Supplementary Materials

Materials and Methods

Animals

The collection and feeding of toads (*Bombina maxima*) were performed following previously described procedures (Xiang et al., 2014). All procedures and the care and handing of animals were approved by the Ethics Committee of the Kunming Institute of Zoology, Chinese Academy of Sciences (IACUC No: IACUC-OE-2021-05-001).

Extracellular vesicle (EV) isolation

The toads were stimulated by electric shock to produce skin secretions, which were added to basal buffer (20 mM Tris-HCl, 0.1 M NaCl, pH 7.8). The samples were centrifuged at 300 ×g for 10 min at 4 °C to remove large particle impurities, then the supernatants were centrifuged at 2 000 ×*g* for 30 min at 4 °C to remove cell debris. The supernatants were again centrifuged (3 000 ×*g*, 30 min, 4 °C) to concentrate the centrifugal filters (100 kDa; Millipore, Massachusetts, USA). The resulting filtrates were collected and defined as sample 1 (proteins <100 kDa). Size exclusion chromatography columns (IZON qEV original/70 nm, iZON Science, Christchurch, New Zealand) were used to isolate the EVs per the manufacturer's protocols. The concentrated supernatants in the centrifugal filters were subjected to size exclusion chromatography. The first 3 mL of the eluent was phosphate-buffered saline (PBS), which was discarded; 3.0–4.5 mL contained EVs; and 4.5–9.0 mL was collected and defined as sample 2 (proteins >100 kDa). Isolated EVs were stored at −80 °C until use. Samples 1 and 2 were defined as non-EV skin secretions and stored at −80 °C until use.

Nanoparticle tracking analysis

The collected EV samples were sent to VivaCell Biosciences (Shanghai, China) to determine concentration and particle size. The samples were diluted 250 times with PBS (Biological Industries, Israel) and measured using a ZetaView PMX 110 instrument (Particle Metrix, Meerbusch, Germany) at 27 °C. Three runs were recorded for each sample, and the results were analyzed using ZetaView v8.04.02 SP2 software.

Western blotting

The EVs were lysed with lysis buffer, then subjected to sodium dodecyl-sulfate polyacrylamide gel electrophoresis (SDS-PAGE). The proteins were transferred to polyvinylidene difluoride (PVDF) membranes. After incubation with 5% skim milk powder for 2 h at room temperature and washing three times with phosphate-buffered saline with Tween-20 (PBST), the membranes were incubated with primary antibodies (final concentration 200 ng/mL) for CD9 (sc-13118, Santa Cruz, USA), CD63 (ab213090, Abcam, Cambridge, UK), CD81 (ab109201, Abcam), and TSG101 (28283-1-AP, Proteintech, Chicago, IL, USA) overnight at 4 °C. The membranes were then washed three times with PBST buffer and incubated with secondary antibodies (final concentration 200 ng/mL; goat-anti-rabbit IgG, SA00001-2, and goat-anti-mouse IgG, SA00001-1; Proteintech) at room temperature for 2 h. After washing three times with PBST buffer, the protein bands were imaged on a Tanon 5200CE Chemi-Image System (Tanon Science and Technology Co., Ltd., Shanghai,

China).

Transmission electron microscopy (TEM)

TEM was performed as described previously (Deng et al., 2020), with some modification. In brief, the isolated EVs were diluted 1:5 with PBS. A drop of EV sample was placed on a 200 mesh carbon-coated nickel grid for 2 min, then blotted with filter paper and air-dried. After staining with 3% uranyl acetate, the nickel grid was visualized using a JEM-1400 PLUS TEM (Japan Electron Optics Laboratory Co., Ltd.).

Coomassie brilliant blue staining

The EV and non-EV samples were freeze-dried using a freeze dryer (Christ, Germany) and proteins were quantified using a Pierce™ BCA Protein Assay Kit (Thermo Fisher Scientific, Cleveland, USA). Equal amounts of EV and non-EV proteins were subjected to SDS-PAGE with Coomassie brilliant blue staining, as described previously (Liu et al., 2008).

