

**Supplementary Table 1 - Proteins identified from the Lysosomal Integral-membrane protein fraction: Peptide Details****1. Metabolism**

	Accession	Calculated MW	1D-gel MW (approx kDa)	Fraction	Intepreted Spectra	Unique Peptides	Peptides*	Abundance factor
Aldehyde dehydrogenase 3-A2	13929028	54.5	55 FT		2	2	IAFGGETDEATR YIAPTILTDVDPNSK	36.7
apyrase	21426787	45.6	65 250mM		2	2	QVGALVPTHGFSSFK AVPWWILSDGDGAVEK	43.9
Arachidonic acid epoxygenase	13929204	57.1	55 FT		4	4	SLDPANPR ACVGESLAR IEEEKDNLK VQEEAWCLVEELQK	70.1
aryl sulfotransferase	1091600	34.2	50 250mM		2	1	(K)CPGVPSGLE TLEETPAPR(L) 955.57(2+), (1142.57)SP(1496.76), 37	29.2
ATP synthase alpha subunit	6729934	55.3	40 250mM		8	4	TGAIVDVPVGDELLGR EVAFAAQFGSDLAATQQLLSR ILGADTSVDLEETGRVLSIGDGIAR EVAFAAQFGSDLAATQQLLSRGVR	72.3
ATP synthase f0 beta subunit	19705465	28.9	40 250mM		2	2	HYLFDVQR LGLIPEEFFQFLYPK	69.2
ATP synthase F1 complex O subunit	20302061	23.4	35 80mM		3	3	VGQLLKDPK VSLAVLNPIYIK LDQVEKELLR	128.2
ATP synthase gamma Chain	39930503	32.9	45 250mM		4	3	HLIIGVSSDR VYGTGSLALYEK THSDQFLVSFK	91.2
Betaine-homocysteine methyltransferase	13540663	45.4	46 250mM		34	5	EATTEQQLR AIAEELAPER VNEAACDIAR AGPWTPEAAVEHPEAVR LNAGEVVIGDGGFVFALEKR	110.1
carbamoyl-phosphate synthetase 1	8393186	165	55 80mM		3	2	IPRWDLDR GQNQPVLNITNR	12.1
Catalase	6978607	60	70 250mM		3	2	LAQEDPDYGLR NFTDVHPDYGAR	33.3
CYP2A1	6978741	56.5	46 FT		4	3	YLPGPQQQIIK DVYSSITQLSER EALVDQAEFEFSGR	53.1
CYP2C13	25453406	56.3	46 FT		3	1	(R)QSLTNFSK(T) 462.66(2+), (381.21)NTLS(796.42), 54	17.8
CYP2C22	19924039	56.7	70 250mM		22	2	YIDFVPIPLPR IQEEVVYLLEALR	35.3
CYP2C29	9506529	57.5	55 FT		1	1	(R)ICAGEALAR(T) 480.68(2+), (430.28)EGAC(847.41), 40	17.4
CYP2D2	6978747	56.8	55 FT		2	1	(K)AVSNVIA SLVYAR(R) 681.77(2+), (708.40)AIVNS(1192.67), 41	17.6
CYP4A3	28461155	59.2	65 250mM		7	2	ELSSPVTFPDGR HSHAYLPFSGGAR	33.8
Cytochrome b5	11560046	15.3	25 80mM		11	5	YYTLEEIQK TYIIGELHPDDR FLEEHPGGEVLR	326.8

dopa/tyrosine sulfotransferase	11968092	34.9	45 250mM	1	ELSKTYIIGELHPDDR EQAGGDATENFEDVGHSTDAR 1 (M)GTAEDVFRK(D) + N-Acetyl (Protein) 532.84(2+), (450.28)VDEA(864.46), 34	28.7
Epoxide hydrolase 1	6978813	47.8	46 FT	7	4 ASPPLEGSR ELEDGGLER LISYSYMER SFYTMTPLLGQR + Oxidation (M)	83.7
glyceraldehyde-3-phosphate dehydrogenase	8393418	36	40 80mM	5	1 (R)GAAQNIIPASTGAAK(A) 685.38(2+), (702.38)IIN(1042.59), 41	27.8
L-gulono-gamma-lactone oxidase	11560006	51.2	46 FT	2	2 NADVFAQAR GDDILLSPCFQR	39.1
Peroxiredoxin 1	16923958	22.3	35 40mM	4	3 IGHPAPSFK ATAVMPDGQFK + Oxidation (M) QITINDLPVGR	134.5
Retinol dehydrogenase type III	31377477	35.9	25 FT	6	5 ELTYFGVK TNVTNMER VLAACLTEK VAIIPEGGFK VVNIASTMGR + Oxidation (M)	139.3
similar to NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 9	34858473	42.6	50 250mM	6	4 EAGVER NFD FEDVFVNIPR SSVSGVVATVFGATGFLGR LMGDLGQLIFLEWDAR	93.9

## 2. Immunity

CD1 antigen	5420461	38.9	55 40mM	12	7 DIKEIVK FHGTSWQK GDQEQGGTHR QEKPAWLSR GLLEAGKPDLEK VPEAPSWLDLPIK TDSVVWLGLDQTHR	179.9
Fc receptor	15375322	40.4	55 40mM	6	6 LLGHLER SKEQLFLEAIR ESEFLTSCPER QNLEWKEPPSMR KESEFLTSCPER ARPGNSGSSVLTCAAFSFYPPELK	148.5
macrophage expressed gene 1	12018298	74.4	40 80mM	7	2 GITNHLVAIDR VQSFGGIPFYPGITLETWQK	26.9
MHC class I alpha chain	940825	39.3	46 FT	1	1 (R)DSSQSSDVSLPDCKA(-) 798.22(2+), (590.26)LSV(889.45), 44	25.4
polymeric immunoglobulin receptor	27151742	86	120 80mM	15	3 SSVTFECDLGR DAPEEEAMESSVR EIQNAGDQAQENR	34.9
similar to Igh-6 protein	34935297	79.9	30 80mM	7	2 HPPAVYLLPPAR GFSPADIFVQWLQR	25.0
Similar to Immunoglobulin joining chain	34876693	26.4	20 40mM	6	3 CYTAMVPLR MVQTALTPDSCYPD	113.6

