Supplementary Table 1: Proteins Identified in the Lysosomal Soluble fraction were Classified according their Function. SC, sequence coverage. MP, number of matched peptides.

Protein Name	Gi Number	MW	ΡΙ	SC%	MP	Mascot Score	Peptides
Peptidases							
cathepsin B	74180941	37	5.8	36	9	337	K.SGVYK.H, K.EIMAEIYK.N, K.EIMAEIYK.N, K.SCEAGYSPSYK.E, K.HEAGDMMGGHAIR.I, R.GENHCGIESEIVAGIPR.T, K.NGPVEGAFTVFSDFLTYK.S, K.EIMAEIYKNGPVEGAFTVFSDFLTYK.S, R.VNVEVSAEDLLTCCGIQCGDGCNGGYPSGAWSF WTK.K
cathepsin C	12832450	52.3	6.44	6	2	103	R.NVQGVNYVSPVR.N, R.NQESCGSCYSFASMGMLEAR.I
cathepsin D	6753556	45.4	6.71	29	10	426	K.QIFGEATK.Q, K.QPGIVFVAAK.F, K.NYELHPDK.Y, K.VSSLPTVYLK.L , K.NIFSFYLNR.D, K.LGGKNYELHPDK.Y, K.NYELHPDKYILK.V, R.DPEGQPGGELMLGGTDSK.Y , K.AIGAVPLIQGEYMIPCEK.V, K.GGCEAIVDTGTSLLVGPVEEVK.E
cathepsin F	4826565	34	6.53	11	4	197	K.IAAWLAQK.G, R.GSGACGVNTMASSAVVN, R.GTLLSLSEQELLDCDK.V, R.GTLLSLSEQELLDCDKVDK.A
cathepsin H	1705636	37.2	8.68	17	4	153	K.GNVVSPVK.N, K.GIMEEDSYPYIGK.D, K.GGLPSQAFEYILYNK.G, K.MLSLAEQQLVDCAQAFNNHGCK.G
cathepsin L	4887002	37.5	6.37	10	2	108	K.ENGGLDSEESYPYEAK.D, K.DRDNHCGLATAASYPVVN
cathepsin S	10946582	39.1	6.16	24	6	249	K.DYWLVK.N, R.YIQLPFGDEDALK.E, K.NSWGLNFGDQGYIR.M, K.NHCGIASYCSYPEI, K.LISLSAQNLVDCSNEEK.Y, K.GPVSVGIDASHSSFFFYK.S

cathepsin Z	11066226	34.8 6.	13 30	8	327	R.IVTSTYK.G, R.VGDYGSLSGR.E, R.NSWGEPWGEK.G, R.NVNGVNYASVTR.N, K.FNQCGTCTEFK.E, K.HGIPDETCNNYQAK.D, K.DQDCDKFNQCGTCTEFK.E, .NQHIPQYCGSCWAHGSTSAMADR.I
dipeptidyl-peptidase 2	9858825	56.2 5.	17 35	11	602	R.FLVSDK.F, R.DAFQQIK.D, K.DLTQLFGFAR.N, K.SLPFGVQSTQR.G, R.DVTADFYGQSPK.C, R.ASNSEDPPSVVEVR.K, R.QDWLQTSFWGGDLK.A, R.LYQSCADPTGCGTGSDAR.A, K.DLFLQGAYDTISQNFGTCQSLSSPK.D, K.YPHLVAGALAASAPVVAVAGLGDSYQFFR.D, R.NAFTVLAMMDYPYPTDFLGPLPANPVK.V
dipeptidyl-peptidase 4	109788	87.4 5.9	96 11	6	223	K.IQLTDHTNVK.C, R.MLQDVQMPSK.K, K.CLSCDLNPER.C, R.YMGLPIPEDNLDHYR.N, K.KYPLLLDVYAGPCSQK.A, K.FFIVNIDSLSSSSSAAPIQIPAPASVAR.G
