Table S3A. Spectrum to peptide matches leading to the identification of MMs proteins isolated from Mouse liver

For each of the proteins or protein groups listed in Table S3B are provided:
the sequences of each peptide mapped to this protein/protein group, as well as the position within the protein of the peptide's 1st residue, its tryptic status (2 for full-tryptic, and 1 for half-tryptic +Met, to account for CNBr cleaved samples),
and whether the peptide is unique to this protein/protein group (*);
the name of the spectrum (MatchID) mapping each peptide with the highest SEQUEST cross-correlation score (XCorr), as well as its charge state (Z), DeltCn, Sp rank, and ion proportion;
the observed (M+H+) and calculated (CalcM+H+) precursor ion mass;
the number of different spectra matched to each peptide/charge state (Count).

rk	ORTHO_GROUPS	GENE_NAME	Locus	Proteins In Group	Description	Sequence Count	Spectrum Count	Coverage	Length	MW	pI	MatchID	Z	XCorr	DeltCN	M+H+	CalcM +H+	SpRk	Ion Proportion	Count	Sequence	Sequence Position	Tryptic	Unique
1	ENSG00000205754:ENSMUSG00000030236:ENSRNOG00000030538	SLCO1B2	gi|14547899|ref|NP_065241.1|	gi|14547899|ref|NP_065241.1|;gi|30102937|ref|NP_839953.1|	solute carrier organic anion transporter family, member 1b2 isoform	3	370	5.4	689	76729	8.7	MmNaOH-MM_liver_CNBrTi_101.3162.3162.2	2	3.1179	0.3076	1792.68	1793.1	1	56.25	4	R.TLGGILAPVYYGALIDR.T	577	2	
1	ENSG00000205754:ENSMUSG00000030236:ENSRNOG00000030538	SLCO1B2	gi|14547899|ref|NP_065241.1|	gi|14547899|ref|NP_065241.1|;gi|30102937|ref|NP_839953.1|	solute carrier organic anion transporter family, member 1b2 isoform	3	370	5.4	689	76729	8.7	MmNaOH-MM_liver_CNBrTi_101.3570.3570.2	2	4.1615	0.4245	2091.9	2092.4	1	50	3	R.GIGETPIVPLGVSYIDDFAK.E	177	2	
1	ENSG00000205754:ENSMUSG00000030236:ENSRNOG00000030538	SLCO1B2	gi|14547899|ref|NP_065241.1|	gi|14547899|ref|NP_065241.1|;gi|30102937|ref|NP_839953.1|	solute carrier organic anion transporter family, member 1b2 isoform	3	370	5.4	689	76729	8.7	MmNaOH-MM_liver_CNBrTi_204.3414.3414.2	2	4.837	0.4216	2091.76	2092.4	1	60.526318	78	R.GIGETPIVPLGVSYIDDFAK.E	177	2	
1	ENSG00000205754:ENSMUSG00000030236:ENSRNOG00000030538	SLCO1B2	gi|14547899|ref|NP_065241.1|	gi|14547899|ref|NP_065241.1|;gi|30102937|ref|NP_839953.1|	solute carrier organic anion transporter family, member 1b2 isoform	3	370	5.4	689	76729	8.7	MmNaOH-MM_liver_CNBrTi_209.2889.2889.3	3	4.9416	0.4017	1792.83	1793.1	1	51.5625	3	R.TLGGILAPVYYGALIDR.T	577	2	
1	ENSG00000205754:ENSMUSG00000030236:ENSRNOG00000030538	SLCO1B2	gi|14547899|ref|NP_065241.1|	gi|14547899|ref|NP_065241.1|;gi|30102937|ref|NP_839953.1|	solute carrier organic anion transporter family, member 1b2 isoform	3	370	5.4	689	76729	8.7	MmNaOH-MM_liver_CNBrTi_211.3370.3370.2	2	3.955	0.4286	1794.83	1793.1	1	59.375	282	R.TLGGILAPVYYGALIDR.T	577	2	
2	ENSG00000205702:ENSMUSG00000014372:ENSRNOG00000029128	NR_002570.2	gi|31981816|ref|NP_034135.2|	gi|31981816|ref|NP_034135.2|	cytochrome P450, family 2, subfamily d, polypeptide 10 [Mus musc	18	214	24	504	57233	6.6	MmNaOH-MM_liver_CNBrTi_209.1365.1365.3	3	3.3945	0.0946	1428.01	1427.6	1	52.272724	1	M.PYTNAVIHEVQR.F	357	1	
2	ENSG00000205702:ENSMUSG00000014372:ENSRNOG00000029128	NR_002570.2	gi|31981816|ref|NP_034135.2|	gi|31981816|ref|NP_034135.2|	cytochrome P450, family 2, subfamily d, polypeptide 10 [Mus musc	18	214	24	504	57233	6.6	MmNaOH-MM_liver_CNBrTi_202.2570.2570.2	2	2.7263	0.083	1317.37	1317.5	7	75	1	R.DIEVQDFLIPK.G	384	2	
2	ENSG00000205702:ENSMUSG00000014372:ENSRNOG00000029128	NR_002570.2	gi|31981816|ref|NP_034135.2|	gi|31981816|ref|NP_034135.2|	cytochrome P450, family 2, subfamily d, polypeptide 10 [Mus musc	18	214	24	504	57233	6.6	MmNaOH-MM_liver_CNBrTi_202.1978.1978.1	1	1.9082	0.1756	1214.68	1213.4	8	55	1	R.FGDIAPLNLPR.I	369	2	*
2	ENSG00000205702:ENSMUSG00000014372:ENSRNOG00000029128	NR_002570.2	gi|31981816|ref|NP_034135.2|	gi|31981816|ref|NP_034135.2|	cytochrome P450, family 2, subfamily d, polypeptide 10 [Mus musc	18	214	24	504	57233	6.6	MmNaOH-MM_liver_CNBrTi_202.2031.2031.2	2	3.4641	0.2767	1213.34	1213.4	1	85	127	R.FGDIAPLNLPR.I	369	2	*
2	ENSG00000205702:ENSMUSG00000014372:ENSRNOG00000029128	NR_002570.2	gi|31981816|ref|NP_034135.2|	gi|31981816|ref|NP_034135.2|	cytochrome P450, family 2, subfamily d, polypeptide 10 [Mus musc	18	214	24	504	57233	6.6	MmNaOH-MM_liver_CNBrTi_201.1847.1847.1	1	2.1455	0.0999	1455.64	1455.7	1	54.166668	1	R.VQQEIDAVIGQVR.H	334	2	
2	ENSG00000205702:ENSMUSG00000014372:ENSRNOG00000029128	NR_002570.2	gi|31981816|ref|NP_034135.2|	gi|31981816|ref|NP_034135.2|	cytochrome P450, family 2, subfamily d, polypeptide 10 [Mus musc	18	214	24	504	57233	6.6	MmNaOH-MM_liver_CNBrTi_203.1850.1850.2	2	3.8934	0.2287	1455.37	1455.7	1	79.16667	2	R.VQQEIDAVIGQVR.H	334	2	
2	ENSG00000205702:ENSMUSG00000014372:ENSRNOG00000029128	NR_002570.2	gi|31981816|ref|NP_034135.2|	gi|31981816|ref|NP_034135.2|	cytochrome P450, family 2, subfamily d, polypeptide 10 [Mus musc	18	214	24	504	57233	6.6	MmNaOH-MM_liver_CNBrTi_206.2997.2997.2	2	4.3018	0.2523	1592.57	1591.8	1	73.07692	1	R.NLTDAFLAEIEKVK.G	273	2	*
2	ENSG00000205702:ENSMUSG00000014372:ENSRNOG00000029128	NR_002570.2	gi|31981816|ref|NP_034135.2|	gi|31981816|ref|NP_034135.2|	cytochrome P450, family 2, subfamily d, polypeptide 10 [Mus musc	18	214	24	504	57233	6.6	MmNaOH-MM_liver_CNBrTi_209.0933.0933.2	2	2.689	0.0808	1159.5	1159.3	1	83.33333	1	R.RSCLGEPLAR.M	444	2	
2	ENSG00000205702:ENSMUSG00000014372:ENSRNOG00000029128	NR_002570.2	gi|31981816|ref|NP_034135.2|	gi|31981816|ref|NP_034135.2|	cytochrome P450, family 2, subfamily d, polypeptide 10 [Mus musc	18	214	24	504	57233	6.6	MmNaOH-MM_liver_CNBrTi_211.1929.1929.2	2	2.5817	0.1741	965.69	966.13	1	85.71429	1	R.RFSVSTLR.N	136	2	
2	ENSG00000205702:ENSMUSG00000014372:ENSRNOG00000029128	NR_002570.2	gi|31981816|ref|NP_034135.2|	gi|31981816|ref|NP_034135.2|	cytochrome P450, family 2, subfamily d, polypeptide 10 [Mus musc	18	214	24	504	57233	6.6	MmNaOH-MM_liver_CNBrTi_104.1894.1894.2	2	3.2706	0.1653	1500.74	1501.7	1	80	5	R.RFEYEDPYLIR.M	197	2	
2	ENSG00000205702:ENSMUSG00000014372:ENSRNOG00000029128	NR_002570.2	gi|31981816|ref|NP_034135.2|	gi|31981816|ref|NP_034135.2|	cytochrome P450, family 2, subfamily d, polypeptide 10 [Mus musc	18	214	24	504	57233	6.6	MmNaOH-MM_liver_CNBrTi_101.4840.4840.2	2	2.5707	0.1714	1776.66	1776.1	6	43.333332	1	M.LNNAVCNVIASLIFAR.R	181	1	
2	ENSG00000205702:ENSMUSG00000014372:ENSRNOG00000029128	NR_002570.2	gi|31981816|ref|NP_034135.2|	gi|31981816|ref|NP_034135.2|	cytochrome P450, family 2, subfamily d, polypeptide 10 [Mus musc	18	214	24	504	57233	6.6	MmNaOH-MM_liver_CNBrTi_106.1418.1418.2	2	2.6953	0.1275	965.99	966.13	1	100	1	R.RFSVSTLR.N	136	2	