Liquid chromatography-tandem mass spectrometry (LC-MS/MS)

The EV and non-EV samples were freeze-dried as described above. The proteins were then treated using an EasyPep™ Mini MS Sample Prep Kit (Thermo Fisher Scientific) following the manufacturer's protocols. After quantification using a Pierce Quantitative Colorimetric Peptide Assay (Thermo Fisher Scientific), an equal dose of peptide mixture from each sample was trapped on a C18 Acclaim PepMap™ 100 trap column (75 μm×2 cm, 3 μm particle size, 100 Å, Thermo Fisher Scientific), with the peptides then separated using a C18 PepMap™ 100 analytical column (75 μm×25 cm, 2 μm particle size, 100 Å; Thermo Fisher Scientific). The UltiMate™ 3000 RSLCnano system was used for peptide separation and an Electrospray Q Exactive quadrupole Orbitrap benchtop mass spectrometer (Thermo Fisher Scientific) was used for data acquisition. The flow rate was set to 300 nL min^{-1} and the acetonitrile gradient was set to: 0–4 min, 2%–8% B; 4–63 min, 8%–25% B, 63–75 min, 25%–35% B; 75–80 min, 35%–99% B; 80–84 min, 99%–99% B; 84–85 min, 99%–2% B; 85–90 min 2%–2% B (A: 2% acetonitrile, 0.1% formic acid; B: 80% acetonitrile, 0.1% formic acid). The mass spectrometer was operated in positive and data-dependent mode. The MS scan parameters were: scan range: m/z 350–1 800; resolution: 70 000 (@ m/z 200); AGC target: 3e6; maximum injection time: 20 ms. The dd-MS2 acquisition parameters were: resolution 17 500; AGC target 1e5; maximum IT 60 ms; isolation window 1.6 m/z. The top 20 parent ions (charge range: $2 \leq z \leq 7$) were selected for fragmentation in higher-energy collisional dissociation mode with collision energy NCE28. Dynamic exclusion was set to 75 s. Other settings were: no sheath and auxiliary gas flow; heated capillary temperature, 320 °C. All data were read using Xcalibur software (v4.0).

Mass spectrometry data processing and analysis

Proteome Discoverer software (v1.3.0.339) was used for raw data processing and protein identification by searching against the protein sequence database of B. maxima skin based on transcriptomes (Zhao et al., 2014). Carbamidomethylation of cysteines was set as a fixed modification; oxidation of methionine and acetylation of protein N-termini were set as variable modifications. Precursor and fragment mass tolerances

were set to 10 ppm and 0.02 Da, respectively. Two or more transcripts annotated in the same protein were considered as one protein, with the highest number of peptides that matched presented. Protein functions were searched in UniProt (https://www.uniprot.org/uniprot) and proteins were classified based on their functions. Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway enrichment analysis was carried out using KOBAS (Bu et al., 2021).

Flow cytometry analysis

Based on previous research (Deng et al., 2020), with some modifications, the EVs were pre-incubated with PKH67 for 5 min in accordance with the instructions of the PKH67 Green Fluorescent Cell Linker Kit (Sigma, Germany). *Bombina maxima* skin fibroblast cells (Xiang et al., 2012) were grown to 70% confluence in a six-well plate, then incubated with PKH67-labeled EVs for 5 h at 37 °C. The cells were washed twice with Ringer's solution (3.42 M NaCl, 1.34 M KCl, 0.9 M $CaCl_2$, 0.6 M $NaHCO_3$, 0.08 M NaH_2PO_4, and 0.01 M glucose) and fixed in 5% paraformaldehyde for 2 h. Finally, the cells were scraped off the plate for flow cytometry analysis.

Statistical analysis

The data in Figure 1F represent mean±standard deviation (SD) and were analyzed using Prism v8.0. Two-sample comparisons were performed using Student's *t*-test; $P<0.05$ was considered statistically significant.