### 3. Biosynthesis

Alpha-mannosidase II	34877940	87	120 FT	36	15 LYQSDPSK AGFSHMLIQR LFQSLNSLEK WWDIIDNPK VLLAPLGDDFR NIIQLSAQEPR TAEILYHLALK IIGDSAFLILK KNIIQLSAQEPR LLAENNEIISNIR FLSSPHYTTLTAR NLGLFQHHDAITGTAK IQFGTLDYFDALK RNLGLFQHHDAITGTAK YGCPWGVPEAISPGNVQSR	172.4
Core 1 beta 1,3-Galactosyltransferase	12621124	42.7	35 FT	10	5 DPTGK FVDAFKTEK YQPALPENILK QGYMSGGAGYVLSK VLCWVMTSPQNLEK	117.1
Elongation factor Tu, similar to RIKEN cDNA 2300002G02	34859187	49.8	70 250mM	2	1 (K)AEAGDNLGALVR(G) 593.31(2+), (387.27)AGLN(742.46), 43	20.1
eukaryotic translation elongation factor 1 alpha	15805031	50.4	60 250mM	4	2 NVSVKDVR IGGIGTVPVGR	39.7
Heat shock 70kD protein 5, GRP78, BiP	25742763	72.2	65 250mM	11	6 ELEEIVQPIISK TWNTPSVQQDIK ITPSYVAFTPEGER IINEPTAAAIAYGLDK IINEPTAAAIAYGLDKR IEIESFFEGEDFSETLTR	83.1
Microsomal glutathione S-transferase 1	19705453	17.5	15 FT	7	2 MMFLSSATAFQR IYHTIAYLTPLPQPNR	114.3
N-acetylglucosaminyltransferase I	13540685	51.8	55 250mM	16	6 GIVTFQFR WALGQIFNK QPDLSNIAVQPDHR LNQQFVPFTQLDLSYLQR EAYDRDFLAQVYGAPQLQVEK FIKLNQQFVPFTQLDLSYLQR	115.8
N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 1; heparan sulfate-N-deacetylase/N-sulfotransferase	13242253	101	70 250mM	8	5 FLHSWTNLR ALFDTQNELR VLTILINPADR LQTLPPVQLAQK	49.5
ppGaNTase-T2	46877109	65	67 FT	3	3 SGQDPYAR QGNPVAPIK NVPYGNISQR	46.2
Protein disulfide isomerase (ER60)	91897	57	75 80mM	1	1 (R)LAPEYEAATR(L) 596.32(2+), (347.20)AAEYEP(1007.48), 89	17.5

Ribophorin I	6981486	68.3	30 80mM	1	1 (R)ASSFVLALEPELESRL) 824.43(2+), (730.37)ELAL(1156.62), 32	14.6
ribosomal protein L13	13592055	24.2	40 250mM	7	3 TIGISVDPR VDTWFNQPAR LATQLTGPVMPPIR	124.0
ribosomal protein L6	16758864	33.6	40 250mM	1	1 (R)YYPTEDVPR(K) 570.30(2+), (272.17)VDETP(813.41), 25	29.8
ribosomal protein L7, cytosolic [validated] - rat	11383729	30.3	40 250mM	7	2 KVLQLLR IALTDNSLVAR	66.0
ribosomal protein S3, cytosolic [validated] - rat	70850	26.8	40 250mM	3	1 (R)ELAEDGYSGVEVR(V) 712.43(2+), (403.23)VGSYGDEA(1181.54), 69	37.3
ribosomal protein S3a, cytosolic [validated] -	8394221	30.1	40 250mM	3	1 (R)VFEVSLADLQNDEVAFR(K) 976.62(2+), (1091.55)DALSVE(1705.84), 66	33.2
<b>ribosomal protein S4</b>	227229	29.8	35 250mM	6	5 LSNIFVIGK GIPHLVTHDAR TIRYPDPLIK HPGSFDVVHVK ECLPLIIFLR	167.8
ribosomal protein S6	6677809	28.8	40 250mM	3	1 (R)MATEVAADALGEEWKGYVVR(I) 732.45(3+), (1036.56)EGLA(1406.74), 44	34.7
<b>Sialyltransferase 1 (ST6Gal1)</b>	115446	47.1	55 FT	60	13 EFQMPK FSVEALR CAVVSSAGSLK VSYKGPGPGVK EIDNHDAVLR TDVCYYHQB LMNSQLVTTEK GSDYEALTLQAK LMNSQLVTTEKR VAMGSASQVVFNSNK FNGAPTDNFQQDVGSK HLNEGTDEDIYLFQK	276.0
Sialyltransferase 4A (ST3Gal1)	6677957	39.3	46 FT	6	2 APTVGFEADVGSR CAVVGNSGNLQ	50.9
Sialyltransferase 8 (GT3 alpha 2,8-sialyltransferase) C	6981540	44.3	55 FT	1	1 (K)ENIFTTPK(Y) 475.18(2+), (244.17)TTFI(706.41), 55	22.6
similar to 60S RIBOSOMAL PROTEIN L3 (L4)	38454246	52.3	40 250mM	3	1 (R)HGSGLFLPR(K) 492.28(2+), (589.35)LSG(846.48), 34	19.1
similar to 60S ribosomal protein L7a (Surfeit locus protein 3) (PLA-X polypeptide)	34853132	33.7	40 250mM	4	3 HWGGNVLGPK  AGVNTVTTLVENK LKVPPAINQFTQALDR	89.0
similar to 60S ribosomal protein L8	27685597	28.3	35 250mM	5	3 DIIHDPGR AVVGVVAGGGR VFRDPYR	106.0
Similar to Heparan sulfate 2-sulfotransferase	34860929	42	46 250mM	3	2 FGDDYRPGLR LVSYYYFLR	47.6
similar to ribosomal protein S8	38049330	24.4	30 250mM	8	2 QWYESHYALPLGR IIDVVYNASNNELVR	82.0
similar to Vesicular integral-membrane protein VIP36 precursor	27682691	40.7	50 250mM	19	6 LFQLTVER DNVDDPTGNFR	147.4