2	ENSG00000205702:ENSMUSG00000014372:ENSRNOG00000029128	NR_002570.2	gi|31981816|ref|NP_034135.2|	gi|31981816|ref|NP_034135.2|	cytochrome P450, family 2, subfamily d, polypeptide 10 [Mus musc	18	214	24	504	57233	6.6	MmNaOH-MM_liver_CNBrTi_203.2749.2749.2	2	4.4631	0.2852	1364.38	1364.5	1	86.36364	50	R.NLTDAFLAEIEK.V	273	2	
2	ENSG00000205702:ENSMUSG00000014372:ENSRNOG00000029128	NR_002570.2	gi|31981816|ref|NP_034135.2|	gi|31981816|ref|NP_034135.2|	cytochrome P450, family 2, subfamily d, polypeptide 10 [Mus musc	18	214	24	504	57233	6.6	MmNaOH-MM_liver_CNBrTi_101.2919.2919.1	1	2.7825	0.2275	1363.75	1364.5	1	68.181816	1	R.NLTDAFLAEIEK.V	273	2	
2	ENSG00000205702:ENSMUSG00000014372:ENSRNOG00000029128	NR_002570.2	gi|31981816|ref|NP_034135.2|	gi|31981816|ref|NP_034135.2|	cytochrome P450, family 2, subfamily d, polypeptide 10 [Mus musc	18	214	24	504	57233	6.6	MmNaOH-MM_liver_CNBrTi_101.2930.2930.2	2	4.2944	0.2241	1364.85	1364.5	1	81.818184	1	R.NLTDAFLAEIEK.V	273	2	
2	ENSG00000205702:ENSMUSG00000014372:ENSRNOG00000029128	NR_002570.2	gi|31981816|ref|NP_034135.2|	gi|31981816|ref|NP_034135.2|	cytochrome P450, family 2, subfamily d, polypeptide 10 [Mus musc	18	214	24	504	57233	6.6	MmNaOH-MM_liver_CNBrTi_101.1967.1967.2	2	3.1832	0.2919	1214.57	1213.4	1	85	1	R.FGDIAPLNLPR.I	369	2	*
2	ENSG00000205702:ENSMUSG00000014372:ENSRNOG00000029128	NR_002570.2	gi|31981816|ref|NP_034135.2|	gi|31981816|ref|NP_034135.2|	cytochrome P450, family 2, subfamily d, polypeptide 10 [Mus musc	18	214	24	504	57233	6.6	MmNaOH-MM_liver_CNBrTi_101.1700.1700.1	1	2.17	0.0907	1500.75	1501.7	2	55	2	R.RFEYEDPYLIR.M	197	2	
2	ENSG00000205702:ENSMUSG00000014372:ENSRNOG00000029128	NR_002570.2	gi|31981816|ref|NP_034135.2|	gi|31981816|ref|NP_034135.2|	cytochrome P450, family 2, subfamily d, polypeptide 10 [Mus musc	18	214	24	504	57233	6.6	MmNaOH-MM_liver_CNBrTi_104.1962.1962.2	2	4.2503	0.4283	1611.76	1611.8	1	69.230774	4	R.RVQQEIDAVIGQVR.H	333	2	
2	ENSG00000205702:ENSMUSG00000014372:ENSRNOG00000029128	NR_002570.2	gi|31981816|ref|NP_034135.2|	gi|31981816|ref|NP_034135.2|	cytochrome P450, family 2, subfamily d, polypeptide 10 [Mus musc	18	214	24	504	57233	6.6	MmNaOH-MM_liver_CNBrTi_101.2775.2775.2	2	3.0833	0.2222	1317.36	1317.5	4	80	1	R.DIEVQDFLIPK.G	384	2	
2	ENSG00000205702:ENSMUSG00000014372:ENSRNOG00000029128	NR_002570.2	gi|31981816|ref|NP_034135.2|	gi|31981816|ref|NP_034135.2|	cytochrome P450, family 2, subfamily d, polypeptide 10 [Mus musc	18	214	24	504	57233	6.6	MmNaOH-MM_liver_CNBrTi_101.1798.1798.3	3	4.9	0.235	1612.58	1611.8	1	53.846157	1	R.RVQQEIDAVIGQVR.H	333	2	
2	ENSG00000205702:ENSMUSG00000014372:ENSRNOG00000029128	NR_002570.2	gi|31981816|ref|NP_034135.2|	gi|31981816|ref|NP_034135.2|	cytochrome P450, family 2, subfamily d, polypeptide 10 [Mus musc	18	214	24	504	57233	6.6	MmNaOH-MM_liver_CNBrTi_101.5386.5386.2	2	4.9068	0.2729	1585.66	1585.8	1	73.07692	3	K.SLLAIVENLLTENR.N	249	2	*
2	ENSG00000205702:ENSMUSG00000014372:ENSRNOG00000029128	NR_002570.2	gi|31981816|ref|NP_034135.2|	gi|31981816|ref|NP_034135.2|	cytochrome P450, family 2, subfamily d, polypeptide 10 [Mus musc	18	214	24	504	57233	6.6	MmNaOH-MM_liver_CNBrTi_102.2012.2012.3	3	4.0934	0.1859	1502.42	1501.7	1	57.5	6	R.RFEYEDPYLIR.M	197	2	
2	ENSG00000205702:ENSMUSG00000014372:ENSRNOG00000029128	NR_002570.2	gi|31981816|ref|NP_034135.2|	gi|31981816|ref|NP_034135.2|	cytochrome P450, family 2, subfamily d, polypeptide 10 [Mus musc	18	214	24	504	57233	6.6	MmNaOH-MM_liver_CNBrTi_102.1994.1994.2	2	3.7553	0.2386	1454.92	1455.7	1	75	1	R.VQQEIDAVIGQVR.H	334	2	
3	ENSG00000008394:ENSMUSG00000008540:ENSRNOG00000007743	MGST1	gi|31981068|ref|NP_064330.2|	gi|31981068|ref|NP_064330.2|	microsomal glutathione S-transferase 1 [Mus musculus]	4	32	29.7	155	17552	9.7	MmNaOH-MM_liver_CNBrTi_102.2699.2699.2	2	3.6221	0.3546	1329.44	1329.6	1	77.27273	1	M.AFTSYATIILTK.M	15	1	*
3	ENSG00000008394:ENSMUSG00000008540:ENSRNOG00000007743	MGST1	gi|31981068|ref|NP_064330.2|	gi|31981068|ref|NP_064330.2|	microsomal glutathione S-transferase 1 [Mus musculus]	4	32	29.7	155	17552	9.7	MmNaOH-MM_liver_CNBrTi_104.2038.2038.2	2	5.4463	0.4434	1897.06	1898.2	1	76.666664	26	R.IYHTIAYLTPLPQPNR.G	115	2	*
3	ENSG00000008394:ENSMUSG00000008540:ENSRNOG00000007743	MGST1	gi|31981068|ref|NP_064330.2|	gi|31981068|ref|NP_064330.2|	microsomal glutathione S-transferase 1 [Mus musculus]	4	32	29.7	155	17552	9.7	MmNaOH-MM_liver_CNBrTi_106.2010.2010.3	3	3.5407	0.146	1897.95	1898.2	4	38.333332	3	R.IYHTIAYLTPLPQPNR.G	115	2	*
3	ENSG00000008394:ENSMUSG00000008540:ENSRNOG00000007743	MGST1	gi|31981068|ref|NP_064330.2|	gi|31981068|ref|NP_064330.2|	microsomal glutathione S-transferase 1 [Mus musculus]	4	32	29.7	155	17552	9.7	MmNaOH-MM_liver_CNBrTi_210.1366.1366.2	2	4.3838	0.3376	1912.35	1912	1	64.70589	2	K.VFANPEDCAGFGKGENAK.K	43	2	*
4	ENSG00000093010:ENSMUSG00000000326:ENSRNOG00000001889	COMT	gi|6680982|ref|NP_031770.1|	gi|6680982|ref|NP_031770.1|	catechol-O-methyltransferase [Mus musculus]	6	61	21.9	265	29496	5.8	MmNaOH-MM_liver_CNBrTi_105.3864.3864.2	2	4.8266	0.3163	2459.32	2459.9	1	50	2	R.KGTVLLADNVIVPGTPDFLAYVR.G	205	2	*
4	ENSG00000093010:ENSMUSG00000000326:ENSRNOG00000001889	COMT	gi|6680982|ref|NP_031770.1|	gi|6680982|ref|NP_031770.1|	catechol-O-methyltransferase [Mus musculus]	6	61	21.9	265	29496	5.8	MmNaOH-MM_liver_CNBrTi_207.2946.2946.3	3	4.053	0.2403	1806.78	1806.1	7	46.42857	3	R.YLPDTLLLEECGLLR.K	190	2	*
4	ENSG00000093010:ENSMUSG00000000326:ENSRNOG00000001889	COMT	gi|6680982|ref|NP_031770.1|	gi|6680982|ref|NP_031770.1|	catechol-O-methyltransferase [Mus musculus]	6	61	21.9	265	29496	5.8	MmNaOH-MM_liver_CNBrTi_101.3215.3215.2	2	4.0755	0.3522	1807.33	1806.1	1	67.85714	7	R.YLPDTLLLEECGLLR.K	190	2	*
4	ENSG00000093010:ENSMUSG00000000326:ENSRNOG00000001889	COMT	gi|6680982|ref|NP_031770.1|	gi|6680982|ref|NP_031770.1|	catechol-O-methyltransferase [Mus musculus]	6	61	21.9	265	29496	5.8	MmNaOH-MM_liver_CNBrTi_102.3098.3098.3	3	5.358	0.3607	2304.46	2304.6	1	42.105263	12	R.EYRPSLVLELGAYCGYSAVR.M	99	2	*
4	ENSG00000093010:ENSMUSG00000000326:ENSRNOG00000001889	COMT	gi|6680982|ref|NP_031770.1|	gi|6680982|ref|NP_031770.1|	catechol-O-methyltransferase [Mus musculus]	6	61	21.9	265	29496	5.8	MmNaOH-MM_liver_CNBrTi_211.3341.3341.2	2	4.6952	0.3921	1805.19	1806.1	1	78.57143	29	R.YLPDTLLLEECGLLR.K	190	2	*