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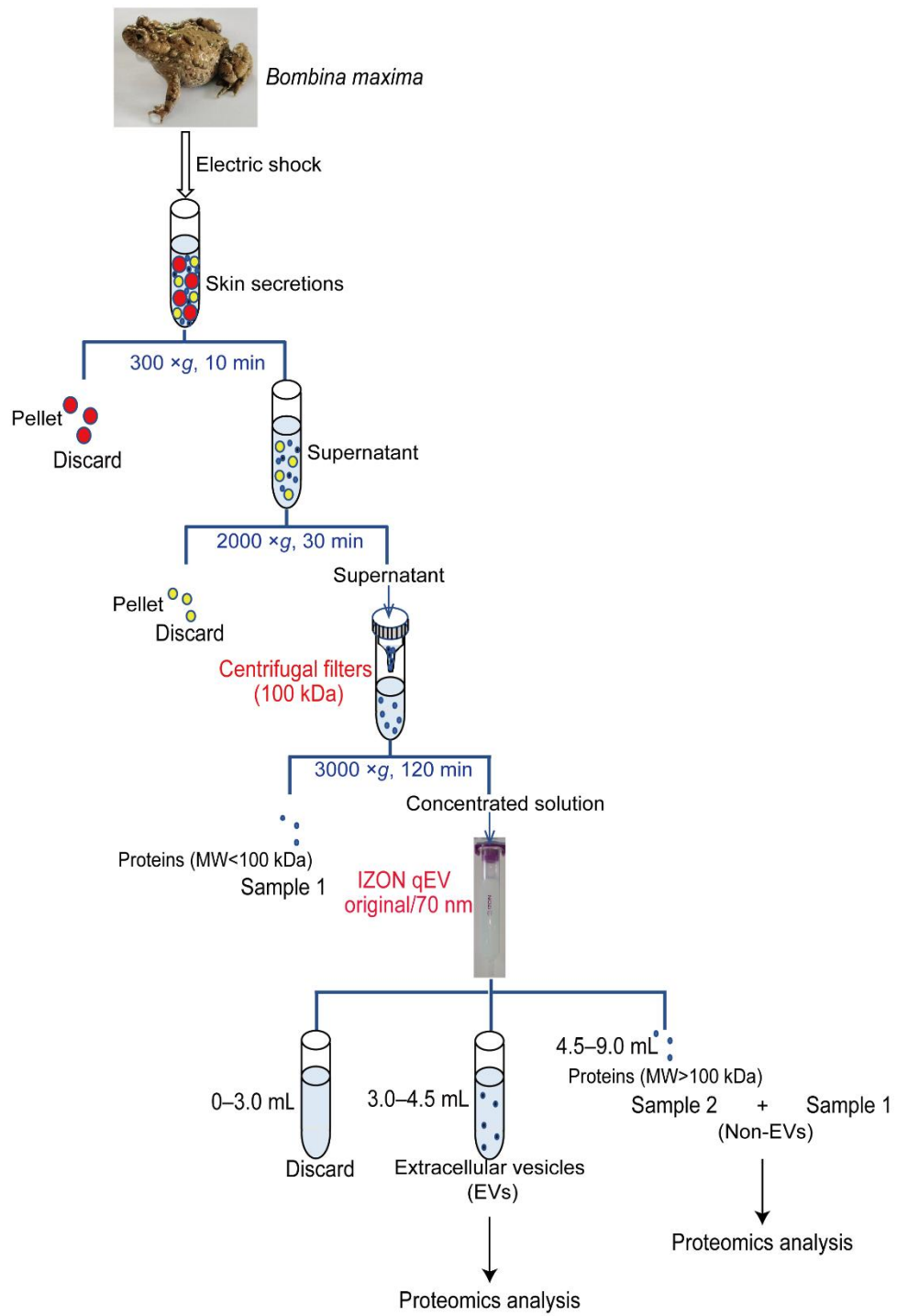
Supplementary Figure S1 Strategy for isolation of EVs from *Bombina maxima* skin secretions

