Disparate proteome reactivity profiles of carbon electrophiles: Supplementary Information

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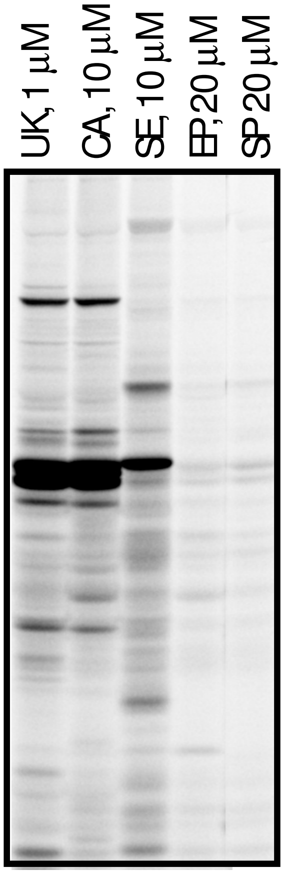
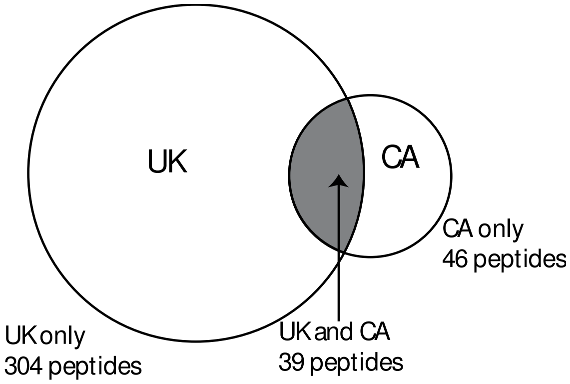
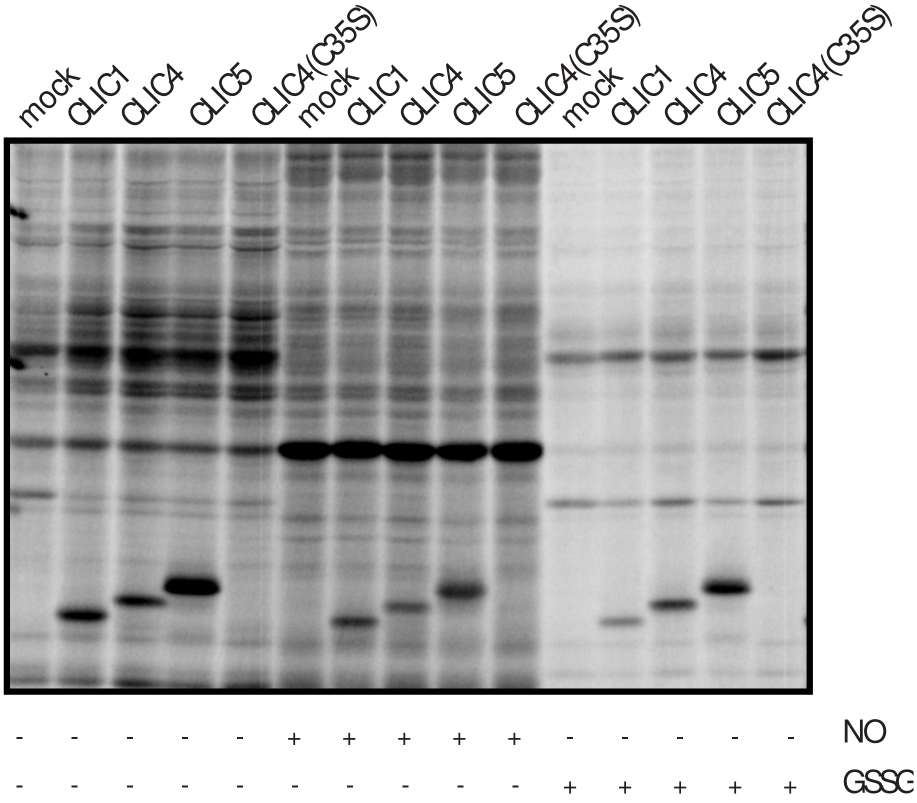
Supplementary Information Figure 1: Gel demonstrating the labeling of a soluble mouse liver proteome (1 mg/ml) using the panel of electrophilic probes (Fig. 1). Fluorescent gel images shown in grayscale after probe labeling for 1 hour, followed by click chemistry with a rhodamine-azide reporter tag.



Supplementary Information Figure 2: Venn-diagram illustrating the overlap between residues labeled by the CA and UK probes.



Supplementary Information, Figure 3: Nitric oxide and oxidized glutathione treatment of CLICs. Lysates were treated with either 5 mM of the nitric oxide donor, diethylamine nitric oxide, sodium salt (DEANO) or 2 mM of oxidized glutathione (GSSG) for 1 hour, followed by addition of 20 μM of the CA probe for 15 minutes. A subsection of the gel is presented in **Fig. 2**; the entire gel is presented here, illustrating the proteome-wide changes that occur in the COS-7 lysates upon treatment with the oxidizing agents.



Supplementary Information Table 1: Functional residues labeled by the SE, CA and UK probes.

IPI number	Description	Peptide	MA	SE	CA	Site of Labeling	Function
IPI00108895	**26S protease regulatory subunit 6B**	GVLMYGPPGC*GK	10	-	-	C210	ATP binding domain (potential)
IPI00109169	**Isocitrate dehydrogenase [NAD] subunit gamma**	HAC*VPVDFEEVHVSSNADEEDIR	22	-	-	C81	NAD binding domain (potential)
IPI00113223	**Fatty acid synthase**	GPSIALDTAC*SSSLLALQNAYQAIR	28	-	75	C161	Active site (for beta-ketoacylsynthase activity)
IPI00115599	**Corticosteroid 11-beta-dehydrogenase 1**	MTQPMIAPY*SASK	-	4	-	Y183	Active site proton acceptor
IPI00116074	**Aconitate hydratase, mitochondrial precursor**	VGLIGSC*TNSSYEDMGR	-	-	8	C385	Iron-sulfur cluster
IPI00116192	**Thioredoxin-dependent peroxide reductase**	AFQFVETHGEVC*PANWTPESPTIKPSPTASK	14	-	-	C230	Disulfide with active-site cysteine
IPI00116489	**Atrial natriuretic factor precursor**	IGAQSGLGC*NSFR	6	-	-	C145	Disulfide bond
IPI00118344	**UDP-glucose 6-dehydrogenase**	ASVGFGGSC*FQK	-	-	18	C276	Active site nucleophile
IPI00118849	**Dual specificity tyrosine-phosphorylation-regulated kinase 1A**	KVYNDGYDDDNY*DYIVK	-	24	-	Y145	Site of phosphorylation
IPI00119112	**Vacuolar ATP synthase catalytic subunit A**	VLDALFPCVQGGTTAIPGAFGC*GK	28	-	-	C254	ATP binding domain (potential)
IPI00119114	**Long-chain specific acyl-CoA dehydrogenase**	GFYYLMQELPQE*R	-	26	-	E291	Active site proton acceptor
IPI00119945	**Nit protein 2**	VGLGIC*YDMR	-	-	125	C153	Active site nucleophile
IPI00120076	**Creatine kinase, sarcomeric mitochondrial precursor**	LGYILTC*PSNLGTGLR	73	-	79	C317	Active site residue
IPI00121566	**GMP reductase 1**	VGVGPGSVC*TTR	11	-	-	C186	Active site thioimidate intermediate
IPI00121639	**Beta-ureidopropionase**	IAVNIC*YGR	-	-	11	C233	Active site nucleophile
IPI00121788	**Peroxiredoxin-1**	HGEVC*PAGWKPGSDTIKPDVNK	95	-	-	C173	Disulfide with active-site cysteine
IPI00122549	**Voltage-dependent anion-selective channel protein 1**	WTEYGLTFTE*K	-	10	-	E86	Hexokinase binding
IPI00125135	**Ubiquitin-conjugating enzyme E2 D2**	IYHPNINSNGSIC*LDILR	29	-	-	C85	Active site glycyl thioester intermediate
IPI00126208	**Hemoglobin, beta adult major chain**	GTFASLSELHC*DK	100	151	332	C94	Metal binding/Site of nitrosylation
IPI00128760	**Ubiquitin-conjugating enzyme E2 L3**	GQVC*LPVISAENWKPATK	21	-	-	C86	Active site glycyl thioester intermediate
IPI00128873	**Nitrilase 1**	VGLAIC*YDMR	-	-	20	C199	Active site nucleophile
IPI00129517	**Peroxiredoxin-5, mitochondrial precursor**	ALNVEPDGTGLTC*SLAPNILSQL GVLFGVPGAFTPGC*SK	25 18	- -	- -	C200 C96	Redox-active disulfide Redox-active disulfide
IPI00130173	**Ubiquitin-like 1-activating enzyme E1B**	VLVVGAGGIGC*ELLK	7	-	-	C30	ATP binding domain

IPI00130521	**Ubiquitin-conjugating enzyme E2 A**	MFHPNVYADGSIC*LDILQNR	15	-	-	C88	Active site glycyl thioester intermediate
IPI00130804	**Delta3,5-delta2,4-dienoyl-CoA isomerase**	EVDMGLAAD*VGTLQR	-	755	-	D204	Active site proton donor
IPI00130950	**Betaine--homocysteine S-methyltransferase**	AGASIVGVNC*HFDPSVSLQTVK	-	-	9	C217	Zinc binding
IPI00131438	**Phosphoenolpyruvate carboxykinase, cytosolic**	YLAAAFPSAC*GK	11	-	22	C288	GTP binding
IPI00132653	**Succinyl-CoA:3-ketoacid-coenzyme A transferase 1**	DIPNGATLLVGGFGLC*GIPENLIGALLK	38	-	23	C67	Coenzyme A binding (potential)
IPI00135977	**Chloride intracellular channel protein 4**	AGSDGESIGNC*PFSQR	-	-	74	C35	Site of nitrosylation
IPI00137533	**6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2**	VFFVESVC*DDPDVIAANILEVK	19	-	-	C161	Active site residue
IPI00153317	**10-formyltetrahydrofolate dehydrogenase**	AVQMGMSSVFFNKGENC*IAAGR	54	-	340	C707	Active site residue
IPI00221400	**Alcohol dehydrogenase 1**	IDGASPLDKVCLIGC*GFSTGYGSAVK	13	-	-	C175	Zinc binding
		VIPLFSPQC*GECR	18	-	-	C98	Zinc binding
		VIPLFSPQCGEC*R	22	-	-	C101	Zinc binding
IPI00226993	**Thioredoxin**	LVVVDFSATWCGPC*K	6	-	-	C35	Active site nucleophile
IPI00229510	**L-lactate dehydrogenase B chain**	ITVVGVGQVGMAC*AISILGK	45	-	-	C36	NAD binding domain
IPI00266614	**Ribosyldihydronicotinamide dehydrogenase**	VLAPQISFGLD*VSSEEER	-	20	-	D194	FAD binding domain
IPI00273164	**Succinate semialdehyde dehydrogenase**	NAGQTC*VCSNR	-	-	19	C328	Active site nucleophile
IPI00273646	**Glyceraldehyde-3-phosphate dehydrogenase**	IVSNASC*TTNCLAPLAK	34	-	37	C150	Active site nucleophile
IPI00314510	**Aspartoacylase-2**	LFSGEDVLYEGDSIVYPVFINE*AAYYEK	-	6	-	E284	Active site residue (potential)
IPI00321375	**Biotinidase**	FGVFTC*FDILFFDPAVR	-	-	12	C222	Active site nucleophile
IPI00461964	**Aldehyde dehydrogenase family 6, subfamily A1**	C*MALSTAILVGEAK	-	24	382	C317	Active site nucleophile
IPI00622235	**Transitional endoplasmic reticulum ATPase**	GVLFYGPPGC*GK	33	-	-	C522	ATP binding domain

Supplementary Information Table 2: Proteins identified from mouse proteomes treated with the SE probe. Mouse proteomes (soluble proteomes of heart, kidney and liver and membrane proteome of liver) were treated with the SE probe (50 µM, 2 hrs) in duplicate. Proteins identified with ≥ 2 spectral counts in ≥ 2 samples are included. * Indicates predicted sites of labeling; Average Xcorr values with associated standard deviation is provided for each assigned labeling site.

	PEPTIDE	HEART 1	HEART 2	KIDNEY 1	KIDNEY 2	LIVER 1	LIVER 2	LIVER MEM 1	LIVER MEM 2	XCORR (average)	STD. DEV.
IPI00110658	**13 days embryo liver cDNA, RIKEN full-length enriched library, clone:2510040B16 product:hemoglobin, beta adult major chain, full insert sequence**										
	IGGH*GAEYGAEALER	0	25	0	18	27	2	2	0	3.368831	0.343294
	IGGHGAE*YGAEALER	1	11	0	13	23	1	2	0	3.629864	0.809313
	IGGHGAEY*GAEALER	47	5	0	18	33	2	4	0	3.757476	0.686705
	IGGHGAEYGAE*ALER	68	4	0	13	12	9	2	0	4.314721	0.911614
	IGGHGAEYGAEALE*R	4	1	1	4	0	0	0	0	3.845813	0.949606
IPI00110850	**Actin, cytoplasmic 1**										
	VAPEEH*PVLLTEAPLNPK	0	0	0	0	0	0	2	3	3.495533	0.536992
IPI00111218	**Aldehyde dehydrogenase, mitochondrial precursor**										
	ELGEYGLQAYTE*VK	0	0	0	0	0	0	3	6	3.312708	0.64171
IPI00111908	**Carbamoyl-phosphate synthase [ammonia], mitochondrial precursor**										
	QADAVYFLPITPQFVT*EVIK	0	0	0	0	0	0	11	2	3.797252	0.6031
	QADAVYFLPITPQFVTE*VIK	0	0	0	0	0	0	13	2	3.880315	0.494176
	S*VGEVMAIGR	0	0	0	0	0	0	4	2	2.797413	0.669073
	SVGE*VMAIGR	0	0	0	0	0	0	5	6	2.934308	0.56647
	TAHIVLE*DGTK	0	0	0	4	0	0	3	2	3.465833	0.57601
	TAHIVLED*GTK	0	0	0	4	0	0	3	2	3.064033	0.68389
IPI00115599	**Corticosteroid 11-beta-dehydrogenase isozyme 1**										
	MTQPMIAPY*SASK	0	0	0	0	0	0	2	2	2.808875	0.671538
IPI00116705	**Fatty acid-binding protein, adipocyte**										
	LVSSENFD*DYMK	2	0	0	0	0	4	0	0	2.732238	0.547574
IPI00118849	**Dual specificity tyrosine-phosphorylation-regulated kinase 1A**										
	KVYNDGYDDDNY*DYIVK	9	2	0	0	0	3	2	8	2.865128	1.100115
IPI00119114	**Long-chain specific acyl-CoA dehydrogenase, mitochondrial precursor**										
	GFYYLMQELPQE*R	9	10	0	0	3	4	0	0	3.525507	0.768354
IPI00120451	**Fatty acid-binding protein, liver**										
	AIGLPE*DLIQK	0	0	7	4	0	0	0	0	2.779891	0.629696
	AIGLPED*LIQK	0	0	5	5	0	0	0	0	3.02239	0.623804
	NEFTLGEEC*ELETMTGEK	0	0	2	2	0	0	0	0	2.860975	0.429258
IPI00121209	**Apolipoprotein A-I precursor**										
	SNPTLNEYH*TR	0	21	0	0	0	0	4	3	2.939579	0.36406
	VAPLGAE*LQESAR	6	0	2	1	4	4	0	1	3.00656	0.884539
	WKED*VELYR	32	5	0	6	1	1	0	0	2.901823	0.912461
IPI00122139	**3-ketoacyl-CoA thiolase B, peroxisomal precursor**										
	DTTPDE*LLSAVLTAVLQDVK	0	0	0	0	0	0	6	8	4.2736	0.601912
	DTTPDELLS*AVLTAVLQDVK	0	0	0	0	0	0	4	4	4.10005	0.408725
IPI00122549	**Isoform PI-VDAC1 of Voltage-dependent anion-selective channel protein 1**										
	WTEYGLTFT*EK	0	0	0	0	0	0	2	7	2.882807	0.671464
	WTEYGLTFTE*K	0	0	0	0	0	0	3	7	3.15006	0.511877
IPI00123176	**PREDICTED: similar to Glyceraldehyde-3-phosphate dehydrogenase**										
	LISWYDNEY*GYSNR	7	0	0	0	0	2	0	0	2.832411	0.846916
IPI00125521	**40S ribosomal protein S5**										
	KAQC*PIVER	0	0	0	0	0	0	2	5	2.65176	0.588363
IPI00126208	**11 days embryo whole body cDNA, RIKEN full-length enriched library, clone:2700082N11 product:hemoglobin, beta adult major chain, full insert sequence**										
	AAVSGLWGK*VNADEVGGEALGR	7	6	0	4	20	8	0	0	4.141633	0.576466
	AAVSGLWGKVNAD*EVGGEALGR	19	1	0	0	20	22	0	0	3.92133	0.633392
	AAVSGLWGKVNADE*VGGEALGR	6	0	0	0	5	16	0	0	4.208527	0.746794
	AAVSGLWGKVNADEVGGE*ALGR	17	0	0	0	15	16	0	0	5.00805	1.128128
	GTFASLSELHC*DK	44	32	3	22	31	16	1	2	2.920061	0.810369
	VITAFNDGLNH*LDSLK	0	2	0	1	1	2	0	0	3.4552	0.337369
	VITAFNDGLNHLDSLKGTFASLSELHC*DK	0	4	0	0	6	0	0	0	4.775125	1.097092
	VNAD*EVGGEALGR	64	9	32	0	50	22	1	1	3.298917	0.746462
	VNADE*VGGEALGR	72	7	28	20	49	22	2	1	3.357731	0.794436
	VNADEVGGE*ALGR	68	15	16	15	41	15	1	9	3.620669	0.720599
	Y*FDSFGDLSSASAIMGNAK	40	22	4	0	5	31	0	0	3.986186	0.758574
	YFD*SFGDLSSASAIMGNAK	19	12	3	0	0	11	0	0	4.113255	0.603852
	YFDS*FGDLSSASAIMGNAK	28	21	3	0	6	20	0	0	4.05001	0.602023
	YFDSFGD*LSSASAIMGNAK	19	14	1	0	14	22	0	0	4.291167	0.904365
IPI00130804	**Delta3,5-delta2,4-dienoyl-CoA isomerase, mitochondrial precursor**										
	EVDMGLAAD*VGTLQR	252	74	200	42	50	42	45	50	3.933302	0.641378
	EVDMGLAAD*VGTLQRLPK	0	0	0	0	8	8	0	0	3.112838	0.638987
	EVDMGLAADVGT*LQR	3	1	2	1	0	0	0	0	3.111558	0.2137
IPI00132347	**Adult male cerebellum cDNA, RIKEN full-length enriched library, clone:1500015I13 product:UBIQUINOL-CYTOCHROME C REDUCTASE BINDING PROTEIN homolog**										
	DDTLHE*TEDVK	0	0	0	0	0	0	3	3	2.9657	0.656413
IPI00133034	**Histidine triad nucleotide-binding protein 2**										
	IS*QAEEDDQQLLGHLLLVAK	0	0	0	0	5	0	4	2	3.961505	0.465516
	ISQAEE*DDQQLLGHLLLVAK	0	0	0	0	4	2	3	4	4.345031	0.858929
	ISQAEEDD*QQLLGHLLLVAK	0	0	0	0	3	1	6	5	4.307644	0.824737
IPI00133456	**Regucalcin**										
	VAVD*APVSSVALR	0	0	11	6	0	0	0	0	3.325346	0.419269
IPI00134746	**Argininosuccinate synthase**										
	EFVEEFIWPAVQSSALY*EDR	0	0	0	0	7	4	0	0	3.89298	0.432658
	EFVEEFIWPAVQSSALYE*DR	0	0	0	0	3	3	0	0	3.793133	0.452609
	EFVEEFIWPAVQSSALYED*R	0	0	0	0	4	3	0	0	3.906375	0.420184
IPI00134961	**Medium-chain specific acyl-CoA dehydrogenase, mitochondrial precursor**										
	AFAGDIANQLAT*DAVQIFGGYGFNTEYPVEK	0	3	0	0	7	0	1	0	4.456584	0.892763
	AFAGDIANQLATDAVQIFGGYGFNT*EYPVEK	0	2	0	0	3	0	0	1	5.338894	1.588239
	IYQIY*EGTAQIQR	5	0	0	0	3	2	0	0	3.169786	0.730981
	IYQIYE*GTAQIQR	6	0	0	0	4	3	0	0	3.416525	0.653121

IPI00169862	**Ubiquinone biosynthesis protein COQ9, mitochondrial precursor**										
	AVLAGIY*NTTELVMMQDSSPDFEDTWR	4	5	0	0	0	0	0	0	5.71694	1.152391
	AVLAGIYNTTE*LVMMQDSSPDFEDTWR	4	5	0	0	0	0	0	0	6.616878	1.907749
	AVLAGIYNTTELVMMQD*SSPDFEDTWR	4	3	0	0	0	0	0	0	4.175925	0.435902
IPI00228630	**Fructose-1,6-bisphosphatase 1**										
	DFD*PAINEYLQR	0	0	0	3	0	2	0	0	3.709242	0.360041
IPI00230212	**Glutathione S-transferase Mu 1**										
	YTMGD*APDFDR	0	0	0	5	0	2	0	0	2.848155	0.734043
IPI00266614	**Ribosyldihydronicotinamide dehydrogenase**										
	VLAPQISFGLD*VSSEEER	8	2	3	0	5	2	0	0	3.532954	0.652788
IPI00271869	**PREDICTED: similar to Glyceraldehyde-3-phosphate dehydrogenase**										
	WGEAGAEYVVE*STGVFTTMEK	2	4	0	0	0	0	0	0	3.916738	0.501891
IPI00283531	**Glutathione S-transferase P 2**										
	FE*DGDLTLYQSNAILR	0	0	6	10	0	0	0	0	3.655657	0.647983
	FED*GDLTLYQSNAILR	0	0	5	5	0	0	0	0	3.14292	0.490743
IPI00308885	**60 kDa heat shock protein, mitochondrial precursor**										
	AAVEEGIVLGGGC*ALLR	11	10	0	0	15	18	7	19	4.27075	0.954116
	ILQSSSEVGYDAMLGDFVNMVE*K	0	0	0	0	0	0	2	4	4.266688	0.556697
	NAGVEGSLIVE*K	0	0	0	2	0	6	0	1	2.913506	0.767052
	SGSSSAYTGYVE*R	0	0	0	0	0	0	3	4	2.792563	0.570409
IPI00314510	**Aspartoacylase-2**										
	LFSGEDVLYEGDSIVYPVFINE*AAYYEK	0	0	0	0	4	2	0	0	4.485513	0.718548
IPI00319973	**Membrane-associated progesterone receptor component 1**										
	FYGPEGPY*GVFAGR	0	0	0	0	0	0	3	2	2.849692	0.805222
IPI00323592	**Malate dehydrogenase, mitochondrial precursor**										
	IQEAGTE*VVK	5	3	0	0	0	3	0	0	2.83022	0.917605
IPI00336324	**Malate dehydrogenase, cytoplasmic**										
	FVE*GLPINDFSR	0	1	0	1	5	5	0	0	2.875425	0.799907
	GE*FITTVQQR	2	0	0	0	2	0	0	0	2.6335	0.671239
IPI00381277	**PREDICTED: similar to zinc finger protein 420 isoform 1**										
	C*SSLRTHQKIHAGEKPHACEKCGK	2	3	3	0	5	13	0	2	3.672296	0.564578
IPI00404014	**Carnitine transporter 2 variant**										
	KARTWASIHLNTFFAIGAMLVALAS*YLLK	2	0	0	0	2	1	0	1	3.917875	0.506869
	KARTWASIHLNTFFAIGAMLVALASY*LLK	2	1	0	1	3	1	0	1	3.953247	0.599483
IPI00461964	**NOD-derived CD11c +ve dendritic cells cDNA, RIKEN full-length enriched library, clone:F630044D15 product:aldehyde dehydrogenase family 6, subfamily A1**										
	C*MALSTAILVGEAK	0	3	0	0	9	7	0	5	3.601511	0.555942
IPI00462072	**Alpha-enolase**										
	VNQIGSVTESLQAC*K	2	3	0	0	0	0	0	0	3.318542	0.494644
IPI00466128	**Alcohol dehydrogenase**										
	GLE*VTAYSPLGSSDR	0	0	0	0	2	6	0	0	3.2112	0.762888
IPI00468481	**ATP synthase subunit beta, mitochondrial precursor**										
	AIAE*LGIYPAVDPLDSTSR	2	1	0	0	0	0	5	7	4.06468	0.81941
	FTQAGSE*VSALLGR	0	2	0	0	0	0	2	1	3.162833	0.660673
	SLQDIIAILGMDELS*EEDK	0	0	0	0	0	0	13	9	3.753479	0.437723
	SLQDIIAILGMDELSEE*DK	0	0	0	0	0	0	2	3	4.663975	0.82379
	SLQDIIAILGMDELSEED*K	0	0	0	0	0	0	16	10	4.606083	0.869303

Supplementary Information Table 3: Proteins identified from mouse proteomes treated with the CA probe. Mouse proteomes (soluble proteomes of heart, kidney and liver and membrane proteome of liver) were treated with the CA probe (50 µM, 2 hrs) in duplicate. Proteins identified with ≥ 2 spectral counts in ≥ 2 samples are included. * Indicates predicted sites of labeling; Average Xcorr values with associated standard deviation is provided for each assigned labeling site.