glutamyl aminopeptidas	e 74147024	108 5.3	28 20	13	703	R.FLLDSK.A, K.GCQIYLK.K, K.KFQFANAK.T, K.LLYGLASVK.D, K.TQDVFTVIR.Y, K.SEMVDDNWK.K, R.MLQDWITPEK.F, K.NNIEWLNVNR.Q, K.SEEDFLPWER.V, K.SEEDFLPWER.V, R.LPDFINPVHYDLEVK.A, K.TSDFWDSLQEASNLPVK.E, R.ETNLLYDPLLSASSNQQR.V
legumain	7242187	49.3 5.9	92 5	2	100	K.VMQFQGMK.H, R.HQADACHAYQIIHR.N
plasma glutamat carboxypeptidase	e 9055234	47.8 6.3	39 27	8	189	R.DDLYK.Y, K.DLGLRPK.R, R.LGLLVDTVGPR.L, R.GEESAVMLEPR.I, K.IIVYNQPYTGYEK.T, K.IPTACITVEDAEMMSR.M, K.YSLVMEADSGTFLPTGLQFTGSDK.A, K.AIQIMYQNLQQDGLENVHLEQVR.I

Prcp protein	32967631	51	6.06	14	7	387	K.SWNVIDK.L, R.KSWNVIDK.L, K.AMLVFAEHR.Y, K.YSVLYFEQK.V, R.KYSVLYFEQK.V, R.AHNAFDPSSVLLSR.L,R.YYGESLPFGQDSFK.D
retinoid-inducible serind carboxypeptidase	e 74151992	45	5.95	10	5	157	K.FNQLK.W, K.SSETAAFVK.S, K.LKWPQLSK.F, K.AGHMVPSDQGEMALK.M, K.WPQLSK.F
tripeptidyl peptidase 1	6753448	61.3	6.1	12	4	246	R.VNTEFMK.A, R.LFGGSFTHQASVAK.V, R.ILNGRPPLGFLNPR.L, K.FRPSFPASSPYVTTVGGTSFK.N
Glycosidases acid beta-galactosidase	e 192185	73.6	7.15	6	2	78	K.SLYPLTFTQVK.Q,K.TVAEALGILCPNGPVK.S
1 alpha-D-mannosidase	1478074	112	7.93	9	9	517	R.FDTPMK.T, R.LLVDDDR.G, K.GQFFTDSNGR.E, R.ATFDSGTGLLMK.I, R.HLVLLSSVSDAAAR.H, R.GVSEPLLETDTGDK.V, R.GRHLVLLSSVSDAAAR.H, R.IYITDGQMQLTVLTDR.S, R.SQGGSSLQDGSLELMVHR.R
alpha-N- acetylgalactosamindase	18203750	47.2	6.02	33	17	594	K.VDMLK.L, R.LIPDPK.R, R.TDMPFR.F, R.LAQDGWR.D, K.DIQDSWK.S, K.SHIEVFK.R, R.LFMEMADR.L, K.LGIYEDMGK.M, K.LDGCFSSSR.E, K.LGIYEDMGK.M , K.INQDPLGIQGR.R, R.CNIDCVEDPK.N, R.TPPMGWLAWER.F, K.MTCMGYPGTTLDK.V, R.FHCSLLELNYPK.G, R.TISPQNMDILQNPLMIK.I, R.TDMPFRFHCSLLELNYPK.G

alpha-N- acetylglucosaminidase	7305299	82.6	6.14	23	16	238	R.AGGLLVYK.L, R.GDTVDLSK.K, R.AVLEAVPR.G, K.QELDLLLR.A, R.YDLLDVTR.Q, R.VFPQVNVIK.L, R.GSTGVAAAAGLHR.Y, R.GVPFQQHEFEK.N, K.QLAGLVADYYQPR.W, R.MGNLHTWDGPLPR.S, R.SWHLSQVYLQHR.I, K.NVFPLEQAFVYNK.K, R.LLGPGPAANFLVSVER.A, R.QAVQELVSLCYEEAR.T, K.AAVSEAEAQFYEQNSR.Y, R.KAAVSEAEAQFYEQNSR.Y