UDP glycosyltransferase 2 family, polypeptide	13928718	61.4	55 FT	8	1 TPATLGPNTR LLDVWTYELPR	16.3
UDP-glucuronosyltransferase 2 family, member 5	34876712	61	55 FT	1	1 (K)IPATLGPNTR(V)  520.23(2+), (487.26)GLTAP(926.51), 52	16.4

#### 4. Membrane receptors/Signaling and Cell adhesion

Asialoglycoprotein receptor 1	7705290	33.4	35 20mM	10	3 ALTTQGER LVESQLEK WVDGTDYETGFK	89.8
Asialoglycoprotein receptor 2	8392926	35.5	67 40mM	5	2 HFPLDLR WVDGTEYR	56.3
carcinoembryonic antigen-related cell adhesion molecule CD59	13929060	50.7	82 FT	5	2 GTTLNPDSEIAR ELGSVTLTCFSK	39.4
	6978635	14.4	15 FT	2	1 (R)CCQADLCNK(S) 584.62(2+), (421.19)LDAQ(848.39), 37	69.4
cell surface antigen RB13-6 - rat	1363274	100.9	60 80mM	7	2 IATLLQWLDLPK NIPQDFFTFNSEEIVR	19.8
<b>E-Selectin ligand, Golgi apparatus protein 1</b>	6677905	137	160 FT	60	21 TMLQCLK LDPALQDK NSELMDPK + Oxidation (M) FCPEADSK EAEKEPK IQVSELCK CNVENLPR ECAEEPVGK GGAGPGGTGGGWK MVEDCEHR MACKEDVLK IQVSELCKK RFCPEADSK HHCAAITPGR QITQNTDYR LSSDCEDQIR FCENTQAGEGR IIQESALDYR ALNEACESVIQTACK QVSSECQGEMLDYR LGEKDAHSQGEVVSCLEK	153.3
guanine nucleotide-binding protein alpha 11	13591951	42.2	60 250mM	1	1 (R)IATVGYLPTQQDVLR(V) 837.48(2+), (956.52)LYGV(1388.75), 36	23.7
Harvey rat sarcoma oncogene, subgroup R	6677819	23.9	20 FT	1	1 (K)ICTVDGIPAR(L) 551.21(2+), (513.31)DVT(828.46), 37	41.8
Lipoprotein receptor-related protein	34865759	523	250 80mM	14	6 GVAGAQPVTLLR TTLLAGDIEHPR	11.5

					AALSGANVLTIEK HTVDQTRPGAFAER DGILFWTDWDASLPR IFFSDIHFGNIQQINDDGSGR	
OX47	111503	34	46 FT	2	2 GNINVEGPPR VLQEDTLPLDQMK	58.8
p21/H-Ras-1 (c-H-ras)	131873	21.6	30 80mM	4	1 (R)QGVEDAFYTLVR(E) 699.37(2+), (274.19)LTYFA(869.49), 56	46.3
phosphatidylinositol 4-kinase type II	16758554	54.7	60 250mM	5	4 IIAVFKPK LVVLDYIIR IYQGSSGSYFVK NDFPEDPEFEVVVR	73.1
Progesterone receptor membrane component	11120720	24.6	25 80mM	3	2 KFYGPEGPYGVFAGR IVRGDQPGASGDNDDEPPPLPR	81.3
protein tyrosine phosphatase, receptor type, F	9507013	212	150 80mM	2	2 TGEQAPSSPPR TDEDVPSGPPR	9.4
Purinergic receptor P2X4	13928806	44.1	67 FT	8	4 AASLCLPR NNIWYPK YVEDYEQGLSGEMNQ TCEVAAWCPVENDVGVPPTPAFLK	90.7
Rap2B	13386338	20.7	30 80mM	1	1 (K)ASVDELFAEIVR(Q) 674.85(2+), (387.27)EAFLED(1091.57), 35	48.3
Rras2, related RAS viral (r-ras) oncogene	13399308	23.6	35 80mM	1	1 (R)QVTQEEGQQLAR(Q) 693.86(2+), (672.38)EEQT(1159.57), 47	42.4
similar to Cux/CDP(1B1); Cux/CDP	34873366	157	55 250mM	2	1 (R)EIAQLVEDVQR(L) 650.34(2+), (745.38)LQA(1057.56), 34	6.4
similar to GTP-binding regulatory protein alpha-13 chain	34875240	45.3	55 250mM	1	1 (R)VFLQYLPAR(A) 610.38(2+), (456.29)LYQL(973.58), 33	22.1
similar to MEK binding partner 1	34860783	13.6	25 40mM	3	2 DGVVPVK ADDLKR + N-Acetyl (Protein)	147.1
<b>similar to pituitary tumor-transforming gene 1 protein-interacting protein</b>	34852416	17.2	20 FT	13	4 SCEECLR ACLDYPVR ILPPASLCK ACLDYPVRK KILPPASLCK	232.6
similar to ras-related C3 botulinum toxin substrate 1 isoform Rac1b	34870449	52.7	25 80mM	7	4 TVFDEAIR AVLCPPPVK AVLCPPPVK LTPITYPQGLAMAK HHCPNTPILVGTK	75.9
similar to RIKEN cDNA 1300006M19	34870394	65.3	35 250mM	1	1 (R)NVVEQFNPGLR(N) 636.92(2+), (442.28)NFQEV(1059.56), 39	15.3
similar to Transferrin receptor protein 2 (TfR2)	34871536	89.5	65 250mM	4	3 SAVGTAILELVR GRLPAAVLAVAQLAGQLLIR HIFLGQGDHTLGALVEHLR	33.5
Toll-like receptor 3	33438238	103	67 40mM	20	10 YLSLKR LTPHSFR SNPFKNQK LDLSSNPLK YNVADCSHLK LEPELCQILPLLK	97.1

