

**Table S1.** Proteins identified by 2-D DIGE and MALDI-TOF-TOF

Spot No <sup>a</sup>	IPI No	Protein description	P-Value ID <sup>b</sup>	Mr (Da)	PI	Coverage (%) <sup>c</sup>	Score <sup>d</sup>	Peptide Hits <sup>e</sup>	Peptides identified
<b>Lipid metabolism</b>									
1572	IPI00197703	Apolipoprotein A-I precursor	4E-23	30043	5.52	71%	270	4	K.VVAEEFR.D K.FGLYSDQMR.E K.WNEEVEAYR.Q K.DSGRDYVSQFESSTLGK.Q
1271	IPI00210823	3-oxo-5-beta-steroid dehydrogenase	4- 6.4E-46	37354	6.18	54%	498	4	K.SLGVSNFNR.R R.HIDGAYVYR.N R.IKENFQIFDFSLTK.E K.YKPVTNQVEC*HPYFTQTK.L
1510	IPI00231767	Triosephosphate isomerase	8.00E-25	26832	6.89	75%	287	2	K.DLGATWVVLGHSER.R K.LPADTEVVC*APPTAYIDFAR.Q
<b>Carbohydrate metabolism</b>									
1280	IPI00198717	Malate dehydrogenase, cytoplasmic	6.4E-39	36460	6.16	46%	428	5	K.ENFSC*LTR.L K.GEFITTVQQR.G K.DLDVAVLVGSMR.R K.FVEGLPINDFSR.E K.SAPSIPKENFSC*LTR.L
1121	IPI00360056	Aldose 1-epimerase	1.30E-11	37869	6.18	42%	155	3	K.EYHLPINR.E K.QPYFGAVVGR.V R.HLQSYHIHGFDHNFCLK
1353	IPI00194324	Pyruvate dehydrogenase component subunit beta	E1 3.2E-11	38957	6.2	34%	151	2	R.IMEGPAFNFLDAPAVR.V K.TYYMSAGLQPVPIVFR.G

**Protein metabolism**

1273	IPI00197900	Translation elongation factor 1- delta subunit (Fragment)	2.00E-14	28748	4.86	49%	183	3	K.LVPVGYGIR.K K.LVPVGYGIR.K K.LVPVGYGIR.K
502	IPI00515829	Kininogen 1	3.20E-20	47734	6.29	32%	241	3	K.HIGLVYSGMGPDYR.V K.SILYDER.S K.LAQQYYLVYQEPIPTAQLVQR.V

**Amino acid and derivative metabolism**

37	IPI00210644	Carbamoyl-phosphate synthase, mitochondrial precursor	5.0E-14	164476	6.33	22%	179	4	K.SLFHYR.Q R.GQNQPVLNITNR.Q R.MC*HPSVDGFTPR.L K.GILIGIQSFRPR.F
1743	IPI00231963	D-dopachrome decarboxylase	1.0E-33	13125	6.09	79%	376	5	R.IPAGLENR.L K.FLTEELSLDQDR.I R.VSVTIRPGMTLLMNK.S R.LC*AATATILDKPEDR.V K.STEPC*AHLLISSIGVVGTAEQNR.S
1708	IPI00324380	Transthyretin precursor	1.0E-10	15710	5.77	20%	146	1	K.ALGISPFHEYAEVVFTANDSGHR.H
1168	IPI00327518	Arginase-1	1.6E-29	36481	6.51	62%	334	3	K.DIVYIGLR.D K.VMEETFSYLLGR.K R.DHGDALAFVDVPNDSPFQIVK.N
564	IPI00475676	Delta-1-pyrroline-5-carboxylate dehydrogenase	1.30E-08	61830	7.14	26%	125	2	K.STGSVVGQQPFGGAR.A K.VANEPILAFTQGSPER.D
1400	IPI00365297	Agmatinase, mitochondrial precursor	4.00E-25	37963	6.71	32%	290	4	R.TLDPYR.Y R.VVQIGIR.G K.SLVPLMAEIR.Q R.VADLGNVNVNLYNLQDSC*R.L

**Response to stimulus**

560	IPI00231742	Catalase		0.0031	59719	7.07	22%	71	1	R.LGPNYLQIPVNCOPYR.A
527	IPI00327469	Alpha-2-HS-glycoprotein precursor		3.2E-06	37958	6.05	21%	101	1	K.VGQPGDAGAAGPVAPLCPGR.V

**Binding**

543	IPI00206624	Glucose-regulated protein precursor	protein	1.30E-40	72302	5.07	50%	445	4	K.SDIDEIVLVGGSTR.I K.DNHLLGTFDLTGIPPAPR.G R.ITPSYVAFTPEGER.L K.VTHAVVTVPAYFNDAQR.Q
1514	IPI00230788	Carbonic anhydrase 3		6.40E-43	29413	6.89	85%	468	5	R.VVFDDTFDR.S R.SLFASAENEPVPLVGNWRPPQPIK.G R.GGPLSGPYR.L K.YAAELHLVHWNPK.Y K.EAPFNHFDPSCLFPACR.D

**Development**

799	IPI00389571	Keratin, type II cytoskeletal 8		1.3e-042	53985	5.83	55%	465	5	K.LALDIEIATYR.K R.LEGLTDEINFLR.Q R.ATLEAAIADAEQRGELAVK.D R.AQYEEIANR.S R.LQAEIDALKGQR.A
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**Unclassified**

1662	IPI00561017	Prdx5 22 kDa protein		6.40E-45	22256	8.54	55%	488	4	K.THLPGFVEQAGALK.A K.GVLFGVPGAFTPGC*SK.T K.ETDLLLDDSLVSLFGNR.R K.GAQVVAC*LSVNDVFVTAEWGR.A
1526	IPI00760117	Comt Isoform 2 of Catechol O-methyltransferase		2.00E-10	24731	5.11	55%	143	2	R.LLQPGAR.L R.EYSPSLVLELGAYC*GYS AVR.M

1563	IPI00392676	Blvrb_predicted reductase B	biliverdin	2.00E-19	22038	6.29	62%	233	3	K.IAIFGATGR.T K.HDLGHFMLR.C K.YVAVMPPHIGDQPLTGAYTVTLDGR. G
1746	IPI00205036	Hemoglobin alpha 2 chain		3.20E-54	15275	8.45	96%	581	5	R.MFAAFPTTK.T K.LRVDPVNFK.F K.IGGHGGGEYGEEALQR.M K.TYFSHIDVSPGSAQVK.A K.AADHVEDLPGALSTLSDLHAHK.L
1453	IPI00231106	3-mercaptopyruvate sulfurtransferase		1.3E-36	32919	5.88	57%	405	4	R.FQGTQPEPR.D R.AQPEHVISQGR.G R.HIPGAAFFDIDR.C R.AFGHHSVSLLDGGFR.Y

<sup>a</sup> Spot No. is the unique number of the position of the spot in the master gel.

<sup>b</sup> *p*-value ID is the best expectation value for the identified protein as calculated by Mascot.

<sup>c</sup> Amino acid sequence coverage for the identified protein.

<sup>d</sup> Score is the protein score based on combined mass and mass/mass spectrums.

<sup>e</sup> Peptide hits is the unique number of MS/MS spectrums which match to the trypsin peptide.