	PEPTIDE	**HEART 1**	**HEART 2**	**KIDNEY 1**	**KIDNEY 2**	**LIVER 1**	**LIVER 2**	**LIVER MEM 1**	**LIVER MEM 2**	**XCORR (average)**	**STD. DEV.**
IPI00108939	**glyceraldehyde-3-phosphate dehydrogenase, spermatogenic**										
	VPTPNVSVVDLTC*R	14	11	10	24	0	0	0	0	4.130756	0.802102
IPI00109061	**ES cells cDNA, RIKEN full-length enriched library, clone:2410129E14 product:tubulin beta-4 chain homolog**										
	LTTPTYGDLNHLVSATMSGVTTC*LR	0	0	5	11	0	0	0	0	4.322249	0.829284
IPI00110042	**Selenium-binding protein 1**										
	C*GPGYSTPLEAMK	0	0	1	2	2	0	0	0	2.843367	0.81476
	GGSVQVLEDQELTC*QPEPLVVK	0	0	0	3	7	0	0	0	4.521031	0.862708
IPI00110753	**Tubulin alpha-1 chain**										
	AVC*MLSNTTAIAEAWAR	2	0	1	3	0	0	0	0	3.751378	0.578757
	TIQFVDWC*PTGFK	3	0	6	9	0	0	0	0	3.376796	0.580338
IPI00111908	**Carbamoyl-phosphate synthase [ammonia], mitochondrial precursor**										
	TSAC*FEPSLDYMVTK	0	0	0	0	2	1	0	2	3.2267	0.764348
	VVAVDC*GIK	0	0	0	0	15	6	1	1	2.832569	1.019222
IPI00113223	**Fatty acid synthase**										
	GPSIALDTAC*SSSLLALQNAYQAIR	2	0	17	21	10	21	3	1	4.833118	1.299959
IPI00114710	**Activated spleen cDNA, RIKEN full-length enriched library, clone:F830201B12 product:pyruvate carboxylase, full insert sequence**										
	FLYEC*PWR	0	0	9	15	8	2	3	1	2.740195	1.180427
IPI00116074	**Aconitate hydratase, mitochondrial precursor**										
	VGLIGSC*TNSSYEDMGR	0	2	4	2	0	0	0	0	4.053017	0.717479
IPI00116591	**Short-chain specific acyl-CoA dehydrogenase, mitochondrial precursor**										
	IGIASQALGIAQASLDC*AVK	0	3	3	1	0	0	0	0	4.3436	1.075734
IPI00117348	**Tubulin alpha-2 chain**										
	AVC*MLSNTTAIAEAWAR	2	0	1	3	0	0	0	0	3.751378	0.578757
	SIQFVDWC*PTGFK	5	3	9	12	0	0	0	0	3.670753	0.685794
IPI00118153	**Cysteine and glycine-rich protein 3**										
	GIGFGQGAGC*LSTDTGEHLGLQFQQSPK	3	2	0	0	0	0	0	0	3.941208	0.669989
IPI00118344	**UDP-glucose 6-dehydrogenase**										
	ASVGFGGSC*FQK	0	0	4	9	2	2	0	1	3.194799	0.879093
IPI00119112	**Vacuolar ATP synthase catalytic subunit A, ubiquitous isoform**										
	YSNSDVIIYVGC*GER	0	0	18	53	0	0	0	0	3.543914	0.637915
IPI00119622	**Cysteine sulfinic acid decarboxylase**										
	FYDVALDTGDKVVQC*GR	0	0	0	0	4	3	0	0	4.749875	1.024211
IPI00119945	**Nit protein 2**										
	VGLGIC*YDMR	8	0	12	47	39	11	7	1	2.773447	1.129454
IPI00120076	**Creatine kinase, sarcomeric mitochondrial precursor**										
	LGYILT*CPSNLGTGLR	3	2	0	0	0	0	0	0	3.5252	0.415846
	LGYILTC*PSNLGTGLR	35	31	0	13	0	0	0	0	4.322031	0.83056
	LGYILTCPS*NLGTGLR	2	2	0	0	0	0	0	0	3.294175	0.267937
IPI00121639	**Beta-ureidopropionase**										
	IAVNIC*YGR	0	0	0	0	8	3	0	0	2.723908	0.740529
IPI00126208	**11 days embryo whole body cDNA, RIKEN full-length enriched library, clone:2700082N11 product:hemoglobin, beta adult major chain, full insert sequence**										
	GTFASLSELHC*DK	87	73	28	80	47	12	4	1	3.244796	0.909914
IPI00126248	**Adult male testis cDNA, RIKEN full-length enriched library, clone:4922505F07 product:ATP citrate lyase, full insert sequence**										
	YIC*TTSAIQNR	0	0	2	0	4	2	0	0	3.051667	0.755569
IPI00126680	**Adult male kidney cDNA, RIKEN full-length enriched library, clone:0610009G07 product:glutathione S-transferase, theta 2, full insert sequence**										
	GQHMSEQFSQVNC*LNK	0	0	0	57	15	8	0	0	4.048783	0.769788
IPI00126940	**Isoform Long of Adenosine kinase**										
	TGC*TFPEKPDFH	0	0	0	0	3	3	0	0	3.255283	0.560802
IPI00127206	**Fructose-bisphosphate aldolase B**										
	TVPAAVPGIC*FLSGGMSEEDATLNLNAINR	0	0	4	17	6	4	0	0	4.106127	0.741567
IPI00128376	**Aldo-keto reductase family 1, member C14**										
	SKDIILVSYC*TLGSSR	0	0	0	1	20	2	0	0	4.44376	0.742406
IPI00128873	**Nitrilase 1**										
	VGLAIC*YDMR	0	0	3	14	3	0	0	0	2.7858	0.881408
IPI00128904	**Poly(rC)-binding protein 1**										
	LVVPATQC*GSLIGK	0	0	0	3	3	0	0	0	2.836967	0.817981
IPI00129011	**Formimidoyltransferase-cyclodeaminase**										
	AC*ALQEGLR	0	0	0	0	6	2	0	0	2.652775	0.733955
IPI00130280	**ATP synthase subunit alpha, mitochondrial precursor**										
	YTIVVSATASDAAPLQYLAPYSGC*SMGEYF	4	2	0	3	0	0	7	1	4.981455	1.395666
IPI00130950	**Betaine--homocysteine S-methyltransferase**										
	AGASIVGVNC*HFDPSVSLQTVK	0	0	0	0	5	4	0	0	4.146553	0.68392
	QVADEGDALVAGGVSQTPSYLSC*K	0	0	0	0	5	5	0	1	5.3209	1.16068
	VNEAAC*DIAR	0	0	0	0	5	2	0	0	3.01099	0.636631
IPI00131438	**Phosphoenolpyruvate carboxykinase, cytosolic**										
	YLAAAFPSAC*GK	0	0	7	6	6	3	0	0	3.480611	0.771934
IPI00131695	**Serum albumin precursor**										
	C*SYDEHAK	1	3	2	6	7	3	0	0	2.670769	1.107526
IPI00132653	**Succinyl-CoA:3-ketoacid-coenzyme A transferase 1, mitochondrial precursor**										
	DIPNGATLLVGGFGLC*GIPENLIGALLK	8	7	0	8	0	0	0	0	3.876715	0.674411
IPI00132950	**40S ribosomal protein S21**										
	TYGIC*GAIR	0	0	1	0	0	0	5	1	2.704907	0.89791
IPI00133903	**Stress-70 protein, mitochondrial precursor**										
	C*ELSSSVQTDINLPYLTMDASGPK	1	0	0	7	0	0	4	1	5.135486	1.351728
IPI00133920	**SEC13-related protein**										
	FASGGC*DNLIK	0	0	2	4	5	0	0	0	3.003452	0.752126
IPI00134599	**40S ribosomal protein S3**										
	GLC*AIAQAESLR	3	1	8	16	11	3	15	2	3.595706	0.835958

	PEPTIDE	HEART 1	HEART 2	KIDNEY 1	KIDNEY 2	LIVER 1	LIVER 2	LIVER MEM 1	LIVER MEM 2	XCORR (average)	STD. DEV.
IPI00134746	**Argininosuccinate synthase**										
	FELTC*YSLAPQIK	0	0	9	17	7	11	1	0	3.452515	0.78576
IPI00135231	**0 day neonate lung cDNA, RIKEN full-length enriched library, clone:E030024J03 product:isocitrate dehydrogenase 1 (NADP+), soluble, full insert sequence**										
	SEGGFIWAC*K	0	0	4	4	2	0	0	0	2.761675	0.906762
IPI00135977	**Chloride intracellular channel protein 4**										
	AGSDGESIGNC*PFSQR	14	9	4	28	10	4	3	2	3.749914	0.767956
IPI00153317	**10-formyltetrahydrofolate dehydrogenase**										
	AVQMGMSSVFFNKGENC*IAAGR	0	0	10	131	12	136	49	2	4.411197	0.997113
IPI00153463	**Dehydrogenase/reductase SDR family member 11 precursor**										
	NIDDGHIININSMC*GHR	10	1	0	10	9	7	0	0	4.64349	1.135088
IPI00172221	**Isoform 2 of Dynamin-1-like protein**										
	IC*YIFHETFGR	2	0	0	0	5	0	0	0	2.707495	0.708201
IPI00221400	**Alcohol dehydrogenase 1**										
	MVATGVC*R	0	0	1	0	11	2	0	0	2.734045	0.885805
IPI00221636	**Adult male aorta and vein cDNA, RIKEN full-length enriched library, clone:A530080C09 product:weakly similar to ALCOHOL SULFOTRANSFERASE**										
	MISQSC*LSNIEK	0	0	0	0	5	2	0	0	3.811675	0.518291
IPI00226993	**Thioredoxin**										
	C*MPTFQFYK	0	0	0	2	6	2	0	0	2.623161	1.011675
IPI00229510	**L-lactate dehydrogenase B chain**										
	GMYGIENEVFLSLPC*ILNAR	0	1	3	12	0	0	0	0	4.473531	0.74263
	VIGSGC*NLDSAR	0	11	12	20	0	0	0	0	3.30604	0.654737
IPI00230034	**D-dopachrome decarboxylase**										
	PFVE*LETNLPASR	1	0	7	8	16	14	0	0	3.209277	0.29961
IPI00230212	**Glutathione S-transferase Mu 1**										
	C*LDAFPNLR	0	0	0	0	6	3	0	0	2.663908	0.809711
IPI00230706	**Phosphoglycerate mutase 2**										
	FC*GWFDAELSEK	21	18	0	0	0	0	0	0	3.041141	0.659126
IPI00230760	**Myoglobin**										
	HGC*TVLTALGTILK	25	18	0	0	0	0	0	0	3.69261	0.640467
IPI00267407	**Aldh8a1 protein**										
	SSFANQGEIC*LCTSR	0	0	0	0	10	3	0	0	3.628142	0.64069
IPI00273164	**Succinate semialdehyde dehydrogenase, mitochondrial precursor**										
	NAGQTC*VCSNR	1	1	4	3	3	1	5	1	3.084797	0.943454
IPI00273646	**Glyceraldehyde-3-phosphate dehydrogenase**										
	IVSNASC*TTNCLAPLAK	8	5	4	11	4	5	0	0	3.31567	0.83853
	VPTPNVSVVDLTC*R	14	11	10	24	8	8	0	0	4.153904	0.860537
IPI00283531	**Glutathione S-transferase P 2**										
	EEVVTIDTWMQGLLKPTC*LYGQLPK	0	0	0	8	5	14	0	1	4.545528	1.025334
IPI00307837	**Elongation factor 1-alpha 1**										
	SGDAAIVDMVPGKPMC*VESFSDYPPLGR	0	0	0	16	3	1	0	0	3.739774	0.611763
IPI00308885	**60 kDa heat shock protein, mitochondrial precursor**										
	AAVEEGIVLGGGC*ALLR	5	7	7	24	5	4	10	2	4.19456	0.980049
	C*EFQDAYVLLSEK	0	0	0	2	5	2	0	0	3.219173	0.823307
IPI00314041	**Villin-1**										
	HVETNSC*DVQR	0	0	2	2	0	0	0	0	3.2118	0.512272
IPI00319994	**L-lactate dehydrogenase A chain**										
	DYC*VTANSK	4	0	0	2	2	1	0	0	2.7288	1.036377
	VIGSGC*NLDSAR	12	0	0	20	4	2	0	0	3.098239	0.879986
IPI00321375	**12 days embryo female mullerian duct includes surrounding region cDNA, RIKEN full-length enriched library, clone:6820408J04 product:biotinidase**										
	FGVFTC*FDILFFDPAVR	0	0	0	0	0	0	10	2	4.373085	0.844608
IPI00323816	**Selenium-binding protein 2**										
	C*GPGYPTPLEAMK	0	0	0	0	8	5	0	0	2.891245	0.75277
	GGSVQVLEDQELTC*QPEPLVVK	0	0	0	0	7	5	0	0	4.869394	1.237034
IPI00323971	**Inosine-5'-monophosphate dehydrogenase 2**										
	HGFC*GIPITDTGR	0	0	0	0	16	4	0	0	3.404316	0.573711
IPI00336324	**Malate dehydrogenase, cytoplasmic**										
	VIVVGNPANTNC*LTASK	4	3	2	3	0	0	0	0	3.450115	0.79349
IPI00378120	**Glutaredoxin-related protein 5**										
	GTPEQPQC*GFSNAVVQILR	0	0	0	1	2	0	3	1	3.6336	0.655941
IPI00395140	**L-xylulose reductase**										
	ALTNHTVYC*STK	0	0	0	3	3	1	0	0	2.895667	0.812925
IPI00409345	**Lambda-crystallin homolog**										
	VILSSSSSC*LLPSK	2	0	9	21	6	2	0	0	3.361205	0.739109
IPI00420718	**Hydroxymethylglutaryl-CoA synthase, mitochondrial precursor**										
	QAGNNQPFTLDDVQYMIFHTPFC*K	0	0	0	0	0	4	4	1	4.285408	0.759121
IPI00454049	**Enoyl-CoA hydratase, mitochondrial precursor**										
	ALNALC*NGLIEELNQALETFEQDPAVGAIVL	15	14	0	33	12	17	15	1	6.075505	2.24612
IPI00461964	**NOD-derived CD11c +ve dendritic cells cDNA, RIKEN full-length enriched library, clone:F630044D15 product:aldehyde dehydrogenase family 6, subfamily A1**										
	C*MALSTAILVGEAK	82	28	26	81	45	47	71	2	3.750005	0.839365
IPI00463392	**RIKEN cDNA E030049G20 gene**										
	EE*PAKITAYQEGLPDEER	0	0	0	2	0	0	4	0	3.602413	0.258302
IPI00466069	**Elongation factor 2**										
	STLTDSLVC*K	0	0	4	2	5	2	0	0	2.627891	1.068592
IPI00467447	**Ras GTPase-activating-like protein IQGAP1**										
	VNTSSALANISLALEQGC*AVTLLK	0	0	10	12	0	0	0	0	5.0236	0.891451
IPI00554931	**4-hydroxyphenylpyruvate dioxygenase**										
	IVFVLC*SALNPWNK	0	0	0	0	0	19	11	2	3.813522	0.688571
IPI00625913	**32 kDa protein**										
	PY*CKLLIVSNPVDILTYVAWK	0	1	1	3	0	3	0	0	3.640283	0.38287
	PYCK*LLIVSNPVDILTYVAWK	0	0	0	4	1	3	0	0	3.635258	0.624515
IPI00653158	**14 days embryo liver cDNA, RIKEN full-length enriched library, clone:I530029G20 product:acetyl-Coenzyme A acyltransferase 2**										
	YAVGSAC*IGGGQGIALIIQNTA	2	5	0	1	5	0	4	2	3.940105	0.849122
IPI00677618	**10, 11 days embryo whole body cDNA, RIKEN full-length enriched library, clone:2810420C16 product:hypothetical Transthyretin containing protein**										
	LEAPC*QQWMELR	0	0	0	0	9	5	0	0	3.431882	0.654789

Supplementary Information Table 4: Proteins identified from mouse proteomes treated with the UK probe. Mouse proteomes (soluble proteomes of heart, kidney and liver and membrane proteome of liver) were treated with the UK probe (50 µM, 2 hrs) in duplicate. Proteins identified with ≥ 2 spectral counts in ≥ 2 samples are included. * Indicates predicted sites of labeling; Average Xcorr values with associated standard deviation is provided for each assigned labeling site.

	PEPTIDE	HEART1	HEART2	LIVER1	LIVER2	KIDNEY1	KIDNEY2	LIVER MEM1	LIVER MEM2	XCORR (average)	STD. DEV.
IPI00108042	**Carbohydrate kinase-like protein**										
	AFPFPVC*FGQDVDAAFGAALVMLQR	0	0	11	11	1	4	0	0	5.111688	1.058886
IPI00108125	**Eukaryotic translation initiation factor 5A-1**										
	YDC*GEEILITVLSAMTEEAAVAIK	15	5	4	1	10	34	22	0	4.719032	1.008221
IPI00108454	**PREDICTED: similar to 40S ribosomal protein S6**										
	LNISFPATGC*QK	0	2	0	0	0	1	0	6	2.734861	1.36287
IPI00108895	**26S protease regulatory subunit 6B**										
	GVLMYGPPGC*GK	2	2	0	1	1	4	0	0	2.92393	1.415906
IPI00108939	**glyceraldehyde-3-phosphate dehydrogenase, spermatogenic**										
	VPTPNVSVVDLT*CR	5	0	0	0	1	3	0	0	3.312478	0.815637
IPI00109061	**ES cells cDNA, RIKEN full-length enriched library, clone:2410129E14 product:tubulin beta-4 chain homolog**										
	LTTPTYGDLNHLVSATMSGVTTC*LR	8	10	3	1	8	0	0	1	4.715728	1.055684
IPI00109142	**S-formylglutathione hydrolase**										
	CPALYWLSGLTC*TEQNFISK	8	19	4	3	20	28	0	0	4.374535	0.908417
	SVSAFAPICNPVLC*SWGK	0	2	0	0	3	4	0	0	3.032133	1.080355
IPI00109169	**Isocitrate dehydrogenase [NAD] subunit gamma, mitochondrial precursor**										
	HAC*VPVDFEEVHVSSNADEEDIR	7	15	0	0	0	0	0	0	5.242754	1.018447
	TSLDLYANVIHC*K	4	3	0	0	0	0	0	0	2.811958	0.979186
IPI00109501	**Ribosome recycling factor, mitochondrial precursor**										
	SPQVILVNMASFPEC*TAAAIK	3	6	0	0	0	0	0	0	4.121858	0.624564
IPI00109536	**Aldo-keto reductase family 1, member C21**										
	CHCVILNDGNFIPVLGFGTALPLEC*PK	0	0	0	0	14	18	0	0	5.281127	1.018804
	VDLC*ATWEAMEK	0	0	0	0	4	4	0	0	2.96265	1.073824
IPI00109655	**Methionine sulfoxide reductase B2**										
	RLDTSLGC*PR	4	6	0	0	0	4	0	0	3.320044	0.99874
IPI00110042	**Selenium-binding protein 1**										
	GGSVQVLEDQELTC*QPEPLVVK	4	0	8	8	0	0	4	4	4.35057	0.813273
IPI00110528	**Probable isomerase MAWBP-1**										
	WFTPEAEFPLC*GHATLASAAVLFQK	0	0	4	4	0	0	0	0	3.983475	0.642507
IPI00110658	**13 days embryo liver cDNA, RIKEN full-length enriched library, clone:2510040B16 product:hemoglobin, beta adult major chain, full insert sequence**										
	TYFPHFDVS*HGSAQVK	5	0	0	0	0	2	0	0	3.002325	0.777108
	IGGH*GAEYGAEALER	17	19	4	3	5	9	0	0	3.638537	0.805639
	TYFPHFDVSH*GSAQVK	4	1	0	0	0	2	0	0	2.8731	0.782135
IPI00110753	**Tubulin alpha-1 chain**										
	AVC*MLSNTTAIAEAWAR	22	25	2	2	20	14	0	0	4.167546	0.969675
	AYHEQLSVAEITNAC*FEPANQMVK	9	31	0	0	4	30	0	0	4.925476	0.947093
	TIQFVDWC*PTGFK	3	6	1	1	3	8	0	1	3.25866	1.328342
	LADQC*TGLQGFLVFHSFGGGTGSGFTSLLMER	3	0	4	0	6	6	0	0	4.694548	1.052013
IPI00110866	**Cytidine deaminase**										
	IFSGCNIENAC*YPLGVCAER	0	0	0	0	2	4	0	0	4.451863	0.59363
IPI00111004	**Uncharacterized protein C7orf24 homolog**										
	NPSAVFC*CVAR	2	3	0	0	3	4	0	0	2.815754	1.403764
IPI00111181	**Vacuolar protein sorting-associated protein 35**										
	IANQC*MDPSLQVQLFIEILNR	4	0	0	0	3	1	0	0	4.613986	0.88635
IPI00111315	**Apolipoprotein A-II precursor**										
	T*HEQLTPLVR	3	3	0	0	0	0	0	0	2.751583	0.758319
	TH*EQLTPLVR	3	3	0	0	0	0	0	0	2.701433	0.654067
IPI00111412	**60S ribosomal protein L4**										
	SGQGAFGNMC*R	0	0	0	0	1	2	3	6	2.681871	1.445144
IPI00111885	**Ubiquinol-cytochrome-c reductase complex core protein I, mitochondrial precursor**										
	YFYDQC*PAVAGYGPIEQLPDYNR	0	3	0	0	0	1	3	0	5.151122	1.044012
IPI00111908	**Carbamoyl-phosphate synthase [ammonia], mitochondrial precursor**										
	TSAC*FEPSLDYMVTK	0	0	2	3	0	0	0	0	3.118942	0.786098
IPI00111981	**Isoform 1 of Putative GTP-binding protein 9**										
	STFFNVLTNSQASAENFPFC*TIDPNESR	0	9	0	0	0	5	0	0	4.570258	0.785186
IPI00112190	**RIKEN cDNA 1810022C23 gene**										
	ATFHTPFSQLSQIPEAC*STYMFPK	0	0	0	0	6	7	0	0	4.553314	0.746329
IPI00112366	**PREDICTED: similar to isochorismatase domain containing 2**										
	IIKEPVPDSGLLSLFQGQSPLTSC*	5	12	0	0	2	4	0	1	4.663911	0.91293
IPI00113223	**Fatty acid synthase**										
	GPSIALDTAC*SSSLLALQNAYQAIR	0	0	6	5	5	8	0	4	4.380412	0.934703
IPI00113347	**Carnitine O-acetyltransferase**										
	SMIDNETLPVEFLGGQPLC*MNQYYQILSSCR	2	12	0	0	0	1	0	0	4.30035	0.983289
IPI00113377	**60S acidic ribosomal protein P1**										
	ALANVNIGSLIC*NVGAGGPAPAAGAAPAGGAAP	1	8	0	0	2	6	18	15	7.388889	2.705562
IPI00114330	**Homogentisate 1,2-dioxygenase**										
	TCSC*LDENYYK	0	0	1	1	2	2	1	3	3.099342	1.340815
IPI00114396	**Isoform Long of Galectin-9**										
	GMPFELC*FLVQR	0	0	0	0	0	0	3	9	3.105272	0.893762