DVGNDAFSWLPHLK  
SLIKLDLSHNGLSSTK  
LGTWVQLENLQELLAK  
YSQLALLDAGFNSISKLEPELCQILPLLK

## 5. Molecular transport

ATP-binding cassette, sub-family B (MDR/TAP), member 6	18034785	93.8	175 80mM	5	3 SHIGVVPQD TVLFNDTIANNIR TILKAPDIILLDEATSALDTSNER VTAGDSEIQAAAQAAGIHDAILSFP EGYETQVGER	32.0
ATP-binding cassette, sub-family C (CFTR/MRP), member 2; Canalicular multispecific organic anion transporter; multidrug resistance associated protein 2	6978669	174	175 80mM	11	5 ALELAHLR YLGGDDLD TSAIR LTIIPQDPILFSGSLR ILESAGGQIIIDGIDVASIGLHDLR SFVSGQLQLGLLSEVTEGGDNLSIGQR	28.7
Chloride ion pump-associated 55 kDa protein	21489987	56.7	50 80mM	1	1 (K)IAIVGAGIGGTSSAYYLR(K) 885.01(2+), (960.48)GGIGAG(1372.69), 30	17.6
Niemann Pick C1	6679104	145	250 80mM	34	4 ALGLLCGR CRPLTPEGK DVEAPSSNEK LQEETLDQQLGR	27.6
Peptide/histidine transporter	21426791	62.6	250 FT	1	1 (R)SGEGLGVFQQSSK(H) 662.30(2+), (449.24)QFVGL(993.54), 32	16.0
similar to 2810423E13Rik protein	34856883	62.5	175 250mM	2	2 SYIAGATSLQER GLVGFAGNVA VVR	32.0
similar to Calcium-binding mitochondrial carrier protein Aralar2 (Solute carrier family 25, member 13) (Citrin)	7657583	74.8	67 80mM	16	8 LQVAGEITTGPR GLLPQLLGVAPEK YLNIFGESQPNPK ITLPAPNPDHVG GYK SSPQFGVTLLTYELLQR IAPLEEGMLPFNLAE AQR FGLGSIAGAVGATAVYPIDLVK HLTYAEFTQFLL EIQLEHAK	107.0
similar to MLN64 N-terminal domain homolog (STARD3 N-terminal like protein)	27686679	26.8	25 FT	1	1 (R)LLLVDASER(A) 572.32(2+), (462.23)DQVL(917.47), 30	37.3
Similar to Proteolipid protein 2	46485405	16.8	15 FT	1	1 (R)HTAAPT DPTDGP(-) 590.15(2+), (116.07)GD(288.12), 33	59.5
similar to putative protein, with at least 9 transmembrane domains, of eukaryotic origin (43.9 kD) (2G415)	34863028	39.6	170 FT	8	1 (R)QSDSSVEPR(Q) 502.69(2+), (587.32)SDS(876.41), 44	25.3
Similar to Solute carrier 31, member 1	19424310	21.2	25 FT	1	1 (R)KSQVSIR(Y) 409.24(2+), (375.24)VQS(689.39), 47	47.2
similar to Tm9sf1 protein	34874167	90.3	35 250mM	2	2 SDELLGLTH TYSVR QAIEELYFFEVVDDLPIR	22.1
similar to transmembrane 9 superfamily	34876089	76.5	250 FT	2	2 TNQIPR FCNPGFPIGCYITDK	26.1
similar to Transmembrane 9 superfamily protein member 4	34859018	75.5	30 250mM	10	3 FEVIPQSIR ITEEYYVHLIADNLPVATR LVAERITEEYYVHLIADNLPVATR	39.7
solute carrier family 25 (mitochondrial phosphate carrier; adenine nucleotide	20806141	39.8	170 80mM	2	1 (R)IQTQPGYANTLR(E) 681.42(2+), (794.42)PQT(1120.58), 46	25.1

translocator), member 3; phosphate carrier, solute carrier family 25, member 4; mitochondrial adenine nucleotide translocator solute carrier family 29 (nucleoside transporters), member 3	32189355	33.1	25 FT	2	2 TAVAPIER YFPTQALNFAFK	60.4
vATPase 100kDa a3 subunit	51036680	52.2	170 FT	3	2 AVHTPPLGPILK DAPSTSSVAPASR	38.3
	7140942	94.1	250 80mM	10	3 IQEETDRLAQELR FTSSSQGIVDAYGVGR DLPTVQQALQSGSSEEGVSAVAHR	31.9
vATPase Subunit B	17105370	56.9	55 FT	2	2 TPVSEDMLGR AVVQVFEGTSGIDAK	35.1
<b>vATPase Subunit D(V0)</b>	3955100	40.7	30 80mM	55	9 MVVEFR + Oxidation (M) SIAELVPK FFEHEVK LKEQECR ADDYEQVK AKIDNYIPF LYPEGLAQLAR NVADYYPEYK LLFEGAGSNPGDK	221.1
vATPase Subunit D(V1)	40786463	28.2	30 250mM	7	3 VNAIEHVIIPR RVNAIEHVIIPR TLAYIITELDER	106.4
vATPase Subunit E	1718091	26.1	30 80mM	3	1 (R)YQVLLDGLVLQGLYQLLEPR(M) 777.46(3+), (272.17)ELLQYLGQLV(1428.82), 73	38.3
vATPase Subunit G	27714615	13.8	20 250mM	1	1 (M)ASQSQGIQQLLQAEKR(A) + N-Acetyl (Protein) 913.99(2+), (303.21)EAQLLQQ(1113.64), 58	72.5
vATPase Subunit H	14318722	56.2	55 FT	3	2 GAVDAAVPTNIIAAK QLQSEQPQTAAAR	35.6
Voltage-dependent anion channel 1	6755963	30.7	35 80mM	11	4 VTQSNFAVGKYK LTFDSSFSPNTGK AVPPTYADLGKSAR + N-Acetyl (Protein) WTEYGLTFTEKWNTDNTLGTEITVEDQLAR	130.3