aspartylglucosamindase	54292135	37	5.99	8	3	68	K.FAESMGFTNEDLSTK.T, R.NCQPNYWR.N, R.NVIPDPSK.Y
beta-glucoronidase	193721	74.2	6.22	19	9	362	K.DFNLLR.W, K.LVQSGPLTTCR.I, R.LQGFEQQWYR.Q, R.HHLEVMEELVR.R, K.AVLENYHSVLDQK.R, K.FLINGKPFYFQGVNK.H, R.TSHYPYSEEVLQLCDR.Y, K.VTTTESVTDYYTLPIGIR.T, K.THQKPIIQSEYGADAIPGIHEDPPR.M
beta-manosidase	13310141	101	6.61	12	10	414	K.IVLSEDK.S, R.FNDLNYR.W, K.DHHTQLTVR.L, K.GECHVNFIR.K, R.SAVQYAECQSK.A, K.VSSQEDWAYNSR.F, K.GSNWIPADSFQDK.V, K.SRPFIASSPTNGMK.T, K.TQQTNDIELQQEQR.I, K.DTIYLTQVMQAQCIK.T
alpha-L-fucosidase	6978861	53.7	5.82	3	2	64	K.YVVLTTK.H, R.DLVGELGAAVR.K
alpha-glucosidase	31982355	107	5.57	10	9	385	R.THFPLDVQWNDLDYMDAR.R, R.THFPLDVQWNDLDYMDAR.R, R.RDFTFNQDSFADFPDMVR.E, R.DFTFNQDSFADFPDMVR.E, R.GTRPFVISR.S, R.YAGHWTGDVR.S, R.WTQLGAFYPFMR.N R.NHNDLNSVPQEPYR.F, R.FSETAQQAMR.K, K.TEVTGYFPK.G

lysosomal sialidase	2731441	44.6	5.67	6	1	46	K.HDHDFNPDECQPYELPDGSVIINAR.N
mannosidase alpha class 2B member 2	6678792	116	6.9	4	4	170	R.IDYDLK.D, R.FIAVEQEFFR.L, R.LWWDGVASEQQK.Q, R.QASALLYAGESMFTR.Y
protective protein for beta-galactosidase	6679437	54.4	5.56	16	6	310	R.FLNKEPY, K.ALHIPESLPR.W, K.GAGHMVPTDKPR.A, R.LYQSMNSQYLK.L, R.RLYQSMNSQYLK.L, R.RPWLVDYGESGEQVAGFVK.E
Sulfatases							
Arylasulfatase A	312269	53.7	5.5	16	7	256	R.AALLTGR.L, R.GYLTGMAGK.W, R.DLMADAQR.Q, K.GTTFEGGVR.E, R.MSNGGCSGLLR.C, K.AQYDAAMTFGPSQIAK.G, K.AHFFTQGSAHSDTTSDPACHAANR.L
N-acetylgalactosamine-4- sulfatase	- 33859510	47.9	8.09	13	3	111	K.EYNNIYSTNIFTK.R, R.DGEEPAKEYNNIYSTNIFTK.R, R.YQIHLGLQHYLIMTCQPSCVPLDEK.L,
N-acetylgalactosamine-6- sulfate sulfatase	- 7576473	58.1	6.16	6	2	116	R.GNTLMAVTLGQYK.A, R.FPLSFHSDEYQDALSR.T
N-sulfoglucosamine sulfohydrolase	6851203	57.3	5.97	7	3	127	R.ADLAAQYTTIGR.M, R.MDQGVGLVLQELR.G, K.VQSLPLLLNQAGVR.T
Lipid metabolism							
acid sphingomyelinase- like phosphodiesterase 3A		50		17	4	130	K.VYNIAHVPVGYLPYATDTPAIR.Q, R.YSSVIAGQFYGHTHR.D, R.DSLMVLSDGNGNPLNSVFVAPAVTPVK.G, K.SLYALVQQFATK.D
