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LA-ICP-MS and nHPLC-ESI-FT-LTQ-MS/MS for the analysis of cisplatin-protein complexes separated by two dimensional gel electrophoresis in biological samples

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SUPPORTING INFORMATION

The present document provides further information on the paper mentioned above.

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1. ADDITIONAL EXPERIMENTAL DETAILS

In vitro incubations of RPTECs with cisplatin and protein extraction

Cytosolic proteins extract preparation

Cell lysates were heated at 100 ºC for 5 minutes, homogenized in ice and centrifuged at 12,000 x *g* for 5 minutes at 4ºC. Supernatant containing cytosolic proteins extract was separated. Proteins were precipitated by adding ten volumes of acetone (-20 ºC) to a volume of 150 µL of extract, and by incubation for 30 min at -20 ºC, followed by centrifugation at 13000 x g at 4ºC for 30 min. The supernatant was removed and discarded and the protein pellet was washed three times with 100 µL 80 % acetone, each washing followed by centrifugation at 13000 x g at 4 ºC for 3 min and removal of supernatant. Finally the protein pellet was resuspended in a buffer containing 8 M urea and 10 mM Tris-HCl pH 7.4.

Electrophoresis

SDS-PAGE

2x Laemmli Sample Buffer (LSB) composition: Tris-HCl (125 mM, pH 6.8), 6 % glycerol, 2 % SDS and 0.025 % bromophenol blue.

Running buffer composition: Tris-HCl (25 mM, pH 8.3), glycine (200 mM) and SDS (0.1 %).

2-DE

The IEF gel for protein separation contained: 9 M urea, 4 % acrylamide, 0,3 % piperazine diacrylamide (PDA), 5 % glycerol, 0,06 % tetramethylethylenediamine (TEMED), 0,02 % ammonium persulfate (APS), 2 % ampholytes (pH 3-11). A 4 % sephadex (GE Healthcare) suspension was placed on top of the gel and then proteins were loaded in the anodic side of the gel rod, followed by a protection solution containing 5 M urea, 5 % glycerol and 2 % ampholytes (pH 2-4). Isoelectric focusing was performed using a cathode solution containing 9 M urea, 5 % glycerol, 5 % ethylenediamine and an anode solution composed of 3 M urea, 5 % phosphoric acid; in a in-house made cell with a Bio-Rad power supply using the following running steps: (i) 100 V for 75 min, (ii) 200 V for 75 min, (iii) 400 V for 75 min, (iv) 600 V for 75 min, (v) 800 V for 10 min and (vi) 1000 V for 5 min. Current and power were set to a maximum of 5 mA and 5 W, respectively and separation was performed at 20 ºC. After separation, gels were equilibrated twice for 5 min with a 3 % SDS, 125 mM Tris-HCl (pH 6.8), 40 % glycerol buffer. For the SDS-PAGE second dimension, the IEF gel grooves were placed onto 1-mm 12.5 % polyacrylamide mini gels, followed by a 200 µL layer of 1 % agarose (Bio-Rad), 125 mM Tris-H_3PO_4 (pH 6.8), 0.1 % SDS and 0.01 % bromophenol blue. Gels were run at 150 V for 75 min at RT.

Protein fixing and CBB-staining

Protein Fixing. A solution containing 50 % ethanol and 10 % acetic acid (Carl Roth GmbH, Karlsruhe, Germany) for 30 min was used.

CBB-staining. Staining was performed overnight, and gels were finally washed with Milli-Q water for 45 min. A rocker was used for both shaking during fixation and staining.

nHPLC-MS/MS

In gel digestion protocol

Protein bands or spots were transferred to 600 µL siliconized Lo-bind Eppendorf tubes and washed for 30 min in 150 µL of 25 mM ammonium bicarbonate (NH_4HCO_3, Carl Roth GmbH, Karlsruhe, Germany) at 22°C. Wash solutions were always discarded onwards. Bands/spots from Coomassie stained gels were unstained in 150 µL of 50% acetonitrile and 25 mM NH_4HCO_3 shaking at 1000 rpm for 30 min, this step being repeated as many times as needed. When completely unstained, the gel slices were washed with 100 µL of 25 mM NH_4HCO_3 for 15 min to keep them completely hydrated during the following step. Then, the gel bands/spots were cut into 1 mm x 1 mm pieces and 50 µL of acetonitrile were added to dehydrate the gel plugs. After 10 min, the solvent was removed and the gel pieces were dried in a Savant SpeedVac concentrator (Thermo Scientific) for 15 min. In the case of protein bands from the rat serum sample and the standard proteins, reduction and alkylation steps were performed. In those cases, gel pieces were reswollen and incubated with 40-50 µL of 10 mM DTT at 37 ºC for 40 min. After that, the solution was discarded and replaced by 40 µL of 55 mM IAA, followed by incubation at room temperature in the darkness for 40 min. Then, gel pieces were washed with 100 µL of 25 mM NH_4HCO_3 for 15 min and dehydrated with 50 µL of ACN. Afterwards, gel pieces were dried in a vacuum centrifuge. The dry gel pieces were rehydrated in 12.5 ng µL^{-1} porcine trypsin (Sequencing Grade Modified Trypsin, Promega, Madison, WI, USA) in 50 mM NH_4HCO_3 (typically 10 µL) at 4 ºC. Once the gel plugs had been completely reswollen, 10-20 µL of 50 mM NH_4HCO_3 were added so that gel pieces were completely immersed in liquid and then incubated at 37 °C for 16 h. After digestion, supernatants were collected and transferred to Lo-Bind eppendorf tubes, and kept at 4 ºC. Peptides remaining in the gels were extracted with 30 µL of 2 % HCOOH, with vortexing, and incubation for 30 min at RT. Extracted peptides were pooled with the original supernatants. Next, 30 µL of a solution containing 50 % ACN and 0.1 % HCOOH were added to the gel plugs, vortexed and incubated for another 30 min at RT. The extraction solution was pooled with the previous ones and samples were evaporated in a vacuum centrifuge to dryness.

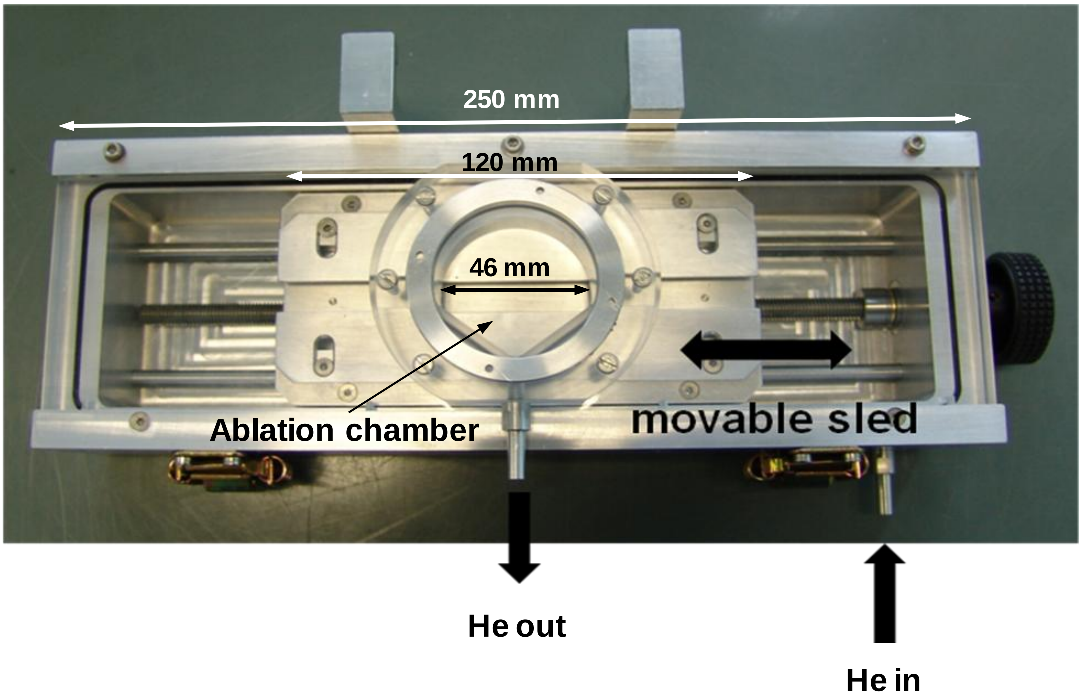

Figure S-1. Laser ablation chamber designed at ETH Zürich, which was employed for gel analysis. This ablation chamber is suitable for large samples. There is one He gas inlet on the right hand side, and a gas outlet on the centre of the ablation window.

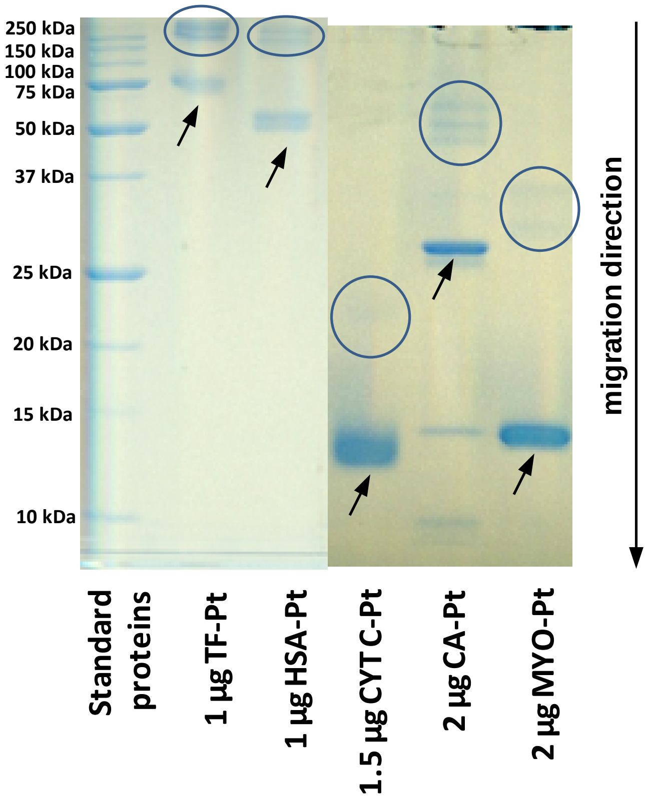

Figure S-2. 12.5% nrSDS-PAGE gel showing the separation of the individual standard proteins (TF, HAS, CA, MYO and CYT C) incubated with cisplatin, along with the molecular weight markers. The main bands corresponding to the standard proteins are indicated by arrows. Bands showing the occurrence of protein polymerization in the incubations have been indicated with circles.