## 6. Membrane structure and Lipid Rafts

<b>CD36 antigen-like 2 (LIMPII)</b>	16758914	54.4	82 40mM	116	10 IVEWNGK AVDQTIEK EIIIEAMLK + Oxidation (M) FQINTYVK RFQINTYVK LDDFVETGNIR GQGSTDEGTADER KLDDFVETGNIR NQSVDGPTVDLIR DETLYIFPSDFCR	183.8
DAMP-1 protein	37693510	19.9	25 FT	10	2 LNQELENLR VSQTQEQQAR	100.5
<b>Flotillin-1</b>	13124118	40.1	70 80mM	54	20 QQIEEQR VQVQVVER SPPVMVAGGR VRKPAAEER	498.8



					GEAEFAVGAR ATYDIEVNTR ISLNTLTINVK KATYDIEVNTR MRGEAEFAVGAR HGVPISVTGIAQVK AQADLAYQLQVAK AQQVAVQEQEIAR VFVLPCIQQIQR RAQADLAYQLQVAK AQQVAVQEQEIARR DIHDDQDYLHSLGK LTGVSIQVNHKPLR QQIEEQRVQVQVVER VTGEVLDILSRLPESVER TEAEIAHIALETLEGHQR	
<b>Flotillin-2</b>	13124119	47.4	46 FT	31	15 ISAPLTK AFELQK TQTAVVQR EVAAPDVGR LKAEAYQK IQQIAEGEK SAFSEEVNIK DADIGVAEAER QVLLAQAEAEK IQQIAEGEKVK QIAVEAQEILR ISLEIMTLQPR + Oxidation (M) VDEIVVLSGDNSK MALVLEALPQIAAK TAEAQLAYELQGAR	316.5
Golgi-associated protein GCP360	20302065	365	250 FT	20	9 KLQAALISR LQVEAQELK LTAALSSSQKR NTLSEETRNLK ILLDDTQSEAAR AAAAEELQALVQR FGDAIQTKEEEV SSSQTQILPTQYQR DLNEVITIKDSQQR	24.7
<b>LAMP1</b>	6981144	42.2	100 FT	213	10 CVSDIR APALFEVK SHAGYQTI AFNINPSDK ALQASVGNSYK GPDTV DSTTDIK CNSEEHIFVSK YSGTCGAQLVTLK ALALNVFSVQVQAFR AFNINPSDKYSGTCGAQLVTLK	237.0
<b>LAMP2</b>	40254785	45.6	100 FT	49	8 HEQVCK	175.4

					TFPGAVPK EQVVSISR HHTGYEQF YLDFIFAVK TFQINTFNLK YLDFIFAVKNEK GILTVIIPVGSQPLGVIFK	
<b>Prohibitin</b>	6679299	29.8	25 80mM	15	9 AVIFDRFR QVAQQEAER QVSDDLTER FVVEKAEQQK IYTSIGEDYDER ELVSRQVSDDLTER NITYLPAGQSVLLQLPQ AAELIANSLATAGDGLIELR AAIISAEGDSKAAELIANSLATAGDGLIELR	302.0
similar to band 7 protein (35.3 kD) (4N53)	34863101	39.4	60 80mM	5	1 (R)ISEIEDAAFLAR(E) 667.89(2+), (648.38)DEIES(1221.61), 51	25.4
Similar to Macrosialin (CD68)	34870966	35.3	82 FT	44	3 LQAAQLPDK ILYLTQGGK ILYLTQGGKK	85.0
similar to MAL2A	32693285	19.4	170 80mM	9	1 (M)SAGGAAPPPNPAPVSPAPR(I) + N-Acetyl (Protein) 1000.11(2+), (1152.62)PPPVA(1613.88), 39	51.5
<b>B-cell associated protein 37; similar to repressor of estrogen receptor activity</b>	34858436	33.3	60 80mM	33	8 LGLDYER FNASQLITQR VLPSIVNEVLK ESVFTVEGGHR LLLGAAYGVVR IPWFQYPIIDIR IGGVQQDTILAEGLHFR IYLTADNLVNLQDESFR	240.2
<b>Stomatin (Erythrocyte band 7 integral membrane protein 7.2b)</b>	7710018	31.5	25 80mM	27	8 LLAQTTLR AMAAEAEAR + Oxidation (M) DVKLPLQLQR VIAAEGEMNASR YLQTLTTIAAEK TISFDIPPQEVLT EASMVITESPAALQLR	254.0
<b><u>7. Hydrolyases/Co-factors</u></b>						
5' nucleotidase, ecto	11024643	64.3	40 80mM	4	2 VIYPAVEGR YGQSTGEFLQVGGIHVYDISR	31.1
beta-galactosidase	192185	73.2	65 FT	2	2 FYWEDR QYFGYVLYR	27.3
beta-glucuronidase	8393510	73.5	60 250mM	3	2 LVQSGPLTTFR LLDEDGKIVAR	27.2
Cathepsin F	34861419	24	25 40mM	6	3 IAAWLAQK ACMGGLPSNAYTAIK GSGACGVNTMASSAVVN + Oxidation (M)	125.0
Cathepsin L	67650	38.2	25 40mM	2	2 GCVTPVK	52.4