carboxylesterase 3	14331135	62	6.34	25	10	480	K.FWANFAR.N, K.APEEILAEK.S, K.IGASTQAAQR.L, K.DGASEEETNLSK.M, K.ISENMIPVVAEK.Y, R.QKTEDELLETSLK.L, R.FAPPQPAEPWSFVK.N, K.ESYPFLPTVIDGVVLPK.A, R.NGNPNGGGLPHWPEYDQK.E, K.AVIGDHGDEIFSVFGSPFLK.D

carboxylesterase 5	32967662	62	5.81	7	3	111	K.LPYTEEEEQLSR.R, R.FAPPEAPEPWSGVR.D, R.LGVLGFFSTGDQHAK.G
sialic acid 9-o acetylesterase	- 5917657	51.1	6.06	20	8	308	K.QTVAYR.L, R.DKQTVAYR.L, R.DSPFGSIHPR.D, R.QTFHYGSQGQTDR.F, R.WHQTADFGHVPNPK.M, K.GVVWYQGESNADYNR.D, K.MPNTFMAVAIDLCDR.D, R.FFPFGFVQLSSYMLK.N
esterase 31-like	21362301	63	5.65	8	3	98	K.VIQPEVDTPLGR.V, R.FSAPLPPQPWEGVR.D, R.DAGCPVFLYEFQHTPSSFAK.F
GM2 ganglioside activator protein	e 71059907	20.8	5.63	31	6	216	R.LGCIK.I, K.IAASLK.G, K.EVAGFWVK.I, R.IQSILSSGGK.R, K.TSVPLTAPQK.V, K.SLTIQPDPIVVPGDVVVSLEGK.T
hexosaminidase A	7110627	60.6	6.09	13	7	162	K.EVIEYAR.L, K.SNPNIQAFMK.K, K.GSFNPVTHIYTAQDVK.E, R.KGSFNPVTHIYTAQDVK.E, R.EEMPVEYMLEMQDITR.A, R.GIQAQPISVGYCEQEFEQT, R.RGIQAQPISVGYCEQEFEQT
hexosaminidase B	226165	61.1	8.3	5	2	72	K.VEPLNFEGSEK.Q + Deamidation, R.GIAAQPLYTGYCNYENK.I + Carbamidomethyl
lysosomal acid lipase	4456671	45.5	7.7	10	4	134	R.LPTALWSGGR.D, K.QFLPQSAMLK.W, K.LYDEIISLMK.K, R.KLQAFDWGSSEK.N
lysosomal phospholipase A2	e 18043186	47.2	6.02	13	5	218	R.HPPVVLVPGDLGNQLEAK.L, R.ATQFPDGVDVR.V, R.APNENGPYFLALR.E, R.IPVIGPLK.I, R.VLLEP
N-acylsphingosine amidohydrolase 1 Asah1	13096822	44.6	8.68	12	5	210	K.DAQWVGFITR.S, K.IMAPVYFILGGK.K, R.WYVVQTNYDR.W, K.NTLFIDDR.R, 0 K.GQFESHLR.D
Niemann Pick type c2	12963667	16.7	7.59	40	6	172	K.LEDDKK.N, K.NEYPSIK.L, K.DKVYSYLNK.L, K.KNNLFCWEIPVQITS, K.EVNVSPCPTDPCQLHK.G, K.SGINCPIQK.D

palmitoyl-protein thioesterase	17225443	35	8.26	43	9	379	K.NLMALK.K, K.SLNAGAYSK.L, K.EGDHLQISK.E, R.LVQAQYWHDPIK.E, K.EIPGIYVLSLEIGK.N, R.CPGESSHICDFIR.K, K.ETIPLQESTLYTEDR.L, K.LQQGYNAIGFSQGGQFLR.A, R.CPTPPMMTLISVGGQHQGVFGLPR.C
palmitoyl-protein thioesterase 2	9506985	34.7	5.92	22	6	182	R.DSFGLK.T, R.EAVVPIMEK.A, K.WLFPTSMR.S, R.TLYDTCIEPWLS, R.ESLRPLWEQVQGFR.E, K.APEGVHLICYSQGGLVCR.A