Supplementary Table S1 Proteins specific to EVs

Proteins identified	Peptides matched
Proteins related to stress (14)	
1 mucus protein; Flags: Precursor	6
2 PREDICTED: heat shock protein 30D-like	5
3 heat shock protein 90 kDa alpha (cytosolic), class B member 1	4
4 PREDICTED: early endosome antigen 1	4
5 heat shock protein 90 kDa alpha (cytosolic), class A member 1, gene 1	3
6 PREDICTED: heat shock 70 kDa protein-like	3
7 PREDICTED: IgGFc-binding protein	2
8 ras-related protein Rab-11A isoform 1	2
9 alpha-2-macroglobulin	2
10 immunoglobulin-associated J chain	1
11 von Willebrand factor A domain containing 5A	1
12 PREDICTED: IgGFc-binding protein-like	1
13 polymeric immunoglobulin receptor	1
14 PREDICTED: similar to FAT tumor suppressor homolog 4	1
Metabolic enzymes (7)	
1 amiloride-sensitive amine oxidase	3
2 rab7 GTPase homolog SUrab7	2
3 ecto-ATP-diphosphohydrolase	1
4 fructose-bisphosphate aldolase A	1
5 D-3-phosphoglycerate dehydrogenase	1
6 aldolase B, fructose-bisphosphate	1
7 phosphoribosyl pyrophosphate synthase-associated protein 2	1
Proteins related to transcription, translation and protein folding (6)	
1 aminoacyl tRNA synthetase complex-interacting multifunctional protein 1	2
2 Isoleucyl-tRNA synthetase, cytoplasmic	2
3 seryl-tRNA synthetase	1
4 cold-inducible RNA-binding protein homolog	1
5 PREDICTED: mismatch repair endonuclease PMS2-like	1
6 phenylalanyl-tRNA synthetase alpha chain A	1
Skeleton proteins (12)	
1 Integumentary mucin B.1	8
2 LOC398083 protein	6
3 keratin 19	3
4 PREDICTED: LOW QUALITY PROTEIN: myosin-9-like	2
5 LOC398555 protein	2
6 PREDICTED: filamin-A isoform 2	2
7 inner-ear cytokeratin	2

8	PREDICTED: keratin, type II cytoskeletal 5-like	1
9	gelsolin	1
10	charged multivesicular body protein 1b	1
11	similar to coronin, actin binding protein 1C	1
12	annexin A1	1

Others (22)

1	integumentary mucin B.1	12
2	PREDICTED: olfactomedin-like	9
3	PREDICTED: protein FAM115-like	8
4	14-3-3 protein	5
5	hCG1818434-like	5
6	PREDICTED: similar to hCG1818434	3
7	Prokineticin Bm8-a	2
8	actin-related protein 2/3 complex subunit 3	2
9	syndecan binding protein (syntenin)	2
10	PREDICTED: hypothetical protein LOC100486853	2
11	MGC64358 protein	2
12	LOC100036918 protein	1
13	PREDICTED: mucin-5AC-like	1
14	PREDICTED: olfactomedin-4-like	1
15	LOC398095 protein	1
16	PREDICTED: mismatch repair endonucl	1
17	prominin-3 transcript variant 2	1
18	PREDICTED: retinoic acid-induced protein 3-like	1
19	PREDICTED: protein S100-A13-like	1
20	alpha(I)-globin	1
21	serotransferrin	1
22	Ferritin heavy chain, oocyte isoform	1

Unknown (1)

1	Unknown	1

Supplementary Table S2 Proteins common to EVs and non-Evs

	Proteins identified	Peptides matched in EVs	Peptides matched in non-EVs
Secretory endolysosome channel (SELC) protein interaction networks (6)			
1	betagamma-cat alpha subunit (BmALP1)	6	12
2	betagamma-cat beta subunit (BmTFF3)	4	9
3	trefoil factor BmTFF2	2	9
4	BmALP3	2	9
5	PREDICTED: trefoil factor 3-like	1	4
6	BmALP2	1	9
Redox proteins (8)			
1	peroxiredoxin 5	5	2
2	peroxiredoxin 6	4	8