	PEPTIDE	HEART1	HEART2	LIVER1	LIVER2	KIDNEY1	KIDNEY2	LIVER MEM1	LIVER MEM2	XCORR (average)	STD. DEV.
IPI00114416	**3,2-trans-enoyl-CoA isomerase, mitochondrial precursor**										
	GVILTSEC*PGIFSAGLDLLEMYGR	33	45	7	4	12	11	0	11	5.570855	1.535658
	LRNPPVNSLSLEC*LTEFTISLEK	13	11	0	0	0	1	0	0	4.217746	0.961346
	GVILTSE*CPGIFSAGLDLLEMYGR	2	3	0	0	0	0	0	0	4.387767	0.638285
	GVILTS*ECPGIFSAGLDLLEMYGR	2	3	0	0	0	0	0	0	4.248042	0.604287
	GVILT*SECPGIFSAGLDLLEMYGR	2	3	0	0	0	0	0	0	3.949758	0.654299
IPI00114472	**PREDICTED: similar to ribosomal protein L27a**										
	NQSFC*PTVNLDKLWTLVSEQTR	0	4	0	0	1	4	16	33	4.383024	0.938454
IPI00115302	**Branched chain ketoacid dehydrogenase E1, beta polypeptide**										
	SGDLFNC*GSLTIR	0	1	0	0	0	2	0	4	2.914358	1.151209
IPI00115569	**Dihydrolipoyl dehydrogenase, mitochondrial precursor**										
	VLGAHILGPGAGEMVNEAALALEYGASC*EDIAR	13	20	0	0	1	8	0	0	6.070539	1.950744
	NETLGGTC*LNVGCIPSK	4	4	0	0	2	4	0	0	3.85835	0.892421
	AEVITCDVLLVC*IGR	5	5	0	0	0	0	0	0	3.58167	0.725865
IPI00115598	**Isoform Short of Estradiol 17-beta-dehydrogenase 8**										
	LLEEVQAC*FSRPPSVVVSCAGITR	2	4	0	0	0	3	0	0	4.445672	0.920765
IPI00115751	**9.5 days embryo parthenogenote cDNA, RIKEN full-length enriched library, clone:B130049K07 product:eukaryotic translation initiation factor 3, subunit 7 (zeta, 66/67 kDa), full i**										
	FMTPVIQDNPSGWGPC*AVPEQFR	0	6	0	0	0	2	9	6	4.182999	0.810356
IPI00115827	**Protein NipSnap2**										
	QYPC*TLVGTWNTWYGEQDQAVHLWR	6	10	0	0	0	0	0	0	3.928352	0.674461
IPI00116074	**Aconitate hydratase, mitochondrial precursor**										
	DVGGIVLANACGPC*IGQWDRK	13	13	0	0	4	9	0	0	4.061127	0.864145
	DVGGIVLANACGPC*IGQWDR	10	13	0	0	4	4	0	0	3.999021	0.87308
	DVGGIVLANAC*GPCIGQWDRK	6	9	0	0	0	1	0	0	3.968172	0.810643
IPI00116170	**NADH-ubiquinone oxidoreductase chain 3**										
	ANPYEC*GFDPTSSAR	0	0	0	0	0	0	3	3	3.050983	0.853272
IPI00116192	**Thioredoxin-dependent peroxide reductase, mitochondrial precursor**										
	AFQFVETHGEVC*PANWTPESPTIKPSPTASK	3	5	0	0	0	6	0	0	5.445049	1.40471
IPI00116222	**3-hydroxyisobutyrate dehydrogenase, mitochondrial precursor**										
	HGYPLILYDVFPDVC*K	9	0	0	0	8	1	0	0	4.102988	0.846446
IPI00116277	**T-complex protein 1 subunit delta**										
	IGLIQFC*LSAPK	4	2	0	2	4	4	0	12	2.780399	1.570238
	SIHDALC*VIR	5	5	0	0	0	5	0	4	2.719598	1.462587
	AQDIEAGDGTTSVVIIAGSLLDSC*TK	2	3	0	0	4	3	0	0	4.236138	0.788975
IPI00116489	**Atrial natriuretic factor precursor**										
	IGAQSGLGC*NSFR	3	3	0	0	0	0	0	0	2.922667	1.064495
IPI00116591	**Short-chain specific acyl-CoA dehydrogenase, mitochondrial precursor**										
	IGIASQALGIAQASLDC*AVK	53	55	0	0	14	17	2	17	4.994401	1.142153
IPI00116613	**CCAAT/enhancer-binding protein beta**										
	AAPAAC*FAGPPAAPAK	0	0	0	0	0	0	2	4	3.435038	0.99822
IPI00116753	**Electron transfer flavoprotein subunit alpha, mitochondrial precursor**										
	TIYAGNALC*TVK	4	2	0	0	2	4	0	0	2.79085	1.437091
IPI00117007	**MKIAA0120 protein (Fragment)**										
	QYDADLEQILIQWITTQC*R	0	0	0	0	3	3	0	0	3.882633	0.546798
IPI00117264	**Protein DJ-1**										
	VTVAGLAGKDPVQC*SR	4	8	0	0	1	1	0	0	3.625497	1.052074
IPI00117281	**Isoform Mitochondrial of Phospholipid hydroperoxide glutathione peroxidase, mitochondrial precursor**										
	ILAFPC*NQFGR	0	0	0	0	2	3	0	0	2.732508	1.02873
IPI00117312	**Aspartate aminotransferase, mitochondrial precursor**										
	NLDKEYLPIGGLAEFC*K	11	30	0	0	2	8	0	0	4.14842	0.871227
	HFIEQGINVCLC*QSYAK	5	14	0	0	0	0	0	0	4.245712	0.762269
IPI00117348	**Tubulin alpha-2 chain**										
	AVC*MLSNTTAIAEAWAR	22	0	2	2	20	14	0	0	4.185585	0.950547
	AYHEQLSVAEITNAC*FEPANQMVK	9	0	0	0	4	30	0	0	4.90386	0.865795
	SIQFVDWC*PTGFK	5	0	1	1	5	10	0	5	3.501743	1.133287
	LADQC*TGLQGFLVFHSFGGGTGSGFTSLLMER	3	0	4	0	6	6	0	0	4.694548	1.052013
IPI00117350	**Tubulin alpha-4 chain**										
	AVC*MLSNTTAIAEAWAR	22	25	0	0	20	14	0	0	4.251594	0.916818
	AYHEQLSVAEITNAC*FEPANQMVK	9	31	0	0	4	30	0	0	4.925476	0.947093
	SIQFVDWC*PTGFK	5	14	0	0	5	10	0	0	3.489249	1.031201
	LSDQC*TGLQGFLVFHSFGGGTGSGFTSLLMER	4	0	0	0	5	7	0	0	4.478826	0.761019
	TIGGGDDSFTTFFC*ETGAGK	0	3	0	0	2	5	0	0	3.552128	0.903349
IPI00117569	**40S ribosomal protein S11**										
	DVQIGDIVTVGEC*RPLSK	0	0	0	0	0	1	2	9	3.661359	0.779485
IPI00117570	**Growth-arrest-specific protein 2**										
	LDNGALLC*QLAATVQEK	0	0	0	0	2	3	0	0	4.072825	0.610875
IPI00118059	**Serine hydroxymethyltransferase, cytosolic**										
	LIIAGTSC*YSR	0	0	2	1	2	0	0	0	2.9954	1.245301
IPI00118153	**Cysteine and glycine-rich protein 3**										
	GIGFGQGAGC*LSTDTGEHLGLQFQQSPK	7	16	0	0	0	0	0	0	4.751402	0.774105
	GIGFGQGAGC*LSTDTGEHLGLQFQQSPKPAR	9	9	0	0	0	0	0	0	4.496267	0.879211
	TCFHCMAC*R	3	2	0	0	0	0	0	0	2.72405	1.087708
IPI00118344	**UDP-glucose 6-dehydrogenase**										
	ISSINSISALC*EATGADVEEVATAIGMDQR	0	0	0	0	2	5	0	0	5.99587	0.709929
IPI00118676	**Eukaryotic initiation factor 4A-I**										
	VVMALGDYMGASCHAC*IGGTNVR	0	0	0	0	0	2	0	3	4.084292	0.699035
IPI00118986	**ATP synthase O subunit, mitochondrial precursor**										
	GEVPC*TVTTASPLDDAVLSELK	0	3	0	0	0	0	6	5	4.598804	0.822757
IPI00119004	**hypothetical protein LOC67732**										
	VILITPPPLC*EAAWEK	0	0	0	0	10	11	0	0	2.83369	1.030208
IPI00119087	**Uroporphyrinogen-III synthase**										
	GLPVSC*TAESPTPQALAAGIR	3	4	0	0	2	4	0	0	4.146138	0.785005
IPI00119112	**Vacuolar ATP synthase catalytic subunit A, ubiquitous isoform**										
	VLDALFPCVQGGTTAIPGAFGC*GK	0	0	0	0	13	15	0	0	3.840205	0.649815
IPI00119113	**Bone marrow macrophage cDNA, RIKEN full-length enriched library, clone:I830083B18 product:ATPase, H+ transporting, V1 subunit B, isoform 2, full insert sequence**										
	GPVVLAEDFLDIMGQPINPQC*R	0	0	0	0	4	8	0	0	5.5092	0.918527
IPI00119219	**Isoform 1 of Estradiol 17-beta-dehydrogenase 12**										
	AFQVWC*VGNEALVGPR	0	0	0	0	0	0	2	18	4.054925	0.688656
IPI00119667	**Elongation factor 1-alpha 2**										
	SGDAAIVEMVPGKPMC*VESFSQYPPLGR	10	13	0	0	0	0	0	0	4.591518	0.691104
	NMITGTSQADC*AVLIVAAGVGEFEAGISK	10	7	0	0	0	0	0	0	4.024329	0.745542
IPI00119842	**Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial precursor**										
	VDASVALLC*DIQNTIINNLFR	7	11	0	0	8	15	1	5	5.085773	1.191275
	ASSTC*QLTFENVKVPETNILGK	1	4	0	0	1	4	0	0	3.985919	0.780317
IPI00119930	**5'-AMP-activated protein kinase subunit gamma-1**										
	EVYLQDSFKPLVC*ISPNASLFDAVSSLIR	4	10	0	0	1	1	0	0	4.708225	0.948917
IPI00120076	**Creatine kinase, sarcomeric mitochondrial precursor**										
	LGYILTC*PSNLGTGLR	34	35	0	0	2	2	0	0	3.942655	0.926466
	SEVELVQIVIDGVNYLVDC*EK	12	16	0	0	0	0	0	0	5.348479	1.135165
	MTPSGYTLDQC*IQTGVDNPGHPFIK	6	10	0	0	0	0	0	0	4.48199	0.688391

	PEPTIDE	HEART1	HEART2	LIVER1	LIVER2	KIDNEY1	KIDNEY2	LIVER MEM1	LIVER MEM2	XCORR (average)	STD. DEV.
IPI00120165	**Peroxisomal carnitine O-octanoyltransferase**										
	AFVFDVLHEGC*LITPPELLR	0	0	0	0	3	7	0	0	3.909005	0.846413
IPI00121280	**12 days embryo embryonic body between diaphragm region and neck cDNA, RIKEN full-length enriched library, clone:9430034P22 product:Glutathione S-transferase Yb-3 (EC 2**										
	KHNLC*GETEEER	3	2	0	0	0	2	0	0	3.099183	1.131248
IPI00121348	**L-serine dehydratase**										
	ETLSAKPGAIVLSVGGGGLLC*GVVQGLR	0	0	6	7	0	0	0	0	5.582112	1.053565
	LQTPLASLVVIVC*GGSNISLAQLQALK	0	0	5	8	0	0	0	0	4.388961	0.747519
IPI00121440	**Electron transfer flavoprotein subunit beta**										
	HSMNPFC*EIAVEEAVR	2	6	0	0	0	0	0	0	3.498983	0.611419
	QAIDDDC*NQTGQMTAGLLDWPQGTFASQVTLE	0	4	0	0	0	2	0	0	5.064938	0.700717
	EIIAVSCGPSQC*QETIR	0	2	0	0	0	2	0	0	3.739975	0.616943
IPI00121566	**GMP reductase 1**										
	VGVGPGSVC*TTR	3	3	0	0	2	3	0	0	2.76755	1.46312
IPI00121758	**TAR DNA-binding protein 43**										
	VTEDENDEPIEIPSEDDGTVLLSTVTAQFPGAC*G	0	1	0	0	0	2	3	0	5.538489	1.098867
IPI00121788	**Peroxiredoxin-1**										
	HGEVC*PAGWKPGSDTIKPDVNK	5	0	12	9	3	65	1	0	4.095454	0.913619
	LNCQVIGASVDSHFC*HLAWINTPK	0	0	22	10	0	1	0	0	4.017392	0.79687
IPI00121833	**3-ketoacyl-CoA thiolase A, peroxisomal precursor**										
	AGLTVNDIDIFEINEAFASQAVYC*VEK	0	0	0	0	1	3	1	4	4.513827	0.841643
IPI00122075	**Mitochondrial antiviral signaling protein**										
	FCCVDVLEILPYLSC*LTASDQDR	0	0	0	0	3	4	0	0	5.4117	1.421662
IPI00122634	**Cytochrome P450, family 2, subfamily a, polypeptide 12**										
	MLQGTC*GAPIDPTIYLSK	0	0	0	0	0	0	3	6	3.926158	0.617994
	IQEEAGC*LIK	0	0	0	0	0	0	2	3	3.025933	0.848702
IPI00122684	**Eno2 protein (Fragment)**										
	SGETEDTFIADLVVGLC*TGQIK	8	9	0	0	0	0	0	0	4.332102	0.836946
IPI00122740	**Protein LRP16**										
	LEVDAIVNAANSSLLGGGGVDGC*IHR	4	3	0	0	0	0	0	0	4.752042	1.016974
IPI00122743	**Aspartyl-tRNA synthetase, cytoplasmic**										
	LEYC*EALAMLR	1	2	3	1	4	6	0	6	3.046305	1.395217
IPI00123006	**GDP-mannose pyrophosphorylase A**										
	LLPAITILGC*R	2	2	0	2	4	6	0	0	2.80744	1.520255
IPI00123619	**Cytochrome P450, family 2, subfamily d, polypeptide 22**										
	VQQEIDEVIGQVQC*PEMADQAR	0	0	0	0	0	0	3	2	4.718667	0.729775
IPI00123651	**ATP-dependent RNA helicase DDX19A**										
	VLVTTNVC*AR	1	2	1	0	2	2	0	2	2.768175	1.570999
IPI00123975	**Glycerol kinase-like protein 2**										
	GIIC*GLTQFTNK	0	0	0	0	3	8	0	0	3.180419	0.823171
IPI00124103	**Copper chaperone for superoxide dismutase**										
	GMGSSQLQNLGAAVAILEGC*GSIQGVVR	2	3	2	2	4	6	0	0	5.224846	1.248554
IPI00124225	**Proteasome activator complex subunit 2**										
	QNLFQEADDFLC*TFLPR	1	10	1	0	4	2	0	0	3.61088	0.984092
IPI00124372	**aldehyde dehydrogenase 9, subfamily A1**										
	TVC*VEMGDVESAF	0	0	0	0	2	4	0	0	2.897563	0.903546
IPI00124444	**Isoform 1 of 6-phosphofructokinase type C**										
	WDC*VSSILQVGGTIIGSAR	0	9	0	0	4	0	0	0	4.127578	0.703725
IPI00124819	**Coronin-1B**										
	NVLLSAGC*DNVVLIWNVGTAEELYR	0	4	0	0	3	1	0	0	4.505086	0.966567
IPI00124900	**Isoform 1 of Methylglutaconyl-CoA hydratase, mitochondrial precursor**										
	SEVPGIFC*AGADLK	2	3	0	0	0	1	0	0	3.050261	1.200662
IPI00125135	**Ubiquitin-conjugating enzyme E2 D2**										
	IYHPNINSNGSIC*LDILR	11	8	0	0	4	5	1	0	3.660672	1.038639
	VLLSICSLLC*DPNPDDPLVPEIAR	4	7	0	0	2	5	0	0	5.158652	1.081996
IPI00125325	**Peroxisomal 2,4-dienoyl-CoA reductase**										
	INILINCAAGNFLC*PASALSFNAFK	0	1	1	0	2	5	1	11	4.948558	1.100794
IPI00125521	**40S ribosomal protein S5**										
	VNQAIWLLC*TGAR	0	0	0	0	3	0	0	18	3.006219	0.881482
IPI00125853	**Mitochondrial ornithine transporter 1**										
	LSDLQNAAAGSFASAFAALVLC*PTELVK	0	1	0	0	0	0	7	20	5.792662	1.12812
IPI00125960	**Protein NDRG1**										
	FALNNPEMVEGLVLMNVNPC*AEGWMDWAASK	0	0	0	0	4	4	0	0	5.01815	0.81445
IPI00126172	**Ester hydrolase C11orf54 homolog**										
	AHIMPAEFSSC*PLNSDEAVNK	2	0	0	1	13	36	1	0	4.05144	0.8907
	APLVC*LPVFVSK	0	0	0	0	6	7	0	0	2.86829	0.97284
IPI00126208	**11 days embryo whole body cDNA, RIKEN full-length enriched library, clone:2700082N11 product:hemoglobin, beta adult major chain, full insert sequence**										
	GTFASLSELHC*DK	25	32	3	4	5	17	2	12	2.727417	1.71339
	AAVSGLWGK*VNADEVGGEALGR	8	15	0	0	4	2	0	0	3.709681	0.609317
	YFDSFGDLSSASAIMGNAK*VK	0	2	1	0	0	2	0	0	3.7747	0.606138
	GTFASLSELHCD*K	3	4	0	0	0	0	0	0	2.862542	0.777655
	VITAFNDGLNHLD*SLK	0	1	0	0	2	2	0	0	2.546733	1.03556
	AAVS*GLWGKVNADEVGGEALGR	8	20	0	0	5	7	0	0	3.87699	0.696279
	YFDSFGDLSSAS*AIMGNAKVK	3	2	0	0	1	2	0	0	3.648383	0.719169
	KVITAFNDGLNH*LDSLK	2	5	0	0	0	1	0	0	3.606697	0.664238
	VITAFNDGLNH*LDSLK	7	14	0	0	2	6	0	0	2.87884	0.841444
	GTFASLSELH*CDK	2	4	0	0	0	0	0	0	2.785	0.674795
	VVAGVAAALAH*K	100	13	0	12	90	18	0	0	2.840191	0.846296
IPI00126680	**Adult male kidney cDNA, RIKEN full-length enriched library, clone:0610009G07 product:glutathione S-transferase, theta 2, full insert sequence**										
	GQHMSEQFSQVNC*LNK	0	0	6	4	11	16	0	0	3.864564	0.850918
	GQHMSEQFSQVNC*LNKVPVLK	0	0	0	2	3	0	0	0	3.759783	0.557783
IPI00126826	**Histamine N-methyltransferase**										
	DDLC*QYVTSSDLAQILDDLGIK	3	5	3	2	6	4	0	0	4.78263	1.042373
IPI00126940	**Isoform Long of Adenosine kinase**										
	TGC*TFPEKPDFH	4	1	2	0	1	4	0	0	3.25764	1.207429
IPI00127206	**Fructose-bisphosphate aldolase B**										
	IADQC*PSSLAIQENANALAR	0	0	0	0	2	8	0	0	5.598113	0.778763
IPI00127625	**Hydroxymethylglutaryl-CoA lyase, mitochondrial precursor**										
	NANC*SIEESFQR	0	1	0	0	2	3	0	0	3.053194	1.018269
IPI00127707	**Isoform 1 of Poly(rC)-binding protein 2**										
	LVVPASQC*GSLIGK	1	1	0	0	3	3	0	1	2.77172	1.462293
	INISEGNC*PER	0	0	0	0	2	3	0	1	2.628922	1.344156
IPI00127989	**Prostaglandin E synthase 3**										
	HLNEIDLFHC*IDPNDSK	4	2	0	0	4	4	0	0	3.665056	0.948684
IPI00128209	**Adenylate kinase isoenzyme 1**										
	KVNAEGTVDTVFSEVC*TYLDSLK	35	85	0	0	0	3	0	0	4.80389	1.032332
	VNAEGTVDTVFSEVC*TYLDSLK	24	37	0	0	2	3	0	0	4.143552	0.935455
IPI00128267	**PREDICTED: similar to 60S ribosomal protein L32**										
	ELEVLLMC*NK	0	0	0	0	0	0	3	5	2.954017	0.909719