phospholipase D family member 3	, 7242181	54.3	6.07	4	2	64	K.LFVVPTDESQAR.I, R.SQLEAVFLR.D
sphingomyelin phosphodiesterase 1,acid lysosomal	6755582 d	70.8	6.76	2	2	78	R.ADSPALCR.H, R.ALTTITDLVR.K
Others							
acid phosphatase 5 tartrate resistant	, 17512394	37	8.99	9	2	97	R.FQETFEDVFSDR.S, R.FVAVGDWGGVPNAPFHTAR.E
Atp5b protein (ATPase beta subunit)	, 23272966	56.6	5.24	9	3	123	K.VALVYGQMNEPPGAR.A, R.IMDPNIVGNEHYDVAR.G, R.IPSAVGYQPTLATDMGTMQER.I

catalase	26344712	60	7.73	43	22	623	K.NLPVGEAGR.L, K.DAQLFIKK.K, R.LFAYPDTHR.H, R.LAQEDPDYGLR.D, K.LVNADGEAVYCK.F, R.FSTVTGESGSADTVR.D, R.SALEHSVQCAVDVK.R, K.NAIHTYTQAGSHMAAK.C K.GAGAFGYFEVTHDITR.Y, R.LGPNYLQIPVNCPYR.A, R.ASQRPDVLTTGGGNPIGE R.GPLLVQDVVFTDEMAHFE R.HMNGYGSHTFKLVNADG K.NPVNYFAEVEQMAFDPSI R.DAILFPSFIHSQK.R	K.EAETFPFNPFDLTK.V, G, DK.L, DR.E, GEAVYCK.F, GEAVYCK.F,
cellular repressor of E1A stimulated gene 1(CREG)		24.5	5.96	21	3	108	K.TEEDYAR.D, R.FVTHVSDWGSLATISTIK	R.IWVLDYFGGPK.V, E
Dnase2a protein	35193201	38.8	7.1	2	1	30	K.LPDLETVIK.N	
ferritin heavy chain 1	15126788	21	5.33	28	5	193	R.QNYHQDAEAAINR.Q, R.IFLQDIK.K, K.ELGDHVTNLR.K	K.YFLHQSHEER.E, K.SVNQSLLELHK.L,
ferritin light chain 1	18044716	21	5.66	43	5	317	R.LLEFQNDR.G, R.QNYSTEVEAAVNR.L, .MTSQIRQNYSTEVEAAVNI R.VAGPQPAQTGAPQGSLG	•

Erp57	6679687	56.5	5.98	33	12	498	K.DPNIVIAK.M, K.LNFAVASR.K, K.QAGPASVPLR.T, K.FVMQEEFSR.D, K.SEPIPESNEGPVK.V, R.ELNDFISYLQR.E, R.EATNPPIIQEEKPK.K, K.MDATANDVPSPYEVK.G, K.VVVAENFDDIVNEEDK.D, K.FIQDSIFGLCPHMTEDNK.D, K.EYDDNGEGITIFRPLHLANK.F, K.FIQDSIFGLCPHMTEDNKDLIQGK.D
fibrinogen, B beta polypeptide	a 21619364	54.7	6.68	8	2	77	R.TPCTVSCNIPVVSGK.E, K.ENENVINEYSSILEDQR.L
lysosomal thiol reductase IP 30	e 9837556	27.7	4.94	4	1	48	R.LNMVEACLLDK.L
mammalian ependymi related protein-2	n 13562142	25.9	7.52	26	5	284	R.QVLYQQSSGHNNR.A, R.ALVSYDGLNQR.V, K.EGVMFQIEQATK.Q, R.SYETWIGVYTAK.D, K.DCYPVQETFIR.N
myeloid bactenecin(neutrophilic granule protein)	2071985	19.7	5.21	28	4	78	R.EDTQETSFNDK.Q, R.LLSATPPSSQNPATNIPLQFR.I, R.AIEAYNQGR.Q, R.EDTQETSFNDKQDVSEK.E
