

Suppl Table S1, List of proteins identified in the 70% ethanol fraction from the mouse liver tissue. Only proteins with a probability > 0.5 have been listed. Color code: **Pink**: observed across all tissue types; **Green**: observed across three tissue types; **Yellow**: observed across two tissue types.

UniRef100 Accession Nb	Protein probability	Percent coverage	Nb unique peptides		Description (S, observed in human serum)
P31786	1	69	16		Acyl-CoA-binding protein
Q3UJW9	1	13.8	4	S	Aldo-keto reductase family 1
P17182	1	56.2	12		Alpha-enolase
Q3UKX6	1	42.2	7	S	Apolipoprotein A-II
P97450	1	55.6	8	S	ATP synthase-coupling factor 6
Q8VBW8	1	21	3		CDNA sequence BC021608
O08997	1	63.2	6		Copper transport protein ATOX1
P48771	1	57.8	5		Cytochrome c oxidase polypeptide VIIa-liver/heart
O35215	1	79.7	15		D-dopachrome decarboxylase
Q6PHC1	1	52.7	7	S	Enolase
P12710	1	76.4	12		Fatty acid-binding protein, liver
P26883	1	34.3	4	S	FK506-binding protein 1A; Peptidyl-prolyl cis-trans isomerase
P19157	1	72.4	37	S	Glutathione S-transferase P 1
P01942	1	50.7	12	S	Hemoglobin subunit alpha
P02088	1	53.7	6	S	Hemoglobin subunit beta
Q91X52	1	33.6	8		L-xylulose reductase
P34884	1	23.5	3	S	Macrophage migration inhibitory factor
P17742	1	55.5	9	S	Peptidyl-prolyl cis-trans isomerase A (Cyclophilin A)
P70296	1	25.1	3		Phosphatidylethanolamine-binding protein 1 (PEBP-1)
P29341	1	5.9	2	S	Polyadenylate-binding protein 1 (Poly(A)-binding protein 1)
Q3TIT5	1	10.3	7		Prosaposin
Q64374	1	41.5	10		Regucalcin
Q63836	1	83.1	23	S	Selenium binding protein 2
P17563	1	82.4	16	S	Selenium-binding protein 1
P07724	1	6.2	3	S	Serum albumin

P08228	1	66.9	18	S	Superoxide dismutase [Cu-Zn]
P20065	1	50	6	S	Thymosin beta-4
Q9D1N0	0.9999	25.2	2		Hypothetical protein
P58044	0.9999	26.4	3		Isopentenyl-diphosphate Delta-isomerase 1
Q3U3C2	0.9999	15.4	3		Niemann Pick type C2
P12815	0.9997	15.7	2	S	Programmed cell death protein 6
Q9CR68	0.9984	6.9	2	S	Ubiquinol-cytochrome c reductase iron-sulfur subunit
P16015	0.9979	4.6	2	S	Carbonic anhydrase 3
Q3TH47	0.9965	44.6	2		Ubiquitin C
A2A513	0.9919	21	7		Keratin 10
P70349	0.9905	11.1	1		Histidine triad nucleotide-binding protein 1
Q63880	0.9858	2.3	1		Liver carboxylesterase 31
P62500	0.983	8.4	1		TSC22 domain family protein 1 (TSC22-related inducible leucine zipper 1b)
P04104	0.9802	7.5	2		Keratin, type II cytoskeletal 1
P62077	0.9719	13.3	1		Mitochondrial import inner membrane translocase subunit Tim8 B
Q14AA6	0.9431	9.7	1		Mammary gland RCB-0527 Jyg-MC(B) cDNA
P49429	0.9222	2.3	1		4-hydroxyphenylpyruvate dioxygenase
P21550	0.9096	16.1	1		Beta-enolase
Q66JR8	0.8915	15.5	1	S	Parathymosin (Ptms protein)
Q3TNH0	0.867	2.9	1	S	Thymopoietin
O08705	0.8626	3.9	1		Sodium/bile acid cotransporter (Na+)/bile acid cotransporter) (Na+) / taurocholate transport protein)
A2A4U6	0.7881	3.1	1		Zinc finger protein 334
A2AQZ2	0.7328	10	1		Phytanoyl-CoA dioxygenase domain containing 1
P99029	0.7264	6.3	1		Peroxiredoxin-5
O35114	0.6877	4.6	1		Lysosome membrane protein 2
Q5DTY0	0.6818	4.5	1		MKIAA1414 protein
P30115	0.6603	4.1	1		Glutathione S-transferase A3
Q9WVA2	0.6239	11.3	1		Mitochondrial import inner membrane translocase subunit Tim8 A
UPI00001C2A77	0.5505	5.5	1		Predicted: hypothetical protein
P51910	0.5474	6.3	1	S	Apolipoprotein D
A2AUA8	0.5051	0.8	1	S	A disintegrin and metalloprotease domain 11
Q3UHH3	0.4753	0.2	1		Perlecan (heparan sulfate proteoglycan 2)
P15327	0.4687	3.9	1		Bisphosphoglycerate mutase

Suppl Table S2, List of proteins identified in the 70% ethanol fraction from the mouse lung tissue. Only proteins with a probability > 0.5 have been listed. Color code: **Pink**: observed across all tissue types; **Green**: observed across three tissue types; **Yellow**: observed across two tissue types.