Cathepsin Y	34328540	34.8	25 80mM	1	1 (R)VG DYGSLSGR(E) 505.77(2+), (319.17)LSGYDG(911.42), 29	28.7
Dipeptidylpeptidase IV	6978773	88.7	100 80mM	87	12 AGAVNPTVK ISLQWLR TVWIPYPK TYTLADYLK VLEDNSALDK GPGLPLYTLHR WEYYDSVYTER LGTLEVEDQIEAAR HSYTASYSIYDLNKR FRPAEPHFTSDGSSFYK LNWATYLASTENIIVASFDGR ADAAFRNLWATYLASTENIIVASFDGR	135.3
GM2 ganglioside activator protein	48976085	21.9	20 40mM	3	2 EVAGFWVK SLTLQPDPIVPGDVIVSAEGK	91.3
kidney aminopeptidase M; Leucine arylaminopeptidase 1	13591914	109	150 80mM	4	2 VVATTQMQAADAR ALGDTAPNIDTTELVER	18.3
<b>Lysosomal Acid Phosphatase</b>	8392842	48.7	67 80mM	22	9 QEVYVR HGDRSPVK LTEPVIPK FVTLLYR FPLGPCPR CPLQDFLR WPQGFGQLTK LLKFPLGPCPR KAPWPLTLPGCPHR	184.8
<b>Nicastrin</b>	27819651	79	100 FT	28	13 VVVAATR EPGAVSY LKGETSR APDVTTLPR LLYGFLVR ADVLVAPR ALADVATVLAR ADVLVAPREPGAVSY LENIDSFVELGQVALR WVLTGPNPPYMLLEGK NQVEDLLVTLEQSGADTPQVVLSR SFFWNVAPGAESAVASFTQLAAAEALHK TLWNELGNLAYDDFSFPIFILLEDENETK	164.6
plasma glutamate carboxypeptidase	13928880	52	90 250mM	2	1 (R)LGLLVDTVGPR(L) 570.36(2+), (529.31)DVLLG(1026.59), 42	19.2
Prosaposin	6981424	62.9	15 FT	5	2 LVTDIQTAVR ACSLLPAPASTK	31.8
Protective protein for beta-galactosidase	6679437	54.4	20 80mM	6	3 FLNKEPY AAFTMFSR + Oxidation (M) RPWLVDYGESGEQVAGFVK	55.1
X-prolyl aminopeptidase (aminopeptidase P) 2, membrane-bound	16924020	76.5	100 80mM	8	6 LVFPAATSGR ENIGPELQR VLMGNIDLSR	78.4

TVHWGTPTAFQK  
 NLIDVSLLSPEQLQYLNR  
 SSDIPYNPFFYSYTLTLDSSIR

## 8. Secreted

Alpha-1-Inhibitor III	12831225	165	250 FT	4	2 VTAS PQSLCGLR VQTVPLTCNNPK	12.1
Alpha-2-HS-glycoprotein (fetuin)	6978477	38.8	67 40mM	8	7 CNLLAEK HLLQGFR LGGEVSVACK QILNQIDKVK VGQPGDAGAAGPVAPLCPGR HAFSPVASVESASGEVLHSPK AQNVPPFPVSTLVEFVIAATDCTGQEVTPAK	180.4
Apolipoprotein A-V	18034777	41.4	60 250mM	25	12 LAQDPEGIR LAQDPEGIRK ELFHPYAER SVAPHAVASPAR HQQVGWNLEGLR QLQQUEEEVSTR LVTGIGHHVQELHR NLDQLRDELSTFIR QLQQUEEEVSTRLEPYMAAK QQLKPYTVELMEQVGLSVQDLQEQLR	289.9
Apolipoprotein b	34863099	539	250 FT	7	4 SPSSSDINK LQDLQVLGK ITDNDVLIALDSAK IAQDGVSTSATTNLK	7.4
Apolipoprotein E	1703338	36	15 80mM	47	10 DRLEEV LGPLVEQGR LEEVG NQAR LGADMEDLR LQAEIFQAR MEEQTQQIR GRLEEVGNQAR TANLGAGAAQPLR TANLGAGAAQPLRDR ELEEQQLGPVAEETR	277.8
Complement component 9	16924006	64.9	15 FT	4	1 (K)GVELSDVKR(C) 501.68(2+), (402.28)DSLE(846.47), 58	15.4
dermcidin precursor; AIDD protein	16751921	11.3	25 20mM	6	5 KAVGGLGK ENAGEDPGLAR DAVEDLESVGK SSLLEKGLDGAK LGKDAVEDLESVGK	442.5
Epithelin/granulin precursor	8393493	68.3	15 FT	30	4 CMDEGYCQK LNTGAWGCCPFTK TQCPDDSTCCCLPTGK CDLEVSCP DGYTCCR + Pyro-cmC (N-term camC)	58.6
ferritin light chain - rat	2119695	20.8	30 80mM	29	8 LVNLHLR	384.6

					DDVALEGVGHFFR QNYSTEVEAAVNR ALFQDVQKPSQDEWGK TSQIRQNYSTEVEAAVNR + N-Acetyl (Protein) VAGPQPAQTGVAQASLGEYLFER RVAGPQPAQTGVAQASLGEYLFER ASYTYLSLGFFDRDDVALEGVGHFFR	
Fibrinogen Gamma-A chain	71829	50.1	80 250mM	3	2 TSTADYAMFR YLQDIYTSNK	39.9
Fibronectin 1	9506703	275	140 80mM	10	4 APITGYIIR ATGVFTTLQPLR WLPSTSPVTGYR VTWAPPPSIELTNLLVR	14.5
inter-alpha-inhibitor H4 heavy chain	9506819	104	140 80mM	6	5 LGDGLVGSR VLGIDYPATR IPAQGGTNINK TTFELIYQELLQR VVEQEGTTPEESPNPDHPR	48.1
Peptidylprolyl isomerase C-associated protein (mama)	20806135	64.6	82 40mM	9	4 LVNGASASEGR SELAVSSELDLLK LASAYGATELQGYCGR AVDQWSTATGASHGDVER	61.9
Pregnancy Zone protein	21955142	168	250 FT	4	4 LLLQEV LQDQSNQIR LADLPGNYITK YNILPEAEGEAPFTLK	23.8
Serum Amyloid P	8392903	26.2	20 40mM	2	2 ESETDYVK SQSLFSYSVNSR	76.3
similar to cellular repressor of E1A-stimulated genes CREG	34880832	25.1	35 80mM	2	1 (R)FVTHVSDWGLATISTR(E) 938.98(2+), (905.51)WDSV(1392.71), 54	39.8
Vitronectin	9507241	55.4	60 250mM	11	3 IYITGSTFR FEDGVLDPDYPR LIQDVWGIEGPIDAAFR	54.2