	PEPTIDE	HEART1	HEART2	LIVER1	LIVER2	KIDNEY1	KIDNEY2	LIVER MEM1	LIVER MEM2	XCORR (average)	STD. DEV.
IPI00128376	**Aldo-keto reductase family 1, member C14**										
	SKDIILVSYC*TLGSSR	0	0	6	3	10	19	0	0	4.258152	0.94793
	SPVLLDDPVLC*AMANK	0	0	2	2	6	7	0	4	3.638078	1.001272
IPI00128518	**S-adenosylmethionine synthetase isoform type-1**										
	TGMVLLC*GEITSVAMVDYQR	0	0	8	8	0	0	0	0	4.634206	0.823943
IPI00128760	**Ubiquitin-conjugating enzyme E2 L3**										
	GQVC*LPVISAENWKPATK	7	2	0	3	6	2	0	1	3.815264	0.97781
IPI00128791	**Heat-shock protein beta-6**										
	FGEGLLEAELASLC*PAAIAPYYLR	29	48	0	0	1	1	0	0	4.529149	0.984369
IPI00128873	**Nitrilase 1**										
	THLC*DVEIPGQGPMR	0	0	0	0	2	4	0	0	3.836775	0.636184
IPI00128904	**Poly(rC)-binding protein 1**										
	LVVPATQC*GSLIGK	5	5	2	2	3	7	0	6	2.874496	1.546735
	GYWASLDASTQTTHELTIPNNLIGC*IIGR	1	4	0	0	3	7	1	0	4.689434	0.881532
	INISEGNC*PER	0	0	0	0	2	3	1	1	2.605392	1.523572
IPI00129164	**Sepiapterin reductase**										
	TVVNISSLC*ALQPYK	15	7	5	3	14	15	0	3	3.58894	1.117575
	SDGALVDC*GTSAQK	1	2	0	0	1	2	0	0	3.001188	1.203694
IPI00129517	**Isoform Mitochondrial of Peroxiredoxin-5, mitochondrial precursor**										
	ALNVEPDGTGLTC*SLAPNILSQL	7	6	0	0	6	6	0	0	3.924354	1.028492
	GVLFGVPGAFTPGC*SK	3	5	0	0	5	5	0	0	3.429605	1.027609
	FEALAAHDALVELSGAMNTAAC*SLMK	6	8	0	0	0	1	0	0	5.027172	1.140451
IPI00130000	**Puromycin-sensitive aminopeptidase**										
	LPAEVSPINYSLC*LKPDLLDFTFEGK	2	12	0	0	0	5	0	0	4.023423	0.724985
IPI00130173	**Ubiquitin-like 1-activating enzyme E1B**										
	VLVVGAGGIGC*ELLK	0	1	0	0	3	3	0	0	3.715422	0.742533
IPI00130280	**ATP synthase subunit alpha, mitochondrial precursor**										
	YTIVVSATASDAAPLQYLAPYSGC*SMGEYFR	19	20	0	0	1	6	13	33	4.880809	1.130696
IPI00130344	**Chloride intracellular channel protein 1**										
	LHIVQVVC*K	0	0	0	0	4	3	0	0	2.761175	1.080245
IPI00130521	**Ubiquitin-conjugating enzyme E2 A**										
	MFHPNVYADGSIC*LDILQNR	4	9	0	0	2	0	0	0	4.269494	0.79749
IPI00130530	**Glyoxylate reductase/hydroxypyruvate reductase**										
	VGYTPGVLTDATAELAVSLLLTTC*R	0	0	4	4	6	9	0	0	4.271638	0.787473
IPI00130950	**Betaine--homocysteine S-methyltransferase**										
	QVADEGDALVAGGVSQTPSYLSC*K	0	0	8	7	0	1	7	12	5.208183	1.20432
IPI00131204	**UDP-glucose pyrophosphorylase 2**										
	LNGGLGTSMGC*K	2	1	0	0	1	0	0	3	2.792625	1.383268
IPI00131357	**11 days embryo whole body cDNA, RIKEN full-length enriched library, clone:2700086E01 product:ribosomal protein S23, full insert sequence**										
	ITAFVPNDGC*LNFIEENDEVLVAGFGR	0	9	0	0	2	11	17	23	4.602263	0.979998
IPI00131438	**Phosphoenolpyruvate carboxykinase, cytosolic**										
	YLAAAFPSAC*GK	0	0	1	0	5	5	0	0	3.184567	0.969835
	FCTPASQC*PIIDPAWESPEGVPIEGIIFGGR	0	0	0	0	3	6	0	0	6.192583	1.283874
IPI00131478	**Arylsulfotransferase ST1A4**										
	IPFLEFSC*PGVPPGLETLK	0	0	5	0	0	0	2	7	3.821921	0.872023
IPI00131695	**Serum albumin precursor**										
	AHCLSEVEHD*TMPADLPAIAADFVEDQEVCK	2	8	0	0	0	0	0	0	5.430644	0.980099
	AHCLS*EVEHDTMPADLPAIAADFVEDQEVCK	2	8	0	0	0	0	0	0	5.826906	1.032668
	AHCLSEVEHDT*MPADLPAIAADFVEDQEVCK	2	8	0	0	0	0	0	0	5.1167	0.935152
	AH*CLSEVEHDTMPADLPAIAADFVEDQEVCK	2	8	0	0	0	0	0	0	6.361644	1.674172
IPI00132042	**Pyruvate dehydrogenase E1 component subunit beta, mitochondrial precursor**										
	TNHLVTVEGGWPQFGVGAEIC*AR	25	54	0	0	7	13	7	0	5.602756	1.420883
IPI00132076	**Isoform Membrane-bound of Catechol O-methyltransferase**										
	EYRPSLVLELGAYC*GYSAVR	12	21	6	5	12	26	3	70	4.297608	0.959212
IPI00132080	**6-phosphogluconolactonase**										
	TGALC*WFLDEAAAR	3	3	0	0	2	1	0	0	3.005788	1.299957
IPI00132388	**Basic leucine zipper and W2 domain-containing protein 1**										
	FDPTQFQDC*IIQGLTETGTDLEAVAK	4	5	1	2	7	8	3	29	5.221656	1.238398
IPI00132653	**Succinyl-CoA:3-ketoacid-coenzyme A transferase 1, mitochondrial precursor**										
	DIPNGATLLVGGFGLC*GIPENLIGALLK	13	7	0	0	7	11	0	0	3.859885	0.888851
IPI00132958	**Thioesterase superfamily member 2**										
	LGTLHGGLTATLVDSISTMALMC*TER	41	18	0	0	12	15	0	0	5.281679	1.20063
IPI00133006	**Acyl carrier protein, mitochondrial precursor**										
	LMC*PQEIVDYIADKK	3	8	0	0	0	0	4	3	4.078357	0.798299
IPI00134599	**40S ribosomal protein S3**										
	GLC*AIAQAESLR	4	7	0	0	3	14	6	56	3.622401	1.0307
IPI00134704	**Quinone oxidoreductase**										
	AGESVLVHGASGGVGLATC*QIAR	0	0	0	0	4	10	0	0	4.497155	0.819364
IPI00134746	**Argininosuccinate synthase**										
	FAELVYTGFWHSPEC*EFVR	0	5	10	16	22	40	12	63	4.432198	0.897114
	FELTC*YSLAPQIK	0	6	6	5	14	19	6	46	3.471591	1.184135
	GSVVLAYSGGLDTSC*ILVWLK	0	0	5	14	24	8	0	0	4.197867	0.783556
IPI00134870	**Acyl-coenzyme A oxidase 2, peroxisomal**										
	LSGLPTLVTQAIASC*TYEGENTVLYLQVAR	0	0	0	0	3	7	0	0	4.970295	0.99517
IPI00135284	**PREDICTED: similar to Glyceraldehyde-3-phosphate dehydrogenase**										
	VIHDNFGIVE*GLMTTVHAITATQK	3	0	3	0	4	0	0	0	4.712386	0.955796
IPI00135708	**Dual specificity mitogen-activated protein kinase kinase 2**										
	LC*DFGVSGQLIDSMANSFVGTR	5	0	0	0	6	6	0	0	5.185746	1.301656
IPI00136134	**Isoform 1 of Protein NDRG2**										
	YFLQGMGYMASSC*MTR	6	7	3	6	0	0	0	2	3.952473	0.913526
IPI00137409	**Transketolase**										
	TVPFC*STFAAFFTR	0	1	0	0	4	7	0	0	2.762657	1.169398
IPI00137533	**6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2**										
	VFFVESVC*DDPDVIAANILEVK	4	10	0	0	2	3	0	0	4.767738	1.004408
IPI00137730	**Phosphatidylethanolamine-binding protein 1**										
	YVWLVYEQEQPLSC*DEPILSNK	3	8	0	0	2	5	0	0	4.710623	0.85463
IPI00139780	**60S ribosomal protein L23**										
	ISLGLPVGAVINC*ADNTGAK	0	5	0	0	1	0	8	8	3.742343	0.993258
IPI00153107	**Bleomycin hydrolase**										
	LNSDPQFVLAQNVGTTHDLLDIC*LR	0	3	0	0	2	2	0	0	3.859689	0.864447
IPI00153144	**Adult male liver tumor cDNA, RIKEN full-length enriched library, clone:C730007N17 product:sulfite oxidase, full insert sequence**										
	VDVSVDGGLTWQEAELEGEEQC*PR	0	0	0	0	0	3	7	0	4.57575	0.796629
IPI00153294	**Xylulose kinase**										
	LGSPVPSC*SVVGTISSYYVQR	0	0	0	0	7	13	0	0	4.555923	0.782317
IPI00153317	**10-formyltetrahydrofolate dehydrogenase**										
	AVQMGMSSVFFNKGENC*IAAGR	0	0	12	18	7	7	4	6	4.580519	0.990345
	SPLIIFADC*DLNK	0	0	4	2	0	0	0	0	3.744038	0.697813
IPI00153376	**Homeodomain-only protein**										
	HPDPTTLC*LIAAEAGLTEEQTQK	4	11	0	0	0	0	0	0	5.133991	0.835559
	VNKHPDPTTLC*LIAAEAGLTEEQTQK	9	5	0	0	0	0	0	0	5.505117	1.347146

	PEPTIDE	HEART1	HEART2	LIVER1	LIVER2	KIDNEY1	KIDNEY2	LIVER MEM1	LIVER MEM2	XCORR (average)	STD. DEV.
IPI00154054	**Acetyl-CoA acetyltransferase, mitochondrial precursor**										
	QATLGAGLPISTPC*TTVNK	5	7	0	0	4	7	0	0	3.767204	0.99578
	IHMGNC*AENTAK	2	3	0	0	0	3	0	0	3.102139	1.183412
IPI00169586	**16 days embryo head cDNA, RIKEN full-length enriched library, clone:C130036H15 product:Kidney-specific protein homolog**										
	AIVAGDEVAQEVDAVAPDC*SFLK	0	0	0	0	7	9	0	0	4.732825	0.977003
	EIYGQTETGLIC*R	0	0	0	0	2	2	0	0	2.962225	0.899414
IPI00172221	**Isoform 2 of Dynamin-1-like protein**										
	LHDAIVEVVTC*LLR	13	6	0	0	6	0	0	0	3.540605	1.044291
IPI00187462	**GTPase, IMAP family member 4 isoform a**										
	VFNSGIC*AK	0	0	0	0	3	3	0	0	2.796367	1.057581
IPI00221400	**Alcohol dehydrogenase 1**										
	VTPGSTC*AVFGLGGVGLSVIIGCK	0	0	15	18	7	9	0	3	4.559669	1.017366
	VCLIGC*GFSTGYGSAVK	0	0	4	2	5	7	0	5	3.81482	0.987705
	VIPLFSPQCGEC*R	0	0	1	5	3	7	2	4	3.020914	1.355322
	VIPLFSPQC*GECR	0	0	4	4	1	3	0	6	2.89947	1.512425
	SDDHVVSGTLVTPLPAVLGHEGAGIVESVGEGVT	0	0	2	1	0	12	0	0	6.511586	1.558183
	IDGASPLDKVCLIGC*GFSTGYGSAVK	0	0	2	1	0	6	1	3	4.541233	0.865373
IPI00221402	**Fructose-bisphosphate aldolase A**										
	ALANSLAC*QGK	3	3	0	0	1	2	0	0	2.78515	1.43399
IPI00221501	**Adult male medulla oblongata cDNA, RIKEN full-length enriched library, clone:6330583A05 product:SH3BGRL2-like protein, full insert sequence**										
	VFVASC*SGFVAIK	0	0	0	0	4	7	0	1	2.990693	1.256207
IPI00221613	**ADP-ribosylation factor 1**										
	NWYIQATC*ATSGDGLYEGLDWLSNQLR	0	0	0	0	2	5	0	4	5.853337	1.509722
	AAMLLGSVGDALGYGNIC*R	14	33	0	0	0	0	0	0	4.859521	0.913457
IPI00221769	**GTP:AMP phosphotransferase mitochondrial**										
	TLTQC*SWLLDGFPR	16	12	0	0	14	11	0	3	4.097678	0.981405
IPI00221890	**Carbonic anhydrase 3**										
	EAPFTHFDPSCLFPAC*R	4	10	22	16	13	16	8	24	3.557952	1.154624
	GKEAPFTHFDPSCLFPAC*R	1	0	31	63	6	0	0	0	3.956287	0.760291
IPI00222306	**Adult male testis cDNA, RIKEN full-length enriched library, clone:4933415I16 product:SERINE/THREONINE PROTEIN PHOSPHATASE 2A, 65 kDa REGULATORY SUBUNIT A, BE**										
	LNIISNLDC*VNEVIGIR	0	4	0	0	2	0	0	0	3.72635	0.701669
IPI00222549	**60S ribosomal protein L30**										
	LVILANNC*PALR	0	1	0	0	0	0	6	7	3.11086	0.963672
IPI00223092	**Hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (Trifunctional protein), alpha subunit**										
	ALMGLYNGQVLC*K	4	3	0	0	0	0	0	0	2.8036	1.048122
IPI00224626	**cell division cycle 10 homolog**										
	EGGVQLLLTIVDTPGFGDAVDNSNC*WQPVIDYI	0	2	0	0	0	6	0	0	5.282525	0.795201
IPI00225100	**12 days embryo embryonic body between diaphragm region and neck cDNA, RIKEN full-length enriched library, clone:9430014L03 product:hypothetical protein, full insert sequ**										
	FSQSLVMAAYSC*QLYPENK	0	0	0	0	2	7	0	0	4.0675	0.700303
IPI00225634	**Adult male kidney cDNA, RIKEN full-length enriched library, clone:0610039M20 product:ribosomal protein S12, full insert sequence**										
	QAHLC*VLASNCDEPMYVK	0	0	0	0	0	0	2	12	3.826113	0.613474
IPI00225961	**D-3-phosphoglycerate dehydrogenase**										
	NAGTC*LSPAVIVGLLR	0	0	0	0	4	7	0	0	3.814209	0.647612
IPI00226218	**17 days embryo head cDNA, RIKEN full-length enriched library, clone:3300001H21 product:hypothetical SAM**										
	LTLLEVGC*GTGANFK	0	3	0	0	0	0	5	14	3.486325	0.902896
IPI00226234	**Phospholipase A-2-activating protein**										
	ILSLIC*NNSSEKPTAQQLQILWK	0	1	0	0	2	3	0	0	4.397511	0.657357
IPI00226521	**9130227C08Rik protein**										
	ITWSELSESGLPLC*DVVINLAGENILNPLR	0	2	0	0	1	6	0	0	5.212933	1.012061
IPI00226993	**Thioredoxin**										
	LVVVDFSATWCGPC*K	0	2	0	0	0	4	0	0	2.945775	0.936227
IPI00228106	**Activated spleen cDNA, RIKEN full-length enriched library, clone:F830212I15 product:hypothetical Glycine cleavage T protein (aminomethyl transferase) containing protein, full**										
	TLYDVILYGLPEC*TEGAPSFLLECDSSVLGALQK	0	7	0	0	1	4	0	0	5.257594	1.115826
IPI00228253	**Acetyl-CoA acetyltransferase, cytosolic**										
	VAPEEVSEVIFGHVLTAGC*GQNPTR	0	1	0	0	7	11	0	0	5.329713	0.943674
IPI00228630	**Fructose-1,6-bisphosphatase 1**										
	YVVCFDPLDGSSNIDC*LVSIGTIFGIYR	0	0	10	8	13	23	5	5	4.953994	1.087544
	KAQGTGELTQLLNSLC*TAIK	0	0	0	2	1	7	0	0	4.03134	0.699046
IPI00228828	**18-day embryo whole body cDNA, RIKEN full-length enriched library, clone:1110048P09 product:guanylate kinase 1, full insert sequence**										
	KTDLC*PIYIFVQPPSLDVLEQR	4	8	0	0	2	0	0	0	4.116138	0.71332
IPI00228883	**PDZ domain-containing protein 1**										
	FSPLLYC*QSQELPNGSVK	0	0	0	0	2	7	0	0	3.781218	0.909895
IPI00229080	**17 days embryo kidney cDNA, RIKEN full-length enriched library, clone:I920059K05 product:heat shock protein 1, beta, full insert sequence**										
	VFIMDSC*DELIPEYLNFIR	5	11	0	1	2	12	0	3	4.108704	0.892693
	GFEVVYMTEPIDEYC*VQQLK	2	3	0	0	2	3	0	0	3.876642	1.039917
IPI00229510	**L-lactate dehydrogenase B chain**										
	ITVVGVGQVGMAC*AISILGK	17	22	0	0	4	2	0	0	3.652919	0.995354
	GMYGIENEVFLSLPC*ILNAR	18	8	0	0	3	7	0	0	4.454749	0.86976
	YSPDC*TIIVVSNPVDILTYVTWK	19	8	0	0	2	3	0	0	5.202877	1.208543
	VIGSGC*NLDSAR	4	3	0	0	4	4	0	0	2.767523	1.429595
IPI00229517	**Galectin-1**										
	FNAHGDANTIVC*NTK	3	2	0	0	0	0	0	0	3.5584	0.873521
IPI00229859	**Eif3s9 protein**										
	FSHQGVQLIDFSPC*ER	0	5	0	0	3	7	8	7	4.07262	0.861084
IPI00230139	**FK506-binding protein 4**										
	ELCFEVGEGESLDLPC*GLEEAIQR	2	6	0	0	1	4	0	0	4.689315	0.887435
IPI00230760	**Myoglobin**										
	HGC*TVLTALGTILK	162	137	0	0	16	46	0	0	3.467396	1.130874
	GLSD*GEWQLVLNVWGK	3	6	0	0	0	0	0	0	3.660475	0.551236
	VEAD*LAGHGQEVLIGLFK	6	13	0	0	0	0	0	0	3.702267	0.611366
	GLSDGE*WQLVLNVWGK	2	3	0	0	0	0	0	0	3.554592	0.283625
	GLS*DGEWQLVLNVWGK	3	4	0	0	0	0	0	0	3.721029	0.493553
	HS*GDFGADAQGAMSK	5	12	0	0	0	0	0	0	3.340224	0.646326
	HGCT*VLTALGTILK	17	15	0	0	0	0	0	0	3.090091	0.723981
	VEADLAGH*GQEVLIGLFK	7	14	0	0	0	0	0	0	3.870418	0.586428
	H*GCTVLTALGTILK	24	17	0	0	0	0	0	0	3.058635	0.680193
	H*SGDFGADAQGAMSK	5	13	0	0	0	0	0	0	3.691167	0.629236

	PEPTIDE	HEART1	HEART2	LIVER1	LIVER2	KIDNEY1	KIDNEY2	LIVER MEM1	LIVER MEM2	XCORR (average)	STD. DEV.
IPI00261627	**Succinyl-CoA ligase [ADP-forming] beta-chain, mitochondrial precursor**										
	ILAC*DDLDEAAK	2	7	0	0	1	2	0	0	2.981034	1.381119
	ICNQVLVC*ER	5	4	0	0	0	2	0	0	3.028048	1.139357
IPI00265025	**galactokinase 1**										
	AEHSFAGVPC*GIMDQLIALLGQK	3	0	0	0	7	8	0	0	4.266074	0.79312
IPI00269076	**Adenylate kinase isoenzyme 2, mitochondrial**										
	GIHC*AIDASQTPDIVFASILAAFSK	4	0	0	0	6	2	5	0	4.88273	0.96959
IPI00269481	**Capping protein**										
	NLSDLIDLVPSLC*EDLLSSVDQPLK	0	1	0	0	3	12	3	6	4.264932	0.807544
IPI00273646	**Glyceraldehyde-3-phosphate dehydrogenase**										
	VPTPNVSVVDLTC*R	32	45	5	4	22	31	0	11	3.932861	0.981726
	IVSNASC*TTNCLAPLAK	6	7	3	3	5	6	0	4	4.079355	0.912938
	IVSNASCTTNC*LAPLAK	10	9	1	1	3	6	0	1	3.195608	1.349841
IPI00274407	**Isoform 1 of Elongation factor Tu, mitochondrial precursor**										
	ELLTEFGYKGEETPVIVGSALC*ALEQR	9	9	0	0	6	10	0	0	4.68751	0.933965
	NMITGTAPLDGC*ILVVAANDGPMPQTR	3	7	0	0	1	0	0	0	4.401365	0.72488
	GEETPVIVGSALC*ALEQR	2	2	0	0	3	0	0	0	4.094789	0.78675
IPI00283531	**Glutathione S-transferase P 2**										
	EEVVTIDTWMQGLLKPTC*LYGQLPK	17	21	11	7	13	16	6	18	4.659184	0.988177
IPI00307837	**Elongation factor 1-alpha 1**										
	NMITGTSQADC*AVLIVAAGVGEFEAGISK	10	7	6	7	14	13	0	3	4.210954	0.925515
	DGSASGTTLLEALDC*ILPPTRPTDKPLR	2	11	1	0	12	13	10	0	4.2036	0.862557
	SGDAAIVDMVPGKPMC*VESFSDYPPLGR	4	6	5	3	5	12	1	6	4.079165	0.924853
IPI00308328	**Cytochrome P450 2F2**										
	DFIDC*FLTK	0	0	0	0	0	0	3	2	2.736258	0.970341
IPI00308885	**60 kDa heat shock protein, mitochondrial precursor**										
	AAVEEGIVLGGGC*ALLR	31	33	5	5	20	32	3	11	4.155146	0.952683
IPI00308938	**Calpain-2 catalytic subunit precursor**										
	RPTEIC*ADPQFIIGGATR	0	2	0	0	0	4	0	0	4.124863	0.911075
IPI00310669	**Dihydroxyacetone kinase**										
	MVNSVEGC*ADDALAGLVASNPDLQLLQGHR	0	0	3	2	1	3	0	0	6.096788	1.430143
IPI00312058	**Catalase**										
	LGPNYLQIPVNC*PYR	0	7	0	0	4	6	11	20	3.765154	0.936415
IPI00313236	**Bile acyl-CoA synthetase**										
	VALVC*TGSEGSSITNSQLDAR	0	0	0	0	0	0	2	7	5.184643	1.143658
IPI00313296	**Ribonuclease inhibitor**										
	ELDLSNNC*MGGPGVLQLLESLK	0	2	0	0	1	2	0	0	4.7711	0.713982
IPI00314189	**3 beta-hydroxysteroid dehydrogenase type 5**										
	LPFIYGEEC*QVTSTTVK	0	0	0	0	0	0	2	15	3.813883	0.867682
IPI00314510	**Aspartoacylase-2**										
	NGIC*LEMGPQPQGVLR	0	0	0	0	4	12	0	0	4.267842	0.606117
IPI00314950	**60S acidic ribosomal protein P0**										
	AGAIAPC*EVTVPAQNTGLGPEK	0	0	0	0	0	0	4	8	4.616881	0.767345
IPI00315488	**Arginyl-tRNA synthetase, cytoplasmic**										
	LQEVFGC*AIR	1	2	0	0	0	5	0	4	2.966269	1.26013
IPI00315550	**Thioredoxin-like protein 2**										
	ELEASEELDTIC*PK	0	2	0	0	0	2	0	0	2.8534	0.804387
IPI00317902	**proteasome (prosome, macropain) subunit, beta type 5**										
	VIEINPYLLGTMAGGAADC*SFWER	3	3	0	0	1	0	0	0	4.367244	0.880207
IPI00318545	**3'(2'),5'-bisphosphate nucleotidase 1**										
	SHSNQLVTDC*ISAMNPDTVLR	0	0	0	0	4	7	0	0	4.375709	0.806476
	LVQMSIC*SSLAR	0	0	0	0	3	6	0	0	2.749042	0.975066
IPI00318614	**Isoform 2 of Isocitrate dehydrogenase [NADP], mitochondrial precursor**										
	NYDGDVQSDILAQGFGSLGLMTSVLVC*PDGK	26	33	0	0	4	12	0	0	5.981039	1.603922
	NILGGTVFREPIIC*K	16	18	0	0	4	7	0	0	3.737878	1.064613
	DLAGC*IHGLSNVK	5	2	0	0	1	0	0	0	2.66559	1.347613
IPI00318841	**Elongation factor 1-gamma**										
	VPAFEGDDGFC*VFESNAIAYYVSNEELR	0	18	0	0	5	14	9	0	5.104426	1.083674
IPI00319652	**Glutathione peroxidase 1**										
	YIIWSPVC*R	0	0	0	0	3	7	0	0	2.758298	1.028405
IPI00319973	**Membrane-associated progesterone receptor component 1**										
	GLATFC*LDKEALKDEYDDLSDLTPAQQETLSDW	0	0	0	0	0	0	4	0	4.3518	0.385024
IPI00319994	**L-lactate dehydrogenase A chain**										
	ITVVGVGAVGMAC*AISILMK	10	2	16	19	10	4	0	0	3.800218	1.053955
	VIGSGC*NLDSAR	4	3	1	1	4	4	0	1	2.720413	1.659779
	IVSSKDYC*VTANSK	3	2	0	0	0	2	0	0	3.432456	0.975638
IPI00320217	**T-complex protein 1 subunit beta**										
	SLHDALC*VLAQTVK	4	3	0	0	0	2	0	0	3.148511	1.224444
IPI00320850	**Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial precursor**										
	SSAAQAIHPGYGFLSENMEFAELC*K	4	6	0	0	2	5	0	0	4.183145	0.818293
IPI00321308	**Alanyl-tRNA synthetase, cytoplasmic**										
	NVGC*LQEALQLATSFAQLR	3	1	0	0	3	0	0	0	4.858378	0.942281
IPI00321978	**Ran-specific GTPase-activating protein (Fragment)**										
	AWVWNTHADFADEC*PKPELLAIR	5	7	0	0	1	4	0	0	4.678419	0.893248
IPI00322931	**Adult male tongue cDNA, RIKEN full-length enriched library, clone:2310022K03 product:peroxisomal delta3, delta2-enoyl-Coenzyme A isomerase, full insert sequence**										
	ATFHTPFSQLGQSPEAC*SSYTFPK	9	10	0	0	4	9	2	6	4.495434	0.929837
IPI00323592	**Malate dehydrogenase, mitochondrial precursor**										
	GC*DVVVIPAGVPR	2	6	0	0	0	0	0	0	3.249142	0.875282
	GYLGPEQLPDC*LK	3	3	0	0	0	1	0	0	3.000589	1.241485
	ETEC*TYFSTPLLLGK	2	2	0	0	0	0	0	0	2.79655	1.085484
IPI00323816	**Selenium-binding protein 2**										
	GGSVQVLEDQELTC*QPEPLVVK	0	5	0	0	7	28	0	0	4.134383	0.734319
	FLHDPSATQGFVGC*ALSSNIQR	0	1	0	0	2	7	0	0	4.218507	0.662488
IPI00323881	**Importin beta-1 subunit**										
	IQFNDLQSLLC*ATLQNVLR	0	0	0	1	4	7	0	0	3.979769	0.677108
IPI00330754	**D-beta-hydroxybutyrate dehydrogenase, mitochondrial precursor**										
	METYC*NSGSTDTSSVINAVTHALTAATPYTR	0	0	0	0	0	0	4	24	5.27419	1.297388
	TIQLNVC*NSEEVEK	0	0	0	0	0	0	2	2	3.2667	0.792733
IPI00330804	**Heat shock protein HSP 90-alpha**										
	VFIMDNC*EELIPEYLNFIR	1	0	0	0	2	2	0	0	3.876267	0.7105
IPI00331066	**Calbindin**										
	AFELYDQDGNGYIDENELDALLKDLC*EK	0	0	0	0	2	3	0	0	5.292667	1.039512
IPI00331094	**Aspartoacylase**										
	VIPLGGDC*TVYPVFVNEAAYYEK	0	0	0	0	3	6	0	0	4.090667	0.655565
IPI00331322	**Microsomal glutathione S-transferase 1**										
	VFANPEDC*AGFGK	1	3	0	0	0	5	12	30	3.093055	1.245377
	VFANPEDC*AGFGKGENAK	0	2	0	0	0	0	9	7	3.748428	0.82794
	ITNKVFANPEDC*AGFGK	0	0	0	0	0	0	10	7	4.04792	0.641619
IPI00331436	**Lap3 protein**										
	LNLPINIIGLAPLC*ENMPSGK	0	5	0	0	4	8	5	5	4.210748	0.845621
	SAGAC*TAAAFLR	2	0	0	0	3	3	0	0	2.825606	1.273069
IPI00331490	**Aflatoxin B1 aldehyde reductase member 2**										
	GHSELDTAFMYC*DGQSENILGGLGLGLGSGDC	0	6	0	0	1	15	0	0	6.236631	1.699934
IPI00331541	**6-phosphofructokinase, muscle type**										
	LPLMEC*VQVTK	10	6	0	0	0	2	0	0	2.971776	1.238983
	SSYLNIVGLVGSIDNDFC*GTDMTIGTDSALHR	2	3	0	0	0	0	0	0	4.792875	0.717206