UniRef100 Accession Nb	Protein probability	Percent coverage	Nb unique peptides		Description (S, observed in human serum)
P31786	1	33.3	4		Acyl-CoA-binding protein
P45376	1	7.9	2		Aldose reductase
Q60590	1	18.4	3	S	Alpha-1-acid glycoprotein 1
P17182	1	28.3	8	S	Alpha-enolase
Q3UKX6	1	42.2	7	S	Apolipoprotein A-II
P06728	1	28.4	10	S	Apolipoprotein A-IV
P51910	1	27.5	4	S	Apolipoprotein D
P97450	1	54.6	6	S	ATP synthase-coupling factor 6
P15327	1	32.8	8		Bisphosphoglycerate mutase
Q91XV3	1	21.2	3		Brain acid soluble protein 1
Q3UKW2	1	57.9	24		Calmodulin 1
P00920	1	71.5	19	S	Carbonic anhydrase 2
O08997	1	63.2	8		Copper transport protein ATOX1
P07310	1	8.1	2	S	Creatine kinase M-type
P12787	1	42.8	4		Cytochrome c oxidase subunit 5A
O35215	1	60.2	7		D-dopachrome decarboxylase
Q6UL10	1	3.7	4		Desmoyokin (AHNAK)
Q99LT0	1	58.6	7		Dpy-30-like protein
A2AVR9	1	29.2	2		Dynein light chain roadblock-type 1
P26883	1	65.7	6	S	FK506-binding protein 1A; Peptidyl-prolyl cis-trans isomerase
P19157	1	43.3	10	S	Glutathione S-transferase P 1
P02088	1	74.1	17	S	Hemoglobin subunit beta
Q8R1H0	1	49.3	4		Homeodomain-only protein
P58044	1	18.9	3		Isopentenyl-diphosphate Delta-isomerase 1
P08074	1	81.1	30		Lung carbonyl reductase [NADPH]

Q91X52	1	27.9	5		L-xylulose reductase
P34884	1	23.5	4	S	Macrophage migration inhibitory factor
Q3U3C2	1	41.6	6		Niemann Pick type C2
P17742	1	74.4	15	S	Peptidyl-prolyl cis-trans isomerase A (Cyclophilin A)
O55103	1	6.3	4		Periaxin
P70296	1	49.2	5		Phosphatidylethanolamine-binding protein 1 (PEBP-1)
Q9DBJ1	1	21.3	6		Phosphoglycerate mutase 1
P50405	1	28.2	16		Pulmonary surfactant-associated protein B (SP-B), (Pulmonary surfactant-associated proteolipid SPL(Phe))
P14069	1	47.2	4		S100-A6 (calcyclin)
P17563	1	78.2	12	S	Selenium-binding protein 1
Q63836	1	55.9	1	S	Selenium-binding protein 2
Q92111	1	21.7	11	S	Serotransferrin
P07724	1	78.8	105	S	Serum albumin
P08228	1	97.4	24	S	Superoxide dismutase [Cu-Zn]
P20065	1	54	12	S	Thymosin beta-4
P62500	1	21.7	2		TSC22 domain family protein 1 (TSC22-related inducible leucine zipper 1b)
Q06318	1	19.8	4		Uteroglobin
P21614	1	17.4	6	S	Vitamin D-binding protein
A2A5G4	1	36.5	2		WAP four-disulfide core domain 2
P16015	0.9999	11.5	3	S	Carbonic anhydrase 3
O08692	0.9999	9.6	2		Myeloid bacterenecin
P61750	0.9998	6.1	2	S	ADP-ribosylation factor 4
Q9CPU0	0.9998	9.2	2		Lactoylglutathione lyase (glyoxalase 1)
O08855	0.9994	14.1	2	S	Apolipoprotein A-I
Q9WVA2	0.9994	28.9	2		Mitochondrial import inner membrane translocase subunit Tim8 A
Q8CB17	0.9992	11.6	2	S	Fetuin beta, Fetuin-B
P48771	0.9925	27.7	2		Cytochrome c oxidase polypeptide VIIa-liver/heart, mitochondrial
P14220	0.9888	18.7	1		Glycophorin A
Q66JR8	0.9888	15.5	1	S	Parathymosin (Ptms protein)
P04939	0.9857	9.8	1		Major urinary protein 3
P08556	0.9821	10.6	1		GTPase NRas
Q3UYC6	0.9804	6.4	2		Hypothetical protein, predicted gene, ENSMUSG00000063087;
P97361	0.9797	10.1	1		Protein Plunc