Table S-1. Proteins identified in the gel bands where Pt was detected during the LA-ICP-MS analysis of serum proteins from a rat treated with 16 mg kg^{-1} cisplatin, separated by nrSDS-PAGE. Bands were in-gel digested and analyzed by nLC-ESI-FT-LTQ-MS/MS. Search was performed with MASCOT, using a *rattus norvegicus* NCBI database.

Sample	Accesion number	Protein	MASCOT score	MW, Da	Identified sequences	Protein coverage, %	pI
B1	gi|21955142	alpha-1-macroglobulin precursor [Rattus norvegicus]	707	167053	63	52.3	6.46
	gi|186972114	fibronectin precursor [Rattus norvegicus]	315	272276	43	20.7	5.44
	gi|12831225	murinoglobulin-1 precursor [Rattus norvegicus]	197	165221	20	17.5	5.68
	gi|83816939	alpha-1-inhibitor 3 precursor [Rattus norvegicus]	190	163670	18	15	5.7
	gi|158138561	complement C3 [Rattus norvegicus]	57	186206	4	2.4	6.06
B2	gi|12831225	murinoglobulin-1 precursor [Rattus norvegicus]	551	165221	45	31.4	5.68
	gi|83816939	alpha-1-inhibitor 3 precursor [Rattus norvegicus]	544	163670	46	33	5.7
	gi|109472532	PREDICTED: alpha-2-macroglobulin [Rattus norvegicus]	350	164809	30	21.5	6.63
	gi|293348303	PREDICTED: hypothetical protein [Rattus norvegicus]	262	45760	14	40.5	6.56
	gi|158186621	complement C4 precursor [Rattus norvegicus]	251	192070	23	14	7.1
	gi|293346859	PREDICTED: Igk protein-like isoform 1 [Rattus norvegicus]	151	26056	8	41.4	7.6
	gi|109468076	PREDICTED: complement C5 [Rattus norvegicus]	118	189700	9	5.8	6.16
	gi|21955142	alpha-1-macroglobulin precursor [Rattus norvegicus]	77	167053	15	11.4	6.46
	gi|158138561	complement C3 [Rattus norvegicus]	47	186206	5	3.2	6.06
B3	gi|61556986	serotransferrin precursor [Rattus norvegicus]	780	76346	39	55.2	7.14
	gi|158138568	serum albumin precursor [Rattus norvegicus]	159	68714	17	30.1	6.09
	gi|16758014	hemopexin precursor [Rattus norvegicus]	158	51258	22	45.4	7.58
	gi|80861401	T-kininogen 1 [Rattus norvegicus]	82	47734	6	16	6.29
	gi|57526868	T-kininogen 2 precursor [Rattus norvegicus]	74	47673	8	21.6	5.94
	gi|57529187	liver carboxylesterase 1 [Rattus norvegicus]	54	60186	3	6.9	5.36
B4	gi|158138568	serum albumin precursor [Rattus norvegicus]	1116	68714	43	68	6.09
	gi|51036655	alpha-1-antiproteinase precursor [Rattus norvegicus]	150	46093	15	45	5.7

Sample	Accesion number	Protein	MASCOT score	MW, Da	Identified sequences	Protein coverage, %	pI
B4	gi|13928716	serine protease inhibitor A3N [Rattus norvegicus]	103	45526	9	30	5.39
	gi|17865327	fetuin-B precursor [Rattus norvegicus]	42	41506	3	10	6.71
B5	gi|8393197	C-reactive protein precursor [Rattus norvegicus]	114	25452	5	31.3	4.89
B6	gi|17985949	hemoglobin subunit beta-1 [Rattus norvegicus]	122	15969	12	89	7.88
	gi|164448680	hemoglobin subunit beta-2 [Rattus norvegicus]	99	15972	12	88	8.91
	gi|57164089	serum amyloid A-4 protein [Rattus norvegicus]	72	14963	10	63	9.2
	gi|6981010	hemoglobin subunit alpha-1/2 [Rattus norvegicus]	65	15319	8	66	7.82
	gi|40445397	beta-glo [Rattus norvegicus]	60	16027	7	55	6.75
B7	gi|145553986	apolipoprotein C-II [Rattus norvegicus]	81	10688	2	18.6	4.57

Table S-2. Proteins identified in Pt spots detected during the LA-ICP-MS imaging of a 2-DE gel where separation of a cytosolic protein extract from RPTECs incubated with cisplatin was performed. Spots were in-gel digested and analyzed by nLC-ESI-FT-LTQ-MS/MS. Search was performed with MASCOT and SEQUEST, using a *sus scrofa* NCBI database.

Spot no	Accesion number	Protein	MASCOT score	MW, Da	Identified sequences	Protein coverage, %	pI
1	gi|335309939	PREDICTED: nucleolin-like [Sus scrofa]	881	78181	32	37.0	4.56
	gi|45269029	cytoskeletal beta actin [Sus scrofa]	172	44763	5	15.3	5.55
2	gi|17865698	Endoplasmin (Ppk 98; a protein kinase [Sus scrofa]	1661	92413	46	48.5	4.75
	gi|335296459	PREDICTED: vimentin-like [Sus scrofa]	232	53635	11	24.2	5.06
	gi|83778524	beta-tropomyosin [Sus scrofa]	170	33326	7	17.8	4.62
	gi|164409	complement cytolysis inhibitor [Sus scrofa]	139	51741	6	15.5	5.62
	gi|3661527	tropomyosin 4 [Sus scrofa]	130	28504	10	26.6	4.67
	gi|1927	cardiac alpha tropomyosin [Sus scrofa]	121	32710	8	25.0	4.67
	gi|45269029	cytoskeletal beta actin [Sus scrofa]	120	44763	7	20.5	5.55
	gi|335309154	PREDICTED: LOW QUALITY PROTEIN: splicing factor 3A subunit 1 isoform 1, partial [Sus scrofa]	104	87117	8	11.0	5.21
	gi|335309520	PREDICTED: tropomyosin alpha-3 chain-like isoform 1 [Sus scrofa]	96	32817	8	24.6	4.68
	gi|343887440	heterogeneous nuclear ribonucleoprotein C (C1/C2) 1 [Sus scrofa]	58	34300	2	6.7	5.00
	gi|311264773	PREDICTED: protein disulfide-isomerase A4-like [Sus scrofa]	55	72864	7	10.4	5.02
	gi|335282871	PREDICTED: epidermal growth factor receptor substrate 15-like 1 [Sus scrofa]	47	99555	1	1.2	4.92
3	gi|311264773	PREDICTED: protein disulfide-isomerase A4-like [Sus scrofa]	1232	72864	47	55.9	5.02
	gi|335281003	PREDICTED: 78 kDa glucose-regulated protein [Sus scrofa]	161	74485	7	12.1	5.17
	gi|45269029	cytoskeletal beta actin [Sus scrofa]	140	44763	5	15.6	5.55
	gi|194034833	PREDICTED: microfibrillar-associated protein 1 [Sus scrofa]	109	51941	5	10.9	4.95
	gi|194035971	PREDICTED: proline-rich protein PRCC isoform 1 [Sus scrofa]	91	52320	5	16.9	4.97
	gi|345441750	heat shock 70kDa protein 8 [Sus scrofa]	84	70822	5	7.4	5.37
	gi|335296459	PREDICTED: vimentin-like [Sus scrofa]	51	53635	3	5.8	5.06
4	gi|290756002	calreticulin [Sus scrofa]	481	48258	23	42.9	4.32