	PEPTIDE	HEART1	HEART2	LIVER1	LIVER2	KIDNEY1	KIDNEY2	LIVER MEM1	LIVER MEM2	XCORR (average)	STD. DEV.
IPI00337893	**Pyruvate dehydrogenase E1 component alpha subunit, somatic form, mitochondrial precursor**										
	NFYGGNGIVGAQVPLGAGIALAC*K	31	35	0	0	6	12	5	9	4.52102	0.958247
	LPCIFIC*ENNR	20	9	0	0	4	5	0	0	3.215484	1.227028
IPI00338561	**Nucleotide exchange factor SIL1 precursor**										
	D*RYRQDLQLSR	1	1	1	0	0	0	3	2	2.729083	1.118925
IPI00350458	**Isoform 1 of UNC45 homolog B**										
	AGVISALAC*MVK	2	2	0	0	0	0	0	0	2.7364	0.932122
IPI00352124	**Flavin containing monooxygenase 5**										
	LLLGPC*TPVQYR	0	1	0	0	0	1	6	8	2.614853	1.480184
	IAVIGAGASGLTC*IK	0	0	0	0	0	0	5	7	3.973296	0.732972
IPI00355265	**PREDICTED: similar to High mobility group protein 1**										
	MSSYAFFVQTC*R	1	0	0	0	3	2	0	0	2.724189	1.198703
IPI00377396	**41 kDa protein**										
	VEAILVNIFGGIVNC*AIIANGITK	4	3	2	3	26	26	0	0	4.652554	0.958456
	IDATQVEVNPFGETPEGQVVC*FDAK	0	3	1	0	3	13	2	0	5.598681	1.438901
IPI00380320	**Lactate dehydrogenase D**										
	LHPAPEATVAATC*AFPSVQAAVDSTVQILQAAVP	0	0	0	0	7	4	0	0	6.852189	1.8107
	DSGLWFPVDPGADASLC*GMAATGASGTNAVR	0	0	0	0	3	4	0	0	4.0419	0.620445
	IEFLDDVMMDAC*NR	0	0	0	0	2	3	0	0	3.9078	0.727091
IPI00403579	**hypothetical protein LOC232078**										
	MGLPIC*LVVAVNR	0	0	0	0	11	3	0	0	3.080794	1.069587
	GDFSLC*EVLR	0	0	0	0	2	3	0	0	2.5919	1.056849
IPI00403810	**Tubulin alpha-6 chain**										
	AVC*MLSNTTAIAEAWAR	0	0	0	0	20	14	0	0	4.367829	0.83905
	AYHEQLTVAEITNAC*FEPANQMVK	0	0	0	0	3	12	0	0	5.159413	0.890058
	LADQC*TGLQGFLVFHSFGGGTGSGFTSLLMER	0	0	0	0	6	6	0	0	5.225492	0.933444
	TIQFVDWC*PTGFK	0	0	0	0	3	8	0	0	3.381308	0.751202
IPI00406419	**Xaa-Pro dipeptidase**										
	IEEDVVVTDSGMELLTC*VPR	0	0	0	0	2	5	0	0	3.883805	0.534416
IPI00406442	**Succinyl-CoA ligase [GDP-forming] subunit alpha, mitochondrial precursor**										
	LIGPNC*PGVINPGECK	3	6	0	0	2	5	0	0	3.326828	1.062384
	LIGPNCPGVINPGEC*K	3	1	0	0	0	4	0	0	3.358886	1.104901
IPI00408378	**Isoform 1 of 14-3-3 protein theta**										
	DNLTLWTSDSAGEEC*DAAEGAEN	0	2	0	0	5	16	0	0	4.2548	0.670962
	YLAEVAC*GDDR	0	2	0	0	2	3	0	0	3.012744	1.134079
IPI00408961	**3-hydroxyanthranilate 3,4-dioxygenase**										
	VTMGGQC*IALAPDDSLLVPAGTSYVWER	0	0	0	0	2	5	0	0	4.878725	1.118091
IPI00409345	**Lambda-crystallin homolog**										
	VILSSSSSC*LLPSK	3	0	0	0	12	12	0	0	3.030617	1.0711
IPI00416303	**Probable aminopeptidase NPEPL1**										
	IVDTPC*NEMNTDIFLEEIIQVGK	0	3	1	0	2	8	0	0	4.530199	1.086409
IPI00420706	**Leucine-rich PPR-motif containing**										
	VFESTC*SSGSPGSNQALLLLR	4	8	0	0	0	6	1	0	4.112996	0.994706
IPI00420718	**Hydroxymethylglutaryl-CoA synthase, mitochondrial precursor**										
	QAGNNQPFTLDDVQYMIFHTPFC*K	0	0	6	7	0	0	0	7	4.040741	0.781135
	MGFCSVQEDINSLC*LTVVQR	0	0	3	2	0	0	0	0	4.696525	1.008244
IPI00420882	**2-oxoglutarate dehydrogenase E1 component, mitochondrial precursor**										
	FGLEGC*EVLIPALK	2	2	0	0	0	0	0	0	3.904675	0.691661
IPI00421223	**Tropomyosin alpha-4 chain**										
	EENVGLHQTLDQTLNELNC*I	0	0	0	0	2	4	0	0	4.323238	0.568567
IPI00454008	**Serine hydroxymethyl transferase 2**										
	GLELIASENFC*SR	0	0	0	0	2	2	0	0	2.9679	1.302816
IPI00454049	**Enoyl-CoA hydratase, mitochondrial precursor**										
	ALNALC*NGLIEELNQALETFEQDPAVGAIVLTGG	38	61	38	15	21	71	15	44	6.033112	1.769244
IPI00458204	**48 kDa protein**										
	LTTPTYGDLNHLVSATMSGVTTC*LR	0	10	0	0	0	15	0	0	4.586763	0.780787
	VSDTVVEPYNATLSVHQLVENTDETYC*IDDEALY	0	2	0	0	0	7	0	0	5.323439	1.164591
	VSDTVVEPYNATLSVHQLVENTDETYCIDDEALY	0	4	0	0	0	4	0	0	5.063538	0.783842
IPI00459725	**Isoform 1 of Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial precursor**										
	TFDLYANVRPC*VSIEGYK	7	13	0	0	0	3	0	0	3.722203	0.873393
	KTFDLYANVRPC*VSIEGYK	5	11	0	0	0	0	0	0	3.899065	0.723312
IPI00461964	**NOD-derived CD11c +ve dendritic cells cDNA, RIKEN full-length enriched library, clone:F630044D15 product:aldehyde dehydrogenase family 6, subfamily A1, full insert sequenc**										
	GYENGNFVGPTIISNVKPSMTC*YK	10	13	1	0	10	20	0	5	4.178024	0.961432
IPI00466069	**Elongation factor 2**										
	VTDGALVVVDCVSGVC*VQTETVLR	26	23	29	20	29	25	2	1	4.696303	1.022286
IPI00467066	**Glycine N-methyltransferase**										
	LSYYPHC*LASFTELVR	0	0	7	7	0	0	4	11	3.863533	0.89392
IPI00467833	**Triosephosphate isomerase**										
	VSHALAEGLGVIAC*IGEK	4	5	0	0	7	8	0	0	4.1506	0.828419
	CLGELIC*TLNAANVPAGTEVVCAPPTAYIDFAR	1	12	0	1	1	6	0	0	5.376593	1.160109
	IIYGGSVTGATC*K	2	1	0	0	2	3	0	0	3.057592	1.261468
IPI00468162	**17 days embryo heart cDNA, RIKEN full-length enriched library, clone:I920020H01 product:protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting prote**										
	K*DLRGQLKMVDSFHRNSFQCGIMCLR	0	0	10	4	0	0	0	0	3.64681	0.391354
	KD*LRGQLKMVDSFHRNSFQCGIMCLR	0	0	12	4	0	0	0	0	3.642608	0.511641
IPI00554933	**Glutathione S-transferase theta-1**										
	VLELYLDLLSQPC*R	0	0	0	2	5	3	0	0	3.559167	0.953856
	VKDC*PPADLIIK	0	0	0	0	2	4	0	0	2.7983	0.977415
IPI00622235	**Transitional endoplasmic reticulum ATPase**										
	GVLFYGPPGC*GK	7	7	0	0	5	6	1	7	2.985151	1.447249
IPI00653158	**14 days embryo liver cDNA, RIKEN full-length enriched library, clone:I530029G20 product:acetyl-Coenzyme A acyltransferase 2**										
	YAVGSAC*IGGGQGIALIIQNTA	24	51	1	4	3	6	0	0	4.052817	0.944295
	VVGYFVSGC*DPTIMGIGPVPAINGALKK	27	29	4	7	7	3	0	0	5.105371	1.322215
	VVGYFVSGC*DPTIMGIGPVPAINGALK	16	27	1	0	5	5	0	0	4.992312	1.268678
	LCGSGFQSIVSGCQEIC*SK	3	9	0	0	0	0	0	0	4.079294	0.620083
IPI00653247	**13 days embryo liver cDNA, RIKEN full-length enriched library, clone:I920064F20 product:tubulin, beta 2, full insert sequence**										
	GSESCD*CLQGFQLTHSLGGGTGSGMGTLLISK	0	2	0	0	0	3	0	0	4.1099	0.596694
	GSE*SCDCLQGFQLTHSLGGGTGSGMGTLLISK	0	2	0	0	0	4	0	0	4.016838	0.577036
IPI00658877	**PREDICTED: similar to F11C1.5a**										
	LGHILVVDEADKAPTNVTC*ILK	7	5	0	0	1	4	0	0	4.869755	1.082044
IPI00663327	**Beta-1-globin (Fragment)**										
	YFDSFGDLSSASAIMGNAK*VK	0	2	0	0	0	2	0	0	3.8373	0.582371
	VH*LTDAEKAAVSGLWGK	4	8	0	0	2	3	0	0	3.620659	0.875939
	GTFASLSELH*CDK	2	4	0	0	0	0	0	0	2.785	0.674795
IPI00750197	**PREDICTED: similar to 14-3-3 protein theta**										
	DNLTLWTSDSAEECD*AAEGAEN	0	1	0	0	5	11	0	0	3.829752	0.586134
IPI00754489	**Bifunctional 3'-phosphoadenosine 5'-phosphosulfate synthetase 2**										
	IHESAGLPFFEIFVDAPLNIC*ESR	0	0	0	0	4	2	0	0	6.024	1.300259

Supplementary Information Table 5: All labeled peptides with total spectral count values across all sampled tissue proteomes for the SE, CA and MA probes.

IPI number	Description	Peptide	SE	CA	UK
IPI00108042	**Carbohydrate kinase-like protein**	AFPFPVC*FGQDVDAAFGAALVMLQR	-	-	27
IPI00108125	**Eukaryotic translation initiation factor 5A-1**	EIEQKYDC*GEEILITVLSAMTEEAAVAIK	-	-	6
		YDC*GEEILITVLSAMTEEAAVAIK	-	-	91
IPI00108454	**PREDICTED: similar to 40S ribosomal protein S6**	LNISFPATGC*QK	-	-	9
IPI00108895	**26S protease regulatory subunit 6B**	GVLMYGPPGC*GK	-	-	10
IPI00108939	**glyceraldehyde-3-phosphate dehydrogenase, sperma**	GKLTGMAFRVPTPNVSVVDLTC*R	-	8	-
		VPTPNVSVVDLT*CR	-	-	9
		VPTPNVSVVDLTC*R	-	59	-
IPI00109061	**ES cells cDNA, RIKEN full-length enriched library, cl**	LTTPTYGDLNHLVSATMSGVTTC*LR	-	16	31
IPI00109142	**S-formylglutathione hydrolase**	CPALYWLSGLTC*TEQNFISK	-	-	82
		SVSAFAPICNPVLC*SWGK	-	-	9
IPI00109169	**Isocitrate dehydrogenase [NAD] subunit gamma, mit**	HAC*VPVDFEEVHVSSNADEEDIR	-	-	22
		TSLDLYANVIHC*K	-	-	7
IPI00109501	**Ribosome recycling factor, mitochondrial precursor**	SPQVILVNMASFPEC*TAAAIK	-	-	9
IPI00109536	**Aldo-keto reductase family 1, member C21**	CHCVILNDGNFIPVLGFGTALPLEC*PK	-	-	32
		VDLC*ATWEAMEK	-	-	8
IPI00109655	**Methionine sulfoxide reductase B2**	RLDTSLGC*PR	-	-	14
IPI00110042	**Selenium-binding protein 1**	C*GPGYSTPLEAMK	-	5	-
		GGSVQVLEDQELTC*QPEPLVVK	-	10	28
IPI00110528	**Probable isomerase MAWBP-1**	WFTPEAEFPLC*GHATLASAAVLFQK	-	-	8
IPI00110658	**13 days embryo liver cDNA, RIKEN full-length enrich**	IGGH*GAEYGAEALER	74	-	57
		IGGHGAE*YGAEALER	51	-	-
		IGGHGAEY*GAEALER	109	-	-
		IGGHGAEYGAE*ALER	108	-	-
		IGGHGAEYGAEALE*R	10	-	-
		TYFPHFDVS*HGSAQVK	-	-	7
		TYFPHFDVSH*GSAQVK	-	-	7
IPI00110753	**Tubulin alpha-1 chain**	AVC*MLSNTTAIAEAWAR	-	6	85
		AYHEQLSVAEITNAC*FEPANQMVK	-	-	74
		LADQC*TGLQGFLVFHSFGGGTGSGFTSLL	-	-	19
		TIQFVDWC*PTGFK	-	18	23
IPI00110850	**Actin, cytoplasmic 1**	VAPEEH*PVLLTEAPLNPK	5	-	-
IPI00110866	**Cytidine deaminase**	IFSGCNIENAC*YPLGVCAER	-	-	6
IPI00111004	**Uncharacterized protein C7orf24 homolog**	NPSAVFC*CVAR	-	-	12
IPI00111181	**Vacuolar protein sorting-associated protein 35**	IANQC*MDPSLQVQLFIEILNR	-	-	8
IPI00111218	**Aldehyde dehydrogenase, mitochondrial precursor**	ELGEYGLQAYTE*VK	9	-	-
IPI00111315	**Apolipoprotein A-II precursor**	T*HEQLTPLVR	-	-	6
		TH*EQLTPLVR	-	-	6
IPI00111412	**60S ribosomal protein L4**	SGQGAFGNMC*R	-	-	12
IPI00111885	**Ubiquinol-cytochrome-c reductase complex core pro**	YFYDQC*PAVAGYGPIEQLPDYNR	-	-	7
IPI00111908	**Carbamoyl-phosphate synthase [ammonia], mitocho**	QADAVYFLPITPQFVT*EVIK	13	-	-
		QADAVYFLPITPQFVTE*VIK	15	-	-
		S*VGEVMAIGR	6	-	-
		SVGE*VMAIGR	11	-	-
		TAHIVLE*DGTK	9	-	-
		TAHIVLED*GTK	9	-	-
		TSAC*FEPSLDYMVTK	-	5	5
		VVAVDC*GIK	-	23	-
IPI00111981	**Isoform 1 of Putative GTP-binding protein 9**	STFFNVLTNSQASAENFPFC*TIDPNESR	-	-	14
IPI00112190	**RIKEN cDNA 1810022C23 gene**	ATFHTPFSQLSQIPEAC*STYMFPK	-	-	13
IPI00112366	**PREDICTED: similar to isochorismatase domain con**	IIKEPVPDSGLLSLFQGQSPLTSC*	-	-	24
IPI00113223	**Fatty acid synthase**	GPSIALDTAC*SSSLLALQNAYQAIR	-	75	28
IPI00113347	**Carnitine O-acetyltransferase**	SMIDNETLPVEFLGGQPLC*MNQYYQILSSC	-	-	15
IPI00113377	**60S acidic ribosomal protein P1**	ALANVNIGSLIC*NVGAGGPAPAAGAAPAG	-	-	50
IPI00114330	**Homogentisate 1,2-dioxygenase**	TCSC*LDENYYK	-	-	10
IPI00114396	**Isoform Long of Galectin-9**	GMPFELC*FLVQR	-	-	12
IPI00114416	**3,2-trans-enoyl-CoA isomerase, mitochondrial precu**	GVILT*SECPGIFSAGLDLLEMYGR	-	-	5
		GVILTS*ECPGIFSAGLDLLEMYGR	-	-	5
		GVILTSE*CPGIFSAGLDLLEMYGR	-	-	5
		GVILTSEC*PGIFSAGLDLLEMYGR	-	-	123
		LRNPPVNSLSLEC*LTEFTISLEK	-	-	25