4	ENSG00000093010:ENSMUSG00000000326:ENSRNOG00000001889	COMT	gi|6680982|ref|NP_031770.1|	gi|6680982|ref|NP_031770.1|	catechol-O-methyltransferase [Mus musculus]	6	61	21.9	265	29496	5.8	MmNaOH-MM_liver_CNBrTi_208.3753.3753.2	2	2.7357	0.2095	2332.19	2331.7	3	35.714287	1	K.GTVLLADNVIVPGTPDFLAYVR.G	206	2	*
4	ENSG00000093010:ENSMUSG00000000326:ENSRNOG00000001889	COMT	gi|6680982|ref|NP_031770.1|	gi|6680982|ref|NP_031770.1|	catechol-O-methyltransferase [Mus musculus]	6	61	21.9	265	29496	5.8	MmNaOH-MM_liver_CNBrTi_104.2878.2878.2	2	4.2531	0.3713	2304.38	2304.6	1	57.894737	7	R.EYRPSLVLELGAYCGYSAVR.M	99	2	*
5	ENSG00000105518:ENSMUSG00000040883:ENSRNOG00000011747	NP_940938.1	gi|31982159|ref|NP_848692.2|	gi|31982159|ref|NP_848692.2|	hypothetical protein LOC235043 [Mus musculus]	1	67	9	189	21180	9.4	MmNaOH-MM_liver_CNBrTi_202.1872.1872.2	2	4.0909	0.4295	1804.62	1805	1	65.625	66	R.GLGTEVPGNFQGPDPYR.Q	125	2	*
5	ENSG00000105518:ENSMUSG00000040883:ENSRNOG00000011747	NP_940938.1	gi|31982159|ref|NP_848692.2|	gi|31982159|ref|NP_848692.2|	hypothetical protein LOC235043 [Mus musculus]	1	67	9	189	21180	9.4	MmNaOH-MM_liver_CNBrTi_101.1843.1843.2	2	2.9536	0.3053	1804.88	1805	1	50	1	R.GLGTEVPGNFQGPDPYR.Q	125	2	*
6	ENSG00000197838:ENSMUSG00000060407:ENSRNOG00000020817	CYP2A13	gi|19526798|ref|NP_598418.1|	gi|19526798|ref|NP_598418.1|	cytochrome P450, family 2, subfamily a, polypeptide 12 [Mus musc	3	158	5.1	492	56179	9.2	MmNaOH-MM_liver_CNBrTi_101.1870.1870.2	2	3.5653	0.3315	1219.45	1219.4	1	80	1	R.FSNFAPLGIPR.R	360	2	
6	ENSG00000197838:ENSMUSG00000060407:ENSRNOG00000020817	CYP2A13	gi|19526798|ref|NP_598418.1|	gi|19526798|ref|NP_598418.1|	cytochrome P450, family 2, subfamily a, polypeptide 12 [Mus musc	3	158	5.1	492	56179	9.2	MmNaOH-MM_liver_CNBrTi_205.1962.1962.2	2	3.8809	0.3646	1219.32	1219.4	1	75	154	R.FSNFAPLGIPR.R	360	2	
6	ENSG00000197838:ENSMUSG00000060407:ENSRNOG00000020817	CYP2A13	gi|19526798|ref|NP_598418.1|	gi|19526798|ref|NP_598418.1|	cytochrome P450, family 2, subfamily a, polypeptide 12 [Mus musc	3	158	5.1	492	56179	9.2	MmNaOH-MM_liver_CNBrTi_202.2314.2314.2	2	4.7392	0.4763	1466.52	1466.6	1	73.07692	1	K.TASNVISSIVFGDR.F	176	2	*
6	ENSG00000197838:ENSMUSG00000060407:ENSRNOG00000020817	CYP2A13	gi|19526798|ref|NP_598418.1|	gi|19526798|ref|NP_598418.1|	cytochrome P450, family 2, subfamily a, polypeptide 12 [Mus musc	3	158	5.1	492	56179	9.2	MmNaOH-MM_liver_CNBrTi_207.1915.1915.1	1	2.5279	0.2829	1218.72	1219.4	1	70	2	R.FSNFAPLGIPR.R	360	2	
7	ENSG00000143819:ENSMUSG00000038776:ENSRNOG00000003515	EPHX1	gi|6753762|ref|NP_034275.1|	gi|6753762|ref|NP_034275.1|	epoxide hydrolase 1, microsomal [Mus musculus]	7	131	7.5	455	52577	8.4	MmNaOH-MM_liver_CNBrTi_203.2137.2137.2	2	3.8738	0.1732	1375.59	1375.6	1	81.818184	117	R.NIYSLTPLLGQR.F	256	2	*
7	ENSG00000143819:ENSMUSG00000038776:ENSRNOG00000003515	EPHX1	gi|6753762|ref|NP_034275.1|	gi|6753762|ref|NP_034275.1|	epoxide hydrolase 1, microsomal [Mus musculus]	7	131	7.5	455	52577	8.4	MmNaOH-MM_liver_CNBrTi_202.2631.2631.1	1	2.8062	0.119	1137.68	1138.3	4	68.75	1	K.DLELLYPFK.E	278	2	*
7	ENSG00000143819:ENSMUSG00000038776:ENSRNOG00000003515	EPHX1	gi|6753762|ref|NP_034275.1|	gi|6753762|ref|NP_034275.1|	epoxide hydrolase 1, microsomal [Mus musculus]	7	131	7.5	455	52577	8.4	MmNaOH-MM_liver_CNBrTi_209.1225.1225.1	1	2.9634	0.2346	1189.43	1190.3	2	70	3	R.GGHFAAFEEPK.L	429	2	*
7	ENSG00000143819:ENSMUSG00000038776:ENSRNOG00000003515	EPHX1	gi|6753762|ref|NP_034275.1|	gi|6753762|ref|NP_034275.1|	epoxide hydrolase 1, microsomal [Mus musculus]	7	131	7.5	455	52577	8.4	MmNaOH-MM_liver_CNBrTi_204.2148.2148.1	1	2.0816	0.1982	1374.66	1375.6	3	59.090908	1	R.NIYSLTPLLGQR.F	256	2	*
7	ENSG00000143819:ENSMUSG00000038776:ENSRNOG00000003515	EPHX1	gi|6753762|ref|NP_034275.1|	gi|6753762|ref|NP_034275.1|	epoxide hydrolase 1, microsomal [Mus musculus]	7	131	7.5	455	52577	8.4	MmNaOH-MM_liver_CNBrTi_105.1399.1399.2	2	2.8852	0.2388	1475.78	1475.6	8	58.333332	1	M.ERGGHFAAFEEPK.L	427	1	*
7	ENSG00000143819:ENSMUSG00000038776:ENSRNOG00000003515	EPHX1	gi|6753762|ref|NP_034275.1|	gi|6753762|ref|NP_034275.1|	epoxide hydrolase 1, microsomal [Mus musculus]	7	131	7.5	455	52577	8.4	MmNaOH-MM_liver_CNBrTi_106.1391.1391.3	3	3.4581	0.2516	1475.46	1475.6	1	47.916664	2	M.ERGGHFAAFEEPK.L	427	1	*
7	ENSG00000143819:ENSMUSG00000038776:ENSRNOG00000003515	EPHX1	gi|6753762|ref|NP_034275.1|	gi|6753762|ref|NP_034275.1|	epoxide hydrolase 1, microsomal [Mus musculus]	7	131	7.5	455	52577	8.4	MmNaOH-MM_liver_CNBrTi_101.2098.2098.2	2	3.3713	0.3178	1375.27	1375.6	1	68.181816	1	R.NIYSLTPLLGQR.F	256	2	*
7	ENSG00000143819:ENSMUSG00000038776:ENSRNOG00000003515	EPHX1	gi|6753762|ref|NP_034275.1|	gi|6753762|ref|NP_034275.1|	epoxide hydrolase 1, microsomal [Mus musculus]	7	131	7.5	455	52577	8.4	MmNaOH-MM_liver_CNBrTi_210.1194.1194.2	2	3.6536	0.2477	1192.55	1190.3	1	70	5	R.GGHFAAFEEPK.L	429	2	*
8	ENSG00000130649:ENSMUSG00000025479:ENSRNOG00000012458	CYP2E1	gi|11276065|ref|NP_067257.1|	gi|11276065|ref|NP_067257.1|	cytochrome P450, family 2, subfamily e, polypeptide 1 [Mus muscu	7	109	14.4	493	56805	8.4	MmNaOH-MM_liver_CNBrTi_204.0683.0683.2	2	2.1288	0.1533	1066.57	1067.2	8	75	1	M.DAVVHEIQR.F	351	1	*
8	ENSG00000130649:ENSMUSG00000025479:ENSRNOG00000012458	CYP2E1	gi|11276065|ref|NP_067257.1|	gi|11276065|ref|NP_067257.1|	cytochrome P450, family 2, subfamily e, polypeptide 1 [Mus muscu	7	109	14.4	493	56805	8.4	MmNaOH-MM_liver_CNBrTi_202.4310.4310.2	2	4.8545	0.3934	1689.41	1687.9	1	73.333336	98	K.DIDLSPVTIGFGSIPR.E	468	2	*
8	ENSG00000130649:ENSMUSG00000025479:ENSRNOG00000012458	CYP2E1	gi|11276065|ref|NP_067257.1|	gi|11276065|ref|NP_067257.1|	cytochrome P450, family 2, subfamily e, polypeptide 1 [Mus muscu	7	109	14.4	493	56805	8.4	MmNaOH-MM_liver_CNBrTi_101.3222.3222.2	2	4.059	0.4166	1689.19	1687.9	1	63.333332	2	K.DIDLSPVTIGFGSIPR.E	468	2	*
8	ENSG00000130649:ENSMUSG00000025479:ENSRNOG00000012458	CYP2E1	gi|11276065|ref|NP_067257.1|	gi|11276065|ref|NP_067257.1|	cytochrome P450, family 2, subfamily e, polypeptide 1 [Mus muscu	7	109	14.4	493	56805	8.4	MmNaOH-MM_liver_CNBrTi_212.2003.2003.2	2	2.8048	0.1729	1215.08	1215.4	6	72.22222	1	R.EAHFLVEELK.K	150	2	*
8	ENSG00000130649:ENSMUSG00000025479:ENSRNOG00000012458	CYP2E1	gi|11276065|ref|NP_067257.1|	gi|11276065|ref|NP_067257.1|	cytochrome P450, family 2, subfamily e, polypeptide 1 [Mus muscu	7	109	14.4	493	56805	8.4	MmNaOH-MM_liver_CNBrTi_205.2898.2898.3	3	3.5421	0.2932	1687.61	1687.9	1	46.666668	1	K.DIDLSPVTIGFGSIPR.E	468	2	*
8	ENSG00000130649:ENSMUSG00000025479:ENSRNOG00000012458	CYP2E1	gi|11276065|ref|NP_067257.1|	gi|11276065|ref|NP_067257.1|	cytochrome P450, family 2, subfamily e, polypeptide 1 [Mus muscu	7	109	14.4	493	56805	8.4	MmNaOH-MM_liver_CNBrTi_104.1978.1978.2	2	3.166	0.0971	992.24	992.21	3	100	3	R.RFSLSILR.D	127	2	*