## 9. Unknown/Uncharacterized

2810022L02Rik protein	15928581	62	45 80mM	1	1 (K)SSGHNKPSEGK(A) + Guanidination (K) 585.32(2+), (938.48)GS(1082.53), 55	16.1
<b>Expressed sequence AV006840</b>	20846843	10.7	25 40mM	7	2 GREPIDV TSALTQGLER + N-Acetyl (Protein)	186.9
hypothetical protein XP_236205	34863318	101	55 20mM	2	2 YEFPDGVDSVIVK EAVVSFQVPLILR	19.8
Mg87 protein	19705543	38.8	30 250mM	2	2 QLQQVGTVSK STWLGVAAALGLAVALGTVAWR	51.5
RIKEN cDNA C730027E14	22122497	34.7	45 80mM	2	1 (R)LLQLACPGTGEADAR(V) 786.42(2+), (873.41)CALQ(1345.62), 34	28.8
similar to Ab2-095	34865464	80	46 FT	15	5 YLGACGR DSGSFLLR CDLLQAMPR ELAQLDQSICK NVYFAQYGEPR	62.5

					CPACFGTSWCR LEALLDECTNPK	
similar to apoptosis related protein APR-3; p18 protein	34862996	21.5	30 FT	10	3 CCLNQK QICQGQK VAAYCEDTSK	139.5
Similar to cDNA 1810037C20	34881760	39.9	20 FT	1	1 (R)IVSGAANVIGPK(I) 563.24(2+), (698.42)AGSV(1012.58), 35	25.1
similar to CG14980-PB	34870407	66.9	55 FT	2	2 MEESLSVVK AAAAAGTGTWAAQEK + N-Acetyl (Protein)	29.9
Similar to Chr14 ORF	34869712	35.6	250 FT	7	3 VCQSPINVEGK CGVCNEATPIK CPCNCLLICK	84.3
similar to E25B protein	27701907	30.8	35 80mM	3	2 YQTIEENIK NLLELLINIK	64.9
similar to FAM3C-like protein	38454280	24.9	20 FT	1	1 (K)TGDVIDTK(Y) 424.65(2+), (248.16)DIVDG(747.39), 37	40.2
similar to grey lethal osteopetrosis; grey-lethal	34853421	46	35 FT	22	2 ALQFQGWAK + Guanidination (K) CAGSLLMADR	43.5
similar to HTGN29 protein; keratinocytes associated transmembrane protein 2	34870715	33.8	46 FT	1	1 (R)LDQNVNEAMPSTK(I) 729.75(2+), (444.28)PMAENV(988.51), 30	29.6
similar to hypothetical protein FLJ38482	34877746	31.2	175 80mM	2	2 LLELATQPAR LLELATQPART	64.1
similar to Hypothetical protein MGC18837	27719651	21.4	170 80mM	2	1 (R)GLGTEVPGSLQGPDPYR(Q) 872.02(2+), (1089.53)PVE(1414.70), 24	46.7
Similar to hypothetical protein MGC29390	34869210	204	90 250mM	7	5 FLQQVDGQR KPLIKVSGISR LLVSPEGLNIR FLVLFSPEDVR SEDVQGISQIR	24.5
<b>similar to hypothetical protein MGC40107</b>	27672946	11.8	150 80mM	4	2 AGVGAAFR + N-Acetyl (Protein) LGALSGAGALSLATYGAHGAQFPDAYGK	169.5
similar to RIKEN cDNA 1100001H23	34858551	68.9	35 80mM	3	3 GDPCSTICCR DQGTVDMSMK EDLNEASPSPGGCYDTK	43.5
similar to RIKEN cDNA 1110055L24	34854713	28.1	25 FT	4	2 TAIPYDKK GNCEMSSVTGTLCK	71.2
Similar to RIKEN cDNA 2010320H07 gene	34853121	83.7	150 80mM	1	1 (R)LLAELVQSSQVAR(V) 707.43(2+), (246.16)VQSSQV(874.47), 41	11.9
Similar to TRIM14 alpha	34868472	59.2	46 80mM	33	7 LWEGTISIPR NTLQTPMDTR LLLDEEEALAK GHPVGLAEAAAAR TPTLDPDTMHAR APVQSDWTGGWR VWDISQVSNPVQLLQAYIATK	118.2
<b>Unknown (protein for MGC:72560)</b>	40018580	17.8	20 40mM	16	6 LLLDPSNTPTK KLLDPSNTPTK TDEQALLSSILAK IAAYAYSALSQIR TASNIIDVSAADSQGMQHEYMDR + Oxidation (M) LPPLPSLTSQPHQVLASEPIPFSDLQQVSR	337.1

Unknown (protein for MGC:72638)	40018550	21.7	25 40mM	1	1 (R)SSDGASALSVPR(K) 573.74(2+), (642.39)SAGD(972.51), 53	46.1
<b>10. Vesicular and protein trafficking</b>						
<b>arl10C</b>	12838871	21.5	25 80mM	5	4 DLPNALDEK MNLSAIQDR + Oxidation (M) GVNAIVYMIDAADR NELHNLLDKPQLQGIPVLVLGNKR	186.0
Cation Dependent M6PR	27713160	31.6	46 40mM	5	4 SVPAAYR SNEKETVVGR HTLAGNFPVSEER SFESTVGQGSPTYIFR	126.6
<b>ergicp53, Mannose-binding lectin 1</b>	16758758	58.2	70 250mM	14	9 IHLEIK DIDSLAQR IAPSLKSQR QLDMILDEQR YVSSLTEEISR QLDMILDEQRR AAFENWEVEVTFR GAGTPGQPGQVSQQELDTVVR GHPDLQGQPADDIFESIGDRELK	154.6
heat shock protein 8; Heat shock cognate protein 70; heat shock 70kD protein 8	13242237	71	80 250mM	9	5 DAGTIAGLNVLR FEELNADLFR ARFEELNADLFR TTPSYVAFTDTER IINEPTAAAIAYGLDK	70.4
RAB11B, member RAS oncogene family	14249144	24.5	30 80mM	3	3 AQIWDTAGQER GTRDDEYDYLK + N-Acetyl (Protein) VVLIGDSGVGK	122.4
<b>Rab1A</b>	4758988	22.9	20 FT	19	7 IQSTPVK YASENVNK MGPGATAGGAEK + Oxidation (M) LLLIGDSGVGK LQIWDTAGQER SSMNPEYDYLK + N-acetyl (Protein); Oxidation (M) NATNVEQSFMTMAAEIK	305.7
Rab2	13929006	23.6	25 80mM	1	1 (K)LQIWDTAGQESFR(S) 775.89(2+), (895.43)DWI(1309.62), 31	42.4
Rab5C	27689505	23.6	30 80mM	11	3 NEPQNAAGAPGR GVDLQESNPASR QASPNIVIALAGNK	127.1
<b>Rab6</b>	17512290	23.6	20 80mM	21	7 SREDMIDIK QVSIEEGERK LVFLGEQSVGK WIDDVRTER SAGGDFGNPLRK + N-Acetyl (Protein) VAAALPGMESTQDR DSAAAVVYDITNVNSFQQTTK	296.6
<b>Rab7</b>	13027392	23	25 80mM	10	6 ATIGADFLTK VIILGDSGVGK	260.9