IPI00114472	**PREDICTED: similar to ribosomal protein L27a**	NQSFC*PTVNLDKLWTLVSEQTR	-	-	58
IPI00114710	**Activated spleen cDNA, RIKEN full-length enriched li**	FLYEC*PWR	-	38	-
IPI00115302	**Branched chain ketoacid dehydrogenase E1, beta pc**	SGDLFNC*GSLTIR	-	-	7
IPI00115569	**Dihydrolipoyl dehydrogenase, mitochondrial precurs**	AEVITCDVLLVC*IGR	-	-	10
		NETLGGTC*LNVGCIPSK	-	-	14
		VLGAHILGPGAGEMVNEAALALEYGASC*ED	-	-	42
IPI00115598	**Isoform Short of Estradiol 17-beta-dehydrogenase 8**	LLEEVQAC*FSRPPSVVVSCAGITR	-	-	9
IPI00115599	**Corticosteroid 11-beta-dehydrogenase isozyme 1**	MTQPMIAPY*SASK	4	-	-
IPI00115751	**9.5 days embryo parthenogenote cDNA, RIKEN full-le**	FMTPVIQDNPSGWGPC*AVPEQFR	-	-	23
IPI00115827	**Protein NipSnap2**	QYPC*TLVGTWNTWYGEQDQAVHLWR	-	-	16
IPI00116074	**Aconitate hydratase, mitochondrial precursor**	DVGGIVLANAC*GPCIGQWDRK	-	-	16
		DVGGIVLANACGPC*IGQWDR	-	-	31
		DVGGIVLANACGPC*IGQWDRK	-	-	39
		VGLIGSC*TNSSYEDMGR	-	8	-
IPI00116170	**NADH-ubiquinone oxidoreductase chain 3**	ANPYEC*GFDPTSSAR	-	-	6
IPI00116192	**Thioredoxin-dependent peroxide reductase, mitocho**	AFQFVETHGEVC*PANWTPESPTIKPSPTAS	-	-	14
IPI00116222	**3-hydroxyisobutyrate dehydrogenase, mitochondrial**	HGYPLILYDVFPDVC*K	-	-	18
IPI00116277	**T-complex protein 1 subunit delta**	AQDIEAGDGTTSVVIIAGSLLDSC*TK	-	-	12
		IGLIQFC*LSAPK	-	-	28
		SIHDALC*VIR	-	-	19
IPI00116489	**Atrial natriuretic factor precursor**	IGAQSGLGC*NSFR	-	-	6
IPI00116591	**Short-chain specific acyl-CoA dehydrogenase, mitoc**	IGIASQALGIAQASLDC*AVK	-	7	158
IPI00116613	**CCAAT/enhancer-binding protein beta**	AAPAAC*FAGPPAAPAK	-	-	6
IPI00116705	**Fatty acid-binding protein, adipocyte**	LVSSENFD*DYMK	6	-	-
IPI00116753	**Electron transfer flavoprotein subunit alpha, mitoch**	TIYAGNALC*TVK	-	-	12
IPI00117007	**MKIAA0120 protein (Fragment)**	QYDADLEQILIQWITTQC*R	-	-	6
IPI00117264	**Protein DJ-1**	VTVAGLAGKDPVQC*SR	-	-	14
IPI00117281	**Isoform Mitochondrial of Phospholipid hydroperoxid**	ILAFPC*NQFGR	-	-	5
IPI00117312	**Aspartate aminotransferase, mitochondrial precurso**	HFIEQGINVCLC*QSYAK	-	-	19
IPI00117312	**Aspartate aminotransferase, mitochondrial precurso**	NLDKEYLPIGGLAEFC*K	-	-	51
IPI00117348	**Tubulin alpha-2 chain**	AVC*MLSNTTAIAEAWAR	-	6	60
		AYHEQLSVAEITNAC*FEPANQMVK	-	-	43
		LADQC*TGLQGFLVFHSFGGGTGSGFTSLL	-	-	19
		SIQFVDWC*PTGFK	-	29	27
IPI00117350	**Tubulin alpha-4 chain**	AVC*MLSNTTAIAEAWAR	-	-	81
		AYHEQLSVAEITNAC*FEPANQMVK	-	-	74
		LSDQC*TGLQGFLVFHSFGGGTGSGFTSLL	-	-	16
		SIQFVDWC*PTGFK	-	-	34
		TIGGGDDSFTTFFC*ETGAGK	-	-	10
IPI00117569	**40S ribosomal protein S11**	DVQIGDIVTVGEC*RPLSK	-	-	12
IPI00117570	**Growth-arrest-specific protein 2**	LDNGALLC*QLAATVQEK	-	-	5
IPI00118059	**Serine hydroxymethyltransferase, cytosolic**	LIIAGTSC*YSR	-	-	5
IPI00118153	**Cysteine and glycine-rich protein 3**	GIGFGQGAGC*LSTDTGEHLGLQFQQSPK	-	5	23
		GIGFGQGAGC*LSTDTGEHLGLQFQQSPKP	-	-	18
		TCFHCMAC*R	-	-	5
IPI00118344	**UDP-glucose 6-dehydrogenase**	ASVGFGGSC*FQK	-	18	-
		ISSINSISALC*EATGADVEEVATAIGMDQR	-	-	7
IPI00118676	**Eukaryotic initiation factor 4A-I**	VVMALGDYMGASCHAC*IGGTNVR	-	-	5
IPI00118849	**Dual specificity tyrosine-phosphorylation-regulated**	KVYNDGYDDDNY*DYIVK	24	-	-
IPI00118986	**ATP synthase O subunit, mitochondrial precursor**	GEVPC*TVTTASPLDDAVLSELK	-	-	14
IPI00119004	**hypothetical protein LOC67732**	VILITPPPLC*EAAWEK	-	-	21
IPI00119087	**Uroporphyrinogen-III synthase**	GLPVSC*TAESPTPQALAAGIR	-	-	13
IPI00119112	**Vacuolar ATP synthase catalytic subunit A, ubiquitou**	VLDALFPCVQGGTTAIPGAFGC*GK	-	-	28
		YSNSDVIIYVGC*GER	-	71	-
IPI00119113	**Bone marrow macrophage cDNA, RIKEN full-length e**	GPVVLAEDFLDIMGQPINPQC*R	-	-	12
IPI00119114	**Long-chain specific acyl-CoA dehydrogenase, mitoc**	GFYYLMQELPQE*R	26	-	-
IPI00119219	**Isoform 1 of Estradiol 17-beta-dehydrogenase 12**	AFQVWC*VGNEALVGPR	-	-	20
IPI00119622	**Cysteine sulfinic acid decarboxylase**	FYDVALDTGDKVVQC*GR	-	7	-
IPI00119667	**Elongation factor 1-alpha 2**	NMITGTSQADC*AVLIVAAGVGEFEAGISK	-	-	17
		SGDAAIVEMVPGKPMC*VESFSQYPPLGR	-	-	23
IPI00119842	**Short/branched chain specific acyl-CoA dehydrogena**	ASSTC*QLTFENVKVPETNILGK	-	-	10
		VDASVALLC*DIQNTIINNLFR	-	-	47
IPI00119923	**17 days pregnant adult female amnion cDNA, RIKEN**	QDLSFVTASC*LDEVLNAAFDGGFPVK	-	-	10
IPI00119930	**5'-AMP-activated protein kinase subunit gamma-1**	EVYLQDSFKPLVC*ISPNASLFDAVSSLIR	-	-	16
IPI00119945	**Nit protein 2**	VGLGIC*YDMR	-	125	-
IPI00120076	**Creatine kinase, sarcomeric mitochondrial precursor**	LGYILT*CPSNLGTGLR	-	5	-
		LGYILTC*PSNLGTGLR	-	79	73
		LGYILTCPS*NLGTGLR	-	4	-
		MTPSGYTLDQC*IQTGVDNPGHPFIK	-	-	16
		SEVELVQIVIDGVNYLVDC*EK	-	-	28
IPI00120165	**Peroxisomal carnitine O-octanoyltransferase**	AFVFDVLHEGC*LITPPELLR	-	-	10
IPI00120451	**Fatty acid-binding protein, liver**	AIGLPE*DLIQK	11	-	-
		AIGLPED*LIQK	10	-	-
		NEFTLGEEC*ELETMTGEK	4	-	-
IPI00121209	**Apolipoprotein A-I precursor**	SNPTLNEYH*TR	28	-	-
		VAPLGAE*LQESAR	18	-	-
		WKED*VELYR	45	-	-
IPI00121280	**12 days embryo embryonic body between diaphragm**	KHNLC*GETEEER	-	-	7
IPI00121348	**L-serine dehydratase**	ETLSAKPGAIVLSVGGGGLLC*GVVQGLR	-	-	13
		LQTPLASLVVIVC*GGSNISLAQLQALK	-	-	13
IPI00121440	**Electron transfer flavoprotein subunit beta**	EIIAVSCGPSQC*QETIR	-	-	4
		HSMNPFC*EIAVEEAVR	-	-	8
		QAIDDDC*NQTGQMTAGLLDWPQGTFASQ	-	-	6
IPI00121566	**GMP reductase 1**	VGVGPGSVC*TTR	-	-	11
IPI00121639	**Beta-ureidopropionase**	IAVNIC*YGR	-	11	-
IPI00121758	**TAR DNA-binding protein 43**	VTEDENDEPIEIPSEDDGTVLLSTVTAQFPG	-	-	6
IPI00121788	**Peroxiredoxin-1**	HGEVC*PAGWKPGSDTIKPDVNK	-	-	95
		LNCQVIGASVDSHFC*HLAWINTPK	-	-	33

IPI00121833	**3-ketoacyl-CoA thiolase A, peroxisomal precursor**	AGLTVNDIDIFEINEAFASQAVYC*VEK	-	-	9
IPI00122075	**Mitochondrial antiviral signaling protein**	FCCVDVLEILPYLSC*LTASDQDR	-	-	7
IPI00122139	**3-ketoacyl-CoA thiolase B, peroxisomal precursor**	DTTPDE*LLSAVLTAVLQDVK	14	-	-
		DTTPDELLS*AVLTAVLQDVK	8	-	-
IPI00122549	**Isoform PI-VDAC1 of Voltage-dependent anion-selec**	WTEYGLTFT*EK	9	-	-
		WTEYGLTFTE*K	10	-	-
IPI00122634	**Cytochrome P450, family 2, subfamily a, polypeptide**	IQEEAGC*LIK	-	-	5
		MLQGTC*GAPIDPTIYLSK	-	-	9
IPI00122684	**Eno2 protein (Fragment)**	SGETEDTFIADLVVGLC*TGQIK	-	-	17
IPI00122740	**Protein LRP16**	LEVDAIVNAANSSLLGGGGVDGC*IHR	-	-	7
IPI00122743	**Aspartyl-tRNA synthetase, cytoplasmic**	LEYC*EALAMLR	-	-	23
IPI00123006	**GDP-mannose pyrophosphorylase A**	LLPAITILGC*R	-	-	16
IPI00123176	**PREDICTED: similar to Glyceraldehyde-3-phosphate**	LISWYDNEY*GYSNR	9	-	-
IPI00123619	**Cytochrome P450, family 2, subfamily d, polypeptide**	VQQEIDEVIGQVQC*PEMADQAR	-	-	5
IPI00123651	**ATP-dependent RNA helicase DDX19A**	VLVTTNVC*AR	-	-	10
IPI00123975	**Glycerol kinase-like protein 2**	GIIC*GLTQFTNK	-	-	11
IPI00124103	**Copper chaperone for superoxide dismutase**	GMGSSQLQNLGAAVAILEGC*GSIQGVVR	-	-	19
IPI00124225	**Proteasome activator complex subunit 2**	QNLFQEADDFLC*TFLPR	-	-	18
IPI00124372	**aldehyde dehydrogenase 9, subfamily A1**	TVC*VEMGDVESAF	-	-	6
IPI00124444	**Isoform 1 of 6-phosphofructokinase type C**	WDC*VSSILQVGGTIIGSAR	-	-	13
IPI00124819	**Coronin-1B**	NVLLSAGC*DNVVLIWNVGTAEELYR	-	-	8
IPI00124900	**Isoform 1 of Methylglutaconyl-CoA hydratase, mitoc**	SEVPGIFC*AGADLK	-	-	6
IPI00125135	**Ubiquitin-conjugating enzyme E2 D2**	IYHPNINSNGSIC*LDILR	-	-	29
		VLLSICSLLC*DPNPDDPLVPEIAR	-	-	18
IPI00125325	**Peroxisomal 2,4-dienoyl-CoA reductase**	INILINCAAGNFLC*PASALSFNAFK	-	-	21
IPI00125521	**40S ribosomal protein S5**	KAQC*PIVER	7	-	-
		VNQAIWLLC*TGAR	-	-	21
IPI00125853	**Mitochondrial ornithine transporter 1**	LSDLQNAAAGSFASAFAALVLC*PTELVK	-	-	28
IPI00125960	**Protein NDRG1**	FALNNPEMVEGLVLMNVNPC*AEGWMDWA	-	-	8
IPI00126172	**Ester hydrolase C11orf54 homolog**	AHIMPAEFSSC*PLNSDEAVNK	-	-	53
		APLVC*LPVFVSK	-	-	13
IPI00126208	**11 days embryo whole body cDNA, RIKEN full-length**	AAVS*GLWGKVNADEVGGEALGR	-	-	40
		AAVSGLWGK*VNADEVGGEALGR	45	-	29
		AAVSGLWGKVNAD*EVGGEALGR	62	-	-
		AAVSGLWGKVNADE*VGGEALGR	27	-	-
		AAVSGLWGKVNADEVGGE*ALGR	48	-	-
		GTFASLSELH*CDK	-	-	6
		GTFASLSELHC*DK	151	332	100
		GTFASLSELHCD*K	-	-	7
		KVITAFNDGLNH*LDSLK	-	-	8
		VITAFNDGLNH*LDSLK	6	-	29
		VITAFNDGLNHLD*SLK	-	-	5
		VITAFNDGLNHLDSLKGTFASLSELHC*DK	10	-	-
		VNAD*EVGGEALGR	179	-	-
		VNADE*VGGEALGR	201	-	-
		VNADEVGGE*ALGR	180	-	-
		VVAGVAAALAH*K	-	-	233
		Y*FDSFGDLSSASAIMGNAK	102	-	-
		YFD*SFGDLSSASAIMGNAK	45	-	-
		YFDS*FGDLSSASAIMGNAK	78	-	-
		YFDSFGD*LSSASAIMGNAK	70	-	-
		YFDSFGDLSSAS*AIMGNAKVK	-	-	8
		YFDSFGDLSSASAIMGNAK*VK	-	-	5
IPI00126248	**Adult male testis cDNA, RIKEN full-length enriched li**	YIC*TTSAIQNR	-	8	-
IPI00126680	**Adult male kidney cDNA, RIKEN full-length enriched**	GQHMSEQFSQVNC*LNK	-	80	37
		GQHMSEQFSQVNC*LNKVPVLK	-	-	5
IPI00126826	**Histamine N-methyltransferase**	DDLC*QYVTSSDLAQILDDLGIK	-	-	23
IPI00126940	**Isoform Long of Adenosine kinase**	TGC*TFPEKPDFH	-	6	12
IPI00127206	**Fructose-bisphosphate aldolase B**	IADQC*PSSLAIQENANALAR	-	-	10
		TVPAAVPGIC*FLSGGMSEEDATLNLNAINR	-	31	-
IPI00127625	**Hydroxymethylglutaryl-CoA lyase, mitochondrial pre**	NANC*SIEESFQR	-	-	6
IPI00127707	**Isoform 1 of Poly(rC)-binding protein 2**	INISEGNC*PER	-	-	6
		LVVPASQC*GSLIGK	-	-	9
IPI00127989	**Prostaglandin E synthase 3**	HLNEIDLFHC*IDPNDSK	-	-	14
IPI00128209	**Adenylate kinase isoenzyme 1**	KVNAEGTVDTVFSEVC*TYLDSLK	-	-	123
		VNAEGTVDTVFSEVC*TYLDSLK	-	-	66
IPI00128267	**PREDICTED: similar to 60S ribosomal protein L32**	ELEVLLMC*NK	-	-	8
IPI00128376	**Aldo-keto reductase family 1, member C14**	SKDIILVSYC*TLGSSR	-	23	38
		SPVLLDDPVLC*AMANK	-	-	21

IPI00128518	**S-adenosylmethionine synthetase isoform type-1**	TGMVLLC*GEITSVAMVDYQR	-	-	16
IPI00128760	**Ubiquitin-conjugating enzyme E2 L3**	GQVC*LPVISAENWKPATK	-	-	21
IPI00128791	**Heat-shock protein beta-6**	FGEGLLEAELASLC*PAAIAPYYLR	-	-	79
IPI00128873	**Nitrilase 1**	THLC*DVEIPGQGPMR	-	-	6
		VGLAIC*YDMR	-	20	-
IPI00128904	**Poly(rC)-binding protein 1**	GYWASLDASTQTTHELTIPNNLIGC*IIGR	-	-	16
		INISEGNC*PER	-	-	7
		LVVPATQC*GSLIGK	-	6	30
IPI00129011	**Formimidoyltransferase-cyclodeaminase**	AC*ALQEGLR	-	8	-
IPI00129164	**Sepiapterin reductase**	SDGALVDC*GTSAQK	-	-	6
		TVVNISSLC*ALQPYK	-	-	62
IPI00129517	**Isoform Mitochondrial of Peroxiredoxin-5, mitochon**	ALNVEPDGTGLTC*SLAPNILSQL	-	-	25
		GVLFGVPGAFTPGC*SK	-	-	18
IPI00129928	**Isoform Mitochondrial of Fumarate hydratase, mitoc**	FEALAAHDALVELSGAMNTAAC*SLMK	-	-	15
IPI00130000	**Puromycin-sensitive aminopeptidase**	LPAEVSPINYSLC*LKPDLLDFTFEGK	-	-	19
IPI00130173	**Ubiquitin-like 1-activating enzyme E1B**	VLVVGAGGIGC*ELLK	-	-	7
IPI00130280	**ATP synthase subunit alpha, mitochondrial precurso**	YTIVVSATASDAAPLQYLAPYSGC*SMGEYF	-	17	92
IPI00130344	**Chloride intracellular channel protein 1**	LHIVQVVC*K	-	-	7
IPI00130521	**Ubiquitin-conjugating enzyme E2 A**	MFHPNVYADGSIC*LDILQNR	-	-	15
IPI00130530	**Glyoxylate reductase/hydroxypyruvate reductase**	VGYTPGVLTDATAELAVSLLLTTC*R	-	-	23
IPI00130804	**Delta3,5-delta2,4-dienoyl-CoA isomerase, mitochond**	EVDMGLAAD*VGTLQR	755	-	-
		EVDMGLAAD*VGTLQRLPK	16	-	-
		EVDMGLAADVGT*LQR	7	-	-
IPI00130950	**Betaine--homocysteine S-methyltransferase**	AGASIVGVNC*HFDPSVSLQTVK	-	9	-
		QVADEGDALVAGGVSQTPSYLSC*K	-	11	35
		VNEAAC*DIAR	-	7	-
IPI00131204	**UDP-glucose pyrophosphorylase 2**	LNGGLGTSMGC*K	-	-	7
IPI00131357	**11 days embryo whole body cDNA, RIKEN full-length**	ITAFVPNDGC*LNFIEENDEVLVAGFGR	-	-	62
IPI00131438	**Phosphoenolpyruvate carboxykinase, cytosolic**	FCTPASQC*PIIDPAWESPEGVPIEGIIFGGR	-	-	9
		YLAAAFPSAC*GK	-	22	11
IPI00131478	**Arylsulfotransferase ST1A4**	IPFLEFSC*PGVPPGLETLK	-	-	14
IPI00131695	**Serum albumin precursor**	AH*CLSEVEHDTMPADLPAIAADFVEDQEVC	-	-	10
		AHCLS*EVEHDTMPADLPAIAADFVEDQEVC	-	-	10
		AHCLSEVEHD*TMPADLPAIAADFVEDQEVC	-	-	10
		AHCLSEVEHDT*MPADLPAIAADFVEDQEVC	-	-	10
		C*SYDEHAK	-	22	-
IPI00132042	**Pyruvate dehydrogenase E1 component subunit bet**	TNHLVTVEGGWPQFGVGAEIC*AR	-	-	106
IPI00132076	**Isoform Membrane-bound of Catechol O-methyltrans**	EYRPSLVLELGAYC*GYSAVR	-	-	155
IPI00132080	**6-phosphogluconolactonase**	TGALC*WFLDEAAAR	-	-	9
IPI00132347	**Adult male cerebellum cDNA, RIKEN full-length enric**	DDTLHE*TEDVK	6	-	-
IPI00132388	**Basic leucine zipper and W2 domain-containing prot**	FDPTQFQDC*IIQGLTETGTDLEAVAK	-	-	59
IPI00132653	**Succinyl-CoA:3-ketoacid-coenzyme A transferase 1,**	DIPNGATLLVGGFGLC*GIPENLIGALLK	-	23	38
IPI00132958	**Thioesterase superfamily member 2**	LGTLHGGLTATLVDSISTMALMC*TER	-	-	86
IPI00133006	**Acyl carrier protein, mitochondrial precursor**	LMC*PQEIVDYIADKK	-	-	18
IPI00133034	**Histidine triad nucleotide-binding protein 2**	IS*QAEEDDQQLLGHLLLVAK	11	-	-
		ISQAEE*DDQQLLGHLLLVAK	13	-	-
		ISQAEEDD*QQLLGHLLLVAK	15	-	-
IPI00133456	**Regucalcin**	VAVD*APVSSVALR	17	-	-
IPI00133903	**Stress-70 protein, mitochondrial precursor**	AKC*ELSSSVQTDINLPYLTMDASGPK	-	9	-
		C*ELSSSVQTDINLPYLTMDASGPK	-	13	-
IPI00133920	**SEC13-related protein**	FASGGC*DNLIK	-	11	-
IPI00134599	**40S ribosomal protein S3**	GLC*AIAQAESLR	-	59	90
IPI00134704	**Quinone oxidoreductase**	AGESVLVHGASGGVGLATC*QIAR	-	-	14
IPI00134746	**Argininosuccinate synthase**	EFVEEFIWPAVQSSALY*EDR	11	-	-
		EFVEEFIWPAVQSSALYE*DR	6	-	-
		EFVEEFIWPAVQSSALYED*R	7	-	-
		FAELVYTGFWHSPEC*EFVR	-	-	168
		FELTC*YSLAPQIK	-	45	102
		GSVVLAYSGGLDTSC*ILVWLK	-	-	51
IPI00134870	**Acyl-coenzyme A oxidase 2, peroxisomal**	LSGLPTLVTQAIASC*TYEGENTVLYLQVAR	-	-	10
IPI00134961	**Medium-chain specific acyl-CoA dehydrogenase, mit**	AFAGDIANQLAT*DAVQIFGGYGFNTEYPVE	11	-	-
		AFAGDIANQLATDAVQIFGGYGFNT*EYPVE	6	-	-
		IYQIY*EGTAQIQR	10	-	-
		IYQIYE*GTAQIQR	13	-	-
IPI00135231	**0 day neonate lung cDNA, RIKEN full-length enriche**	SEGGFIWAC*K	-	10	-
IPI00135284	**PREDICTED: similar to Glyceraldehyde-3-phosphate**	VIHDNFGIVE*GLMTTVHAITATQK	-	-	10
IPI00135708	**Dual specificity mitogen-activated protein kinase kin**	LC*DFGVSGQLIDSMANSFVGTR	-	-	17
IPI00135977	**Chloride intracellular channel protein 4**	AGSDGESIGNC*PFSQR	-	74	-
IPI00136134	**Isoform 1 of Protein NDRG2**	YFLQGMGYMASSC*MTR	-	-	24
IPI00137091	**Osteoclast-like cell cDNA, RIKEN full-length enriche**	HRRRPS*KRKR	-	-	12
IPI00137409	**Transketolase**	TVPFC*STFAAFFTR	-	-	12
IPI00137533	**6-phosphofructo-2-kinase/fructose-2,6-biphosphata**	VFFVESVC*DDPDVIAANILEVK	-	-	19
IPI00137730	**Phosphatidylethanolamine-binding protein 1**	YVWLVYEQEQPLSC*DEPILSNK	-	-	18
IPI00139780	**60S ribosomal protein L23**	ISLGLPVGAVINC*ADNTGAK	-	-	22
IPI00153107	**Bleomycin hydrolase**	LNSDPQFVLAQNVGTTHDLLDIC*LR	-	-	7
IPI00153144	**Adult male liver tumor cDNA, RIKEN full-length enric**	VDVSVDGGLTWQEAELEGEEQC*PR	-	-	10
IPI00153294	**Xylulose kinase**	LGSPVPSC*SVVGTISSYYVQR	-	-	20
IPI00153317	**10-formyltetrahydrofolate dehydrogenase**	AVQMGMSSVFFNKGENC*IAAGR	-	340	54
		SPLIIFADC*DLNK	-	-	6
IPI00153376	**Homeodomain-only protein**	HPDPTTLC*LIAAEAGLTEEQTQK	-	-	15
		VNKHPDPTTLC*LIAAEAGLTEEQTQK	-	-	14
IPI00153463	**Dehydrogenase/reductase SDR family member 11 pr**	NIDDGHIININSMC*GHR	-	37	-
IPI00154054	**Acetyl-CoA acetyltransferase, mitochondrial precurs**	IHMGNC*AENTAK	-	-	8
		QATLGAGLPISTPC*TTVNK	-	-	23
IPI00169586	**16 days embryo head cDNA, RIKEN full-length enrich**	AIVAGDEVAQEVDAVAPDC*SFLK	-	-	16
		EIYGQTETGLIC*R	-	-	4