	gi|346716193	nucleosome assembly protein 1-like 1 [Sus scrofa]	114	45346	2	9.0	4.36
	gi|335296459	PREDICTED: vimentin-like [Sus scrofa]	91	53635	5	10.3	5.06
4	gi|89574051	mitochondrial ATP synthase, H+ transporting F1 complex beta subunit [Sus scrofa]	50	47060	5	16.7	4.99
	gi|335282758	PREDICTED: UV excision repair protein RAD23 homolog A-like [Sus scrofa]	50	39638	4	10.2	4.56
5	gi|311273928	PREDICTED: nucleophosmin-like isoform 2 [Sus scrofa]	920	29561	15	47.0	4.45
	gi|346644699	protein SET [Sus scrofa]	130	32084	8	23.8	4.12
	gi|311258852	PREDICTED: MARCKS-related protein-like isoform 2 [Sus scrofa]	79	20954	3	16.7	4.62
	gi|335286747	PREDICTED: hepatoma-derived growth factor-like [Sus scrofa]	44	27088	1	4.1	4.67
6	gi|335281333	PREDICTED: 60S acidic ribosomal protein P2-like [Sus scrofa]	576	11686	8	81.7	4.44
	gi|47606435	RecName: Full=Myosin light polypeptide 6; AltName: Full=17 kDa myosin light chain	153	16919	7	49.7	4.56
7	gi|335281003	PREDICTED: 78 kDa glucose-regulated protein [Sus scrofa]	5719	74485	53	58.5	5.17
	gi|345441750	heat shock 70kDa protein 8 [Sus scrofa]	1408	70822	29	53.1	5.37
	gi|335296459	PREDICTED: vimentin-like [Sus scrofa]	771	53635	33	68.9	5.06
	gi|45269029	cytoskeletal beta actin [Sus scrofa]	340	44763	14	43.8	5.55
	gi|335307643	PREDICTED: sorting nexin-2 [Sus scrofa]	192	62429	8	16.8	5.15
	gi|335293906	PREDICTED: annexin A5-like [Sus scrofa]	133	36112	2	7.8	4.94
	gi|135435	RecName: Full=Tubulin alpha-1A chain; AltName: Full=Alpha-tubulin 1	128	50036	6	18.2	4.91
	gi|71559141	tubulin alpha 3 [Sus scrofa]	118	50134	7	22.2	4.94
	gi|343488538	cytoplasmic dynein 1 intermediate chain 2 [Sus scrofa]	111	68437	3	7.0	5.17
	gi|301016767	protein disulfide isomerase P5 [Sus scrofa]	93	48044	1	3.2	5.00
	gi|335283403	PREDICTED: lamin-B1 [Sus scrofa]	80	66446	2	4.1	5.08
8	gi|335296459	PREDICTED: vimentin-like [Sus scrofa]	3412	53635	56	90.3	5.06
	gi|89574051	mitochondrial ATP synthase, H+ transporting F1 complex beta subunit [Sus scrofa]	632	47060	17	50.8	4.99
	gi|71559141	tubulin alpha 3 [Sus scrofa]	268	50134	10	33.0	4.94
	gi|335296366	PREDICTED: heterogeneous nuclear ribonucleoprotein K-like [Sus scrofa]	122	51300	3	10.1	5.37
	gi|311275781	PREDICTED: drebrin-like protein-like [Sus scrofa]	72	47866	3	8.7	5.04

	gi|217031226	solute carrier family 9 (sodium/hydrogen exchanger) member 3 regulator 1 [Sus scrofa]	61	39281	2	6.8	5.27
	gi|301016767	protein disulfide isomerase P5 [Sus scrofa]	49	48044	1	3.9	5.00
9	gi|335296459	PREDICTED: vimentin-like [Sus scrofa]	5579	53635	58	91.6	5.06
9	gi|89574051	mitochondrial ATP synthase, H+ transporting F1 complex beta subunit [Sus scrofa]	414	47060	15	47.6	4.99
	gi|311267185	PREDICTED: polymerase I and transcript release factor-like [Sus scrofa]	375	43556	8	22.4	5.42
	gi|45269029	cytoskeletal beta actin [Sus scrofa]	185	44763	9	31.9	5.55
	gi|346986349	glial fibrillary acidic protein [Sus scrofa]	93	49406	4	7.2	5.32
	gi|335296366	PREDICTED: heterogeneous nuclear ribonucleoprotein K-like [Sus scrofa]	91	51300	3	11.4	5.37
	gi|71559141	tubulin alpha 3 [Sus scrofa]	90	50134	2	7.3	4.94
10	gi|335296459	PREDICTED: vimentin-like [Sus scrofa]	8684	53635	58	90.3	5.06
	gi|194037554	PREDICTED: ATP synthase subunit beta, mitochondrial [Sus scrofa]	1081	56300	22	62.3	5.15
	gi|311267185	PREDICTED: polymerase I and transcript release factor-like [Sus scrofa]	365	43556	9	24.2	5.42
	gi|45269029	cytoskeletal beta actin [Sus scrofa]	125	44763	6	19.1	5.55
11	gi|335296459	PREDICTED: vimentin-like [Sus scrofa]	5698	53635	72	95.3	5.06
	gi|2959454	desmin [Sus scrofa]	689	52627	14	23.6	5.21
	gi|311267185	PREDICTED: polymerase I and transcript release factor-like [Sus scrofa]	668	43556	8	27.2	5.42
	gi|45269029	cytoskeletal beta actin [Sus scrofa]	369	44763	12	37.9	5.55
	gi|335296366	PREDICTED: heterogeneous nuclear ribonucleoprotein K-like [Sus scrofa]	205	51300	3	12.7	5.37
12	gi|194037554	PREDICTED: ATP synthase subunit beta, mitochondrial [Sus scrofa]	5543	56300	31	75.4	5.15
	gi|335296459	PREDICTED: vimentin-like [Sus scrofa]	1529	53635	37	74.9	5.06
	gi|301016767	protein disulfide isomerase P5 [Sus scrofa]	310	48044	7	17.7	5.00
	gi|71559141	tubulin alpha 3 [Sus scrofa]	196	50134	6	19.5	4.94
	gi|45269029	cytoskeletal beta actin [Sus scrofa]	195	44763	7	20.5	5.55
	gi|335282162	PREDICTED: nucleobindin-2 isoform 2 [Sus scrofa]	84	49991	5	12.9	5.07
	gi|217031226	solute carrier family 9 (sodium/hydrogen exchanger) member 3 regulator 1 [Sus scrofa]	78	39281	1	3.8	5.27
13	gi|45269029	cytoskeletal beta actin [Sus scrofa]	633	44763	17	51.2	5.55

	gi|790202	skeletal alpha actin [Sus scrofa]	488	42024	13	34.5	5.23
	gi|7288863	ubiquitous tropomodulin U-Tmod [Sus scrofa]	73	39615	4	13.1	4.98
	gi|194037554	PREDICTED: ATP synthase subunit beta, mitochondrial [Sus scrofa]	60	56300	2	5.7	5.15
	gi|311274741	PREDICTED: RNA-binding protein Raly isoform 1 [Sus scrofa]	48	33990	1	3.7	8.93
14	gi|45269029	cytoskeletal beta actin [Sus scrofa]	2007	44763	23	65.8	5.55
	gi|164669	succinyl-CoA synthetase beta-subunit [Sus scrofa]	418	45103	12	34.1	5.46
14	gi|335296459	PREDICTED: vimentin-like [Sus scrofa]	327	53635	22	48.7	5.06
	gi|71057496	ribosomal protein SA [Sus scrofa]	155	32907	3	15.3	4.80
	gi|7288863	ubiquitous tropomodulin U-Tmod [Sus scrofa]	154	39615	7	23.6	4.98
	gi|89574051	mitochondrial ATP synthase, H+ transporting F1 complex beta subunit [Sus scrofa]	146	47060	6	19.9	4.99
	gi|311274741	PREDICTED: RNA-binding protein Raly isoform 1 [Sus scrofa]	97	33990	5	14.7	8.93
	gi|311254260	PREDICTED: interleukin enhancer-binding factor 2 [Sus scrofa]	69	43023	2	6.4	5.19
	gi|335281686	PREDICTED: UBX domain-containing protein 1-like [Sus scrofa]	65	36550	2	6.4	5.55
	gi|311245972	PREDICTED: stomatin-like protein 2-like isoform 1 [Sus scrofa]	49	38621	1	4.2	7.71
15	gi|45269029	cytoskeletal beta actin [Sus scrofa]	2811	44763	26	58.4	5.55
	gi|790202	skeletal alpha actin [Sus scrofa]	1598	42024	20	51.5	5.23
	gi|164669	succinyl-CoA synthetase beta-subunit [Sus scrofa]	529	45103	21	47.0	5.46
	gi|335296459	PREDICTED: vimentin-like [Sus scrofa]	240	53635	13	27.3	5.06
	gi|343790893	creatine kinase, brain [Sus scrofa]	117	42630	2	7.1	5.47
	gi|311274741	PREDICTED: RNA-binding protein Raly isoform 1 [Sus scrofa]	75	33990	4	11.3	8.93
	gi|311245972	PREDICTED: stomatin-like protein 2-like isoform 1 [Sus scrofa]	61	38621	3	10.7	7.71
	gi|311254260	PREDICTED: interleukin enhancer-binding factor 2 [Sus scrofa]	58	43023	2	6.4	5.19
	gi|335281686	PREDICTED: UBX domain-containing protein 1-like [Sus scrofa]	55	36550	1	3.6	5.55
16	gi|311275365	PREDICTED: caldesmon [Sus scrofa]	560	100803	24	25.8	6.02
	gi|45269029	cytoskeletal beta actin [Sus scrofa]	427	44763	17	48.5	5.55
	gi|335278839	PREDICTED: ezrin [Sus scrofa]	426	69328	22	39.0	5.79
	gi|83778522	procollagen-proline 2-oxoglutarate-4-dioxygenase [Sus scrofa]	311	60897	10	23.8	5.70
	gi|66352014	lamin A [Sus scrofa]	307	74174	12	20.0	6.73
	gi|39777368	heat shock protein 70.2 [Sus scrofa]	287	70055	9	15.9	5.60
	gi|301016769	glucose regulated protein 58 [Sus scrofa]	241	56823	22	44.4	5.93