Q9D6P8	0.9749	39.6	1	S	Calmodulin-like protein 3
P04104	0.972	7.0	2		Keratin, type II cytoskeletal 1
UPI0000693A01	0.9653	0.9	2	S	Phosphodiesterase 4D interacting protein isoform 1 (myomegalin)
Q8R527	0.9626	10.2	1		Rho-related GTP-binding protein RhoQ
P56395	0.9592	9.0	1	S	Cytochrome b5
Q920F6	0.9553	1.9	1	S	Structural maintenance of chromosomes protein 1B
Q8CAI1	0.9532	4.8	1		Hypothetical protein LOC243510
A6PW73	0.9488	34.0	1		Dehydrogenase/reductase SDR family member 11
Q3TIT5	0.9084	17.5	0		Prosaposin
Q61012	0.8895	10.8	1		Guanine nucleotide-binding protein G(T) gamma-T1 subunit
Q3TCR9	0.8714	2.1	1		Zyxin
Q3UD53	0.861	10.8	1		Calcium regulated heat stable protein 1
Q3TCS0	0.8425	1.8	1		Prolyl endopeptidase
P08207	0.8109	14.4	1		S100-A10 (calpactin)
P97371	0.8004	5.6	1		Proteasome activator complex subunit 1
Q3U449	0.788	3.6	1	S	Bisphosphate 3'-nucleotidase 1
P26807	0.7689	4.5	1	S	Gag polyprotein (Core polyprotein) [Contains: Matrix protein p15; RNA- binding phosphoprotein p12; Capsid protein p30; Nucleocapsid protein p10]
A2A8R7	0.7549	1.6	1		Zinc finger, CCHC domain containing 11
Q3TH47	0.7435	44.6	1		Ubiquitin C
UPI0000195319	0.74	26.6	1		Predicted: similar to ubiquitin A-52 residue ribosomal protein fusion product 1
P62077	0.7178	13.3	1		Mitochondrial import inner membrane translocase subunit Tim8 B
Q8BHT4	0.6854	5.1	1		Serine/threonine-protein kinase RIO2
P10639	0.678	11.4	1	S	Thioredoxin
Q925F2	0.6438	5.8	1		Endothelial cell-selective adhesion molecule
A2CEL1	0.6012	24.4	0		Major urinary protein 1
Q3UHH3	0.5983	0.2	1		Perlecan (heparan sulfate proteoglycan 2)
Q3UGT3	0.5845	20	1		COMM domain containing 1
Q9CQZ1	0.5807	25	1	S	Heat shock factor-binding protein 1
UPI00001C2A77	0.5768	5.5	1		Predicted: hypothetical protein
P23275	0.576	1.6	1		Olfactory receptor 15
Q9DCC7	0.5678	7.1	1		Isochorismatase domain-containing protein 2B
P01942	0.5553	42.3	0	S	Hemoglobin subunit alpha

Q61017	0.5258	29	1	Guanine nucleotide-binding protein G(I)/G(S)/G(O) gamma-T2 subunit
A2ACI8	0.4738	6.5	1	Actin, gamma

Suppl Table S3, List of proteins identified in the 70% ethanol fraction from the mouse kidney tissue. Only proteins with a probability > 0.5 have been listed. Color code: **Pink**: observed across all tissue types; **Green**: observed across three tissue types; **Yellow**: observed across two tissue types.

Uniref100 accession Nb	Protein probability	Percent coverage	Nb unique peptides		Description (S, observed in human serum)
P25444	1	5.4	2		40S ribosomal protein S2
P99027	1	25.2	3		60S acidic ribosomal protein P2
P31786	1	54.0	6		Acyl-CoA-binding protein
Q3UJW9	1	73.8	34	S	Aldo-keto reductase family 1, member A4 (aldehyde reductase)
P45376	1	36.7	13		Aldose reductase
P17182	1	66.8	27	S	Alpha-enolase
Q3UKX6	1	42.2	3	S	Apolipoprotein A-II
P51910	1	20.1	2	S	Apolipoprotein D
Q91XE4	1	41.8	13		Aspartoacylase-2
P97450	1	55.6	9	S	ATP synthase-coupling factor 6
P15327	1	25.5	6		Bisphosphoglycerate mutase
Q3UKW2	1	43.1	9		Calmodulin 1
P13634	1	36.8	6	S	Carbonic anhydrase 1
P00920	1	62.7	18	S	Carbonic anhydrase 2
P16015	1	52.3	12	S	Carbonic anhydrase 3
O08997	1	69.1	9		Copper transport protein ATOX1
O35215	1	99.2	22		D-dopachrome decarboxylase
P98078	1	12.6	5		Disabled homolog 2
A2AVR9	1	54.2	3		Dynein light chain roadblock-type 1
Q91V76	1	30.8	7		Ester hydrolase C11orf54 homolog
P26883	1	82.4	7	S	FK506-binding protein 1A
Q3TJ66	1	6.3	3	S	Fructose-bisphosphate aldolase
Q9QUH0	1	43.9	3	S	Glutaredoxin-1
P02088	1	85.7	15	S	Hemoglobin subunit beta
Q9QXN5	1	36.5	10		Inositol oxygenase

P58044	1	18.9	3		Isopentenyl-diphosphate Delta-isomerase 1
Q91X52	1	47.1	10		L-xylulose reductase
P34884	1	23.5	4	S	Macrophage migration inhibitory factor
Q4FZG7	1	17.5	2		Mitochondrial import inner membrane translocase subunit Tim8A-B
Q91WK9	1	26.4	3		Msra protein (methionine-S-oxide reductase) (PMSR)
Q3U3C2	1	41.6	5		Niemann Pick type C2
P17742	1	81.7	27	S	Peptidyl-prolyl cis-trans isomerase A (Cyclophilin A)
P70296	1	80.2	17		Phosphatidylethanolamine-binding protein 1 (PEBP-1)
O70250	1	28.5	6		Phosphoglycerate mutase 2
P29341	1	12.5	3	S	Polyadenylate-binding protein 1, (Poly(A)-binding protein 1)
P17563	1	74.8	38	S	Selenium-binding protein 1
Q63836	1	56.4	1	S	Selenium-binding protein 2
P077249	1	53.3	35	S	Serum albumin
P08228	1	97.4	19	S	Superoxide dismutase [Cu-Zn]
P10639	1	38.1	3	S	Thioredoxin
Q3TNH0	1	3.4	2	S	Thymopoietin
P20065	1	50.0	8	S	Thymosin beta-4
Q9D8Z2	1	18.4	2		TP53-regulated inhibitor of apoptosis 1
P17751	1	22.1	4	S	Triosephosphate isomerase
Q5I0T6	0.9999	8.4	2		Aldo-keto reductase family 1, member C19
P48771	0.9997	17.3	2		Cytochrome c oxidase polypeptide VIIa-liver/heart
P40124	0.9996	3.8	1	S	Adenylyl cyclase-associated protein 1
A0JLR7	0.9996	11.6	3		Desmoyokin (AHNAK)
Q99PT1	0.9996	8.3	2		Rho GDP-dissociation inhibitor 1
P10126	0.9995	4.1	2	S	Elongation factor 1-alpha 1
Q3TGW8	0.9991	2.9	2		Suppression of tumorigenicity 13 (Hsc70-interacting protein)
Q3TH47	0.999	32.8	2		Ubiquitin C
Q9CR68	0.9989	6.9	2	S	Ubiquinol-cytochrome c reductase iron-sulfur subunit
A2A5Y6	0.9974	6.6	2		Microtubule-associated protein tau
P56391	0.9959	30.2	2		Cytochrome c oxidase subunit VIb isoform 1
P29699	0.9909	4.9	1	S	Alpha-2-HS-glycoprotein
Q91WU5	0.99	4.8	1		Arsenite methyltransferase (EC 2.1.1.137), (S-adenosyl-L-methionine : arsenic(III) methyltransferase)
P62075	0.99	14.7	1		Mitochondrial import inner membrane translocase subunit Tim13
Q91XL1	0.9891	4.1	1	S	Leucine-rich alpha-2-glycoprotein