IPI00169862	**Ubiquinone biosynthesis protein COQ9, mitochondri**	AVLAGIY*NTTELVMMQDSSPDFEDTWR	9	-	-
		AVLAGIYNTTE*LVMMQDSSPDFEDTWR	9	-	-
		AVLAGIYNTTELVMMQD*SSPDFEDTWR	7	-	-
IPI00172221	**Isoform 2 of Dynamin-1-like protein**	IC*YIFHETFGR	-	7	-
		LHDAIVEVVTC*LLR	-	-	25
IPI00187462	**GTPase, IMAP family member 4 isoform a**	VFNSGIC*AK	-	-	6
IPI00221400	**Alcohol dehydrogenase 1**	IDGASPLDKVCLIGC*GFSTGYGSAVK	-	-	13
		MVATGVC*R	-	14	-
		SDDHVVSGTLVTPLPAVLGHEGAGIVESVG	-	-	15
		VCLIGC*GFSTGYGSAVK	-	-	23
		VIPLFSPQC*GECR	-	-	18
		VIPLFSPQCGEC*R	-	-	22
		VTPGSTC*AVFGLGGVGLSVIIGCK	-	-	52
IPI00221402	**Fructose-bisphosphate aldolase A**	ALANSLAC*QGK	-	-	9
IPI00221501	**Adult male medulla oblongata cDNA, RIKEN full-leng**	VFVASC*SGFVAIK	-	-	12
IPI00221613	**ADP-ribosylation factor 1**	NWYIQATC*ATSGDGLYEGLDWLSNQLR	-	-	11
IPI00221629	**ADP-ribosylhydrolase**	AAMLLGSVGDALGYGNIC*R	-	-	47
IPI00221636	**Adult male aorta and vein cDNA, RIKEN full-length e**	MISQSC*LSNIEK	-	7	-
IPI00221769	**GTP:AMP phosphotransferase mitochondrial**	TLTQC*SWLLDGFPR	-	-	56
IPI00221890	**Carbonic anhydrase 3**	EAPFTHFDPSCLFPAC*R	-	-	113
		GKEAPFTHFDPSCLFPAC*R	-	-	101
IPI00222306	**Adult male testis cDNA, RIKEN full-length enriched li**	LNIISNLDC*VNEVIGIR	-	-	6
IPI00222549	**60S ribosomal protein L30**	LVILANNC*PALR	-	-	14
IPI00223092	**Hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl**	ALMGLYNGQVLC*K	-	-	7
IPI00224626	**cell division cycle 10 homolog**	EGGVQLLLTIVDTPGFGDAVDNSNC*WQPV	-	-	8
IPI00225100	**12 days embryo embryonic body between diaphragm**	FSQSLVMAAYSC*QLYPENK	-	-	9
IPI00225634	**Adult male kidney cDNA, RIKEN full-length enriched**	QAHLC*VLASNCDEPMYVK	-	-	14
IPI00225961	**D-3-phosphoglycerate dehydrogenase**	NAGTC*LSPAVIVGLLR	-	-	11
IPI00226218	**17 days embryo head cDNA, RIKEN full-length enrich**	LTLLEVGC*GTGANFK	-	-	22
IPI00226234	**Phospholipase A-2-activating protein**	ILSLIC*NNSSEKPTAQQLQILWK	-	-	6
IPI00226521	**9130227C08Rik protein**	ITWSELSESGLPLC*DVVINLAGENILNPLR	-	-	9
IPI00226993	**Thioredoxin**	C*MPTFQFYK	-	10	-
		LVVVDFSATWCGPC*K	-	-	6
IPI00228106	**Activated spleen cDNA, RIKEN full-length enriched li**	TLYDVILYGLPEC*TEGAPSFLLECDSSVLG	-	-	12
IPI00228253	**Acetyl-CoA acetyltransferase, cytosolic**	VAPEEVSEVIFGHVLTAGC*GQNPTR	-	-	19
IPI00228630	**Fructose-1,6-bisphosphatase 1**	DFD*PAINEYLQR	5	-	-
		KAQGTGELTQLLNSLC*TAIK	-	-	10
		YVVCFDPLDGSSNIDC*LVSIGTIFGIYR	-	-	64
IPI00228828	**18-day embryo whole body cDNA, RIKEN full-length**	KTDLC*PIYIFVQPPSLDVLEQR	-	-	14
IPI00228883	**PDZ domain-containing protein 1**	FSPLLYC*QSQELPNGSVK	-	-	9
IPI00229080	**17 days embryo kidney cDNA, RIKEN full-length enri**	GFEVVYMTEPIDEYC*VQQLK	-	-	10
		VFIMDSC*DELIPEYLNFIR	-	-	34
IPI00229510	**L-lactate dehydrogenase B chain**	GMYGIENEVFLSLPC*ILNAR	-	16	36
		ITVVGVGQVGMAC*AISILGK	-	-	45
		VIGSGC*NLDSAR	-	43	15
		YSPDC*TIIVVSNPVDILTYVTWK	-	-	32
IPI00229517	**Galectin-1**	FNAHGDANTIVC*NTK	-	-	5
IPI00229859	**Eif3s9 protein**	FSHQGVQLIDFSPC*ER	-	-	30
IPI00230034	**D-dopachrome decarboxylase**	PFVE*LETNLPASR	-	46	-
IPI00230139	**FK506-binding protein 4**	ELCFEVGEGESLDLPC*GLEEAIQR	-	-	13
IPI00230212	**Glutathione S-transferase Mu 1**	C*LDAFPNLR	-	9	-
		YTMGD*APDFDR	7	-	-
IPI00230706	**Phosphoglycerate mutase 2**	FC*GWFDAELSEK	-	39	-
IPI00230760	**Myoglobin**	GLS*DGEWQLVLNVWGK	-	-	7
		GLSD*GEWQLVLNVWGK	-	-	9
		GLSDGE*WQLVLNVWGK	-	-	5
		H*GCTVLTALGTILK	-	-	41
		H*SGDFGADAQGAMSK	-	-	18
		HGC*TVLTALGTILK	-	43	361
		HGCT*VLTALGTILK	-	-	32
		HS*GDFGADAQGAMSK	-	-	17
		VEAD*LAGHGQEVLIGLFK	-	-	19
		VEADLAGH*GQEVLIGLFK	-	-	21
IPI00261627	**Succinyl-CoA ligase [ADP-forming] beta-chain, mitoc**	ICNQVLVC*ER	-	-	11
		ILAC*DDLDEAAK	-	-	12
IPI00265025	**galactokinase 1**	AEHSFAGVPC*GIMDQLIALLGQK	-	-	18
IPI00266614	**Ribosyldihydronicotinamide dehydrogenase**	VLAPQISFGLD*VSSEEER	20	-	-
IPI00267407	**Aldh8a1 protein**	SSFANQGEIC*LCTSR	-	13	-
IPI00269076	**Adenylate kinase isoenzyme 2, mitochondrial**	GIHC*AIDASQTPDIVFASILAAFSK	-	-	17
IPI00269481	**Capping protein**	NLSDLIDLVPSLC*EDLLSSVDQPLK	-	-	25
IPI00271869	**PREDICTED: similar to Glyceraldehyde-3-phosphate**	WGEAGAEYVVE*STGVFTTMEK	6	-	-
IPI00273164	**Succinate semialdehyde dehydrogenase, mitochond**	NAGQTC*VCSNR	-	19	-
IPI00273646	**Glyceraldehyde-3-phosphate dehydrogenase**	IVSNASC*TTNCLAPLAK	-	37	34
		IVSNASCTTNC*LAPLAK	-	-	31
		VPTPNVSVVDLTC*R	-	75	150

IPI00274407	**Isoform 1 of Elongation factor Tu, mitochondrial pre**	ELLTEFGYKGEETPVIVGSALC*ALEQR	-	-	34
		GEETPVIVGSALC*ALEQR	-	-	7
		NMITGTAPLDGC*ILVVAANDGPMPQTR	-	-	11
IPI00283531	**Glutathione S-transferase P 2**	EEVVTIDTWMQGLLKPTC*LYGQLPK	-	28	109
		FE*DGDLTLYQSNAILR	16	-	-
		FED*GDLTLYQSNAILR	10	-	-
IPI00307837	**Elongation factor 1-alpha 1**	DGSASGTTLLEALDC*ILPPTRPTDKPLR	-	-	49
		NMITGTSQADC*AVLIVAAGVGEFEAGISK	-	-	60
		SGDAAIVDMVPGKPMC*VESFSDYPPLGR	-	20	42
IPI00308328	**Cytochrome P450 2F2**	DFIDC*FLTK	-	-	5
IPI00308885	**60 kDa heat shock protein, mitochondrial precursor**	AAVEEGIVLGGGC*ALLR	80	64	140
		C*EFQDAYVLLSEK	-	9	-
		ILQSSSEVGYDAMLGDFVNMVE*K	6	-	-
		NAGVEGSLIVE*K	9	-	-
IPI00308938	**Calpain-2 catalytic subunit precursor**	RPTEIC*ADPQFIIGGATR	-	-	6
IPI00309073	**Microsomal triglyceride transfer protein large subuni**	SGSSSAYTGYVE*R	7	-	-
IPI00310669	**Dihydroxyacetone kinase**	MVNSVEGC*ADDALAGLVASNPDLQLLQGH	-	-	9
IPI00312058	**Catalase**	LGPNYLQIPVNC*PYR	-	-	48
IPI00313236	**Bile acyl-CoA synthetase**	VALVC*TGSEGSSITNSQLDAR	-	-	9
IPI00313296	**Ribonuclease inhibitor**	ELDLSNNC*MGGPGVLQLLESLK	-	-	5
IPI00314041	**Villin-1**	HVETNSC*DVQR	-	4	-
IPI00314189	**3 beta-hydroxysteroid dehydrogenase type 5**	LPFIYGEEC*QVTSTTVK	-	-	17
IPI00314510	**Aspartoacylase-2**	LFSGEDVLYEGDSIVYPVFINE*AAYYEK	6	-	-
		NGIC*LEMGPQPQGVLR	-	-	16
IPI00314950	**60S acidic ribosomal protein P0**	AGAIAPC*EVTVPAQNTGLGPEK	-	-	12
IPI00315488	**Arginyl-tRNA synthetase, cytoplasmic**	LQEVFGC*AIR	-	-	12
IPI00315550	**Thioredoxin-like protein 2**	ELEASEELDTIC*PK	-	-	4
IPI00317902	**proteasome (prosome, macropain) subunit, beta typ**	VIEINPYLLGTMAGGAADC*SFWER	-	-	7
IPI00318545	**3'(2'),5'-bisphosphate nucleotidase 1**	LVQMSIC*SSLAR	-	-	9
		SHSNQLVTDC*ISAMNPDTVLR	-	-	11
IPI00318614	**Isoform 2 of Isocitrate dehydrogenase [NADP], mitoc**	DLAGC*IHGLSNVK	-	-	8
		NILGGTVFREPIIC*K	-	-	45
		NYDGDVQSDILAQGFGSLGLMTSVLVC*PD	-	-	75
IPI00318841	**Elongation factor 1-gamma**	VPAFEGDDGFC*VFESNAIAYYVSNEELR	-	-	46
IPI00319652	**Glutathione peroxidase 1**	YIIWSPVC*R	-	-	10
IPI00319973	**Membrane-associated progesterone receptor compo**	FYGPEGPY*GVFAGR	5	-	-
IPI00319994	**L-lactate dehydrogenase A chain**	DYC*VTANSK	-	9	-
		ITVVGVGAVGMAC*AISILMK	-	-	61
		IVSSKDYC*VTANSK	-	-	7
		VIGSGC*NLDSAR	-	38	18
IPI00320217	**T-complex protein 1 subunit beta**	SLHDALC*VLAQTVK	-	-	9
IPI00320850	**Methylcrotonoyl-CoA carboxylase subunit alpha, mit**	SSAAQAIHPGYGFLSENMEFAELC*K	-	-	17
IPI00321308	**Alanyl-tRNA synthetase, cytoplasmic**	NVGC*LQEALQLATSFAQLR	-	-	7
IPI00321375	**12 days embryo female mullerian duct includes surr**	FGVFTC*FDILFFDPAVR	-	12	-
IPI00321978	**Ran-specific GTPase-activating protein (Fragment)**	AWVWNTHADFADEC*PKPELLAIR	-	-	17
IPI00322931	**Adult male tongue cDNA, RIKEN full-length enriched**	ATFHTPFSQLGQSPEAC*SSYTFPK	-	-	40
IPI00323592	**Malate dehydrogenase, mitochondrial precursor**	ETEC*TYFSTPLLLGK	-	-	4
		GC*DVVVIPAGVPR	-	-	8
		GYLGPEQLPDC*LK	-	-	7
		IQEAGTE*VVK	11	-	-
IPI00323816	**Selenium-binding protein 2**	C*GPGYPTPLEAMK	-	13	-
		FLHDPSATQGFVGC*ALSSNIQR	-	-	10
		GGSVQVLEDQELTC*QPEPLVVK	-	12	40
IPI00323881	**Importin beta-1 subunit**	IQFNDLQSLLC*ATLQNVLR	-	-	12
IPI00323971	**Inosine-5'-monophosphate dehydrogenase 2**	HGFC*GIPITDTGR	-	20	-
IPI00330754	**D-beta-hydroxybutyrate dehydrogenase, mitochondr**	METYC*NSGSTDTSSVINAVTHALTAATPYT	-	-	28
		TIQLNVC*NSEEVEK	-	-	4
IPI00330804	**Heat shock protein HSP 90-alpha**	VFIMDNC*EELIPEYLNFIR	-	-	5
IPI00331066	**Calbindin**	AFELYDQDGNGYIDENELDALLKDLC*EK	-	-	5
IPI00331094	**Aspartoacylase**	VIPLGGDC*TVYPVFVNEAAYYEK	-	-	9
IPI00331322	**Microsomal glutathione S-transferase 1**	ITNKVFANPEDC*AGFGK	-	-	17
		VFANPEDC*AGFGK	-	-	51
		VFANPEDC*AGFGKGENAK	-	-	18
IPI00331436	**Lap3 protein**	LNLPINIIGLAPLC*ENMPSGK	-	-	27
		SAGAC*TAAAFLR	-	-	8
IPI00331490	**Aflatoxin B1 aldehyde reductase member 2**	GHSELDTAFMYC*DGQSENILGGLGLGLGS	-	-	22
IPI00331541	**6-phosphofructokinase, muscle type**	LPLMEC*VQVTK	-	-	18
		SSYLNIVGLVGSIDNDFC*GTDMTIGTDSAL	-	-	5
IPI00336324	**Malate dehydrogenase, cytoplasmic**	FVE*GLPINDFSR	12	-	-
		GE*FITTVQQR	4	-	-
		VIVVGNPANTNC*LTASK	-	12	-
IPI00337893	**Pyruvate dehydrogenase E1 component alpha subu**	LPCIFIC*ENNR	-	-	38
		NFYGGNGIVGAQVPLGAGIALAC*K	-	-	98
IPI00350458	**Isoform 1 of UNC45 homolog B**	AGVISALAC*MVK	-	-	4
IPI00352124	**Flavin containing monooxygenase 5**	IAVIGAGASGLTC*IK	-	-	12
		LLLGPC*TPVQYR	-	-	16

IPI00355265	**PREDICTED: similar to High mobility group protein 1**	MSSYAFFVQTC*R	-	-	6
IPI00377396	**41 kDa protein**	IDATQVEVNPFGETPEGQVVC*FDAK	-	-	22
		VEAILVNIFGGIVNC*AIIANGITK	-	-	64
IPI00378120	**Glutaredoxin-related protein 5**	GTPEQPQC*GFSNAVVQILR	-	7	-
IPI00380320	**Lactate dehydrogenase D**	DSGLWFPVDPGADASLC*GMAATGASGTN	-	-	7
		IEFLDDVMMDAC*NR	-	-	5
		LHPAPEATVAATC*AFPSVQAAVDSTVQILQ	-	-	11
IPI00381277	**PREDICTED: similar to zinc finger protein 420 isofor**	C*SSLRTHQKIHAGEKPHACEKCGK	28	-	-
IPI00395140	**L-xylulose reductase**	ALTNHTVYC*STK	-	7	-
IPI00403579	**hypothetical protein LOC232078**	GDFSLC*EVLR	-	-	5
		MGLPIC*LVVAVNR	-	-	14
IPI00403810	**Tubulin alpha-6 chain**	AVC*MLSNTTAIAEAWAR	-	-	34
		AYHEQLTVAEITNAC*FEPANQMVK	-	-	15
		LADQC*TGLQGFLVFHSFGGGTGSGFTSLL	-	-	12
		TIQFVDWC*PTGFK	-	-	11
IPI00404014	**Carnitine transporter 2 variant**	KARTWASIHLNTFFAIGAMLVALAS*YLLK	6	-	-
		KARTWASIHLNTFFAIGAMLVALASY*LLK	9	-	-
IPI00406419	**Xaa-Pro dipeptidase**	IEEDVVVTDSGMELLTC*VPR	-	-	7
IPI00406442	**Succinyl-CoA ligase [GDP-forming] subunit alpha, m**	LIGPNC*PGVINPGECK	-	-	16
		LIGPNCPGVINPGEC*K	-	-	8
IPI00408378	**Isoform 1 of 14-3-3 protein theta**	DNLTLWTSDSAGEEC*DAAEGAEN	-	-	23
		YLAEVAC*GDDR	-	-	7
IPI00408961	**3-hydroxyanthranilate 3,4-dioxygenase**	VTMGGQC*IALAPDDSLLVPAGTSYVWER	-	-	7
IPI00409345	**Lambda-crystallin homolog**	VILSSSSSC*LLPSK	-	40	27
		VILSSSSSC*LLPSK	-	40	-
IPI00420706	**Leucine-rich PPR-motif containing**	VFESTC*SSGSPGSNQALLLLR	-	-	19
IPI00420718	**Hydroxymethylglutaryl-CoA synthase, mitochondrial**	MGFCSVQEDINSLC*LTVVQR	-	-	5
		QAGNNQPFTLDDVQYMIFHTPFC*K	-	9	20
IPI00420882	**2-oxoglutarate dehydrogenase E1 component, mitoc**	FGLEGC*EVLIPALK	-	-	4
IPI00421223	**Tropomyosin alpha-4 chain**	EENVGLHQTLDQTLNELNC*I	-	-	6
IPI00454008	**Serine hydroxymethyl transferase 2**	GLELIASENFC*SR	-	-	4
IPI00454049	**Enoyl-CoA hydratase, mitochondrial precursor**	ALNALC*NGLIEELNQALETFEQDPAVGAIVL	-	107	303
IPI00458204	**48 kDa protein**	LTTPTYGDLNHLVSATMSGVTTC*LR	-	-	25
		VSDTVVEPYNATLSVHQLVENTDETYC*IDD	-	-	9
		VSDTVVEPYNATLSVHQLVENTDETYCIDD	-	-	8
IPI00459725	**Isoform 1 of Isocitrate dehydrogenase [NAD] subuni**	KTFDLYANVRPC*VSIEGYK	-	-	16
		TFDLYANVRPC*VSIEGYK	-	-	23
IPI00461964	**NOD-derived CD11c +ve dendritic cells cDNA, RIKEN**	C*MALSTAILVGEAK	24	382	-
		C*MALSTAILVGEAKK	-	70	-
		GYENGNFVGPTIISNVKPSMTC*YK	-	-	59
IPI00462072	**Alpha-enolase**	VNQIGSVTESLQAC*K	5	-	-
IPI00463392	**RIKEN cDNA E030049G20 gene**	EE*PAKITAYQEGLPDEER	-	6	-
IPI00466069	**Elongation factor 2**	STLTDSLVC*K	-	13	-
		VTDGALVVVDCVSGVC*VQTETVLR	-	-	155
IPI00466128	**Alcohol dehydrogenase**	GLE*VTAYSPLGSSDR	8	-	-
IPI00467066	**Glycine N-methyltransferase**	LSYYPHC*LASFTELVR	-	-	29
IPI00467447	**Ras GTPase-activating-like protein IQGAP1**	VNTSSALANISLALEQGC*AVTLLK	-	22	-
IPI00467833	**Triosephosphate isomerase**	CLGELIC*TLNAANVPAGTEVVCAPPTAYID	-	-	21
		IIYGGSVTGATC*K	-	-	8
		VSHALAEGLGVIAC*IGEK	-	-	24
IPI00468481	**ATP synthase subunit beta, mitochondrial precursor**	AIAE*LGIYPAVDPLDSTSR	15	-	-
		FTQAGSE*VSALLGR	5	-	-
		SLQDIIAILGMDELS*EEDK	22	-	-
		SLQDIIAILGMDELSEE*DK	5	-	-
		SLQDIIAILGMDELSEED*K	26	-	-
IPI00554931	**4-hydroxyphenylpyruvate dioxygenase**	IVFVLC*SALNPWNK	-	32	-
IPI00554933	**Glutathione S-transferase theta-1**	VKDC*PPADLIIK	-	-	6
		VLELYLDLLSQPC*R	-	-	10
IPI00622235	**Transitional endoplasmic reticulum ATPase**	GVLFYGPPGC*GK	-	-	33
IPI00625913	**32 kDa protein**	PY*CKLLIVSNPVDILTYVAWK	-	8	-
		PYCK*LLIVSNPVDILTYVAWK	-	8	-
IPI00653158	**14 days embryo liver cDNA, RIKEN full-length enrich**	LCGSGFQSIVSGCQEIC*SK	-	-	12
		VVGYFVSGC*DPTIMGIGPVPAINGALK	-	-	54
		VVGYFVSGC*DPTIMGIGPVPAINGALKK	-	-	77
		YAVGSAC*IGGGQGIALIIQNTA	-	19	89
IPI00653247	**13 days embryo liver cDNA, RIKEN full-length enrich**	GSE*SCDCLQGFQLTHSLGGGTGSGMGTL	-	-	6
		GSESCD*CLQGFQLTHSLGGGTGSGMGTL	-	-	5
IPI00658877	**PREDICTED: similar to F11C1.5a**	LGHILVVDEADKAPTNVTC*ILK	-	-	17
IPI00663327	**Beta-1-globin (Fragment)**	GTFASLSELH*CDK	-	-	6
		VH*LTDAEKAAVSGLWGK	-	-	17
		YFDSFGDLSSASAIMGNAK*VK	-	-	4
IPI00677618	**10, 11 days embryo whole body cDNA, RIKEN full-le**	LEAPC*QQWMELR	-	14	-
IPI00750197	**PREDICTED: similar to 14-3-3 protein theta**	DNLTLWTSDSAEECD*AAEGAEN	-	-	17
IPI00754489	**Bifunctional 3'-phosphoadenosine 5'-phosphosulfat**	IHESAGLPFFEIFVDAPLNIC*ESR	-	-	6
			-	-	-

Supplementary Information Methods:

All reagents were purchased from Sigma-Aldrich unless otherwise noted. Dry solvents were obtained by passing commercially available pre-dried, oxygen-free formulations through activated alumina columns. NMR spectra were obtained in deuterated chloroform on a Varian Inova-400 instrument. NMR chemical shifts are reported in ppm downfield relative to the internal solvent peak and *J* values are reported in Hz. High resolution mass spectrometry experiments (HRMS) were performed at The Scripps Research Institute Mass Spectrometery Core on an Agilent mass spectrometer using ESI-TOF (electrospray ionization – time of flight).