	gi|335296459	PREDICTED: vimentin-like [Sus scrofa]	223	53635	18	42.1	5.06
	gi|335281003	PREDICTED: 78 kDa glucose-regulated protein [Sus scrofa]	182	74485	9	15.9	5.17
	gi|335310868	PREDICTED: t-complex protein 1 subunit epsilon, partial [Sus scrofa]	182	53588	3	7.2	5.78
	gi|345441750	heat shock 70kDa protein 8 [Sus scrofa]	177	70822	9	16.1	5.37
	gi|311250237	PREDICTED: stress-70 protein, mitochondrial [Sus scrofa]	128	73605	5	9.1	5.81
	gi|335304211	PREDICTED: annexin A6-like [Sus scrofa]	122	14541	2	15.9	8.53
	gi|343478174	T-complex protein 1 subunit alpha [Sus scrofa]	107	60317	5	10.8	5.71
16	gi|335296241	PREDICTED: ladinin-1-like [Sus scrofa]	85	54511	5	12.1	9.38
	gi|335305150	PREDICTED: zyxin [Sus scrofa]	80	61098	6	16.0	6.37
	gi|52631987	annexin A2 [Sus scrofa]	78	38510	5	18.6	6.49
	gi|1165145	annexin I [Sus scrofa]	68	38216	1	3.2	6.47
	gi|335286672	PREDICTED: transgelin-2-like isoform 1 [Sus scrofa]	63	22363	1	6.0	8.41
	gi|121118	RecName: Full=Gelsolin; AltName: Full=Actin-depolymerizing factor; Short=ADF; AltName: Full=Brevin; Flags: Precursor	61	84723	3	5.6	5.93
	gi|335296116	PREDICTED: hypothetical protein LOC100525245, partial [Sus scrofa]	52	60667	6	11.2	7.12
17	gi|66352014	lamin A [Sus scrofa]	526	74174	22	35.8	6.73
	gi|335278839	PREDICTED: ezrin [Sus scrofa]	477	69328	23	39.7	5.79
	gi|83778522	procollagen-proline 2-oxoglutarate-4-dioxygenase [Sus scrofa]	337	60897	7	17.4	5.70
	gi|45269029	cytoskeletal beta actin [Sus scrofa]	238	44763	12	40.6	5.55
	gi|311275365	PREDICTED: caldesmon [Sus scrofa]	146	100803	9	11.1	6.02
	gi|345441801	TNF receptor-associated protein 1 [Sus scrofa]	136	79808	5	8.4	6.58
	gi|335296459	PREDICTED: vimentin-like [Sus scrofa]	72	53635	8	16.7	5.06
	gi|335305150	PREDICTED: zyxin [Sus scrofa]	56	61098	8	19.2	6.37
	gi|335296241	PREDICTED: ladinin-1-like [Sus scrofa]	56	54511	3	6.3	9.38
18	gi|304365428	protein disulfide-isomerase A3 [Sus scrofa]	848	56823	35	54.9	5.93
	gi|335296459	PREDICTED: vimentin-like [Sus scrofa]	630	53635	27	59.4	5.06
	gi|45269029	cytoskeletal beta actin [Sus scrofa]	281	44763	13	40.1	5.55
	gi|311270290	PREDICTED: v-type proton ATPase subunit B, brain isoform-like [Sus scrofa]	256	56577	8	20.7	5.57
	gi|55668280	Hsp27 [Sus scrofa]	246	22928	6	32.4	6.23
	gi|187370717	cardiac muscle ATP synthase H+ transporting mitochondrial F1	243	59651	10	21.2	9.21

		complex alpha subunit 1 [Sus scrofa]					
	gi|335310868	PREDICTED: t-complex protein 1 subunit epsilon, partial [Sus scrofa]	218	53588	10	19.5	5.78
	gi|81295909	mitochondrial aldehyde dehydrogenase 2 [Sus scrofa]	160	56885	7	14.4	6.43
	gi|335296366	PREDICTED: heterogeneous nuclear ribonucleoprotein K-like [Sus scrofa]	147	51300	2	9.0	5.37
	gi|335300183	PREDICTED: serine/threonine-protein kinase PAK 2-like [Sus scrofa]	75	63676	3	6.7	7.91
	gi|83778522	procollagen-proline 2-oxoglutarate-4-dioxygenase [Sus scrofa]	72	60897	2	5.8	5.70
	gi|343478174	T-complex protein 1 subunit alpha [Sus scrofa]	63	60317	3	5.6	5.71
	gi|89574051	mitochondrial ATP synthase, H+ transporting F1 complex beta subunit [Sus scrofa]	50	47060	5	16.7	4.99
19	gi|304365428	protein disulfide-isomerase A3 [Sus scrofa]	728	56823	32	52.7	5.93
	gi|335296459	PREDICTED: vimentin-like [Sus scrofa]	329	53635	18	38.6	5.06
	gi|81295909	mitochondrial aldehyde dehydrogenase 2 [Sus scrofa]	208	56885	10	21.7	6.43
	gi|50916342	heat shock protein 27kDa [Sus scrofa]	126	14211	3	33.1	5.94
	gi|225382133	fascin [Sus scrofa]	77	54649	2	4.5	6.04
	gi|45269029	cytoskeletal beta actin [Sus scrofa]	56	44763	6	18.3	5.55
	gi|335293262	PREDICTED: cytosol aminopeptidase-like [Sus scrofa]	48	44357	1	2.9	6.00
20	gi|118627572	F-actin capping protein subunit alpha 1 [Sus scrofa]	487	32996	12	51.4	5.53
	gi|148613355	F-actin capping protein subunit alpha 2 [Sus scrofa]	331	32961	13	50.0	5.57
	gi|52631987	annexin A2 [Sus scrofa]	131	38510	7	23.9	6.49
	gi|121149	RecName: Full=Gamma-glutamyltranspeptidase 1	68	61278	1	1.9	6.52
	gi|311267703	PREDICTED: myeloperoxidase [Sus scrofa]	59	83997	2	3.8	9.64
	gi|335286959	PREDICTED: filaggrin-2-like [Sus scrofa]	54	188792	2	0.8	6.44
	gi|56244527	desmoglein 1 precursor [Sus scrofa]	51	113247	1	1.8	4.87
21	gi|66352014	lamin A [Sus scrofa]	1439	74174	41	52.1	6.73
	gi|2988346	catalase [Sus scrofa]	401	57277	13	26.6	6.26
	gi|335296459	PREDICTED: vimentin-like [Sus scrofa]	309	53635	10	24.2	5.06
	gi|297591975	ATP synthase subunit alpha, mitochondrial [Sus scrofa]	223	59651	7	15.7	9.21
	gi|85720739	beta-enolase 3 [Sus scrofa]	215	47100	2	7.4	8.05
	gi|346644874	T-complex protein 1 subunit gamma [Sus scrofa]	147	60615	3	6.1	6.43
	gi|347300243	glutamate dehydrogenase 1, mitochondrial [Sus scrofa]	133	61269	9	17.9	8.03

	gi|45269029	cytoskeletal beta actin [Sus scrofa]	112	44763	6	17.8	5.55
	gi|52631987	annexin A2 [Sus scrofa]	95	38510	6	18.0	6.49
	gi|311276168	PREDICTED: ATP-dependent RNA helicase DDX3X isoform 2 [Sus scrofa]	95	71378	2	3.6	6.28
	gi|159502444	transketolase [Sus scrofa]	86	67795	5	10.4	7.21
	gi|311259162	PREDICTED: far upstream element-binding protein 1 [Sus scrofa]	79	67534	7	11.3	7.18
	gi|335286672	PREDICTED: transgelin-2-like isoform 1 [Sus scrofa]	63	22363	3	15.6	8.41
	gi|335279197	PREDICTED: heterogeneous nuclear ribonucleoprotein Q isoform 1 [Sus scrofa]	53	74547	6	8.3	9.11
	gi|118675	RecName: Full=Dihydrolipoyl dehydrogenase, mitochondrial;	52	54151	6	13.2	7.59
22	gi|297591975	ATP synthase subunit alpha, mitochondrial [Sus scrofa]	2079	59651	34	59.7	9.21
22	gi|347300243	glutamate dehydrogenase 1, mitochondrial [Sus scrofa]	958	61269	26	42.3	8.03
	gi|2988346	catalase [Sus scrofa]	570	57277	18	38.2	6.26
	gi|335295650	PREDICTED: dihydrolipoyl dehydrogenase, mitochondrial-like [Sus scrofa]	366	54185	13	33.4	7.59
	gi|85720739	beta-enolase 3 [Sus scrofa]	314	47100	4	10.1	8.05
	gi|335285938	PREDICTED: y-box-binding protein 2-like [Sus scrofa]	274	38094	8	29.2	10.75
	gi|335291628	PREDICTED: nuclease-sensitive element-binding protein 1-like [Sus scrofa]	269	36215	5	23.7	10.00
	gi|311262396	PREDICTED: septin-11 [Sus scrofa]	203	49340	5	14.5	6.36
	gi|45269029	cytoskeletal beta actin [Sus scrofa]	172	44763	6	17.8	5.55
	gi|335296459	PREDICTED: vimentin-like [Sus scrofa]	171	53635	9	21.5	5.06
	gi|335290597	PREDICTED: delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial-like, partial [Sus scrofa]	165	41972	11	32.1	6.40
	gi|335291061	PREDICTED: adenylyl cyclase-associated protein 1-like [Sus scrofa]	148	31290	5	19.4	5.70
	gi|311271945	PREDICTED: serine protease HTRA1-like [Sus scrofa]	135	51225	7	18.7	7.83
	gi|89574051	mitochondrial ATP synthase, H+ transporting F1 complex beta subunit [Sus scrofa]	122	47060	3	10.5	4.99
	gi|52631987	annexin A2 [Sus scrofa]	119	38510	5	17.7	6.49
	gi|311255743	PREDICTED: serine hydroxymethyltransferase, mitochondrial-like [Sus scrofa]	109	53515	2	4.6	7.63
	gi|66352014	lamin A [Sus scrofa]	101	74174	4	6.5	6.73