3	glutathione S-transferase mu 2	4	8
4	Superoxide dismutase A	2	5
5	Novel glutathione S-transferase omega protein	2	10
6	prostaglandin reductase 1, gene 2	1	12
7	catalase, gene 2	1	11
8	PREDICTED: uncharacterized oxidoreductase C663.06c-like	1	1

Proteins related to stress (7)

1	IgGFc-binding protein	12	24
2	heat shock cognate 70	4	1
3	scavenger receptor cysteine-rich protein	2	2
4	macrophage migration inhibitory factor	1	2
5	Lysozyme	1	3
6	PREDICTED: alpha-2-macroglobulin	1	1
7	PREDICTED: galectin-1-like	1	5

Metabolic enzymes (16)

1	PREDICTED: insulin-degrading enzyme isoform 1	5	7
2	aldehyde dehydrogenase class 1	3	1
3	PREDICTED: nicotinamide N-methyltransferase-like	3	9
4	peptidylaminoacyl-L/D-isomerase precursor	2	2
5	PREDICTED: amiloride-sensitive amine oxidase	2	7
6	betaine--homocysteine S-methyltransferase 1	2	7
7	phosphoglucomutase 2	1	2
8	PREDICTED: tyrosinase-like	1	3
9	ectonucleotide pyrophosphatase/phosphodiesterase 6	1	7
10	glucosamine (N-acetyl)-6-sulfatase	1	5
11	peptidylprolyl isomerase A (cyclophilin A)	1	2
12	L-lactate dehydrogenase B chain	1	2
13	Nicotinamide N-methyltransferase	1	1
14	selenium-binding protein 1-B	1	11
15	PREDICTED: fatty acid-binding protein, brain-like	1	4
16	PREDICTED: peptidyl-prolyl cis-trans isomerase-like isoform 1	1	4

Proteins related to transcription, translation and protein folding (3)

1	urokinase plasminogen activator surface receptor precursor	4	1
2	elongation factor 1-alpha, somatic form	1	1

3	RAN binding protein 1	1	3

Proteasome, protease and protease inhibitor (7)

1	MGC81160 protein	8	13
2	PREDICTED: neuroendocrine convertase 1-like	4	25
3	LOC733291 protein	1	8
4	trypsin inhibitor BMTI	1	2
5	carboxypeptidase E	1	1
6	LOC100036845 protein	1	2
7	proteasome beta 1 subunit	1	5

Skeleton protein (4)

1	annexin A2	3	14
2	ezrin	2	1
3	PREDICTED: actin, cytoplasmic 2-like	2	3
4	charged multivesicular body protein 2a	1	1

Others (13)

1	MGC69066 protein	5	1
2	Maximins-S type D	2	1
3	YWHAZ protein	2	2
4	ID14 protein	2	2
5	integumentary mucin A.1 precursor	2	5
6	sodefrin-like protein precursor	1	6
7	ighx protein	1	10
8	retinitis pigmentosa GTPase regulator-like protein	1	1
9	XCP3 protein	1	1
10	PREDICTED: extracellular matrix protein 1-like	1	4
11	Gapd-prov protein	1	6
12	PREDICTED: mucin-5B-like	1	1
13	bombinakinin M variant precursor	1	1

Unknown (5)

1	Unknown	2	6
2	Unknown	2	2
3	Unknown	1	3
4	Unknown	1	2
5	Unknown	1	12

Supplementary Table S3 Proteins specific to non-EVs

	Proteins identified	Peptides matched
Redox proteins (11)		
1	thioredoxin domain containing 5	7
2	thioredoxin	4
3	PREDICTED: prostaglandin-E (2) 9-reductase-like	4

4	crystallin, zeta (quinone reductase)	3
5	selenoprotein W	1
6	LOC496089 protein	1
7	PREDICTED: myeloperoxidase-like	1
8	quinoid dihydropteridine reductase	1
9	glutathione peroxidase 3 a	1
10	thioredoxin-like 1	1
11	15 kDa selenoprotein	1