					NNIPYFETSAK DPENFPFVVLGNK EAINVEQAFQTIAR NALKQETEVELYNEFPEPIK	
RIKEN cDNA 1500016L11	21312151	25.1	30 250mM	6	3 MDLLFGR + N-Acetyl (Protein) ANIQAVSLK KTPEELLR	119.5
RIKEN cDNA 3930401E15	38083573	25.5	25 40mM	2	2 AEDLNTR QCFYEDITQGTK	78.4
similar to ankyrin repeat hooked to a zinc finger motif long form	34873095	131	100 FT	4	2 ESGAAEQVDNK	15.3
similar to EH-domain containing 1	34861835	62.9	75 250mM	1	1 (R)HLIEQDFPGMR(I) 671.86(2+), (850.39)EIL(1205.60), 36	15.9
similar to golgi phosphoprotein 4; type II Golgi membrane protein; 130 kDa golgi-localized phosphoprotein; cis Golgi-localized calcium- binding protein	34857091	73.1	90 250mM	16	6 LHGQLLR YLQLQKEK QQQQQQYLAR SPYEEQLEQQR LREHQEALHQQR YLQLQQEKEQELSK	82.1
similar to golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1	34863597	210	250 FT	3	2 GVRFTQSSQK AASSSSPGSPVASSPSK	9.5
similar to gp25L2 protein	34873639	27.1	35 80mM	1	1 (R)QLVEQVEQIQK(E) 671.39(2+), (275.17)IQEVQEV(1100.60), 57	36.9
similar to hypothetical protein 5031407H10	34851786	63.5	67 FT	2	2 TPQSAAQLR TAASDSSPTGEPQR	31.5
similar to LRG-47	27670133	45.1	60 250mM	8	2 NTLQTDLSNIR IIGHEEDASAPTGVVR	44.3
similar to NIPSNAP1 protein	34879019	33.6	25 250mM	8	2 AGPNIYELR GWDENVYYTVPLVR	59.5
similar to Procollagen (type III) N-	34851987	24.2	25 80mM	2	1 (R)VYAENAIR(K) 468.30(2+), (359.24)NEAY(836.43), 41	41.3
similar to Rab18	27687387	23.2	25 80mM	1	1 (K)LAIWDTAGQER(F) 630.33(2+), (304.16)QGATDWI(1075.52), 53	43.1
Similar to Rab5B	34862219	35.2	25 40mM	3	2 SEPQNPGGAAGR QASPSIVIALAGNK	56.8
similar to RET-II	34867583	82.3	75 250mM	3	2 LQEADQVLSSR QNLAEAVTLAER	24.3
similar to RIKEN cDNA 2010012F05	34859075	23.7	35 250mM	4	2 LRDTEEMLSK QLAQIDGTLSTIEFQR	42.2
Sorting Nexin 3A	4507143	18.8	20 250mM	2	2 AETVADTRR + N-Acetyl (Protein) QLPFRGDDGIFDDNFIEER	106.4
SNAP alpha	2143586	33.5	40 80mM	4	2 TIQGDEEDLR LDQWLTTMLLR	59.7
Syntaxin 7	11177920	29.8	35 80mM	4	4 TLNQLGTPQDTPELR ITQCSAEIQR SYTPGIGGDPQAQLAQR + N-Acetyl (Protein) QQLQQEQQYTNQLAK	134.2
syntaxin 8; syntaxin-like protein 3I35	13928908	27.1	35 80mM	7	4 RVTLVDR QNLDDLVTR QITQLEGDRR GTPNPWLCEEPEETRGLGFDEIR	147.6



TGN38	20301976	41	100 20mM	14	6 SGQKFTK IIAFALEGK SSEPTEDVETK LKETLQQLLPVDPK VLGPSSSENQEGTLTDSMKDEK EIEEGDTEPEEGSPLEEEENEK	146.3
Ubitquitin	70637	8.4		20	5 EGIPPDQQR ESTLHLVLR TLSDYNIQK IQDKEGIPPDQQR TITLEVEPSDTIENVK	595.2
Vamp2B	4894188	14.5	20 40mM	2	2 LSELDDR ADALQAGASQFETSAAK	137.9
<b>VAMP8</b>	13929182	11.3	20 40mM	27	8 GENLDHLR NLQSEVEGVK NIMTQNVER MEASGSAGNDRVR + N-Acetyl (Protein) TEDLEATSEHFK ILARGENLDHLR NKTEDLEATSEHFK NLQSEVEGVKNIMTQNVER	708.0
vesicle transport through interaction with t-SNAREs 1B homolog	34866243	36.3	30 80mM	7	3 ALLLQGTESLNR GLLEDLQGVPER IAAETDQIGSEIIEELGEQRDQLER	82.6
Vps24p protein	27229308	25.1	25 250mM	1	1 (K)IPEIQATMR(E) 529.86(2+), (407.21)AQIEP(945.48), 41	39.8

\*For proteins identified with one unique peptide, additional information provided is: precursor ion and charge, sequence tag of y-ions, Mascot score.