	gi|147223383	phosphoglycerate dehydrogenase [Sus scrofa]	79	56774	5	9.8	6.44
	gi|335284299	PREDICTED: t-complex protein 1 subunit zeta-like isoform 1 [Sus scrofa]	79	57934	4	8.3	6.32
	gi|164423	succinyl-CoA:alpha-ketoacid coenzyme A transferase [Sus scrofa]	69	56371	3	6.5	8.47
	gi|335292434	PREDICTED: pyruvate kinase isozymes M1/M2 [Sus scrofa]	46	67726	5	8.0	8.63
23	gi|52631987	annexin A2 [Sus scrofa]	710	38510	20	54.9	6.49
	gi|335302034	PREDICTED: PDZ and LIM domain protein 1-like [Sus scrofa]	197	35180	7	31.0	8.32
	gi|343780936	heterogeneous nuclear ribonucleoprotein H3 [Sus scrofa]	182	36903	6	19.7	6.37
	gi|999617	Chain A, Refined Structure Of Mitochondrial Malate Dehydrogenase From Porcine Heart And The Consensus Structure For Dicarboxylic Acid Oxidoreductases	136	33061	3	12.7	8.55
	gi|311248892	PREDICTED: lysosomal alpha-mannosidase-like isoform 1 [Sus scrofa]	132	113836	8	8.3	6.51
	gi|335294174	PREDICTED: heterogeneous nuclear ribonucleoprotein D-like, partial [Sus scrofa]	78	23996	1	7.4	8.93
23	gi|5733715	hnRNP A2/B1 protein [Sus scrofa]	68	9535	1	11.9	5.78
	gi|335292913	PREDICTED: legumain [Sus scrofa]	62	45125	3	7.8	6.20
	gi|11611545	aldose 1-epimerase [Sus scrofa]	59	37792	4	13.5	6.31
	gi|1165145	annexin I [Sus scrofa]	53	38216	1	3.2	6.47
24	gi|335305545	PREDICTED: heterogeneous nuclear ribonucleoproteins A2/B1-like isoform 2 [Sus scrofa]	821	37407	18	49.3	8.97
	gi|2506849	RecName: Full= Malate dehydrogenase, mitochondrial; Flags: Precursor	521	35573	13	45.0	8.93
	gi|2506441	RecName: Full=Glyceraldehyde-3-phosphate dehydrogenase;	479	35813	14	44.7	8.51
	gi|116175259	heterogeneous nuclear ribonucleoprotein A1 [Sus scrofa]	381	34175	10	32.2	9.27
	gi|4454537	L-3-hydroxyacyl-CoA dehydrogenase [Sus scrofa]	105	34140	9	29.9	9.02
25	gi|194039772	PREDICTED: histone H2B type 1-B-like [Sus scrofa]	772	13942	7	47.6	10.31
	gi|194039782	PREDICTED: histone H2B type 1-like isoform 1 [Sus scrofa]	771	13898	7	47.6	10.31
	gi|54039371	RS18_PIG RecName: Full=40S ribosomal protein S18	293	17708	13	57.2	10.99
	gi|51317314	RecName: Full=Histone H4	174	11360	6	57.3	11.36
	gi|194042185	PREDICTED: peptidyl-prolyl cis-trans isomerase F, mitochondrial [Sus scrofa]	134	22008	2	10.6	9.56

	gi|18643343	histone H3.3A [Sus scrofa]	130	15318	9	33.1	11.27
	gi|51702802	RecName: Full=60S ribosomal protein L31	118	14454	4	32.8	10.54
	gi|194039770	PREDICTED: histone H2A type 1-like [Sus scrofa]	111	14127	3	26.9	11.05
	gi|409074	heparin binding protein [Sus scrofa]	102	14750	3	23.4	9.21
	gi|194039746	PREDICTED: histone H2A type 1-A-like [Sus scrofa]	88	14237	3	29.8	10.86
	gi|56244527	desmoglein 1 precursor [Sus scrofa]	85	113247	1	1.8	4.87
	gi|343432668	RNA binding motif (RNP1, RRM) protein 3 [Sus scrofa]	75	17025	1	11.5	8.86
	gi|158514031	RL27_PIG RecName: Full=60S ribosomal protein L27	74	15788	9	58.1	10.56
	gi|298104126	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8 [Sus scrofa]	69	20017	3	20.9	8.09
	gi|187606917	RS26_PIG RecName: Full=40S ribosomal protein S26	64	13007	2	20.9	11.01
	gi|194042179	PREDICTED: 40S ribosomal protein S24 isoform 4 [Sus scrofa]	55	15444	1	9.0	10.81
	gi|311264034	PREDICTED: 40S ribosomal protein S25-like isoform 1 [Sus scrofa]	48	13734	2	15.2	10.12
	gi|1628608	ubiquitin/ribosomal fusion protein [Sus scrofa]	46	14719	1	12.5	9.87
26	gi|194039782	PREDICTED: histone H2B type 1-like isoform 1 [Sus scrofa]	1084	13898	10	60.3	10.31
26	gi|194039772	PREDICTED: histone H2B type 1-B-like [Sus scrofa]	1058	13942	10	60.3	10.31
	gi|51317314	RecName: Full=Histone H4	228	11360	7	58.3	11.36
	gi|194039746	PREDICTED: histone H2A type 1-A-like [Sus scrofa]	228	14237	3	29.8	10.86
	gi|194039770	PREDICTED: histone H2A type 1-like [Sus scrofa]	208	14127	4	35.4	11.05
	gi|409074	heparin binding protein [Sus scrofa]	174	14750	4	35.2	9.21
	gi|335289786	PREDICTED: 40S ribosomal protein S19-like isoform 1 [Sus scrofa]	127	25106	8	21.4	10.17
	gi|2500494	RecName: Full=40S ribosomal protein S19	112	15086	9	41.2	10.20
	gi|226256	peptidyl-Pro cis trans isomerase	111	17858	5	32.3	8.34
	gi|60394813	RecName: Full=40S ribosomal protein S16	107	16435	6	38.4	10.21
	gi|38492168	ribosomal protein S23 [Sus scrofa]	101	15807	2	15.4	10.50
	gi|18643343	histone H3.3A [Sus scrofa]	95	15318	7	30.9	11.27
	gi|311246039	PREDICTED: golgi-associated plant pathogenesis-related protein 1-like [Sus scrofa]	93	17215	2	16.9	9.50
	gi|311256688	PREDICTED: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12-like isoform 1 [Sus scrofa]	82	17126	1	11.7	9.60
	gi|117661119	RPS20 [Sus scrofa]	78	13324	4	27.7	9.95

	gi|311259030	PREDICTED: small nuclear ribonucleoprotein Sm D1-like [Sus scrofa]	68	13273	1	10.9	11.56
	gi|343887362	small nuclear ribonucleoprotein Sm D2 [Sus scrofa]	55	13518	3	22.0	9.92
	gi|51338616	RecName: Full=60S ribosomal protein L23; AltName: Full=Ribosomal protein L17	47	14856	3	22.9	10.51
27	gi|335309939	PREDICTED: nucleolin-like [Sus scrofa]	2358	78181	58	43.8	4.56
	gi|45269029	cytoskeletal beta actin [Sus scrofa]	80	44763	7	18.6	5.55
28	gi|17865698	Endoplasmin (Ppk 98; a protein kinase [Sus scrofa]	1891	92413	60	56.6	4.75
	gi|3661527	tropomyosin 4 [Sus scrofa]	475	28504	21	54.4	4.67
	gi|45272586	tropomyosin 3 [Sus scrofa]	337	29015	17	53.2	4.75
	gi|1927	cardiac alpha tropomyosin [Sus scrofa]	298	32710	17	46.1	4.67
	gi|311264773	PREDICTED: protein disulfide-isomerase A4-like [Sus scrofa]	269	72864	13	17.0	5.02
	gi|45269029	cytoskeletal beta actin [Sus scrofa]	134	44763	7	19.3	5.55
	gi|335296459	PREDICTED: vimentin-like [Sus scrofa]	119	53635	8	15.9	5.06
29	gi|311264773	PREDICTED: protein disulfide-isomerase A4-like [Sus scrofa]	1469	72864	56	57.1	5.02
	gi|3661527	tropomyosin 4 [Sus scrofa]	367	28504	14	37.1	4.67
	gi|335296459	PREDICTED: vimentin-like [Sus scrofa]	331	53635	22	43.6	5.06
	gi|335281003	PREDICTED: 78 kDa glucose-regulated protein [Sus scrofa]	239	74485	17	29.0	5.17
29	gi|45272586	tropomyosin 3 [Sus scrofa]	219	29015	15	49.6	4.75
	gi|194034833	PREDICTED: microfibrillar-associated protein 1 [Sus scrofa]	167	51941	16	35.5	4.95
	gi|311254132	PREDICTED: ubiquilin-4 isoform 1 [Sus scrofa]	156	63888	2	6.0	5.14
	gi|194036322	PREDICTED: Na(+)/H(+) exchange regulatory cofactor NHE-RF3 isoform 1 [Sus scrofa]	112	56715	4	9.3	5.29
	gi|335296374	PREDICTED: ubiquilin-1 [Sus scrofa]	109	62452	3	7.5	5.02
	gi|45269029	cytoskeletal beta actin [Sus scrofa]	97	44763	7	18.6	5.55
	gi|345441750	heat shock 70kDa protein 8 [Sus scrofa]	83	70822	6	9.8	5.37
	gi|194035971	PREDICTED: proline-rich protein PRCC isoform 1 [Sus scrofa]	47	52320	5	16.9	4.97
30	gi|290756002	calreticulin [Sus scrofa]	844	48258	28	53.2	4.32
	gi|335296459	PREDICTED: vimentin-like [Sus scrofa]	147	53635	16	35.2	5.06
	gi|346716193	nucleosome assembly protein 1-like 1 [Sus scrofa]	85	45346	4	14.8	4.36
	gi|89574051	mitochondrial ATP synthase, H+ transporting F1 complex beta subunit [Sus scrofa]	65	47060	5	15.3	4.99