8	ENSG00000130649:ENSMUSG00000025479:ENSRNOG00000012458	CYP2E1	gi|11276065|ref|NP_067257.1|	gi|11276065|ref|NP_067257.1|	cytochrome P450, family 2, subfamily e, polypeptide 1 [Mus muscu	7	109	14.4	493	56805	8.4	MmNaOH-MM_liver_CNBrTi_104.1438.1438.2	2	3.1565	0.3226	1520.76	1521.7	2	54.166668	2	K.LHEEIDRVIGPSR.A	325	2	*
8	ENSG00000130649:ENSMUSG00000025479:ENSRNOG00000012458	CYP2E1	gi|11276065|ref|NP_067257.1|	gi|11276065|ref|NP_067257.1|	cytochrome P450, family 2, subfamily e, polypeptide 1 [Mus muscu	7	109	14.4	493	56805	8.4	MmNaOH-MM_liver_CNBrTi_101.1746.1746.2	2	3.2945	0.2417	1708.78	1709	2	57.14286	1	R.FINLVPSNLPHEATR.D	360	2	*
9	ENSG00000005421:ENSMUSG00000002588:ENSRNOG00000008902	PON1	gi|7242183|ref|NP_035264.1|	gi|7242183|ref|NP_035264.1|	paraoxonase 1 [Mus musculus]	2	81	4.8	355	39531	5.2	MmNaOH-MM_liver_CNBrTi_203.2293.2293.2	2	3.8323	0.2633	1854.57	1855.1	1	70	80	R.IFFYDAENPPGSEVLR.I	291	2	*
9	ENSG00000005421:ENSMUSG00000002588:ENSRNOG00000008902	PON1	gi|7242183|ref|NP_035264.1|	gi|7242183|ref|NP_035264.1|	paraoxonase 1 [Mus musculus]	2	81	4.8	355	39531	5.2	MmNaOH-MM_liver_CNBrTi_105.2260.2260.2	2	3.4256	0.3031	2010.79	2011.2	1	50	1	M.RIFFYDAENPPGSEVLR.I	290	1	*
10	ENSG00000205702:ENSMUSG00000068086:ENSRNOG00000029128	NR_002570.2	gi|6753584|ref|NP_034136.1|	gi|6753584|ref|NP_034136.1|	cytochrome P450, family 2, subfamily d, polypeptide 9 [Mus muscu	15	66	21.6	504	56949	6.3	MmNaOH-MM_liver_CNBrTi_202.4743.4743.2	2	3.3238	0.2798	1227.31	1227.4	2	85	31	R.FGDIVPVNLPR.I	369	2	*
10	ENSG00000205702:ENSMUSG00000068086:ENSRNOG00000029128	NR_002570.2	gi|6753584|ref|NP_034136.1|	gi|6753584|ref|NP_034136.1|	cytochrome P450, family 2, subfamily d, polypeptide 9 [Mus muscu	15	66	21.6	504	56949	6.3	MmNaOH-MM_liver_CNBrTi_106.1418.1418.2	2	2.6953	0.1275	965.99	966.13	1	100	1	R.RFSVSTLR.N	136	2	
10	ENSG00000205702:ENSMUSG00000068086:ENSRNOG00000029128	NR_002570.2	gi|6753584|ref|NP_034136.1|	gi|6753584|ref|NP_034136.1|	cytochrome P450, family 2, subfamily d, polypeptide 9 [Mus muscu	15	66	21.6	504	56949	6.3	MmNaOH-MM_liver_CNBrTi_104.2438.2438.3	3	4.155	0.299	1485.52	1485.7	1	60.000004	5	R.RFEYEDPFLIR.M	197	2	
10	ENSG00000205702:ENSMUSG00000068086:ENSRNOG00000029128	NR_002570.2	gi|6753584|ref|NP_034136.1|	gi|6753584|ref|NP_034136.1|	cytochrome P450, family 2, subfamily d, polypeptide 9 [Mus muscu	15	66	21.6	504	56949	6.3	MmNaOH-MM_liver_CNBrTi_211.1929.1929.2	2	2.5817	0.1741	965.69	966.13	1	85.71429	1	R.RFSVSTLR.N	136	2	
10	ENSG00000205702:ENSMUSG00000068086:ENSRNOG00000029128	NR_002570.2	gi|6753584|ref|NP_034136.1|	gi|6753584|ref|NP_034136.1|	cytochrome P450, family 2, subfamily d, polypeptide 9 [Mus muscu	15	66	21.6	504	56949	6.3	MmNaOH-MM_liver_CNBrTi_201.1870.1870.2	2	4.3508	0.3048	1513.37	1513.7	1	83.33333	2	R.VQQEIDEVIGQVR.H	334	2	
10	ENSG00000205702:ENSMUSG00000068086:ENSRNOG00000029128	NR_002570.2	gi|6753584|ref|NP_034136.1|	gi|6753584|ref|NP_034136.1|	cytochrome P450, family 2, subfamily d, polypeptide 9 [Mus muscu	15	66	21.6	504	56949	6.3	MmNaOH-MM_liver_CNBrTi_209.1365.1365.3	3	3.3945	0.0946	1428.01	1427.6	1	52.272724	1	M.PYTNAVIHEVQR.F	357	1	
10	ENSG00000205702:ENSMUSG00000068086:ENSRNOG00000029128	NR_002570.2	gi|6753584|ref|NP_034136.1|	gi|6753584|ref|NP_034136.1|	cytochrome P450, family 2, subfamily d, polypeptide 9 [Mus muscu	15	66	21.6	504	56949	6.3	MmNaOH-MM_liver_CNBrTi_105.0172.0172.3	3	3.9365	0.1965	2754.04	2752.3	2	28.125	2	K.VLEQSLTEVSGLIPEVLNAFPILLR.I	211	2	*
10	ENSG00000205702:ENSMUSG00000068086:ENSRNOG00000029128	NR_002570.2	gi|6753584|ref|NP_034136.1|	gi|6753584|ref|NP_034136.1|	cytochrome P450, family 2, subfamily d, polypeptide 9 [Mus muscu	15	66	21.6	504	56949	6.3	MmNaOH-MM_liver_CNBrTi_102.2694.2694.2	2	3.1936	0.2709	1485.56	1485.7	1	70	5	R.RFEYEDPFLIR.M	197	2	
10	ENSG00000205702:ENSMUSG00000068086:ENSRNOG00000029128	NR_002570.2	gi|6753584|ref|NP_034136.1|	gi|6753584|ref|NP_034136.1|	cytochrome P450, family 2, subfamily d, polypeptide 9 [Mus muscu	15	66	21.6	504	56949	6.3	MmNaOH-MM_liver_CNBrTi_101.1831.1831.3	3	4.7299	0.1621	1670.86	1669.9	1	59.615387	1	R.RVQQEIDEVIGQVR.H	333	2	
10	ENSG00000205702:ENSMUSG00000068086:ENSRNOG00000029128	NR_002570.2	gi|6753584|ref|NP_034136.1|	gi|6753584|ref|NP_034136.1|	cytochrome P450, family 2, subfamily d, polypeptide 9 [Mus muscu	15	66	21.6	504	56949	6.3	MmNaOH-MM_liver_CNBrTi_109.6644.6644.3	3	3.5172	0.3386	3119.94	3118.7	1	25	1	K.VLEQSLTEVSGLIPEVLNAFPILLRIPR.L	211	2	*
10	ENSG00000205702:ENSMUSG00000068086:ENSRNOG00000029128	NR_002570.2	gi|6753584|ref|NP_034136.1|	gi|6753584|ref|NP_034136.1|	cytochrome P450, family 2, subfamily d, polypeptide 9 [Mus muscu	15	66	21.6	504	56949	6.3	MmNaOH-MM_liver_CNBrTi_105.0143.0143.2	2	4.1589	0.3287	2752.82	2752.3	1	39.583336	6	K.VLEQSLTEVSGLIPEVLNAFPILLR.I	211	2	*
10	ENSG00000205702:ENSMUSG00000068086:ENSRNOG00000029128	NR_002570.2	gi|6753584|ref|NP_034136.1|	gi|6753584|ref|NP_034136.1|	cytochrome P450, family 2, subfamily d, polypeptide 9 [Mus muscu	15	66	21.6	504	56949	6.3	MmNaOH-MM_liver_CNBrTi_101.1918.1918.2	2	4.7454	0.2964	1513.59	1513.7	1	83.33333	1	R.VQQEIDEVIGQVR.H	334	2	
10	ENSG00000205702:ENSMUSG00000068086:ENSRNOG00000029128	NR_002570.2	gi|6753584|ref|NP_034136.1|	gi|6753584|ref|NP_034136.1|	cytochrome P450, family 2, subfamily d, polypeptide 9 [Mus muscu	15	66	21.6	504	56949	6.3	MmNaOH-MM_liver_CNBrTi_101.4768.4768.2	2	3.2156	0.3318	1619.72	1619.9	1	61.538464	1	K.SFIAILDNLLTENR.T	249	2	*
10	ENSG00000205702:ENSMUSG00000068086:ENSRNOG00000029128	NR_002570.2	gi|6753584|ref|NP_034136.1|	gi|6753584|ref|NP_034136.1|	cytochrome P450, family 2, subfamily d, polypeptide 9 [Mus muscu	15	66	21.6	504	56949	6.3	MmNaOH-MM_liver_CNBrTi_101.1920.1920.1	1	3.2311	0.2937	1512.86	1513.7	1	62.5	1	R.VQQEIDEVIGQVR.H	334	2	
10	ENSG00000205702:ENSMUSG00000068086:ENSRNOG00000029128	NR_002570.2	gi|6753584|ref|NP_034136.1|	gi|6753584|ref|NP_034136.1|	cytochrome P450, family 2, subfamily d, polypeptide 9 [Mus muscu	15	66	21.6	504	56949	6.3	MmNaOH-MM_liver_CNBrTi_205.1975.1975.1	1	2.1344	0.1479	1227.78	1227.4	2	60.000004	1	R.FGDIVPVNLPR.I	369	2	*
10	ENSG00000205702:ENSMUSG00000068086:ENSRNOG00000029128	NR_002570.2	gi|6753584|ref|NP_034136.1|	gi|6753584|ref|NP_034136.1|	cytochrome P450, family 2, subfamily d, polypeptide 9 [Mus muscu	15	66	21.6	504	56949	6.3	MmNaOH-MM_liver_CNBrTi_101.1818.1818.2	2	4.5551	0.3848	1670.01	1669.9	1	69.230774	4	R.RVQQEIDEVIGQVR.H	333	2	