Q66JR8	0.9891	15.5	1	S	Parathymosin (Ptms protein)
P62500	0.9891	8.4	1		TSC22 domain family protein 1 (TSC22-related inducible leucine zipper 1b)
Q64105	0.9873	7.3	1		Sepiapterin reductase
P04104	0.9867	5.7	1		Keratin, type II cytoskeletal 1
A2AD20	0.9846	10.3	1	S	G protein-coupled receptor
P50543	0.9846	16.3	1		S100-A11 (calgizzarin)
A2CEK3	0.9819	2.1	1	S	Phosphoglucomutase 2
UPI00000231BE	0.9794	35.2	1		Unknown
Q3TIB8	0.9784	9.8	1	S	Transgelin 2
P07744	0.9754	5.1	2		Keratin, type II cytoskeletal 4
P97328	0.9749	13.8	1		Ketohexokinase
P32921	0.974	2.9	1	S	Tryptophanyl-tRNA synthetase
A2ARV4	0.9731	12.8	1	S	Low density lipoprotein receptor-related protein 2
P19157	0.9688	5.2	1	S	Glutathione S-transferase P 1
P97816	0.9581	54.4	4	S	S100-G (calbindin)
P09036	0.9547	40.0	2		Serine protease inhibitor Kazal-type 3
P12787	0.9467	6.2	1		Cytochrome c oxidase subunit 5A
Q64374	0.9467	4.3	1		Regucalcin
Q9D6F8	0.9361	19.6	1	S	Glutaredoxin 1 (thioltransferase)
Q501L6	0.9313	8.0	1		Tbrg3 protein
P01942	0.9229	70.4	0	S	Hemoglobin subunit alpha
P09041	0.9223	3.6	1	S	Phosphoglycerate kinase 2
Q9DB15	0.9215	12.4	1		39S ribosomal protein L12
Q3TIT5	0.9125	24.3	0		Prosaposin
Q3TTY5	0.9089	6.1	1		Keratin, type II cytoskeletal 2 epidermal
Q8R4H2	0.9066	1.7	1	S	Rho guanine nucleotide exchange factor 12
O35988	0.8847	8.1	1		Syndecan-4
Q5DTY0	0.8436	4.5	1		MKIAA1414 protein
P28271	0.8348	2.0	1		Iron-responsive element-binding protein 1
A2ACI8	0.8315	6.5	1		Actin, gamma
Q62266	0.8192	27.8	2		Cornifin-A
P11679	0.8175	4.5	1		Keratin, type II cytoskeletal 8
P70349	0.7989	11.1	1		Histidine triad nucleotide-binding protein 1
O88568	0.773	2.2	1	S	Heterogenous nuclear ribonucleoprotein U

P15864	0.7672	4.7	1		Histone H1.2
P99029	0.7483	24.7	0		Peroxiredoxin 5
Q4U2R1	0.6955	0.8	1		E3 ubiquitin-protein ligase HERC2 (probable)
Q3UFJ2	0.6952	0.9	1		Glutamyl-prolyl-tRNA synthetase
Q3U0K5	0.6377	2.2	1		Hypothetical RNA-binding region RNP-1
Q9D6X2	0.6226	10.9	0	S	Peroxiredoxin 6
P16125	0.6066	10.9	1		L-lactate dehydrogenase B chain
A2AKN9	0.578	25	0		Major urinary protein 2
P14069	0.5612	9.0	1		S100-A6 (calcyclin)
A2AN84	0.5605	6.3	1		Membrane protein, palmitoylated
P16381	0.5123	2.1	2		Putative ATP-dependent RNA helicase P110

Suppl Table S4, List of proteins identified in the 70% ethanol fraction from the mouse brain tissue. Only proteins with a probability > 0.5 have been listed. Color code: **Pink**: observed across all tissue types; **Green**: observed across three tissue types; **Yellow**: observed across two tissue types.