31	gi|311273928	PREDICTED: nucleophosmin-like isoform 2 [Sus scrofa]	872	29561	14	60.5	4.45
	gi|1927	cardiac alpha tropomyosin [Sus scrofa]	217	32710	16	33.1	4.67
	gi|311258852	PREDICTED: MARCKS-related protein-like isoform 2 [Sus scrofa]	191	20954	5	37.8	4.62
	gi|83778524	beta-tropomyosin [Sus scrofa]	182	33326	14	31.4	4.62
	gi|346644699	protein SET [Sus scrofa]	171	32084	7	21.7	4.12
	gi|45269029	cytoskeletal beta actin [Sus scrofa]	123	44763	8	22.5	5.55
	gi|335286747	PREDICTED: hepatoma-derived growth factor-like [Sus scrofa]	88	27088	6	26.7	4.67
	gi|346986339	small glutamine-rich tetratricopeptide repeat-containing protein alpha [Sus scrofa]	63	34168	4	15.3	4.87
	gi|343488474	elongation factor 1-beta [Sus scrofa]	56	24789	1	5.8	4.51
32	gi|335281333	PREDICTED: 60S acidic ribosomal protein P2-like [Sus scrofa]	710	11686	10	75.7	4.44
	gi|47606435	RecName: Full=Myosin light polypeptide 6; AltName: Full=17 kDa myosin light chain	197	16919	8	51.0	4.56
33	gi|335281003	PREDICTED: 78 kDa glucose-regulated protein [Sus scrofa]	4800	74485	57	60.7	5.17
	gi|345441750	heat shock 70kDa protein 8 [Sus scrofa]	1317	70822	31	45.7	5.37
	gi|335296459	PREDICTED: vimentin-like [Sus scrofa]	370	53635	19	41.6	5.06
	gi|45269029	cytoskeletal beta actin [Sus scrofa]	196	44763	10	28.0	5.55
	gi|335307643	PREDICTED: sorting nexin-2 [Sus scrofa]	119	62429	5	9.8	5.15
34	gi|335296459	PREDICTED: vimentin-like [Sus scrofa]	4716	53635	69	91.2	5.06
34	gi|89574051	mitochondrial ATP synthase, H+ transporting F1 complex beta subunit [Sus scrofa]	1394	47060	26	79.9	4.99
	gi|71559141	tubulin alpha 3 [Sus scrofa]	409	50134	10	33.0	4.94
	gi|311267185	PREDICTED: polymerase I and transcript release factor-like [Sus scrofa]	307	43556	7	22.1	5.42
	gi|45269029	cytoskeletal beta actin [Sus scrofa]	260	44763	10	32.4	5.55
	gi|335296366	PREDICTED: heterogeneous nuclear ribonucleoprotein K-like [Sus scrofa]	207	51300	6	18.7	5.37
	gi|301016767	protein disulfide isomerase P5 [Sus scrofa]	114	48044	1	3.2	5.00
	gi|217031226	solute carrier family 9 (sodium/hydrogen exchanger) member 3 regulator 1 [Sus scrofa]	105	39281	2	6.8	5.27
35	gi|335296459	PREDICTED: vimentin-like [Sus scrofa]	5430	53635	60	90.1	5.06
	gi|89574051	mitochondrial ATP synthase, H+ transporting F1 complex beta subunit	1117	47060	20	69.6	4.99

		[Sus scrofa]					
	gi|311267185	PREDICTED: polymerase I and transcript release factor-like [Sus scrofa]	433	43556	7	21.6	5.42
	gi|45269029	cytoskeletal beta actin [Sus scrofa]	139	44763	8	23.5	5.55
	gi|346986349	glial fibrillary acidic protein [Sus scrofa]	79	49406	5	9.8	5.32
	gi|71559141	tubulin alpha 3 [Sus scrofa]	73	50134	3	11.8	4.94
	gi|217031226	solute carrier family 9 (sodium/hydrogen exchanger) member 3 regulator 1 [Sus scrofa]	61	39281	2	6.8	5.27
36	gi|335296459	PREDICTED: vimentin-like [Sus scrofa]	7444	53635	62	92.3	5.06
	gi|311267185	PREDICTED: polymerase I and transcript release factor-like [Sus scrofa]	338	43556	6	17.8	5.42
	gi|89574051	mitochondrial ATP synthase, H+ transporting F1 complex beta subunit [Sus scrofa]	167	47060	8	27.7	4.99
	gi|335296366	PREDICTED: heterogeneous nuclear ribonucleoprotein K-like [Sus scrofa]	144	51300	2	6.4	5.37
	gi|45269029	cytoskeletal beta actin [Sus scrofa]	137	44763	5	15.3	5.55
37	gi|335296459	PREDICTED: vimentin-like [Sus scrofa]	8215	53635	72	5.06	5.06
	gi|311267185	PREDICTED: polymerase I and transcript release factor-like [Sus scrofa]	553	43556	8	5.42	5.42
	gi|45269029	cytoskeletal beta actin [Sus scrofa]	175	44763	12	5.55	5.55
	gi|335296366	PREDICTED: heterogeneous nuclear ribonucleoprotein K-like [Sus scrofa]	174	51300	3	5.37	5.37
	gi|346986349	glial fibrillary acidic protein [Sus scrofa]	134	49406	4	5.32	5.32
38	gi|194037554	PREDICTED: ATP synthase subunit beta, mitochondrial [Sus scrofa]	6481	56300	31	75.8	5.15
	gi|335296459	PREDICTED: vimentin-like [Sus scrofa]	1821	53635	44	74.7	5.06
38	gi|71559141	tubulin alpha 3 [Sus scrofa]	201	50134	5	17.5	4.94
	gi|301016767	protein disulfide isomerase P5 [Sus scrofa]	99	48044	2	5.5	5.00
39	gi|335296459	PREDICTED: vimentin-like [Sus scrofa]	4744	53635	69	91.8	5.06
	gi|194037554	PREDICTED: ATP synthase subunit beta, mitochondrial [Sus scrofa]	3325	56300	31	77.1	5.15
	gi|311267185	PREDICTED: polymerase I and transcript release factor-like [Sus scrofa]	303	43556	8	20.9	5.42
	gi|335310032	PREDICTED: dynactin subunit 2-like isoform 3 [Sus scrofa]	288	55871	7	17.8	5.57
	gi|45269029	cytoskeletal beta actin [Sus scrofa]	215	44763	10	32.7	5.55
	gi|311247879	PREDICTED: 26S protease regulatory subunit 6A [Sus scrofa]	176	49172	7	18.2	5.13
	gi|301016767	protein disulfide isomerase P5 [Sus scrofa]	116	48044	2	5.5	5.00

	gi|217031226	solute carrier family 9 (sodium/hydrogen exchanger) member 3 regulator 1 [Sus scrofa]	98	39281	4	11.2	5.27
	gi|71559141	tubulin alpha 3 [Sus scrofa]	97	50134	2	7.3	4.94
	gi|311249564	PREDICTED: heterogeneous nuclear ribonucleoprotein H [Sus scrofa]	94	49198	1	3.8	5.89
	gi|335282162	PREDICTED: nucleobindin-2 isoform 2 [Sus scrofa]	93	49991	4	11.2	5.07
40	gi|45269029	cytoskeletal beta actin [Sus scrofa]	604	44763	17	44.8	5.55
	gi|790202	skeletal alpha actin [Sus scrofa]	469	42024	14	33.4	5.23
	gi|335286959	PREDICTED: filaggrin-2-like [Sus scrofa]	89	188792	1	0.6	6.44
	gi|311259696	PREDICTED: LOW QUALITY PROTEIN: desmoplakin-like [Sus scrofa]	82	331222	11	3.3	6.51
	gi|56244527	desmoglein 1 precursor [Sus scrofa]	53	113247	1	1.8	4.87
41	gi|45269029	cytoskeletal beta actin [Sus scrofa]	1185	44763	25	52.2	5.55
	gi|790202	skeletal alpha actin [Sus scrofa]	685	42024	20	40.1	5.23
	gi|335296459	PREDICTED: vimentin-like [Sus scrofa]	600	53635	26	51.9	5.06
	gi|7288863	ubiquitous tropomodulin U-Tmod [Sus scrofa]	416	39615	17	57.7	4.98
	gi|164669	succinyl-CoA synthetase beta-subunit [Sus scrofa]	354	45103	10	28.3	5.46
	gi|311274741	PREDICTED: RNA-binding protein Raly isoform 1 [Sus scrofa]	103	33990	7	21.7	8.93
42	gi|45269029	cytoskeletal beta actin [Sus scrofa]	1733	44763	26	52.7	5.55
	gi|790202	skeletal alpha actin [Sus scrofa]	1274	42024	21	39.5	5.23
	gi|164669	succinyl-CoA synthetase beta-subunit [Sus scrofa]	733	45103	23	53.2	5.46
	gi|335286108	PREDICTED: protein NDRG1-like [Sus scrofa]	114	42505	1	4.1	5.10
	gi|335281686	PREDICTED: UBX domain-containing protein 1-like [Sus scrofa]	105	36550	2	6.4	5.55
	gi|311274741	PREDICTED: RNA-binding protein Raly isoform 1 [Sus scrofa]	104	33990	9	26.9	8.93
	gi|311254260	PREDICTED: interleukin enhancer-binding factor 2 [Sus scrofa]	53	43023	2	6.4	5.19
43	gi|45269029	cytoskeletal beta actin [Sus scrofa]	2278	44763	30	55.2	5.55
	gi|790202	skeletal alpha actin [Sus scrofa]	1537	42024	24	43.2	5.23
	gi|164669	succinyl-CoA synthetase beta-subunit [Sus scrofa]	587	45103	24	52.5	5.46
	gi|343790893	creatine kinase, brain [Sus scrofa]	216	42630	2	10.0	5.47
	gi|311245972	PREDICTED: stomatin-like protein 2-like isoform 1 [Sus scrofa]	141	38621	4	17.4	7.71
	gi|194045136	PREDICTED: immunoglobulin-binding protein 1 isoform 2 [Sus scrofa]	138	39098	6	23.5	5.21
	gi|311274741	PREDICTED: RNA-binding protein Raly isoform 1 [Sus scrofa]	122	33990	7	25.1	8.93
	gi|345091002	nuclear distribution gene C homolog [Sus scrofa]	54	38284	2	7.8	5.34