11	ENSG00000101856:ENSMUSG00000006373:ENSRNOG00000012786	PGRMC1	gi|31980806|ref|NP_058063.2|	gi|31980806|ref|NP_058063.2|;gi|5729875|ref|NP_006658.1|	progesterone receptor membrane component [Mus musculus]	4	21	12.3	195	21694	4.7	MmNaOH-MM_liver_CNBrTi_106.1938.1938.2	2	4.9422	0.5068	1645.68	1645.9	1	78.57143	8	R.KFYGPEGPYGVFAGR.D	105	2	
11	ENSG00000101856:ENSMUSG00000006373:ENSRNOG00000012786	PGRMC1	gi|31980806|ref|NP_058063.2|	gi|31980806|ref|NP_058063.2|;gi|5729875|ref|NP_006658.1|	progesterone receptor membrane component [Mus musculus]	4	21	12.3	195	21694	4.7	MmNaOH-MM_liver_CNBrTi_105.1911.1911.3	3	4.0885	0.3585	1645.79	1645.9	1	51.785713	4	R.KFYGPEGPYGVFAGR.D	105	2	
11	ENSG00000101856:ENSMUSG00000006373:ENSRNOG00000012786	PGRMC1	gi|31980806|ref|NP_058063.2|	gi|31980806|ref|NP_058063.2|;gi|5729875|ref|NP_006658.1|	progesterone receptor membrane component [Mus musculus]	4	21	12.3	195	21694	4.7	MmNaOH-MM_liver_CNBrTi_208.1276.1276.2	2	2.9693	0.1003	1105.52	1105.2	5	87.5	3	R.RDFTPAELR.R	71	2	
11	ENSG00000101856:ENSMUSG00000006373:ENSRNOG00000012786	PGRMC1	gi|31980806|ref|NP_058063.2|	gi|31980806|ref|NP_058063.2|;gi|5729875|ref|NP_006658.1|	progesterone receptor membrane component [Mus musculus]	4	21	12.3	195	21694	4.7	MmNaOH-MM_liver_CNBrTi_208.1992.1992.2	2	3.8444	0.4743	1517.53	1517.7	1	80.769226	6	K.FYGPEGPYGVFAGR.D	106	2	
12	ENSG00000197446:ENSMUSG00000052974:ENSRNOG00000032805	CYP2F1	gi|124001560|ref|NP_031843.2|	gi|124001560|ref|NP_031843.2|	cytochrome P450, family 2, subfamily f, polypeptide 2 [Mus muscul	9	49	22.6	491	55949	7.9	MmNaOH-MM_liver_CNBrTi_101.2903.2903.2	2	3.617	0.3583	1525.58	1525.7	1	65.38461	1	R.SVSNIICSVVFGSR.F	174	2	*
12	ENSG00000197446:ENSMUSG00000052974:ENSRNOG00000032805	CYP2F1	gi|124001560|ref|NP_031843.2|	gi|124001560|ref|NP_031843.2|	cytochrome P450, family 2, subfamily f, polypeptide 2 [Mus muscul	9	49	22.6	491	55949	7.9	MmNaOH-MM_liver_CNBrTi_212.1912.1912.2	2	3.2474	0.1803	1186.26	1185.4	2	83.33333	1	R.RLCLGEPLAR.M	434	2	*
12	ENSG00000197446:ENSMUSG00000052974:ENSRNOG00000032805	CYP2F1	gi|124001560|ref|NP_031843.2|	gi|124001560|ref|NP_031843.2|	cytochrome P450, family 2, subfamily f, polypeptide 2 [Mus muscul	9	49	22.6	491	55949	7.9	MmNaOH-MM_liver_CNBrTi_206.0453.0453.2	2	3.2009	0.2331	1395.32	1395.4	1	68.181816	8	R.EHQDSLDPNSPR.D	251	2	*
12	ENSG00000197446:ENSMUSG00000052974:ENSRNOG00000032805	CYP2F1	gi|124001560|ref|NP_031843.2|	gi|124001560|ref|NP_031843.2|	cytochrome P450, family 2, subfamily f, polypeptide 2 [Mus muscul	9	49	22.6	491	55949	7.9	MmNaOH-MM_liver_CNBrTi_204.3599.3599.2	2	4.1267	0.3204	2490.49	2492.8	1	45.454548	3	M.DTLLMTTHNLLFGGTETVGTTLR.H	286	1	*
12	ENSG00000197446:ENSMUSG00000052974:ENSRNOG00000032805	CYP2F1	gi|124001560|ref|NP_031843.2|	gi|124001560|ref|NP_031843.2|	cytochrome P450, family 2, subfamily f, polypeptide 2 [Mus muscul	9	49	22.6	491	55949	7.9	MmNaOH-MM_liver_CNBrTi_211.2111.2111.2	2	4.2405	0.2492	1428.52	1428.6	1	86.36364	3	M.PYTDAVIHEVQR.F	347	1	*
12	ENSG00000197446:ENSMUSG00000052974:ENSRNOG00000032805	CYP2F1	gi|124001560|ref|NP_031843.2|	gi|124001560|ref|NP_031843.2|	cytochrome P450, family 2, subfamily f, polypeptide 2 [Mus muscul	9	49	22.6	491	55949	7.9	MmNaOH-MM_liver_CNBrTi_104.1566.1566.2	2	3.0808	0.1812	1185.66	1185.4	1	83.33333	3	R.RLCLGEPLAR.M	434	2	*
12	ENSG00000197446:ENSMUSG00000052974:ENSRNOG00000032805	CYP2F1	gi|124001560|ref|NP_031843.2|	gi|124001560|ref|NP_031843.2|	cytochrome P450, family 2, subfamily f, polypeptide 2 [Mus muscul	9	49	22.6	491	55949	7.9	MmNaOH-MM_liver_CNBrTi_101.4231.4231.2	2	3.8322	0.2663	2490.14	2492.8	1	43.18182	1	M.DTLLMTTHNLLFGGTETVGTTLR.H	286	1	*
12	ENSG00000197446:ENSMUSG00000052974:ENSRNOG00000032805	CYP2F1	gi|124001560|ref|NP_031843.2|	gi|124001560|ref|NP_031843.2|	cytochrome P450, family 2, subfamily f, polypeptide 2 [Mus muscul	9	49	22.6	491	55949	7.9	MmNaOH-MM_liver_CNBrTi_106.4271.4271.3	3	3.1783	0.1896	1885.52	1884.2	4	41.666664	1	M.YNIFPSVLDWIPGPHK.R	217	1	*
12	ENSG00000197446:ENSMUSG00000052974:ENSRNOG00000032805	CYP2F1	gi|124001560|ref|NP_031843.2|	gi|124001560|ref|NP_031843.2|	cytochrome P450, family 2, subfamily f, polypeptide 2 [Mus muscul	9	49	22.6	491	55949	7.9	MmNaOH-MM_liver_CNBrTi_105.4270.4270.2	2	3.5071	0.3437	1883.09	1884.2	1	53.333336	3	M.YNIFPSVLDWIPGPHK.R	217	1	*
12	ENSG00000197446:ENSMUSG00000052974:ENSRNOG00000032805	CYP2F1	gi|124001560|ref|NP_031843.2|	gi|124001560|ref|NP_031843.2|	cytochrome P450, family 2, subfamily f, polypeptide 2 [Mus muscul	9	49	22.6	491	55949	7.9	MmNaOH-MM_liver_CNBrTi_102.4210.4210.2	2	4.7091	0.258	1518.6	1518.8	1	83.33333	24	R.ILEEGSFLLEVLR.K	146	2	*
12	ENSG00000197446:ENSMUSG00000052974:ENSRNOG00000032805	CYP2F1	gi|124001560|ref|NP_031843.2|	gi|124001560|ref|NP_031843.2|	cytochrome P450, family 2, subfamily f, polypeptide 2 [Mus muscul	9	49	22.6	491	55949	7.9	MmNaOH-MM_liver_CNBrTi_211.1977.1977.2	2	2.9136	0.2115	1300.39	1300.5	6	70	1	R.VQEEIDRVVGR.S	324	2	
13	NA:ENSMUSG00000060613:ENSRNOG00000021924	CYP2C22	gi|21703982|ref|NP_663474.1|	gi|21703982|ref|NP_663474.1|	cytochrome P450, family 2, subfamily c, polypeptide 70 [Mus musc	5	90	6.3	489	56068	8.2	MmNaOH-MM_liver_CNBrTi_209.1003.1003.2	2	2.4013	0.189	1013.28	1014.2	5	81.25	1	K.PTVVLHGYK.A	73	2	*
13	NA:ENSMUSG00000060613:ENSRNOG00000021924	CYP2C22	gi|21703982|ref|NP_663474.1|	gi|21703982|ref|NP_663474.1|	cytochrome P450, family 2, subfamily c, polypeptide 70 [Mus musc	5	90	6.3	489	56068	8.2	MmNaOH-MM_liver_CNBrTi_202.4710.4710.2	2	3.0103	0.2176	1304.62	1304.5	1	75	85	R.YIDFVPIPSPR.K	357	2	*
13	NA:ENSMUSG00000060613:ENSRNOG00000021924	CYP2C22	gi|21703982|ref|NP_663474.1|	gi|21703982|ref|NP_663474.1|	cytochrome P450, family 2, subfamily c, polypeptide 70 [Mus musc	5	90	6.3	489	56068	8.2	MmNaOH-MM_liver_CNBrTi_212.1931.1931.2	2	4.2017	0.3291	1265.61	1265.5	1	90	1	K.IQEEIAHVIGR.H	322	2	*
13	NA:ENSMUSG00000060613:ENSRNOG00000021924	CYP2C22	gi|21703982|ref|NP_663474.1|	gi|21703982|ref|NP_663474.1|	cytochrome P450, family 2, subfamily c, polypeptide 70 [Mus musc	5	90	6.3	489	56068	8.2	MmNaOH-MM_liver_CNBrTi_212.1933.1933.1	1	2.6661	0.1269	1264.71	1265.5	2	60.000004	1	K.IQEEIAHVIGR.H	322	2	*
13	NA:ENSMUSG00000060613:ENSRNOG00000021924	CYP2C22	gi|21703982|ref|NP_663474.1|	gi|21703982|ref|NP_663474.1|	cytochrome P450, family 2, subfamily c, polypeptide 70 [Mus musc	5	90	6.3	489	56068	8.2	MmNaOH-MM_liver_CNBrTi_101.2100.2100.1	1	1.9003	0.1004	1305.64	1304.5	6	55	1	R.YIDFVPIPSPR.K	357	2	*