myosin,heavy peptide,1	62656256	234	5.61	6	9	277	R.LQTESGEYSR.Q, R.TKYETDAIQR.T, K.IQHELEEAEER.A, R.ANLLQAEIEELR.A, R.LQDAEEHVEAVNAK.C, R.LEEAGGATSAQIEMNK.K, K.VLNASAIPEGQFIDSK.K, K.QREEQAEPDGTEVADK.A, .MSSDAEMAVFGEAAPYLR.K
prolyl 4-hydroxylase beta polypeptide	, 62533148	57	4.79	34	13	583	K.DGVVLFK.K, K.QLAPIWDK.L, R.NNFEGEITK.E, K.DHENIIIAK.M, K.SNFEEALAAHK.Y, K.MDSTANEVEAVK.V, K.YQLDKDGVVLFK.K, K.VLVGANFEEVAFDEK.K, K.LGETYKDHENIIIAK.M, K.VDATEESDLAQQYGVR.G, K.HNQLPLVIEFTEQTAPK.I, K.IKPHLMSQEVPEDWDKQPVK.V, K.FLESGGQDGAGDDEDLDLEEALEPDMEEDDDQK. A

ribonuclease 1	Γ2	71681319	30	5.92	17	5	200	K.HEWVK.H, K.QIDLNSVLQK.F K.HGTCAAQVDALNSEK.K, K.FGIKPSINYYQLADFK.D,
Selenium bind 2	ding protei	n 9507079	53.2	5.78	29	10	363	K.HEWVKHGTCAAQVDALNSEK.K K.VIQVPSK.K, K.QFYPDLIR.E, K.NEEGTWSVEK.V K.LNPNFLVDFGK.E, R.QYDISNPQKPR.L R.EEIVYLPCIYR.N, R.IPGGPQMIQLSLDGK.R K.DGFNPAHVEAGLYGSR.I, R.NTGTEAPDYLATVDVDPK.S, R.GGSVQVLEDQELTCQPEPLVVK.G
similar to lami	inin A	12004583	66.2	5.77	15	6	200	K.TAELYK.T, R.AHGGIDVK.V R.DQSLVEDMDAMVR.L, R.VLTILEQIPGMVVVADK.T, R.SDLNPANGSYPFQALHQR.A, R.YNDFLHDPLSLCEACNPKPNAENAISAR.S
thrombospond	din	554390	55.3	4.72	5	5	165	R.DLASVAR.L, K.GQDLSSPAFR.I K.DNTGQIFSVVSNGK.A, R.KDNTGQIFSVVSNGK.A, K.DCVGDVTENQVCNK.Q
translation factor eIF-5A	initiatio	n 109296	16.8	5.8	14	1	95	R.NDFQLIGIQDGYLSLLQDSGEVR.E
vitamin protein	D-bindin	g 193446	53	5.26	24	9	225	R.TSELSVK.S, K.VLEPTLK.T, R.QLTSFIEK.G K.TPNTSPAELK.D, R.VCSQYAAYGK.E R.TQVPEVFLSK.V, R.ECCDTQDSVACFSTQSPLLK.R, R.CCESTSEDCMASELPEHTIK.I, K.NYLSMVGSCCTSANPTVCFVK.E
Armet		28913725	19.3	8.38	16	2	105	K.QIDLSTVDLK.K, K.DRDVTFSPATIEEELIK.F
fibrinogen, polypeptide	B bet	a 21619364	54.7	6.68	8	2	77	R.TPCTVSCNIPVVSGK.E, K.ENENVINEYSSILEDQR.L

prolyl 4-hydroxylase beta polypeptide		57	4.79	34	13	583	K.DGVVLFK.K, K.QLAPIWDK.L, R.NNFEGEITK.E, K.DHENIIIAK.M, K.SNFEEALAAHK.Y, K.MDSTANEVEAVK.V, K.YQLDKDGVVLFK.K, K.VLVGANFEEVAFDEK.K, K.LGETYKDHENIIIAK.M, K.VDATEESDLAQQYGVR.G, K.HNQLPLVIEFTEQTAPK.I, K.IKPHLMSQEVPEDWDKQPVK.V, K.FLESGGQDGAGDDEDLDLEEALEPDMEEDDDQK. A