Uniref100 accession Nb	Protein probability	Percent coverage	Nb unique peptides		Description (S, observed in human serum)
P31786	1	65.5	14		Acyl-CoA-binding protein
Q3UJW9	1	10.8	3	S	Aldo-keto reductase family 1, member A4 (aldehyde reductase)
P17182	1	81.1	38	S	Alpha-enolase
P97450	1	55.6	12	S	ATP synthase-coupling factor 6
Q91XV3	1	66.4	12		Brain acid soluble protein 1
P63054	1	41.9	3		Brain-specific polypeptide PEP-19
Q63810-2	1	78.1	7		Calcineurin subunit B isoform 1
Q3UKW2	1	58.4	28		Calmodulin 1
P00920	1	55.0	10	S	Carbonic anhydrase 2
Q9JKC6	1	26.8	4		Cell cycle exit and neuronal differentiation protein 1
O08997	1	63.2	7		Copper transport protein ATOX1
P01193	1	34.0	4		Corticotropin-lipotropin precursor (Pro-opiomelanocortin) (POMC)
Q04447	1	43.3	16	S	Creatine kinase B-type
P12787	1	34.5	6		Cytochrome c oxidase subunit 5A
O35215	1	92.4	10		D-dopachrome decarboxylase
Q7TQ15	1	47.5	4		Dpy-30, dosage compensation-related protein
A2AVR9	1	29.2	2		Dynein light chain roadblock-type 1
P26883	1	82.4	9	S	FK506-binding protein 1A
P17183	1	83.4	33		Gamma-enolase
P19157	1	31.0	4	S	Glutathione S-transferase P 1
Q9JMF3	1	46.3	3		Guanine nucleotide-binding protein G(I)/G(S)/G(O) gamma-13 subunit
UPI0000003F4E	1	66.0	8	S	Hemoglobin subunit beta
A2A7R5	1	30.4	3	S	Hippocalcin
O55023	1	39.7	9		Inositol-1(or 4)-monophosphatase

Q9CPU0	1	18.5	3		Lactoylglutathione lyase (glyoxalase 1)
P34884	1	23.5	6	S	Macrophage migration inhibitory factor
Q9WVA2	1	28.9	3		Mitochondrial import inner membrane translocase subunit Tim8 A
P62077	1	34.9	3		Mitochondrial import inner membrane translocase subunit Tim8 B
P32848	1	51.8	6		Parvalbumin alpha
P17742	1	85.4	33	S	Peptidyl-prolyl cis-trans isomerase A (Cyclophilin A)
P70296	1	80.2	17		Phosphatidylethanolamine-binding protein 1 (PEBP-1)
O70250	1	13.2	2		Phosphoglycerate mutase 2
Q9QXV0	1	37.6	13		ProSAAS precursor (pro-SAAS), (Proprotein convertase subtilisin/kexin type 1 inhibitor)
P12660	1	48.5	4		Purkinje cell protein 2
P16014	1	7.6	6		Secretogranin-1
Q03517	1	14.1	6		Secretogranin-2
P17563	1	27.5	10	S	Selenium-binding protein 1
P07724	1	43.6	28	S	Serum albumin
P60041	1	20.7	2		Somatostatin
P08228	1	63	18	S	Superoxide dismutase [Cu-Zn]
P10639	1	43.8	4	S	Thioredoxin
P20065	1	50.0	11	S	Thymosin beta-4
P17751	1	64.3	11	S	Triosephosphate isomerase
P62500	1	25.2	4		TSC22 domain family protein 1 (TSC22-related inducible leucine zipper 1b)
Q8C2K3	1	60.1	7		Ubiquitin polyprotein
P35455	1	19.6	3	S	Vasopressin-neurophysin 2-copeptin precursor (AVP-NPII)
Q0VGU4	1	14.9	4		VGF nerve growth factor inducible
Q3TVC0	1	58.1	9		Visinin-like 1
Q3UKX6	0.9999	37.3	2	S	Apolipoprotein A-II
P51910	0.9999	20.6	3	S	Apolipoprotein D
P63040	0.9999	33.6	3		Complexin-1
Q9CXP8	0.9996	48.5	2		Guanine nucleotide-binding protein G(I)/G(S)/G(O) gamma-10 subunit
Q9WV98	0.9995	43.8	2		Mitochondrial import inner membrane translocase subunit Tim9
Q3SXD3	0.9994	25.6	3		HD domain containing 2
P29341	0.9994	5.9	2	S	Polyadenylate-binding protein 1, (Poly(A)-binding protein 1)
Q8CF11	0.9993	42.6	2		UPF0366 protein C11orf67 homolog