Proteins related to stress (20)

1	alpha-2-macroglobulin a	6
2	maximin-H16 antimicrobial peptide precursor	5
3	von Hippel-Lindau binding protein 1	4
4	PREDICTED: programmed cell death 1 ligand 1-like	4
5	dnajb9 protein	3
6	PREDICTED: galectin-4-like	3
7	GLI pathogenesis-related 2	3
8	programmed cell death 5	3
9	bactericidal/permeability-increasing protein	2
10	interferon, gamma-inducible protein 30	2
11	cytochrome c	1
12	PREDICTED: similar to scavenger receptor cysteine-rich protein isoform 1	1
13	tumor protein D52	1
14	s100 calcium binding protein	1
15	stathmin 1/oncoprotein 18	1
16	PREDICTED: heat shock cognate 71 kDa protein-like	1
17	lectin, galactoside-binding, soluble, 3 (galectin 3)	1
18	PREDICTED: alpha-2-macroglobulin-like	1
19	Bombesin OS = Bombina orientalis	1
20	Von Willebrand factor homolog	1

Metabolic enzymes (76)

1	PREDICTED: 78 kDa glucose-regulated protein-like	11
2	triosephosphate isomerase	8
3	adenosine kinase	6
4	phosphoglycerate mutase 1 (brain)	5
5	PREDICTED: pancreatic lipase-related protein 2-like isoform 1	5
6	PREDICTED: glutamyl aminopeptidase-like	4
7	cysteine conjugate-beta lyase 2	4
8	glyoxalase 1	4
9	nucleoside diphosphate kinase	4
10	hypoxanthine phosphoribosyltransferase 1 (Lesch-Nyhan syndrome)	4
11	glutamic-oxaloacetic transaminase 1, soluble (aspartate	4

	aminotransferase 1)	
12	transketolase	4
13	phosphoglucomutase 1	3
14	3-hydroxybutyrate dehydrogenase type 2	3
15	Putative phospholipase B-like 2	3
16	Probable L-xylulose reductase	3
17	Rho GDP dissociation inhibitor (GDI) alpha	3
18	D-dopachrome decarboxylase-A	2
19	S-phase kinase-associated protein 1A	2
20	carboxymethylenebutenolidase homolog	2
21	PREDICTED: pancreatic alpha-amylase-like isoform 2	2
22	LOC495027 protein	2
23	Thiamin pyrophosphokinase 1	2
24	ester hydrolase C11orf54 homolog	2
25	glutathione synthetase	2
26	alcohol dehydrogenase [NADP+]	2
27	membrane metallo-endopeptidase-like 1	2
28	serine protease ami precursor	2
29	notum pectinacetylesterase homolog	2
30	thiosulfate sulfurtransferase	2
31	PREDICTED: pancreatic triacylglycerol lipase-like	2
32	aldo-keto reductase family 1, member B1 (aldose reductase)	2
33	alcohol dehydrogenase 5 (class III), chi polypeptide	1
34	PREDICTED: ribose-5-phosphate isomerase isoform 1	1
35	citrate synthase, mitochondrial precursor	1
36	PREDICTED: interferon-induced very large GTPase 1-like	1
37	Glutamate dehydrogenase 1	1
38	abhydrolase domain containing 14B	1
39	inositol(myo)-1(or 4)-monophosphatase 1	1
40	enolase 3	1
41	stress-induced-phosphoprotein 1	1
42	PREDICTED: (4)-(beta-N-acetylglucosaminyl)-L-asparaginase-like	1
43	Gssls-A-prov protein	1
44	lysyl-tRNA synthetase	1
45	aminoacylase 1, gene 1	1
46	ST3 beta-galactoside alpha-2,3-sialyltransferase 5	1
47	ribonuclease T2	1
48	arginase	1
49	Bleomycin hydrolase	1
50	3'(2'), 5'-bisphosphate nucleotidase 1	1
51	GTP cyclohydrolase 1 feedback regulatory protein	1
52	retinoblastoma binding protein 9	1
53	Argininosuccinate lyase	1