Synthesis of undec-10-ynyl benzenesulfonate [sulfonate ester (SE) probe, 1]: This probe was synthesized using a previously published protocol.[1]

Synthesis of *N*-(hex-5-ynyl)-4-(oxiran-2-yl)butanamide [linear epoxide (EP) probe, 2]: To a solution of hex-5-enoic acid (100 µL, 0.9 mmol) in acetonitrile (10 mL) was added 1-hydroxybenzotriazole (HOBT) (150 mg, 1.1 mmol, 1.2 equiv) and *N*-Ethyl-*N'*-(3-dimethylaminopropyl)carbodiimide (EDC) (171 mg, 1.1 mmol, 1.2 equiv). This mixture was stirred at room temperature for 2 hours, followed by addition of hex-5-yne-1-amine[2] (175 mg, 1.8 mmol, 2.0 equiv) and diisopropylethylamine (313 µL, 1.8 mmol, 2.0 equiv). After stirring at room temperature for 2 hours, the reaction was quenched with water and extracted three times with ethyl acetate. The combined organic phases were washed with saturated sodium chloride and dried over anhydrous magnesium sulfate to provide *N*-(hex-5-ynyl)hex-5-enamide as a white solid, which was carried on to the oxidation reaction without further purification.

N-(hex-5-ynyl)hex-5-enamide (50 mg, 0.26 mmol) from above, was dissolved in CH_2Cl_2 and cooled to 0 ^{0}C in an ice bath. A solution of *m*-chloroperoxibenzoic acid (mCPBA, 75% w/w solution in water) (54 mg, 0.32 mmol, 1.2 equiv) was added and the mixture was stirred at 0 ^{0}C for 20 min and warmed to room temperature over 1 hour. The reaction was quenched with saturated sodium bicarbonate solution, washed with water and saturated sodium chloride and dried over anhydrous magnesium sulfate. The crude mixture was purified with column chromatography 1:1 ethylacetate:hexanes to provide **3** as a white solid (40 mg, 73% yield). ^{1}H NMR (400 MHz, $CDCl_3$) δ 1.45 (m, 1H), 1.59 (m, 4H), 1.74 (m, 1H), 1.83 (m, 2H), 1.97 (t, *J* = 2.6 Hz, 1H), 2.24 (m, 4H), 2.48 (dd, *J* = 4.9 Hz, 2.7 Hz, 1H), 2.76 (dd, *J* = 4.9 Hz, 4.0 Hz, 1H), 2.93 (m, 1H), 3.28 (m, 2H). ^{13}C NMR (100 MHz, $CDCl_3$) δ 18.27, 22.69, 25.88, 28.89, 31.78, 36.26, 39.08, 46.90, 52.36, 68.91, 84.19, 172.68. HRMS *m/z* calcd for $C_{12}H_{19}NO_2$ ($M+H^+$): 210.1488. Found: 210.1487.

Synthesis of 2-chloro-*N*-(hex-5-ynyl)acetamide [α-chloroacetamide (CA) probe, 3]: To a solution of hex-5-yne-1-amine[2] (200 mg, 2.0 mmol, 1.0 equiv) in CH_2Cl_2 (5 mL) was added triethylamine (150 µL, 2.2 mmol, 1.1 equiv). The solution was cooled to 0 ºC in an ice bath with constant stirring. Chloroacetyl chloride (200 µL, 2.5 mmol, 1.2 equiv) was added to the cooled solution, which was stirred at 0 ºC for 1 hour, then warmed to room temperature and stirred for an additional 2 hours. The reaction was quenched with

10 mL of H_2O and extracted three times with 10 mL of CH_2Cl_2. The CH_2Cl_2 layers were combined, washed successively with 10% HCl and saturated sodium chloride solutions and dried over anhydrous magnesium sulfate. The CH_2Cl_2 layer was then concentrated by rotary evaporation and purified by preparatory C18 reverse-phase HPLC using a gradient of 5 – 100% buffer B in buffer A over 25 minutes at a flow rate of 5 mL/minute (Buffer A: 95% H_2O, 5% acetonitrile, 0.1% trifluoroacetic acid, Buffer B: 5% H_2O, 95% acetonitrile, 0.1% trifluoroacetic acid), visualizing by UV absorption at 220 nm. The desired product eluted at 27 minutes and was concentrated by rotary evaporation to afford a yellow oil (170 mg, 50% yield). ^{1}H NMR (400 MHz, $CDCl_3$) δ 1.58 (m, 2H), 1.70 (m, 2H), 1.98 (t, J = 2.6 Hz, 1H), 2.24 (td, J = 6.9 Hz, 2.6 Hz, 2H), 3.35 (m, 2H), 4.06 (s, 2H), 6.64 (br s, 1H). ^{13}C NMR (100 MHz, $CDCl_3$) δ 18.24, 25.75, 28.57, 39.49, 42.86, 69.05, 83.98, 166.02. HRMS *m/z* calcd for $C_8H_{12}ClNO$ ($M+Na^+$): 196.0535. Found: 196.0507.

Synthesis of oct-1-en-7-yn-3-one [α,β-unsaturated ketone (UK) probe, 4]: This probe was synthesized following the exact procedure outlined in Kusama et al[3] for the synthesis of non-1-en-7-yn-3-one as a colorless oil. ^{1}H NMR (400 MHz, $CDCl_3$) δ 1.79 (m, 2H), 1.91 (t, J = 2.5 Hz, 1H), 2.20 (m, 2H), 2.68 (t, J = 7.2 Hz, 2H), 5.78 (d, J = 10.3 Hz, 1H), 6.18 (d, J = 17.6, 1H), 6.30 (dd, J = 17.6 Hz, 10.4 Hz, 1H) ^{13}C NMR (100 MHz, $CDCl_3$) δ 17.99, 22.59, 38.09, 53.61, 69.24, 83.78, 128.38, 136.74.

Synthesis of 4-(pent-4-ynyl)-1-oxaspiro[2.5]octane [spiroepoxide (SP) probe, 5]: This probe was synthesized following the exact procedure outlined in Gansauer et al[4], for the synthesis of 4-(but-3-ynyl)-1-oxaspiro[2.5]octane as a colorless oil in a diastereomeric ratio of 63:37. ^{1}H NMR (400 MHz, $CDCl_3$) An asterisk (*) denotes signals from the minor diastereoisomer. The word 'both' indicates overlapping signals for two diasteroisomers. δ 2.70 (d, J = 4.8 Hz, 1H)*, 2.67 (d, J = 4.6 Hz, 1H), 2.51 (d, J = 4.7 Hz, 1H) both, 2.15-2.20 (m, 3H) both, 1.95 (m, 1H), 1.91 (m, 1H)*, 1.18-1.73 (m, 12H). ^{13}C NMR (100 MHz, $CDCl_3$) δ 18.82*, 18.86, 22.47*, 23.07, 25.19*, 25.25, 26.71*, 26.73, 27.83*, 28.72, 29.60*, 30.14, 32.10*, 32.75, 40.25*, 40.94, 52.00*, 53.74, 61.43*, 61.48, 68.49*, 68.56, 84.55*, 84.67.

Preparation of mouse proteomes: Mouse tissues (heart, liver and kidney) were harvested and immediately flash frozen in liquid nitrogen. The tissues were then Dounce homogenized in 1X Phosphate Buffered Saline (PBS), pH 7.4. Centrifugation at 100,000 x *g* (45 min) provided soluble fractions (supernatant) and membrane fractions (pellet). The mouse liver membrane pellet was resuspended in PBS with sonication. Protein concentrations for each proteome were obtained using the Bio-Rad Dc Protein Assay and stored at -80 ºC till use.

Protein labeling and click chemistry: Proteome samples were diluted to a 2 mg protein/ml solution in PBS. Each sample (4 x 0.5 mL aliquots) was treated with 50 μM of probe (CA, SE or UK) using 2.5 μL of a 10 mM stock in DMSO. The labeling reactions were incubated at room temperature for 2 hours. Click chemistry was performed by the addition of 100 μM of the TEV-biotin tag (50X stock in DMSO, synthesis reported previously)[5, 6], 1 mM TCEP (fresh 50X stock in water), 100 μM ligand (17X stock in

DMSO:t-Butanol 1:4) and 1 mM $CuSO_4$ (50X stock in water). Samples were allowed to react at room temperature for 1 hour. Tubes were combined pairwise and centrifuged (5900 x *g*, 4 min, 4 ºC) to pellet the precipitated proteins. The pellets were resuspended in cold MeOH by sonication and tubes combined pairwise. Centrifugation was followed by a second methanol wash, after which the pellet was solubilized in PBS containing 1.2% SDS via sonication and heating (5 min, 80 ºC).

Streptavidin enrichment of probe-labeled proteins: The SDS-solubilized, probe-labeled proteome samples were diluted with 5 mL of PBS for a final SDS concentration of 0.2 %. The solutions were then incubated with 100 μL of streptavidin-agarose beads (Pierce) for 3 hours at room temperature. The beads were washed with 10 mL 0.2% SDS/PBS, 3 x 10 mL PBS and 3 x 10 mL H_2O and the beads were pelleted by centrifugation (1300 x *g*, 2 min) between washes.

On-bead trypsin and TEV digestion: The washed beads from above were suspended in 500 μL of 6 M urea/PBS and 10 mM TCEP (from 20X stock in H_2O) and placed in a 65 ºC heat block for 15 minutes. 20 mM iodoacetamide (from 50X stock in H_2O) was then added and allowed to react at 37 ºC for 30 minutes. Following reduction and alkylation, the beads were pelleted by centrifugation (1300 x *g*, 2 min) and resuspended in 150 μL of 2 M urea/PBS, 1 mM $CaCl_2$ (100X stock in H_2O), and trypsin (2 μg). The digestion was allowed to proceed overnight at 37 ºC. The digest was separated from the beads using a Micro Bio-Spin column and the beads were then washed with 3 x 500 μL PBS, 3 x 500 μL H_2O and 1 x 150 μL of TEV digest buffer. The washed beads were then resuspended in 150 μL of TEV digest buffer with AcTEV Protease (Invitrogen, 5 μL) for 12 hours at 29 ºC. The eluted peptides were separated from the beads using a Micro Bio-Spin column and the beads washed with H_2O (2 x 75 μL). Formic acid (15 μL) was added to the sample, which was stored at -20 ºC until mass spectrometry analysis.

Liquid chromatography-mass spectrometry (LC-MS) analysis: LC-MS analysis was performed on an LTQ ion trap mass spectrometer (ThermoFisher) coupled to an Agilent 1100 series HPLC. TEV digests were pressure loaded onto a 250 μm fused silica desalting column packed with 4 cm of Aqua C18 reverse phase resin (Phenomenex). The peptides were then eluted onto a biphasic column (100 μm fused silica with a 5 μm tip, packed with 10 cm C18 and 3 cm Partisphere strong cation exchange resin (SCX, Whatman) using a gradient 5-100% Buffer B in Buffer A (Buffer A: 95% water, 5% acetonitrile, 0.1% formic acid; Buffer B: 20% water, 80% acetonitrile, 0.1% formic acid). The peptides were then eluted from the SCX onto the C18 resin and into the mass spectrometer using four salt steps as outlined in Speers et al[6] and Weerapana et al[5].

The flow rate through the column was set to ~0.25 μL/min and the spray voltage was set to 2.75 kV. One full MS scan (400-1800 MW) was followed by 18 data dependent scans of the n^{th} most intense ions with dynamic exclusion disabled.

MS Data Analysis: The generated tandem MS data were searched using the SEQUEST algorithm against version 3.23 of the mouse IPI database. A static modification of +57 on Cys was specified to account for iodoacetamide alkylation. For the SE-labeled samples, a differential modification of +435.3 was specified on Arg, Asp, Glu, His, Lys, Ser, Thr and Tyr, with a modification of +378.3 on Cys. CA-labeled samples were searched with a differential modification of +422.3 on Arg, Asp, Glu, His, Lys, Ser, Thr and Tyr and +365.3 on Cys. UK-labeled samples were searched with a differential modification of +407.3 on Arg, Asp, Glu, His, Lys, Ser, Thr and Tyr and +350.3 on Cys. SEQUEST output files were filtered using DTASelect with default parameters as described in the DTASelect Manual v1.9 [min Xcorr = 1.8 (+1), 2.5 (+2), 3.5 (+3), min DeltaCN = 0.08]. Reported peptides were also required to be fully tryptic and contain the desired probe modification. For each probe, datasets were obtained for 4 different mouse proteomes (soluble heart, kidney, liver and liver membranes) with two independent MS runs, resulting in 8 datasets for each probe. This data was collated into an excel file format and further analysis was performed to screen for peptides that appeared in two or more datasets with two or more spectral counts in each dataset. Peptides that contained two or more missed tryptic cleavage sites within the peptide were removed. These data were then analyzed for peptides with >90% of spectral counts assigned to a single amino acid, which yielded the dataset plotted in **Figure 1b**. The full list of labeled peptides is shown in **Supplementary Information Tables 2, 3, 4** and **5,** which include peptides for which multiple sites of labeling were assigned.

Solution reactivity studies: Amino acid derivatives containing C- and N-terminal protecting groups were purchased from Bachem: Ac-Phe-NH_2, Ac-Asp-OMe, Ac-Lys-NH_2, Ac-Tyr-NH_2 and Cys and His derivatives Ac-cystamine and Ac-histamine were purchased from Sigma. 1 M stocks of each amino acid was made in DMSO and diluted into PBS, pH 7.4 to yield a 10 mM solution. Ac-Phe-NH_2 (10 mM) was used as an internal standard. The pH of these solutions was adjusted to 7.4 and each of the electrophiles (SE, CA and UK) were added at 500 µM final concentration. The reactions were allowed to proceed at room temperature and analyzed by LC/MS after 1 hour and 12 hours using a gradient of 0 to 100% Buffer B in Buffer A in 45 minutes (Buffer A: 95% H_2O, 5% acetonitrile, 0.1% formic acid; Buffer B: 5% H_2O, 95% acetonitrile, 0.1% formic acid).

Generation of X-Press tagged ALDH-1 constructs and mutants: The ALDH-1 construct for subcloning into the eukaryotic expression vector pcDNA4 max/His, which results in the expression of N-terminally X-press/His tagged proteins, was generated as previously reported.[7] Point mutations were generated using the Quickchange procedure (Stratagene). All mutant cDNAs were sequenced and found to contain only the desired mutation.

Recombinant expression of enzymes in eukaryotic cells: ALDH-1 constructs in pcDNA4 max/His were recombinantly expressed in COS-7 cells by transient transfection. COS-7 cells were grown in 100-mm dishes in complete medium (DMEM with L-glutamine, nonessential amino acids, sodium pyruvate and FBS). The cells were transiently transfected using the FuGENE 6 transfection system (Roche) following the manufacturer's protocol. Cells were washed three times with PBS, collected by scraping, suspended in 400 µL of PBS and lysed by sonication. The soluble and membrane fractions were separated by centrifugation at 64,000 *g* for 45 minutes. Protein concentrations for the cytosolic fractions were obtained using the Bio-Rad Dc Protein Assay and stored at -80 ºC till use.

Labeling of ALDH-1 and mutants: For SE-labeling, rhodamine-tagged SE probe (PS-Rh, synthesized as previously described[8]) was used. Protein samples (50 µL of a 2mg/ml solution) were treated with 10 µM of PS-Rh (500 µM stock in DMSO) and the reactions were incubated for 1 hour at room temperature before quenching with 50 µL of 2X SDS-PAGE loading buffer (reducing). Quenched reactions were separated by SDS-PAGE (30 µL of sample/lane) and visualized in-gel using a Hitachi FMBio IIe flatbed laser-induced fluorescence scanner (MiraiBio, Alameda, CA).

For CA labeling, protein samples (50 µL of a 2mg/ml solution) were treated with 10 µM of the CA probe (500 µM stock in DMSO) and the reactions were incubated for 1 hour at room temperature. Click chemistry was performed with 20 µM rhodamine azide, 1 mM TCEP (fresh 50X stock in water), 100 µM ligand (17X stock in DMSO:t-Butanol 1:4) and 1 mM $CuSO_4$ (50X stock in water). The reaction was allowed to proceed at room temperature for 1 hour before quenching with 50 µL of 2X SDS-PAGE loading buffer (reducing). Quenched reactions were separated by SDS-PAGE (30 µL of sample/lane) and visualized in-gel using a Hitachi FMBio IIe flatbed laser-induced fluorescence scanner (MiraiBio, Alameda, CA).

Western blot analysis of ALDH-1 expression: The SDS-PAGE gels from above were transferred by electroblotting onto nitrocellulose membranes, which were blocked in Tris-buffered saline (TBS) with 1% Tween (TBS-Tween) and 3% (w/v) non-fat dry milk overnight at 4 ºC. Blots were then treated with α-X-press antibody (Invitrogen, 1:5000) in TBS-Tween for 1 hour at room temperature. The blot was washed with TBS-Tween three times (10 min/wash), then treated with goat α-mouse IgG horseradish peroxidase conjugate (Bio-Rad, 1:10,000) for 30 min at 25 ºC. Blots were washed with TBS-Tween three times (10 min/wash), treated with SuperSignal chemiluminescence reagents (Pierce) and exposed to film for 0.1 minutes before development.

Generation of Myc/His tagged CLIC constructs and mutants: cDNAs corresponding to mouse CLIC1, CLIC4 and CLIC5 were purchased as expressed sequence tages (Open Biosystems). The constructs for subcloning into the eukaryotic expression vector pcDNA3 myc/His, which results in the expression of C-terminally myc/His tagged proteins, were generated by polymerase chain reaction (PCR) from the corresponding cDNA using the following primers:

CLIC1
Sense primer, 5’-GAAGGATCCATGGCTGAAGAACAACCT-3’
Antisense primer, 5’-CGGCTCGAGTTTGAGAGCCCTGGCCAC-3’

CLIC4
Sense primer, 5’-GAAGGATCCATGGCGCTGTCGATGCCC-3’
Antisense primer, 5’- CGGCTCGAGCTTGGTAAGTCTCTTGGC-3’

CLIC5

Sense primer, 5'-GAAGGATCCATGACGGACTCAGCGACAACT-3'
Antisense primer, 5'-CGGCTCGAGCGATCGGCTGAGGC-3'

The PCR product was digested with *BamHI-XhoI* and subcloned into a *BamHI-XhoI* digested pcDNA3 myc/his-B vector and sequenced. The CLIC4 C35S mutant was generated using the Quickchange procedure (Stratagene). The mutant cDNA was sequenced and found to contain only the desired mutation.

Recombinant expression of CLIC proteins in eukaryotic cells: CLIC1, CLIC4, CLIC5 and CLIC4 C35S constructs in pcDNA3 myc/His were recombinantly expressed in COS-7 cells by transient transfection. COS-7 cells were grown in 100-mm dishes in complete medium (DMEM with L-glutamine, nonessential amino acids, sodium pyruvate and FBS). The cells were transiently transfected using the FuGENE 6 transfection system (Roche) following the manufacturer's protocol. Cells were washed three times with PBS, collected by scraping, suspended in 400 µL of PBS and lysed by sonication. The soluble and membrane fractions were separated by centrifugation at 64,000 *g* for 45 minutes. Protein concentrations for the cytosolic fractions were obtained using the Bio-Rad Dc Protein Assay and stored at -80 ºC till use.

***In vitro* labeling of CLIC proteins:** Protein samples (50 µL of a 1 mg/ml solution) were treated with 20 µM of the CA probe (1000 µM stock in DMSO) and the reactions were incubated for 1 hour at room temperature. Click chemistry was performed with 25 µM rhodamine azide, 1 mM TCEP (fresh 50X stock in water), 100 µM ligand (17X stock in DMSO:t-Butanol 1:4) and 1 mM $CuSO_4$ (50X stock in water). The reaction was allowed to proceed at room temperature for 1 hour before quenching with 50 µL of 2X SDS-PAGE loading buffer (reducing). Quenched reactions were separated by SDS-PAGE (30 µL of sample/lane) and visualized in-gel using a Hitachi FMBio IIe flatbed laser-induced fluorescence scanner (MiraiBio, Alameda, CA).

***In situ* labeling of CLIC proteins:** COS-7 cells grown in 100 mm dishes were transfected with CLIC1, CLIC4, CLIC5 and CLIC4 C35S constructs using Fugene as described previously. The media was removed from the cells and replaced with 10 mL of fresh complete medium containing 20 µM of the CA probe (20 µL of a 10 mM stock in DMSO). The cells were incubated with probe-containing media for 1 hour, washed three times with PBS, collected by scraping, suspended in 400 µL of PBS and lysed by sonication. The soluble and membrane fractions were separated by centrifugation at 64,000 *g* for 45 minutes. Protein concentrations for the cytosolic fractions were obtained using the Bio-Rad Dc Protein Assay and stored at -80 ºC till use. Click chemistry was performed as described above.

Nitric oxide treatment of lysates: Lysates of COS-7 cells overexpressing CLIC 1, CLIC 4, CLIC 5 and CLIC 4 C35S (50 µL of 0.5 mg/ml) were treated with 5 mM diethylamine nitric oxide sodium salt (DEANO, Invitrogen). A 250 mM stock of DEANO was made in 10 mM NaOH and diluted 1:50 into the 50 µL reaction. The lysates were treated with

DEANO for 1 hour, followed by addition of 20 μM of the CA probe for 15 minutes. Click chemistry was performed as described above.

Oxidized glutathione (GSSG) treatment of lysates: Lysates of COS-7 cells overexpressing CLIC 1, CLIC 4, CLIC 5 and CLIC 4 C35S (50 μL of 0.5 mg/ml) were treated with 2 mM GSSG for 1 hour, followed by addition of 20 μM of CA for 15 minutes. Click chemistry was performed as described above.

Western blot analysis of CLIC expression: The SDS-PAGE gels from above were transferred by electroblotting onto nitrocellulose membranes, which were blocked in Tris-buffered saline (TBS) with 1% Tween (TBS-Tween) and 3% (w/v) non-fat dry milk overnight at 4 ºC. Blots were then treated with α-myc antibody (Invitrogen, 1:5000) in TBS-Tween for 1 hour at room temperature. The blot was washed with TBS-Tween three times (10 min/wash), then treated with goat α-mouse IgG horseradish peroxidase conjugate (Bio-Rad, 1:10,000) for 30 min at 25 ºC. Blots were washed with TBS-Tween three times (10 min/wash), treated with SuperSignal chemiluminescence reagents (Pierce) and exposed to film for 0.1 minutes before development.

References:

1. Speers, A. E. & Cravatt, B. F. *Chem. Biol.* **11**, 535-46 (2004).
2. Muller, T. E., Lercher, A. A., Nhu, N, V. *AIChE Journal* **49**, 214-224 (2003).
3. Kusama, H., Yamabe, H., Onizawa, Y., Hoshino, T. & Iwasawa, N. *Angew. Chem. Int. Ed. Engl.* **44**, 468-70 (2005).
4. Gansauer, G., Pierobon, M, Bluhm, H. *Synthesis* **16**, 2500-2520 (2001).
5. Weerapana, E., Speers, A. E. & Cravatt, B. F. *Nat. Protoc.* **2**, 1414-25 (2007).
6. Speers, A. E. & Cravatt, B. F. *J. Am. Chem. Soc.* **127**, 10018-9 (2005).
7. Adam, G. C., Burbaum, J., Kozarich, J. W., Patricelli, M. P. & Cravatt, B. F. *J. Am. Chem. Soc.* **126**, 1363-8 (2004).
8. Adam, G. C., Sorensen, E. J. & Cravatt, B. F. *Nat. Biotechnol.* **20**, 805-9 (2002).