P32883	0.9986	13.8	2		GTPase KRas
Q9CW88	0.9984	41.4	2		Protein phosphatase 1 regulatory (inhibitor) subunit 1A
P57774	0.9967	29.9	2		Neuropeptide Y precursor
P62774	0.9905	14.4	1	S	Myotrophin
P02802	0.9886	19.7	1		Metallothionein-1
Q8BGZ1	0.9875	19.9	1		Hippocalcin-like protein 4
P45376	0.9858	4.4	1		Aldose reductase
Q66JR8	0.9858	15.5	1	S	Parathyrosin (Ptms protein)
P56376	0.984	13.1	1		Acylphosphatase-1
P50114	0.9789	16.3	2		S100-B (S-100 protein beta chain)
Q32NY7	0.9765	22.2	1		Short coiled coil protein (Scoc)
P31650	0.973	2.9	1		Sodium and chloride-dependent GABA transporter 4
Q11136	0.9711	3.9	1		Xaa-Pro dipeptidase
P29595	0.9702	23.5	1		NEDD8 (neddylin)
Q3ULW0	0.9684	6.5	1		Mammary gland RCB-0527 Jyg-MC(B) cDNA
Q3TIT5	0.9558	15.2	0		Prosaposin
Q8R1H0	0.9455	13.7	1		Homeodomain-only protein
Q61206	0.9218	6.1	1	S	Platelet-activating factor acetylhydrolase IB subunit beta
Q561M1	0.921	7.6	1		Acp1 protein, (Low molecular weight phosphotyrosine protein phosphatase)
P48771	0.9088	12	1		Cytochrome c oxidase polypeptide VIIa-liver/heart
P01942	0.9062	42.3	0	S	Hemoglobin subunit alpha
P02798	0.9016	19.7	1		Metallothionein-2
Q3U3C2	0.9	8.1	1		Niemann Pick type C2
Q9R1Z7	0.8945	9.0	1	S	6-pyruvoyl tetrahydrobiopterin synthase
Q35619	0.8898	13.8	1		Vesicle associated membrane protein 2
P12815	0.8867	8.5	1	S	Programmed cell death protein 6
P46664	0.867	6.2	1	S	Adenylosuccinate synthetase isozyme 2
UPI0000161D7A	0.8531	7.8	1		Mitochondrial import inner membrane translocase 13 homolog
P13595	0.8446	1.9	1	S	Neural cell adhesion molecule 1
P04104	0.7973	6.1	1		Keratin, type II cytoskeletal 1
Q3TAS8	0.7918	2.9	1	S	Dihydropyrimidinase-like 3
A2A8R7	0.7799	1.6	1		Zinc finger, CCHC domain containing 11
P01216	0.7518	12.5	1		Glycoprotein hormones alpha chain
P14069	0.7164	9.0	1		Protein S100-A6 (calcyclin)

P22005	0.6659	9.0	1		Proenkephalin A
P12961	0.6335	5.7	1		Secretogranin-5 (Neuroendocrine protein 7B2), (Secretory granule endocrine protein I)
Q3UJH8	0.6313	4.6	2	S	Aspartate aminotransferase
Q6PDJ1	0.5889	1.3	1		VWFA (cache domain-containing protein 1)
P06837	0.5769	8.7	1	S	Neuromodulin
Q8CFV4	0.5442	13.4	1		Neuritin
P63328	0.4982	6.7	1		.Serine/threonine-protein phosphatase 2B catalytic subunit alpha isoform
Q5DTY0	0.4899	4.5	1		MKIAA1414 protein (HEAT repeat containing 5B)

Suppl Table S5, List of proteins identified in common in the 70% ethanol fraction from mouse liver (Li), lung (Lu), kidney (K) and brain

tissue. Only proteins with a probability > 0.5 have been listed. Color code: **Pink**: observed across all tissue types; **Green**: observed across three tissue types; **Yellow**: observed across two tissue types.

Commonality across organs	Description (S, observed in human serum)
All 4 organs	Acyl-CoA-binding protein
All 4 organs	S Alpha-enolase
All 4 organs	S Apolipoprotein A-II
All 4 organs	S Apolipoprotein D
All 4 organs	S ATP synthase-coupling factor 6
All 4 organs	Copper transport protein ATOX1
All 4 organs	Cytochrome c oxidase polypeptide VIIa-liver/heart
All 4 organs	D-dopachrome decarboxylase
All 4 organs	S FK506-binding protein 1A; Peptidyl-prolyl cis-trans isomerase
All 4 organs	S Glutathione S-transferase P 1
All 4 organs	S Hemoglobin subunit alpha
All 4 organs	S Hemoglobin subunit beta
All 4 organs	Keratin, type II cytoskeletal 1
All 4 organs	S Macrophage migration inhibitory factor
All 4 organs	Mitochondrial import inner membrane translocase subunit Tim8 B
All 4 organs	Mitochondrial import inner membrane translocase subunit Tim8 A
All 4 organs	Niemann Pick type C2
All 4 organs	S Parathyrosin (Ptms protein)
All 4 organs	S Peptidyl-prolyl cis-trans isomerase A (Cyclophilin A)
All 4 organs	Phosphatidylethanolamine-binding protein 1 (PEBP-1)
All 4 organs	Prosaposin
All 4 organs	S Selenium-binding protein 1
All 4 organs	S Serum albumin
All 4 organs	S Superoxide dismutase [Cu-Zn]
All 4 organs	S Thymosin beta-4

All 4 organs					TSC22 domain family protein 1
All 4 organs					Ubiquitin C
Serum related proteins found common in all four organs: 15/27 = 56%					
Li		K	B	S	Aldo-keto reductase family 1
	Lu	K	B		Aldose reductase
Li	Lu	K			Bisphosphoglycerate mutase
	Lu	K	B		Calmodulin 1
	Lu	K	B	S	Carbonic anhydrase 2
Li	Lu	K		S	Carbonic anhydrase 3
	Lu	K	B		Cytochrome c oxidase subunit 5A
	Lu	K	B		Dynein light chain roadblock-type 1
Li	Lu	K			Isopentenyl-diphosphate Delta-isomerase 1
Li	Lu	K			Keratins, type II cytoskeletal
Li	Lu	K			L-xylulose reductase
Li		K	B		MKIAA1414 protein
Li		K	B	S	Polyadenylate-binding protein 1 (Poly(A)-binding protein 1)
	Lu	K	B		S100-A6 (calyculin)
Li	Lu	K		S	Selenium-binding protein 2
	Lu	K	B	S	Thioredoxin
Serum related proteins found common in three organs: 6/16 = 38%					
	Lu	K			Actin, gamma
	Lu		B		Brain acid soluble protein 1
	Lu	K			Desmoyokin (AHNAK)
	Lu		B		Dpy-30-like protein
	Lu		B		Guanine nucleotide-binding protein
Li		K			Histidine triad nucleotide-binding protein 1
	Lu		B		Homeodomain-only protein
	Lu		B		Lactoylglutathione lyase, glyoxalase 1
Li			B		Mammary gland RCB-0527 Jyg-MC(B) cDNA
	K		B		Mitochondrial import inner membrane translocase subunit Tim13
Li	Lu				Perlecan (heparan sulfate proteoglycan 2)
Li		K			Peroxiredoxin-5
		K	B		Phosphoglycerate mutase 2
Li	Lu				Predicted: hypothetical protein