	gi|335281686	PREDICTED: UBX domain-containing protein 1-like [Sus scrofa]	53	36550	1	3.6	5.55
44	gi|311275365	PREDICTED: caldesmon [Sus scrofa]	2522	100803	61	42.9	6.02
	gi|335278839	PREDICTED: ezrin [Sus scrofa]	1134	69328	33	46.5	5.79
	gi|121118	RecName: Full=Gelsolin; AltName: Full=Actin-depolymerizing factor	549	84723	23	32.0	5.93
	gi|335296459	PREDICTED: vimentin-like [Sus scrofa]	462	53635	22	46.8	5.06
	gi|45269029	cytoskeletal beta actin [Sus scrofa]	429	44763	17	48.5	5.55
	gi|66352014	lamin A [Sus scrofa]	423	74174	18	27.3	6.73
	gi|335296116	PREDICTED: hypothetical protein LOC100525245, partial [Sus scrofa]	345	60667	13	24.1	7.12
	gi|301016769	glucose regulated protein 58 [Sus scrofa]	305	56823	16	37.0	5.93
	gi|83778522	procollagen-proline 2-oxoglutarate-4-dioxygenase [Sus scrofa]	201	60897	10	23.2	5.70
	gi|52631987	annexin A2 [Sus scrofa]	148	38510	6	19.5	6.49
	gi|13399613	Chain A, X-Ray Structure Of Full-Length Annexin 1	148	38720	5	22.8	6.37
	gi|999617	Chain A, Refined Structure Of Mitochondrial Malate Dehydrogenase From Porcine Heart And The Consensus Structure For Dicarboxylic Acid Oxidoreductases	144	33061	2	9.6	8.55
	gi|1978	heat shock protein 70 [Sus scrofa]	99	71065	4	7.5	5.77
	gi|311250237	PREDICTED: stress-70 protein, mitochondrial [Sus scrofa]	96	73605	3	5.4	5.81
	gi|345441750	heat shock 70kDa protein 8 [Sus scrofa]	93	70822	6	11.5	5.37
	gi|343478174	T-complex protein 1 subunit alpha [Sus scrofa]	90	60317	3	5.6	5.71
	gi|335281003	PREDICTED: 78 kDa glucose-regulated protein [Sus scrofa]	68	74485	5	10.5	5.17
	gi|346421409	transgelin [Sus scrofa]	63	22566	2	11.4	8.87
	gi|55668280	Hsp27 [Sus scrofa]	53	22928	3	16.4	6.23
45	gi|304365428	protein disulfide-isomerase A3 [Sus scrofa]	811	56823	34	57.6	5.93
	gi|335296459	PREDICTED: vimentin-like [Sus scrofa]	612	53635	30	67.2	5.06
	gi|297591975	ATP synthase subunit alpha, mitochondrial [Sus scrofa]	329	59651	9	19.5	9.21
45	gi|335310868	PREDICTED: t-complex protein 1 subunit epsilon, partial [Sus scrofa]	145	53588	4	8.6	5.78
	gi|55668280	Hsp27 [Sus scrofa]	106	22928	5	30.0	6.23
	gi|311270290	PREDICTED: v-type proton ATPase subunit B, brain isoform-like [Sus scrofa]	89	56577	3	6.8	5.57
	gi|45269029	cytoskeletal beta actin [Sus scrofa]	78	44763	5	14.1	5.55
46	gi|297591975	ATP synthase subunit alpha, mitochondrial [Sus scrofa]	382	59651	7	16.0	9.21

	gi|335296459	PREDICTED: vimentin-like [Sus scrofa]	128	53635	6	10.5	5.06
	gi|81295909	mitochondrial aldehyde dehydrogenase 2 [Sus scrofa]	92	56885	8	16.9	6.43
	gi|304365428	protein disulfide-isomerase A3 [Sus scrofa]	73	56823	13	31.3	5.93
47	gi|311275365	PREDICTED: caldesmon [Sus scrofa]	2095	100803	57	43.2	6.02
	gi|66352014	lamin A [Sus scrofa]	2009	74174	38	56.5	6.73
	gi|127236	RecName: Full=Moesin; AltName: Full=Membrane-organizing extension spike protein	854	67619	35	46.8	6.30
	gi|131821	RecName: Full=Radixin; AltName: Full=Moesin-B	841	68507	32	44.1	5.95
	gi|335278839	PREDICTED: ezrin [Sus scrofa]	765	69328	34	48.0	5.79
	gi|345441801	TNF receptor-associated protein 1 [Sus scrofa]	522	79808	15	27.1	6.58
	gi|13399613	Chain A, X-Ray Structure Of Full-Length Annexin 1	295	38720	10	37.6	6.37
	gi|335296459	PREDICTED: vimentin-like [Sus scrofa]	212	53635	15	29.8	5.06
	gi|45269029	cytoskeletal beta actin [Sus scrofa]	195	44763	14	37.4	5.55
	gi|999617	Chain A, Refined Structure Of Mitochondrial Malate Dehydrogenase From Porcine Heart And The Consensus Structure For Dicarboxylic Acid Oxidoreductases	176	33061	2	9.6	8.55
	gi|194041525	PREDICTED: dihydropyrimidinase-related protein 2-like isoform 2 [Sus scrofa]	130	73485	9	19.1	5.94
	gi|335288522	PREDICTED: gamma-enolase isoform 1 [Sus scrofa]	106	47167	2	7.4	4.90
	gi|335305150	PREDICTED: zyxin [Sus scrofa]	103	61098	12	26.8	6.37
	gi|311276168	PREDICTED: ATP-dependent RNA helicase DDX3X isoform 2 [Sus scrofa]	100	71378	1	1.9	6.28
	gi|335305515	PREDICTED: glycyl-tRNA synthetase-like [Sus scrofa]	87	60506	5	12.1	8.11
	gi|335305498	PREDICTED: glycyl-tRNA synthetase-like [Sus scrofa]	87	20937	2	16.8	5.57
	gi|194038728	PREDICTED: pyruvate kinase isozymes M1/M2 isoform 1 [Sus scrofa]	73	57841	1	2.4	7.96
	gi|335296116	PREDICTED: hypothetical protein LOC100525245, partial [Sus scrofa]	69	60667	2	2.9	7.12
	gi|640350	Chain A, Crystal Structures Of Medium Chain Acyl-Coa Dehydrogenase From Pig Liver Mitochondria With And Without Substrate	63	42344	3	10.4	6.46
47	gi|335296241	PREDICTED: ladinin-1-like [Sus scrofa]	59	54511	4	8.3	9.38
	gi|311259162	PREDICTED: far upstream element-binding protein 1 [Sus scrofa]	56	67534	6	10.4	7.18
	gi|335286672	PREDICTED: transgelin-2-like isoform 1 [Sus scrofa]	51	22363	2	11.6	8.41
48	gi|66352014	lamin A [Sus scrofa]	1725	74174	43	58.1	6.73

	gi|131821	RecName: Full=Radixin; AltName: Full=Moesin-B	516	68507	27	38.8	5.95
	gi|297591975	ATP synthase subunit alpha, mitochondrial [Sus scrofa]	362	59651	8	20.3	9.21
	gi|13399613	Chain A, X-Ray Structure Of Full-Length Annexin 1	349	38720	12	41.3	6.37
	gi|127236	RecName: Full=Moesin; AltName: Full=Membrane-organizing extension spike protein	327	67619	25	38.6	6.30
	gi|52631987	annexin A2 [Sus scrofa]	196	38510	7	20.9	6.49
	gi|335296459	PREDICTED: vimentin-like [Sus scrofa]	191	53635	12	22.7	5.06
	gi|45269029	cytoskeletal beta actin [Sus scrofa]	187	44763	10	27.0	5.55
	gi|311259162	PREDICTED: far upstream element-binding protein 1 [Sus scrofa]	178	67534	13	21.0	7.18
	gi|335288522	PREDICTED: gamma-enolase isoform 1 [Sus scrofa]	145	47167	2	6.0	4.90
	gi|335297289	PREDICTED: septin-9-like [Sus scrofa]	141	71414	11	21.2	8.94
	gi|73535956	Chain A, Crystal Structure Of Mitochondrial Respiratory Complex Ii From Porcine Heart At 2.4 Angstroms	132	68184	7	13.7	6.32
	gi|194038728	PREDICTED: pyruvate kinase isozymes M1/M2 isoform 1 [Sus scrofa]	122	57841	4	10.9	7.96
	gi|335286672	PREDICTED: transgelin-2-like isoform 1 [Sus scrofa]	122	22363	3	16.1	8.41
	gi|311276168	PREDICTED: ATP-dependent RNA helicase DDX3X isoform 2 [Sus scrofa]	94	71378	4	6.5	6.28
	gi|84028183	RecName: Full=Catalase	86	59846	5	16.1	6.32
	gi|335296241	PREDICTED: ladinin-1-like [Sus scrofa]	71	54511	4	7.7	9.38
49	gi|66352015	lamin C [Sus scrofa]	2721	65132	51	68.9	6.40
	gi|66352014	lamin A [Sus scrofa]	2533	74174	51	58.0	6.73
	gi|297591975	ATP synthase subunit alpha, mitochondrial [Sus scrofa]	291	59651	9	19.3	9.21
	gi|335296459	PREDICTED: vimentin-like [Sus scrofa]	247	53635	13	28.3	5.06
	gi|194041525	PREDICTED: dihydropyrimidinase-related protein 2-like isoform 2 [Sus scrofa]	244	73485	15	30.6	5.94
	gi|45269029	cytoskeletal beta actin [Sus scrofa]	206	44763	11	24.8	5.55
	gi|13399613	Chain A, X-Ray Structure Of Full-Length Annexin 1	198	38720	7	26.3	6.37
	gi|346644874	T-complex protein 1 subunit gamma [Sus scrofa]	164	60615	5	9.9	6.43
	gi|335281609	PREDICTED: stress-induced-phosphoprotein 1-like [Sus scrofa]	158	62424	12	21.5	6.36
	gi|73535956	Chain A, Crystal Structure Of Mitochondrial Respiratory Complex Ii From Porcine Heart At 2.4 Angstroms	128	68184	9	14.5	6.32
49	gi|335284299	PREDICTED: t-complex protein 1 subunit zeta-like isoform 1 [Sus	113	57934	4	8.1	6.32