13	NA:ENSMUSG00000060613:ENSRNOG00000021924	CYP2C22	gi|21703982|ref|NP_663474.1|	gi|21703982|ref|NP_663474.1|	cytochrome P450, family 2, subfamily c, polypeptide 70 [Mus musc	5	90	6.3	489	56068	8.2	MmNaOH-MM_liver_CNBrTi_101.2083.2083.2	2	2.9112	0.2621	1304.65	1304.5	2	65	1	R.YIDFVPIPSPR.K	357	2	*
14	ENSG00000166347:ENSMUSG00000024646:ENSRNOG00000015205	CYB5A	gi|13385268|ref|NP_080073.1|	gi|13385268|ref|NP_080073.1|	cytochrome b-5 [Mus musculus]	7	18	47.8	134	15241	5.1	MmNaOH-MM_liver_CNBrTi_101.0086.0086.2	2	4.8992	0.4416	2207.56	2207.2	1	52.499996	4	R.EQAGGDATENFEDVGHSTDAR.E	53	2	*
14	ENSG00000166347:ENSMUSG00000024646:ENSRNOG00000015205	CYB5A	gi|13385268|ref|NP_080073.1|	gi|13385268|ref|NP_080073.1|	cytochrome b-5 [Mus musculus]	7	18	47.8	134	15241	5.1	MmNaOH-MM_liver_CNBrTi_212.1972.1972.1	1	1.875	0.2165	1428.7	1429.6	5	54.545456	1	K.TYIIGELHPDDR.S	78	2	*
14	ENSG00000166347:ENSMUSG00000024646:ENSRNOG00000015205	CYB5A	gi|13385268|ref|NP_080073.1|	gi|13385268|ref|NP_080073.1|	cytochrome b-5 [Mus musculus]	7	18	47.8	134	15241	5.1	MmNaOH-MM_liver_CNBrTi_211.1943.1943.2	2	4.8362	0.4365	2207.37	2207.2	1	47.5	6	R.EQAGGDATENFEDVGHSTDAR.E	53	2	*
14	ENSG00000166347:ENSMUSG00000024646:ENSRNOG00000015205	CYB5A	gi|13385268|ref|NP_080073.1|	gi|13385268|ref|NP_080073.1|	cytochrome b-5 [Mus musculus]	7	18	47.8	134	15241	5.1	MmNaOH-MM_liver_CNBrTi_212.1905.1905.1	1	3.2337	0.3436	1512.71	1512.7	1	66.66667	2	K.FLEEHPGGEEVLR.E	40	2	*
14	ENSG00000166347:ENSMUSG00000024646:ENSRNOG00000015205	CYB5A	gi|13385268|ref|NP_080073.1|	gi|13385268|ref|NP_080073.1|	cytochrome b-5 [Mus musculus]	7	18	47.8	134	15241	5.1	MmNaOH-MM_liver_CNBrTi_212.1900.1900.2	2	3.8896	0.3389	1512.65	1512.7	1	66.66667	2	K.FLEEHPGGEEVLR.E	40	2	*
14	ENSG00000166347:ENSMUSG00000024646:ENSRNOG00000015205	CYB5A	gi|13385268|ref|NP_080073.1|	gi|13385268|ref|NP_080073.1|	cytochrome b-5 [Mus musculus]	7	18	47.8	134	15241	5.1	MmNaOH-MM_liver_CNBrTi_108.1488.1488.2	2	2.568	0.218	1121.34	1121.3	2	75	1	K.STWVILHHK.V	25	2	*
14	ENSG00000166347:ENSMUSG00000024646:ENSRNOG00000015205	CYB5A	gi|13385268|ref|NP_080073.1|	gi|13385268|ref|NP_080073.1|	cytochrome b-5 [Mus musculus]	7	18	47.8	134	15241	5.1	MmNaOH-MM_liver_CNBrTi_201.0702.0702.2	2	2.2495	0.1231	1189.19	1187.3	3	75	1	K.YYTLEEIQK.H	11	2	*
14	ENSG00000166347:ENSMUSG00000024646:ENSRNOG00000015205	CYB5A	gi|13385268|ref|NP_080073.1|	gi|13385268|ref|NP_080073.1|	cytochrome b-5 [Mus musculus]	7	18	47.8	134	15241	5.1	MmNaOH-MM_liver_CNBrTi_212.1971.1971.2	2	4.1332	0.3408	1430.58	1429.6	1	86.36364	1	K.TYIIGELHPDDR.S	78	2	*
15	ENSG00000205702:ENSMUSG00000022445:ENSRNOG00000008988	CYP2D7P1	gi|13386414|ref|NP_083838.1|	gi|13386414|ref|NP_083838.1|	cytochrome P450, family 2, subfamily d, polypeptide 26 [Mus musc	15	57	23.6	500	56950	6.6	MmNaOH-MM_liver_CNBrTi_103.2315.2315.3	3	3.9966	0.3302	1521.56	1520.6	1	62.5	5	R.RFEYEDPFFNR.M	197	2	*
15	ENSG00000205702:ENSMUSG00000022445:ENSRNOG00000008988	CYP2D7P1	gi|13386414|ref|NP_083838.1|	gi|13386414|ref|NP_083838.1|	cytochrome P450, family 2, subfamily d, polypeptide 26 [Mus musc	15	57	23.6	500	56950	6.6	MmNaOH-MM_liver_CNBrTi_209.0933.0933.2	2	2.689	0.0808	1159.5	1159.3	1	83.33333	1	R.RSCLGEPLAR.M	444	2	
15	ENSG00000205702:ENSMUSG00000022445:ENSRNOG00000008988	CYP2D7P1	gi|13386414|ref|NP_083838.1|	gi|13386414|ref|NP_083838.1|	cytochrome P450, family 2, subfamily d, polypeptide 26 [Mus musc	15	57	23.6	500	56950	6.6	MmNaOH-MM_liver_CNBrTi_209.1365.1365.3	3	3.3945	0.0946	1428.01	1427.6	1	52.272724	1	M.PYTNAVIHEVQR.F	357	1	
15	ENSG00000205702:ENSMUSG00000022445:ENSRNOG00000008988	CYP2D7P1	gi|13386414|ref|NP_083838.1|	gi|13386414|ref|NP_083838.1|	cytochrome P450, family 2, subfamily d, polypeptide 26 [Mus musc	15	57	23.6	500	56950	6.6	MmNaOH-MM_liver_CNBrTi_102.2326.2326.2	2	3.4256	0.387	1519.95	1520.6	1	70	3	R.RFEYEDPFFNR.M	197	2	*
15	ENSG00000205702:ENSMUSG00000022445:ENSRNOG00000008988	CYP2D7P1	gi|13386414|ref|NP_083838.1|	gi|13386414|ref|NP_083838.1|	cytochrome P450, family 2, subfamily d, polypeptide 26 [Mus musc	15	57	23.6	500	56950	6.6	MmNaOH-MM_liver_CNBrTi_101.2622.2622.2	2	4.4227	0.4263	1377.61	1377.6	1	83.33333	1	K.AVSNVIASLIYAR.R	184	2	*
15	ENSG00000205702:ENSMUSG00000022445:ENSRNOG00000008988	CYP2D7P1	gi|13386414|ref|NP_083838.1|	gi|13386414|ref|NP_083838.1|	cytochrome P450, family 2, subfamily d, polypeptide 26 [Mus musc	15	57	23.6	500	56950	6.6	MmNaOH-MM_liver_CNBrTi_104.1558.1558.3	3	4.2747	0.2555	1531.83	1531.7	1	56.25	5	R.VHQEIDEVIGHVR.H	334	2	*
15	ENSG00000205702:ENSMUSG00000022445:ENSRNOG00000008988	CYP2D7P1	gi|13386414|ref|NP_083838.1|	gi|13386414|ref|NP_083838.1|	cytochrome P450, family 2, subfamily d, polypeptide 26 [Mus musc	15	57	23.6	500	56950	6.6	MmNaOH-MM_liver_CNBrTi_106.1418.1418.2	2	2.6953	0.1275	965.99	966.13	1	100	1	R.RFSVSTLR.N	136	2	
15	ENSG00000205702:ENSMUSG00000022445:ENSRNOG00000008988	CYP2D7P1	gi|13386414|ref|NP_083838.1|	gi|13386414|ref|NP_083838.1|	cytochrome P450, family 2, subfamily d, polypeptide 26 [Mus musc	15	57	23.6	500	56950	6.6	MmNaOH-MM_liver_CNBrTi_105.1579.1579.2	2	4.988	0.3504	1532.67	1531.7	1	83.33333	6	R.VHQEIDEVIGHVR.H	334	2	*

rk	ORTHO_GROUPS	GENE_NAME	Locus	Proteins In Group	Description	Sequence Count	Spectrum Count	Coverage	Length	MW	pI	MatchID	Z	XCorr	DeltCN	M+H+	CalcM +H+	SpRk	Ion Proportion	Count	Sequence	Sequence Position	Tryptic	Unique
15	ENSG00000205702:ENSMUSG00000022445:ENSRNOG00000008988	CYP2D7P1	gi|13386414|ref|NP_083838.1|	gi|13386414|ref|NP_083838.1|	cytochrome P450, family 2, subfamily d, polypeptide 26 [Mus musc	15	57	23.6	500	56950	6.6	MmNaOH-MM_liver_CNBrTi_101.3027.3027.2	2	4.1509	0.3634	1350.53	1351.5	1	86.36364	1	R.DLTDAFLAEVEK.A	273	2	
15	ENSG00000205702:ENSMUSG00000022445:ENSRNOG00000008988	CYP2D7P1	gi|13386414|ref|NP_083838.1|	gi|13386414|ref|NP_083838.1|	cytochrome P450, family 2, subfamily d, polypeptide 26 [Mus musc	15	57	23.6	500	56950	6.6	MmNaOH-MM_liver_CNBrTi_101.1716.1716.2	2	2.1475	0.2273	1236.91	1237.4	1	65	1	R.FSFSVPDGQPR.P	467	2	*
15	ENSG00000205702:ENSMUSG00000022445:ENSRNOG00000008988	CYP2D7P1	gi|13386414|ref|NP_083838.1|	gi|13386414|ref|NP_083838.1|	cytochrome P450, family 2, subfamily d, polypeptide 26 [Mus musc	15	57	23.6	500	56950	6.6	MmNaOH-MM_liver_CNBrTi_109.2188.2188.2	2	5.0977	0.4576	1687.98	1687.9	1	80.769226	1	R.RVHQEIDEVIGHVR.H	333	2	*
15	ENSG00000205702:ENSMUSG00000022445:ENSRNOG00000008988	CYP2D7P1	gi|13386414|ref|NP_083838.1|	gi|13386414|ref|NP_083838.1|	cytochrome P450, family 2, subfamily d, polypeptide 26 [Mus musc	15	57	23.6	500	56950	6.6	MmNaOH-MM_liver_CNBrTi_109.2189.2189.3	3	4.7976	0.2828	1687.99	1687.9	1	55.76923	1	R.RVHQEIDEVIGHVR.H	333	2	*