Li		B	S	Programmed cell death protein 6
Li	K			Regucalcin
Li	K		S	Thymopoietin
	K	B	S	Triosephosphate isomerase
Li	K		S	Ubiquinol-cytochrome c reductase iron-sulfur subunit
	Lu	B		Zinc finger, CCHC domain containing 11
Serum related proteins found common in two organs: 4/20 = 20%				

Suppl Table S6, List of proteins identified in the 80% ethanol fraction from the mouse liver tissue. Only proteins with a probability > 0.5 have been listed. The proteins highlighted in **Blue** are unique to the 80% fraction with respect to the 70% liver fraction.

Uniref100 accession Nb	Protein probability	Percent coverage	Nb unique peptides	Description
P31786	1	66.7	9	Acyl-CoA-binding protein
Q3UKX6	1	42.2	3	Apolipoprotein A-II
P97450	1	28.7	4	ATP synthase-coupling factor 6
P16015	1	46.9	12	Carbonic anhydrase 3
O08997	1	47.1	4	Copper transport protein ATOX1
P12710	1	45.7	6	Fatty acid-binding protein
P19157	1	72.9	36	Glutathione S-transferase P 1
P01942	1	50.7	11	Hemoglobin subunit alpha
UPI0000003F4E	1	77.6	13	Hemoglobin, beta
Q02257	1	7.2	4	Junction plakoglobin (desmoplakin-3)
P34884	1	17.4	3	Macrophage migration inhibitory factor
P70296	1	20.9	2	Phosphatidylethanolamine-binding protein 1 (PEBP-1)
Q64374	1	44.1	13	Regucalcin
UPI0000029BFE	1	64.8	10	Selenium binding protein 2
P17563	1	49.2	1	Selenium-binding protein 1
P07724	1	17.8	9	Serum albumin
P08228	1	55.8	7	Superoxide dismutase [Cu-Zn]
Q3UJW9	0.9999	7.7	2	Aldo-keto reductase family 1 member A4, (aldehyde reductase), (Alcohol dehydrogenase [NADP+])
Q3TIT5	0.9999	3.6	2	Prosaposin
A2A513	0.9988	18.2	10	Keratin 10
P04104	0.9984	7.5	2	Keratin, type II cytoskeletal 1
P17742	0.9924	16.5	1	Peptidyl-prolyl cis-trans isomerase A
Q66JR8	0.9834	15.5	1	Parathyrosin (Ptms protein)
Q63880	0.9768	2.3	1	Liver carboxylesterase 31
O35215	0.9753	33.1	2	D-dopachrome decarboxylase

Q9CR68	0.9736	6.9	2	Ubiquinol-cytochrome c reductase iron-sulfur subunit
Q99MS7	0.9448	1.2	2	EH domain-binding protein 1-like protein 1
P62500	0.9392	8.4	1	TSC22 domain family protein 1; (MKIAA1994 protein), (TSC22-related inducible leucine zipper 1b)
Q8BGZ7	0.8722	9.8	1	Cytokeratin homolog
P11679	0.8357	4.9	1	Keratin, type II cytoskeletal 8
Q5NBY9	0.6256	12.3	1	Zinc finger protein 278
A2A8R7	0.6253	1.6	1	Zinc finger, CCHC domain containing 1, (MKIAA0191 protein)
Q9QWL7	0.6238	23.6	0	Keratin, type I cytoskeletal 17
UPI00001C2A77	0.5864	5.5	1	Predicted: hypothetical protein
Q792Z1	0.5717	14.6	1	Trypsinogen 10
Q8C170	0.5503	1.6	1	Myosin IXa isoform 2
Q6ZQF0	0.5366	1.5	1	DNA topoisomerase II-binding protein 1
P32043	0.5114	2.3	1	Homeobox protein Hox-C5

Suppl Table S7, List of proteins identified in the 80% ethanol fraction from the mouse lung tissue. Only proteins with a probability > 0.5 have been listed. The proteins highlighted in **Blue** are unique to the 80% fraction with respect to the 70% lung fraction.