54	PREDICTED: NADP-dependent alcohol dehydrogenase-like	1
55	carboxylesterase 3	1
56	PREDICTED: aldehyde oxidase	1
57	histidine triad nucleotide binding protein 1	1
58	PREDICTED: similar to Os11g0297800	1
59	FK506 binding protein 3, 25kDa	1
60	acylglycerol kinase, mitochondrial precursor	1
61	PMR-1 protein	1
62	cytidylate kinase	1
63	malate dehydrogenase 2, NAD (mitochondrial)	1
64	selenoprotein P, plasma, 1	1
65	calcineurin-like phosphoesterase domain-containing protein 1	1
66	PREDICTED: phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit delta isoform-like	1
67	sphingomyelin phosphodiesterase, acid-like 3A	1
68	regucalcin	1
69	PREDICTED: LOW QUALITY PROTEIN: lysosomal alpha-glucosidase-like	1
70	vanin 2	1
71	PREDICTED: maleylacetoacetate isomerase	1
72	ranaspumin-4	1
73	cathepsin F-like cysteine protease	1
74	LOC495504 protein	1
75	amylase, alpha 2B (pancreatic)	1
76	phospholipase D3	1

Proteasomes, proteases and protease inhibitors (28)

1	peptidyl-glycine alpha-amidating monooxygenase B	15
2	proteasome alpha 7 subunit	7
3	proteasome (prosome, macropain) subunit, alpha type, 5	7
4	serpin peptidase inhibitor, clade B (ovalbumin), member 4	7
5	calpastatin	7
6	proteasome alpha 4 subunit	7
7	cytosol aminopeptidase	5
8	PREDICTED: serpin B11-like	4
9	PREDICTED: proteasome subunit alpha type-1-like	4
10	thimet oligopeptidase 1	3
11	Proteasome subunit alpha type-6	3
12	peptidase D	2
13	proteasome subunit Y	2
14	proteasome (prosome, macropain) subunit, alpha type, 2	2
15	proteasome (prosome, macropain) subunit, beta type, 7, gene 2	1
16	serine peptidase inhibitor, Kunitz type, 2	1
17	cystatin B (stefin B)	1

18	leukocyte elastase inhibitor	1
19	PREDICTED: WAP four-disulfide core domain protein 2-like	1
20	REDICTED: ovomucoid-like	1
21	serpin peptidase inhibitor, clade B (ovalbumin), member 6	1
22	PREDICTED: proteasome subunit beta type-5	1
23	oviduct protein p20	1
24	PREDICTED: proteasome subunit beta type-7-like	1
25	cystatin-C	1
26	proteasome (prosome, macropain) 28 subunit, alpha	1
27	cathepsin L2	1
28	proteasome (prosome, macropain) subunit, beta type, 2	1

Proteins related to transcription, translation and protein folding (16)

1	nascent polypeptide-associated complex subunit alpha	3
2	PREDICTED: ubiquitin-60S ribosomal protein L40-like	2
3	TPA: TPA_inf: HN1-like protein	2
4	FK506 binding protein 2, 13kDa	2
5	prefoldin subunit 6	2
6	eukaryotic translation initiation factor 5A	1
7	LOC100145615 protein	1
8	Vg1 mRNA binding protein 40	1
9	PREDICTED: transcription factor BTF3 homolog 4-like	1
10	cold-inducible RNA-binding protein B	1
11	prefoldin subunit 2	1
12	eukaryotic translation initiation factor 4H	1
13	alanyl-tRNA synthetase	1
14	eukaryotic translation elongation factor 2, gene 1	1
15	eukaryotic translation initiation factor 3 subunit J	1
16	TATA box-binding protein-associated factor, RNA polymerase I, subunit C	1

Skeleton proteins (12)