15	ENSG00000205702:ENSMUSG00000022445:ENSRNOG00000008988	CYP2D7P1	gi|13386414|ref|NP_083838.1|	gi|13386414|ref|NP_083838.1|	cytochrome P450, family 2, subfamily d, polypeptide 26 [Mus musc	15	57	23.6	500	56950	6.6	MmNaOH-MM_liver_CNBrTi_105.1586.1586.1	1	3.4531	0.2697	1531.74	1531.7	1	58.333332	1	R.VHQEIDEVIGHVR.H	334	2	*
15	ENSG00000205702:ENSMUSG00000022445:ENSRNOG00000008988	CYP2D7P1	gi|13386414|ref|NP_083838.1|	gi|13386414|ref|NP_083838.1|	cytochrome P450, family 2, subfamily d, polypeptide 26 [Mus musc	15	57	23.6	500	56950	6.6	MmNaOH-MM_liver_CNBrTi_106.1982.1982.2	2	3.5257	0.2643	1835.9	1836.1	1	60.714287	2	R.FYPEHFLDAQGHFVK.H	418	2	
15	ENSG00000205702:ENSMUSG00000022445:ENSRNOG00000008988	CYP2D7P1	gi|13386414|ref|NP_083838.1|	gi|13386414|ref|NP_083838.1|	cytochrome P450, family 2, subfamily d, polypeptide 26 [Mus musc	15	57	23.6	500	56950	6.6	MmNaOH-MM_liver_CNBrTi_211.1929.1929.2	2	2.5817	0.1741	965.69	966.13	1	85.71429	1	R.RFSVSTLR.N	136	2	
15	ENSG00000205702:ENSMUSG00000022445:ENSRNOG00000008988	CYP2D7P1	gi|13386414|ref|NP_083838.1|	gi|13386414|ref|NP_083838.1|	cytochrome P450, family 2, subfamily d, polypeptide 26 [Mus musc	15	57	23.6	500	56950	6.6	MmNaOH-MM_liver_CNBrTi_208.2010.2010.2	2	3.4279	0.2797	1357.74	1358.6	3	68.181816	4	K.GVILAPYGPEWR.E	121	2	*
15	ENSG00000205702:ENSMUSG00000022445:ENSRNOG00000008988	CYP2D7P1	gi|13386414|ref|NP_083838.1|	gi|13386414|ref|NP_083838.1|	cytochrome P450, family 2, subfamily d, polypeptide 26 [Mus musc	15	57	23.6	500	56950	6.6	MmNaOH-MM_liver_CNBrTi_206.2576.2576.2	2	4.5224	0.3966	1377.34	1377.6	1	79.16667	22	K.AVSNVIASLIYAR.R	184	2	*
16	ENSG00000172828:ENSMUSG00000069922:ENSRNOG00000026731	CES3	gi|82919057|ref|XP_920143.1|	gi|82919057|ref|XP_920143.1|;gi|82919063|ref|XP_928645.1|	PREDICTED: similar to Es31 protein isoform 5 [Mus musculus]	7	88	16.6	571	63318	6.1	MmNaOH-MM_liver_CNBrTi_210.1874.1874.2	2	2.7695	0.2449	1580.7	1581.8	8	53.846157	8	R.FSAPLPPQPWEGVR.D	78	2	
16	ENSG00000172828:ENSMUSG00000069922:ENSRNOG00000026731	CES3	gi|82919057|ref|XP_920143.1|	gi|82919057|ref|XP_920143.1|;gi|82919063|ref|XP_928645.1|	PREDICTED: similar to Es31 protein isoform 5 [Mus musculus]	7	88	16.6	571	63318	6.1	MmNaOH-MM_liver_CNBrTi_101.2998.2998.1	1	2.2124	0.1937	1060.64	1061.3	2	66.66667	2	R.GFLDVVAALR.W	201	2	
16	ENSG00000172828:ENSMUSG00000069922:ENSRNOG00000026731	CES3	gi|82919057|ref|XP_920143.1|	gi|82919057|ref|XP_920143.1|;gi|82919063|ref|XP_928645.1|	PREDICTED: similar to Es31 protein isoform 5 [Mus musculus]	7	88	16.6	571	63318	6.1	MmNaOH-MM_liver_CNBrTi_101.3007.3007.2	2	3.7566	0.3162	1061.38	1061.3	1	83.33333	1	R.GFLDVVAALR.W	201	2	
16	ENSG00000172828:ENSMUSG00000069922:ENSRNOG00000026731	CES3	gi|82919057|ref|XP_920143.1|	gi|82919057|ref|XP_920143.1|;gi|82919063|ref|XP_928645.1|	PREDICTED: similar to Es31 protein isoform 5 [Mus musculus]	7	88	16.6	571	63318	6.1	MmNaOH-MM_liver_CNBrTi_109.7037.7037.2	2	4.7742	0.3548	2348.85	2348.8	2	45	4	R.YALQELLGDITLVIPTLIFSK.Y	407	2	
16	ENSG00000172828:ENSMUSG00000069922:ENSRNOG00000026731	CES3	gi|82919057|ref|XP_920143.1|	gi|82919057|ref|XP_920143.1|;gi|82919063|ref|XP_928645.1|	PREDICTED: similar to Es31 protein isoform 5 [Mus musculus]	7	88	16.6	571	63318	6.1	MmNaOH-MM_liver_CNBrTi_103.5494.5494.2	2	3.25	0.3673	2590.81	2592	1	45.238094	1	K.GLPPWPQLNQLEQYLEIGLEPR.T	513	2	
16	ENSG00000172828:ENSMUSG00000069922:ENSRNOG00000026731	CES3	gi|82919057|ref|XP_920143.1|	gi|82919057|ref|XP_920143.1|;gi|82919063|ref|XP_928645.1|	PREDICTED: similar to Es31 protein isoform 5 [Mus musculus]	7	88	16.6	571	63318	6.1	MmNaOH-MM_liver_CNBrTi_101.3946.3946.2	2	3.6867	0.2705	1910.85	1910.3	1	55.88235	1	M.VNVFLGIPFAQAPLGPLR.F	60	1	
16	ENSG00000172828:ENSMUSG00000069922:ENSRNOG00000026731	CES3	gi|82919057|ref|XP_920143.1|	gi|82919057|ref|XP_920143.1|;gi|82919063|ref|XP_928645.1|	PREDICTED: similar to Es31 protein isoform 5 [Mus musculus]	7	88	16.6	571	63318	6.1	MmNaOH-MM_liver_CNBrTi_208.2679.2679.2	2	3.9338	0.3156	1061.14	1061.3	3	83.33333	62	R.GFLDVVAALR.W	201	2	
16	ENSG00000172828:ENSMUSG00000069922:ENSRNOG00000026731	CES3	gi|82919057|ref|XP_920143.1|	gi|82919057|ref|XP_920143.1|;gi|82919063|ref|XP_928645.1|	PREDICTED: similar to Es31 protein isoform 5 [Mus musculus]	7	88	16.6	571	63318	6.1	MmNaOH-MM_liver_CNBrTi_203.2077.2077.2	2	3.5459	0.2255	1292.34	1291.5	1	77.77778	8	R.LQFWTETLPR.K	544	2	
16	ENSG00000172828:ENSMUSG00000069922:ENSRNOG00000026731	CES3	gi|82919057|ref|XP_920143.1|	gi|82919057|ref|XP_920143.1|;gi|82919063|ref|XP_928645.1|	PREDICTED: similar to Es31 protein isoform 5 [Mus musculus]	7	88	16.6	571	63318	6.1	MmNaOH-MM_liver_CNBrTi_101.2062.2062.2	2	3.3006	0.2567	1291.26	1291.5	1	77.77778	1	R.LQFWTETLPR.K	544	2	
17	ENSG00000167165:ENSMUSG00000054545:ENSRNOG00000018740	UGT1A9	gi|47059135|ref|NP_964007.1|	gi|47059135|ref|NP_964007.1|	UDP glucuronosyltransferase 1 family, polypeptide A1 [Mus muscu	6	91	8.6	535	60066	8.7	MmNaOH-MM_liver_CNBrTi_101.2367.2367.2	2	4.3721	0.4968	1768.61	1769	1	66.66667	1	R.VVYSPYGSLATEILQK.E	227	2	*
17	ENSG00000167165:ENSMUSG00000054545:ENSRNOG00000018740	UGT1A9	gi|47059135|ref|NP_964007.1|	gi|47059135|ref|NP_964007.1|	UDP glucuronosyltransferase 1 family, polypeptide A1 [Mus muscu	6	91	8.6	535	60066	8.7	MmNaOH-MM_liver_CNBrTi_202.1938.1938.2	2	3.0695	0.243	1313.54	1312.5	1	75	3	R.TAFNQDSFLLR.V	100	2	*
17	ENSG00000167165:ENSMUSG00000054545:ENSRNOG00000018740	UGT1A9	gi|47059135|ref|NP_964007.1|	gi|47059135|ref|NP_964007.1|	UDP glucuronosyltransferase 1 family, polypeptide A1 [Mus muscu	6	91	8.6	535	60066	8.7	MmNaOH-MM_liver_CNBrTi_207.0602.0602.2	2	2.7701	0.2575	1208	1208.4	1	70	1	R.YTGTRPSNLAK.N	339	2	
17	ENSG00000167165:ENSMUSG00000054545:ENSRNOG00000018740	UGT1A9	gi|47059135|ref|NP_964007.1|	gi|47059135|ref|NP_964007.1|	UDP glucuronosyltransferase 1 family, polypeptide A1 [Mus muscu	6	91	8.6	535	60066	8.7	MmNaOH-MM_liver_CNBrTi_202.2526.2526.2	2	5.0454	0.5237	1768.65	1769	1	73.333336	25	R.VVYSPYGSLATEILQK.E	227	2	*
17	ENSG00000167165:ENSMUSG00000054545:ENSRNOG00000018740	UGT1A9	gi|47059135|ref|NP_964007.1|	gi|47059135|ref|NP_964007.1|	UDP glucuronosyltransferase 1 family, polypeptide A1 [Mus muscu	6	91	8.6	535	60066	8.7	MmNaOH-MM_liver_CNBrTi_202.2536.2536.3	3	4.3394	0.4032	1769.05	1769	1	46.666668	1	R.VVYSPYGSLATEILQK.E	227	2	*
17	ENSG00000167165:ENSMUSG00000054545:ENSRNOG00000018740	UGT1A9	gi|47059135|ref|NP_964007.1|	gi|47059135|ref|NP_964007.1|	UDP glucuronosyltransferase 1 family, polypeptide A1 [Mus muscu	6	91	8.6	535	60066	8.7	MmNaOH-MM_liver_CNBrTi_203.5853.5853.2	2	3.0751	0.2046	1013.35	1013.2	1	92.85714	57	R.IPQTVLWR.Y	331	2	