Possible Contaminants		22.4	10.2	17	4	40	IV OLDVIDGI VIELITOVANIV A
ribosomal protein L17	28174920	22.4	10.3		1	48	K.GLDVDSLVIEHIQVNK.A
ribosomal protein L3	337580	45.4	10.1		1	69	R.ERLEQQVPVNQVFGQDEMIDVIGVTK.G
ribosomal protein L37a	56540988	10	10.4	21	1	40	K.TVAGGAWTYNTTSAVTVK.S
ribosomal protein L6	6755353	32.5	10.8	2	1	43	K.KPFSQHVR.R
ribosomal protein L8	3851579	28	11.3	10	2	54	R.TELFIAAEGIHTGQFVYCGK.K, K.RTELFIAAEGIHTGQFVYCGK.K
							KINTELI II NEGITT GQI VI CGKIN
60s ribosomal proteir L10a	1709973	18.8	9.73	18	2	86	K.FLETVELQISLK.N, K.KYDAFLASESLIK.Q
aldehyde dehydrogenase family 6, subfamily A1	e 19527258	58.3	8.29	19	6	258	R.FVAVGDWGGVPNAPFHTAR.E , K.EGASILLDGR.R, K.TLADAEGDVFR.G, K.AISFVGSNQAGEYIFER.G, R.VNAGDQPGADLGPLITPQAK.E, K.IVNDNPYGNGTAIFTTNGATAR.K
carbonic anhydrase 3	226778	29	7.86	9	2	51	K.GDNQSPIELHTK.D, K.EPMTVSSDQMAK.L
cellular glutathione peroxidase 1	2 121666	22.6	6.74	8	1	43	R.NALPTPSDDPTALMTDPK.Y
glutamate dehydrogenase 1	6680027	61.7	8.05	13	7	229	K.MVEGFFDR.G, R.DDGSWEVIEGYR.A, K.LQHGSILGFPK.A, K.VYEGSILEADCDILIPAASEK.Q, K.HGGTIPVVPTAEFQDR.I, R.TAAYVNAIEK.V
malate dehydrogenase 2,NAD	31982186	35.6	8.93	13	3	148	K.EGVVECSFVQSK.E, K.GYLGPEQLPDCLK.G, K.VDFPQDQLATLTGR.I

manganese su dismutase	iperoxide 53450	24.9 8.8	16	2	126	K.GDVTTQVALQPALK.F, K.F	IHAAYVNNLNATEEK.Y
ornithine transcarbamylas	762985 e	39.8 8.96	5 23	5	232	K.LAEQYAK.E, K.FGMHLQAATPK.G, R.LQAFQGYQVTMK.T	R.SLVFPEAENR.K, K.LSMTNDPLEAAR.G,
peroxiredoxin 1	6754976	22.3 8.26	13	2	79	R.LVQAFQFTDK.H, K.QGGL	GPMNIPLISDPK.R
peroxiredoxin 3	6680690	28.3 7.15	15	3	28	K.GTAVVNGEFK.E, R.GLFIIDPNGVVK.H	K.HLSVNDLPVGR.S,
plasma glu peroxidase	utathione 11700039	25.3 8.26	5 5	1	27	K.FLVGPDGIPVMR.W	
urate oxidase	6678509	35.6 8.48	3 20	6	227	R.DIVLQK.F, K.NDEVEFVR R.CFATQVYCK.W, K.KDYLHGDNSDIIPTDTIK.N	K.EEVLLPLDNPYGK.I,