1	TPM3 protein	3
2	tropomyosin 3	3
3	Annexin A1	3
4	charged multivesicular body protein 4b	2
5	PREDICTED: LOW QUALITY PROTEIN: actin, alpha skeletal muscle-like	2
6	keratin 10	1
7	F-actin capping protein alpha-1 subunit	1
8	tubulin polymerization-promoting protein family member 3	1
9	Annexin A3	1
10	Sporozoite surface protein 2	1
11	cornulin	1
12	annexin A7	1

Others (71)

1	prolyl 4-hydroxylase, beta polypeptide	8
2	angiotensin I converting enzyme 1	7
3	Maximins 2/H1	6
4	PREDICTED: Golgi apparatus protein 1-like	6
5	protein S100-A13-like	4
6	riddle 2	4
7	DJ-1	4
8	PREDICTED: gastric intrinsic factor-like	4
19	cathepsin C	4
10	glutaredoxin (thioltransferase)	4
11	PREDICTED: calmodulin-like	4
12	Dpp3-A-prov protein	4
13	MGC80873 protein	3
14	MGC115064 protein	3
15	Complement factor B	3
16	ubiquitin-conjugating enzyme	3
17	serotransferrin precursor	3
18	cadherin 2, type 1, N-cadherin (neuronal)	3
19	serotransferrin-B precursor	3
20	Prokineticin	3
21	Chain A, Solution Structure Of Ufm1, A Ubiquitin-Fold Modifier	2
22	diazepam binding inhibitor	2
23	Serotransferrin-A	2
24	brain abundant, membrane attached signal protein 1	2
25	OTTXETP00000006605	2
26	PREDICTED: hypothetical protein LOC100490435	2
27	Armet protein	2
28	BCL2-associated athanogene 3	2
29	MGC84775 protein	2
30	PREDICTED: ig kappa chain V region Mem 5	2
31	LOC496142 protein	2
32	LOC100135142 protein	2
33	14-3-3 protein epsilon	2
34	nucleobindin 1	2
35	PREDICTED: toll interacting protein	1
36	protein CutA homolog	1
37	PREDICTED: similar to ovulatory protein-2	1
38	MGC83153 protein	1
39	MGC68953 protein	1
40	Gdi2-prov protein	1
41	PREDICTED: dynein light chain roadblock-type 1-like	1
42	S100-A11	1

43	PREDICTED: nuclear transport factor 2-like	1
44	neuromedin U precursor	1
45	PREDICTED: breast carcinoma-amplified sequence 1-like	1
46	PREDICTED: protocadherin-18	1
47	high-mobility group box 3	1
48	PREDICTED: calcium-regulated heat stable protein 1 isoform 1	1
49	PREDICTED: small ubiquitin-related modifier 2-like	1
50	FR10	
51	repeat-containing protein 1-A	1
52	myotrophin	1
53	Ubiquitin	1
54	renin binding protein	1
55	PREDICTED: protein S100-P	1
56	High mobility group protein B2	1
57	lysosomal-associated membrane protein 1	1
58	MGC68927 protein	1
59	vaccinia related kinase 1	1
60	EF hand domain family, member D1	1
61	multiple coagulation factor deficiency 2	1
62	protection of telomeres protein 1	1
63	PREDICTED: structural maintenance of chromosomes protein 4	1
64	apolipoprotein CI	1
65	PREDICTED: hypothetical protein LOC100496032	1
66	PREDICTED: protein canopy homolog 1-like isoform 1	1
67	pirin (iron-binding nuclear protein)	1
68	PREDICTED: LOW QUALITY PROTEIN: uncharacterized protein C20orf117-like	1
69	PREDICTED: NSFL1 cofactor p47-like	1
70	PREDICTED: coagulation factor XIII B chain-like	1
71	insulin-like growth factor-binding protein 2	1

Unknown (10)

1	Unknown	27
2	Unknown	7
3	Unknown	6
4	Unknown	3
5	Unknown	2
6	Unknown	2
7	Unknown	1
8	Unknown	1
9	Unknown	1
10	Unknown	1