Uniref100 accession Nb	Protein probability	Percent coverage	Nb unique peptides	Description
P99027	1	31.3	3	60S acidic ribosomal protein P2
Q6UL10	1	10.6	11	AHNAK (desmoyokin)
A2AP12	1	10.8	2	Aldo-keto reductase family 1 member A4 (Alcohol dehydrogenase [NADP+])
P45376	1	13	4	Aldose reductase
Q3V2G1	1	20.5	4	Apolipoprotein A-I
Q3UKX6	1	42.2	6	Apolipoprotein A-II
P97450	1	26.9	5	ATP synthase-coupling factor 6
P15327	1	20.1	3	Bisphosphoglycerate mutase
Q3UD53	1	10.8	2	Calcium regulated heat stable protein 1
Q3UKW2	1	46.7	8	Calmodulin 1
P13634	1	24.1	5	Carbonic anhydrase 1
P00920	1	35.8	7	Carbonic anhydrase 2
O08997	1	63.2	5	Copper transport protein ATOX1
P12787	1	22.8	4	Cytochrome c oxidase subunit 5A
A2AC16	1	16.1	3	Dicarbonyl L-xylulose reductase
Q7TQ15	1	31.3	2	Dosage compensation-related protein DPY30
P19157	1	31.4	4	Glutathione S-transferase P 1
Q9CY06	1	71.8	13	Hemoglobin subunit beta
Q8R1H0	1	43.8	2	Homeodomain-only protein
P08074	1	47.1	10	Lung carbonyl reductase [NADPH]
A2AKN9	1	8.9	2	Major urinary protein 2
O08692	1	9.6	2	Myeloid bactenecin, (Myeloid secondary granule protein)
P17742	1	57.9	9	Peptidyl-prolyl cis-trans isomerase A
O55103	1	8.6	5	Periaxin
P70296	1	25.1	3	Phosphatidylethanolamine-binding protein 1 (PEBP-1)
P29341	1	7.6	2	Polyadenylate-binding protein 1 (Poly(A)-binding protein 1)

Q3TIT5	1	6.3	4	Prosaposin
P50405	1	16.5	11	Pulmonary surfactant-associated protein B precursor (SP-B), (Pulmonary surfactant-associated proteolipid SPL(Phe))
P14069	1	25.8	5	S100-A6 (calcylin)
P17563	1	64	29	Selenium-binding protein 1
Q92111	1	8.2	4	Serotransferrin
P07724	1	59	48	Serum albumin
P08228	1	56.5	12	Superoxide dismutase [Cu-Zn]
P20065	1	50	10	Thymosin beta-4 (T beta 4)
P62500	1	25.2	3	TSC22 domain family protein 1 (TSC22-related inducible leucine zipper 1b)
Q06318	1	29.2	7	Uteroglobin
P17182	0.9999	12.8	2	Alpha-enolase
P26883	0.9999	21.3	2	FK506-binding protein 1A
Q3TUI9	0.9999	9.1	2	Proteasome subunit alpha type
P61750	0.9997	17.2	2	ADP-ribosylation factor 4
P04104	0.997	6.1	1	Keratin, type II cytoskeletal 1
Q9CQZ1	0.9966	42.1	2	Heat shock factor-binding protein 1
Q9WVA2	0.9945	40.2	1	Mitochondrial import inner membrane translocase subunit Tim8 A
P33622	0.9941	19.2	1	Apolipoprotein C-III precursor
P10107	0.9935	4	1	Annexin A1
P52795	0.9935	8	1	Ephrin-B1
P14220	0.9935	18.7	1	Glycophorin
A0AUP0	0.9924	13.5	1	Apolipoprotein A-IV (Efhc1 protein)
P34884	0.9924	9.6	1	Macrophage migration inhibitory factor
Q8BUR9	0.9906	20.5	1	Hypothetical 8.4 kDa protein homolog
Q3TUU0	0.9844	2	2	hypothetical protein
Q63918	0.982	3.1	1	Serum deprivation-response protein
Q00915	0.969	7.4	1	Retinol-binding protein I
Q66JR8	0.9612	15.5	1	Parathyrosin (Ptms protein)
P05533	0.9601	17.2	1	Lymphocyte antigen 6A-2/6E-1
A2BFA6	0.9363	2.2	1	Alpha-N-acetylglucosaminidase
P07310	0.9161	4.5	1	Creatine kinase M-type
Q61017	0.9125	29	1	Guanine nucleotide-binding protein G(I)/G(S)/G(O) gamma-T2 subunit
UPI0001553888	0.9009	0.7	1	MKIAA1116 protein isoform 1

Q792Z1	0.8911	10.6	1	Trypsinogen 10 (Trypsin 10)
Q5DU18	0.8862	1.6	1	MKIAA0715 protein
Q3U0Q9	0.8776	1.6	1	Tensin
Q91WK9	0.8729	8.3	1	MsrA protein (Peptide methionine sulfoxide reductase), (Protein-methionine-S-oxide reductase), (Peptide-methionine (S)-S-oxide reductase), (Peptide Met(O) reductase)
Q9WU28	0.8635	10.4	1	Prefoldin subunit 5
P11679	0.8337	4.9	2	Keratin, type II cytoskeletal 8
A2ACI8	0.7982	6.5	1	Actin, gamma
Q3TU22	0.7654	1.6	1	Chromatin assembly factor 1, subunit A (p150)
P58044	0.7631	9.7	1	Isopentenyl-diphosphate Delta-isomerase 1
Q3TKT4	0.6952	1.4	1	SWI/SNF related matrix associated actin dependent regulator of chromatin subfamily a member 4
Q8CAI1	0.6784	4.8	1	Hypothetical protein LOC243510
Q3TCS0	0.6712	3.1	1	Prolyl endopeptidase
Q8BZG8	0.6443	2	1	Gamma-2 syntrophin homolog
Q8BJC6	0.6111	10.8	1	Brain MY039 protein homolog
O35444	0.5476	7.7	1	RAGE (Advanced glycosylation end product-specific receptor)
Q9DA16	0.5283	9	1	Hypothetical protein LOC75510 isoform 4