		scrofa]					
	gi|194038728	PREDICTED: pyruvate kinase isozymes M1/M2 isoform 1 [Sus scrofa]	105	57841	3	8.9	7.96
	gi|52631987	annexin A2 [Sus scrofa]	101	38510	5	15.6	6.49
	gi|335288522	PREDICTED: gamma-enolase isoform 1 [Sus scrofa]	97	47167	2	6.0	4.90
	gi|335297168	PREDICTED: paraspeckle component 1 [Sus scrofa]	94	40645	10	26.3	6.02
	gi|347300243	glutamate dehydrogenase 1, mitochondrial [Sus scrofa]	90	61269	6	12.0	8.03
	gi|311276168	PREDICTED: ATP-dependent RNA helicase DDX3X isoform 2 [Sus scrofa]	73	71378	1	1.9	6.28
	gi|335286672	PREDICTED: transgelin-2-like isoform 1 [Sus scrofa]	64	22363	2	11.6	8.41
	gi|159502444	transketolase [Sus scrofa]	63	67795	2	6.6	7.21
	gi|84028183	RecName: Full=Catalase	62	59846	8	22.6	6.32
	gi|311259162	PREDICTED: far upstream element-binding protein 1 [Sus scrofa]	55	67534	2	3.3	7.18
	gi|118675	RecName: Full=Dihydrolipoyl dehydrogenase, mitochondrial	49	54151	4	8.3	7.59
50	gi|85720739	beta-enolase 3 [Sus scrofa]	454	47100	6	16.6	8.05
	gi|311262396	PREDICTED: septin-11 [Sus scrofa]	229	49340	4	9.1	6.36
	gi|335291628	PREDICTED: nuclease-sensitive element-binding protein 1-like [Sus scrofa]	221	36215	3	17.0	10.00
	gi|335310645	PREDICTED: n-acetylglucosamine-6-sulfatase-like, partial [Sus scrofa]	80	21003	1	6.5	5.27
	gi|311251336	PREDICTED: elongation factor Tu, mitochondrial-like [Sus scrofa]	64	49420	1	2.7	6.72
	gi|171920012	pre-mRNA processing factor 19 [Sus scrofa]	60	55146	5	11.7	6.14
	gi|1165145	annexin I [Sus scrofa]	59	38216	1	3.2	6.47
	gi|37693471	polypeptide chain elongation factor 1alpha [Sus scrofa]	52	11971	1	9.9	6.06
	gi|52631987	annexin A2 [Sus scrofa]	52	38510	1	2.0	6.49
	gi|335286672	PREDICTED: transgelin-2-like isoform 1 [Sus scrofa]	46	22363	1	5.5	8.41
51	gi|335291628	PREDICTED: nuclease-sensitive element-binding protein 1-like [Sus scrofa]	527	36215	9	43.8	10.00
	gi|85720739	beta-enolase 3 [Sus scrofa]	511	47100	8	24.9	8.05
	gi|311262396	PREDICTED: septin-11 [Sus scrofa]	170	49340	8	21.4	6.36
	gi|311256155	PREDICTED: DNA-binding protein A-like isoform 1 [Sus scrofa]	166	40625	4	8.7	9.64
	gi|311251336	PREDICTED: elongation factor Tu, mitochondrial-like [Sus scrofa]	119	49420	3	8.0	6.72
	gi|335304480	PREDICTED: sorting nexin-5 isoform 2 [Sus scrofa]	53	34915	1	3.7	8.58
52	gi|297591975	ATP synthase subunit alpha, mitochondrial [Sus scrofa]	900	59651	22	39.1	9.21

52	gi|118675	RecName: Full=Dihydrolipoyl dehydrogenase, mitochondrial	204	54151	7	14.7	7.59
	gi|347300243	glutamate dehydrogenase 1, mitochondrial [Sus scrofa]	194	61269	14	26.3	8.03
	gi|85720739	beta-enolase 3 [Sus scrofa]	128	47100	1	4.1	8.05
	gi|335290597	PREDICTED: delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial-like, partial [Sus scrofa]	48	41972	1	3.4	6.40
53	gi|297591975	ATP synthase subunit alpha, mitochondrial [Sus scrofa]	2701	59651	37	60.8	9.21
	gi|347300243	glutamate dehydrogenase 1, mitochondrial [Sus scrofa]	464	61269	22	40.3	8.03
	gi|335291061	PREDICTED: adenylyl cyclase-associated protein 1-like [Sus scrofa]	127	31290	4	19.4	5.70
	gi|118675	RecName: Full=Dihydrolipoyl dehydrogenase, mitochondrial	90	54151	5	10.2	7.59
	gi|2988346	catalase [Sus scrofa]	84	57277	2	4.4	6.26
54	gi|13399613	Chain A, X-Ray Structure Of Full-Length Annexin 1	839	38720	24	59.0	6.37
	gi|311248892	PREDICTED: lysosomal alpha-mannosidase-like isoform 1 [Sus scrofa]	101	113836	9	7.6	6.51
	gi|160858224	CArG-binding factor A [Sus scrofa]	55	31942	1	4.6	8.31
	gi|52631987	annexin A2 [Sus scrofa]	52	38510	6	22.1	6.49
55	gi|2506441	RecName: Full=Glyceraldehyde-3-phosphate dehydrogenase	1050	35813	20	53.2	8.51
	gi|2506849	RecName: Full= Malate dehydrogenase, mitochondrial; Flags: Precursor	563	33061	14	45.0	8.55
	gi|116175259	heterogeneous nuclear ribonucleoprotein A1 [Sus scrofa]	376	34175	6	23.1	9.27
	gi|335305543	PREDICTED: heterogeneous nuclear ribonucleoproteins A2/B1-like isoform 1 [Sus scrofa]	272	35984	10	33.7	8.67
	gi|4454537	L-3-hydroxyacyl-CoA dehydrogenase [Sus scrofa]	117	34140	11	28.0	9.02
56	gi|194039772	PREDICTED: histone H2B type 1-B-like [Sus scrofa]	793	13942	11	62.7	10.31
	gi|194039782	PREDICTED: histone H2B type 1-like isoform 1 [Sus scrofa]	783	13898	11	62.7	10.31
	gi|226256	peptidyl-Pro cis trans isomerase	350	17858	7	35.4	8.34
	gi|51702802	RecName: Full=60S ribosomal protein L31	250	14454	9	56.0	10.54
	gi|51317314	RecName: Full=Histone H4	246	11360	7	58.3	11.36
	gi|194039812	PREDICTED: histone H2A type 1-like [Sus scrofa]	88	14083	4	35.4	10.90
	gi|409074	heparin binding protein [Sus scrofa]	85	14750	3	23.4	9.21
	gi|18643343	histone H3.3A [Sus scrofa]	83	15318	8	33.8	11.27
	gi|117661156	RPS26 [Sus scrofa]	77	13007	3	33.9	11.01
	gi|51338616	RecName: Full=60S ribosomal protein L23; AltName: Full=Ribosomal	75	14856	2	17.1	10.51

		protein L17					
	gi|194039746	PREDICTED: histone H2A type 1-A-like [Sus scrofa]	72	14237	3	29.8	10.86
57	gi|335287018	PREDICTED: histone H2B type 2-E-like [Sus scrofa]	1318	13912	16	77.8	10.31
	gi|194039790	PREDICTED: histone H2B type 1-like [Sus scrofa]	1317	13898	16	77.8	10.31
	gi|51317314	RecName: Full=Histone H4	302	11360	10	63.1	11.36
	gi|194039812	PREDICTED: histone H2A type 1-like [Sus scrofa]	284	14083	8	40.0	10.90
	gi|194039746	PREDICTED: histone H2A type 1-A-like [Sus scrofa]	225	14237	6	39.7	10.86
	gi|335289786	PREDICTED: 40S ribosomal protein S19-like isoform 1 [Sus scrofa]	131	25106	8	23.9	10.17
	gi|409074	heparin binding protein [Sus scrofa] (60S ribosomal protein L22)	116	14750	6	46.1	9.21
	gi|47522626	histone H3.3 [Sus scrofa]	113	15318	12	36.8	11.27
	gi|226256	peptidyl-Pro cis trans isomerase	113	17858	3	27.4	8.34
	gi|51338616	RecName: Full=60S ribosomal protein L23; AltName: Full=Ribosomal protein L17	80	14856	2	17.1	10.51
	gi|2500494	RecName: Full=40S ribosomal protein S19	76	15086	8	33.1	10.20
	gi|194018718	40S ribosomal protein S20 [Sus scrofa]	68	13324	4	27.7	9.95
	gi|311259030	PREDICTED: small nuclear ribonucleoprotein Sm D1-like [Sus scrofa]	64	13273	1	10.9	11.56
	gi|343887362	small nuclear ribonucleoprotein Sm D2 [Sus scrofa]	47	13518	2	13.6	9.92