17	ENSG00000167165:ENSMUSG00000054545:ENSRNOG00000018740	UGT1A9	gi|47059135|ref|NP_964007.1|	gi|47059135|ref|NP_964007.1|	UDP glucuronosyltransferase 1 family, polypeptide A1 [Mus muscu	6	91	8.6	535	60066	8.7	MmNaOH-MM_liver_CNBrTi_101.1890.1890.2	2	3.0537	0.2986	1312.46	1312.5	1	80	1	R.TAFNQDSFLLR.V	100	2	*
17	ENSG00000167165:ENSMUSG00000054545:ENSRNOG00000018740	UGT1A9	gi|47059135|ref|NP_964007.1|	gi|47059135|ref|NP_964007.1|	UDP glucuronosyltransferase 1 family, polypeptide A1 [Mus muscu	6	91	8.6	535	60066	8.7	MmNaOH-MM_liver_CNBrTi_204.1766.1766.1	1	2.3725	0.1664	1012.57	1013.2	3	78.57143	2	R.IPQTVLWR.Y	331	2	
18	ENSG00000212695:ENSMUSG00000045128:ENSRNOG00000018795	Q76N54	gi|149240702|ref|XP_001476096.1|	gi|149240702|ref|XP_001476096.1|;gi|58037465|ref|NP_0840	PREDICTED: hypothetical protein [Mus musculus]	1	12	7.4	176	20762	10.7	MmNaOH-MM_liver_CNBrTi_201.1295.1295.2	2	3.3839	0.3271	1456.06	1456.6	1	70.83333	3	R.DLTTAGAVTQCYR.D	99	2	
18	ENSG00000212695:ENSMUSG00000045128:ENSRNOG00000018795	Q76N54	gi|149240702|ref|XP_001476096.1|	gi|149240702|ref|XP_001476096.1|;gi|58037465|ref|NP_0840	PREDICTED: hypothetical protein [Mus musculus]	1	12	7.4	176	20762	10.7	MmNaOH-MM_liver_CNBrTi_101.0539.0539.2	2	3.7912	0.3679	1456.46	1456.6	1	75	9	R.DLTTAGAVTQCYR.D	99	2	
19	ENSG00000140284:ENSMUSG00000027359:ENSRNOG00000010128	SLC27A2	gi|113374154|ref|NP_036108.2|	gi|113374154|ref|NP_036108.2|	solute carrier family 27 (fatty acid transporter), member 2 [Mus mu	10	70	18.7	620	70423	8.9	MmNaOH-MM_liver_CNBrTi_202.2707.2707.2	2	3.593	0.3387	2334.39	2334.6	1	45.238094	2	R.SEVTFTTPAVYIYTSGTTGLPK.A	212	2	*
19	ENSG00000140284:ENSMUSG00000027359:ENSRNOG00000010128	SLC27A2	gi|113374154|ref|NP_036108.2|	gi|113374154|ref|NP_036108.2|	solute carrier family 27 (fatty acid transporter), member 2 [Mus mu	10	70	18.7	620	70423	8.9	MmNaOH-MM_liver_CNBrTi_105.1598.1598.2	2	3.4359	0.3232	1611.18	1611.8	1	68.181816	2	M.IDRENFVYFHDR.V	469	1	*
19	ENSG00000140284:ENSMUSG00000027359:ENSRNOG00000010128	SLC27A2	gi|113374154|ref|NP_036108.2|	gi|113374154|ref|NP_036108.2|	solute carrier family 27 (fatty acid transporter), member 2 [Mus mu	10	70	18.7	620	70423	8.9	MmNaOH-MM_liver_CNBrTi_211.2109.2109.2	2	3.103	0.2626	1227.43	1227.3	1	87.5	3	R.ENFVYFHDR.V	472	2	*
19	ENSG00000140284:ENSMUSG00000027359:ENSRNOG00000010128	SLC27A2	gi|113374154|ref|NP_036108.2|	gi|113374154|ref|NP_036108.2|	solute carrier family 27 (fatty acid transporter), member 2 [Mus mu	10	70	18.7	620	70423	8.9	MmNaOH-MM_liver_CNBrTi_109.2692.2692.3	3	3.4408	0.2262	1961.94	1962.3	1	45	1	K.LFQHIAEYLPSYARPR.F	542	2	*
19	ENSG00000140284:ENSMUSG00000027359:ENSRNOG00000010128	SLC27A2	gi|113374154|ref|NP_036108.2|	gi|113374154|ref|NP_036108.2|	solute carrier family 27 (fatty acid transporter), member 2 [Mus mu	10	70	18.7	620	70423	8.9	MmNaOH-MM_liver_CNBrTi_109.2689.2689.2	2	3.2878	0.2662	1961.04	1962.3	1	46.666668	1	K.LFQHIAEYLPSYARPR.F	542	2	*
19	ENSG00000140284:ENSMUSG00000027359:ENSRNOG00000010128	SLC27A2	gi|113374154|ref|NP_036108.2|	gi|113374154|ref|NP_036108.2|	solute carrier family 27 (fatty acid transporter), member 2 [Mus mu	10	70	18.7	620	70423	8.9	MmNaOH-MM_liver_CNBrTi_110.4796.4796.3	3	4.7197	0.3623	3985.64	3983.4	1	22.222223	1	R.WKGENVATTEVADIVGLVDFVEEVNVYGVPVPGHEGR.I	487	2	*
19	ENSG00000140284:ENSMUSG00000027359:ENSRNOG00000010128	SLC27A2	gi|113374154|ref|NP_036108.2|	gi|113374154|ref|NP_036108.2|	solute carrier family 27 (fatty acid transporter), member 2 [Mus mu	10	70	18.7	620	70423	8.9	MmNaOH-MM_liver_CNBrTi_101.4499.4499.2	2	4.2078	0.499	2164.6	2165.5	1	50	1	K.VLLASPDLQEAVEEVLPTLK.K	154	2	*
19	ENSG00000140284:ENSMUSG00000027359:ENSRNOG00000010128	SLC27A2	gi|113374154|ref|NP_036108.2|	gi|113374154|ref|NP_036108.2|	solute carrier family 27 (fatty acid transporter), member 2 [Mus mu	10	70	18.7	620	70423	8.9	MmNaOH-MM_liver_CNBrTi_104.1372.1372.2	2	2.4381	0.1834	1022.49	1023.2	1	81.25	1	R.ALHDQLGLR.Q	94	2	*
19	ENSG00000140284:ENSMUSG00000027359:ENSRNOG00000010128	SLC27A2	gi|113374154|ref|NP_036108.2|	gi|113374154|ref|NP_036108.2|	solute carrier family 27 (fatty acid transporter), member 2 [Mus mu	10	70	18.7	620	70423	8.9	MmNaOH-MM_liver_CNBrTi_208.1164.1164.1	1	1.9727	0.1844	1022.62	1023.2	1	68.75	1	R.ALHDQLGLR.Q	94	2	*
19	ENSG00000140284:ENSMUSG00000027359:ENSRNOG00000010128	SLC27A2	gi|113374154|ref|NP_036108.2|	gi|113374154|ref|NP_036108.2|	solute carrier family 27 (fatty acid transporter), member 2 [Mus mu	10	70	18.7	620	70423	8.9	MmNaOH-MM_liver_CNBrTi_208.1124.1124.2	2	2.6656	0.1477	1023.08	1023.2	1	87.5	5	R.ALHDQLGLR.Q	94	2	*
19	ENSG00000140284:ENSMUSG00000027359:ENSRNOG00000010128	SLC27A2	gi|113374154|ref|NP_036108.2|	gi|113374154|ref|NP_036108.2|	solute carrier family 27 (fatty acid transporter), member 2 [Mus mu	10	70	18.7	620	70423	8.9	MmNaOH-MM_liver_CNBrTi_206.3659.3659.2	2	5.5277	0.4093	2164.75	2165.5	1	68.42105	51	K.VLLASPDLQEAVEEVLPTLK.K	154	2	*
19	ENSG00000140284:ENSMUSG00000027359:ENSRNOG00000010128	SLC27A2	gi|113374154|ref|NP_036108.2|	gi|113374154|ref|NP_036108.2|	solute carrier family 27 (fatty acid transporter), member 2 [Mus mu	10	70	18.7	620	70423	8.9	MmNaOH-MM_liver_CNBrTi_105.2428.2428.2	2	2.2109	0.0838	1708.65	1709	1	50	1	K.LFQHIAEYLPSYAR.P	542	2	*
20	ENSG00000115275:ENSMUSG00000030036:ENSRNOG00000008648	GCS1	gi|31981106|ref|NP_065644.2|	gi|31981106|ref|NP_065644.2|	glucosidase 1 [Mus musculus]	10	72	10.2	834	91831	9	MmNaOH-MM_liver_CNBrTi_203.1641.1641.1	1	2.0191	0.117	1084.7	1085.3	8	62.5	1	R.VPPEFLVQR.A	495	2	*
20	ENSG00000115275:ENSMUSG00000030036:ENSRNOG00000008648	GCS1	gi|31981106|ref|NP_065644.2|	gi|31981106|ref|NP_065644.2|	glucosidase 1 [Mus musculus]	10	72	10.2	834	91831	9	MmNaOH-MM_liver_CNBrTi_203.1963.1963.2	2	3.6406	0.3366	1702.6	1702	1	53.333336	1	R.GPSGQGQFLIQQVTLK.A	309	2	*
20	ENSG00000115275:ENSMUSG00000030036:ENSRNOG00000008648	GCS1	gi|31981106|ref|NP_065644.2|	gi|31981106|ref|NP_065644.2|	glucosidase 1 [Mus musculus]	10	72	10.2	834	91831	9	MmNaOH-MM_liver_CNBrTi_102.3278.3278.3	3	3.3103	0.3593	1831.22	1832.1	1	44.642857	1	R.GFLWDEGFHQLVVQR.W	444	2	*
20	ENSG00000115275:ENSMUSG00000030036:ENSRNOG00000008648	GCS1	gi|31981106|ref|NP_065644.2|	gi|31981106|ref|NP_065644.2|	glucosidase 1 [Mus musculus]	10	72	10.2	834	91831	9	MmNaOH-MM_liver_CNBrTi_204.2367.2367.2	2	4.1969	0.3358	1268.88	1269.5	1	86.36364	44	R.LGPLLDVLADSR.H	706	2	*
20	ENSG00000115275:ENSMUSG00000030036:ENSRNOG00000008648	GCS1	gi|31981106|ref|NP_065644.2|	gi|31981106|ref|NP_065644.2|	glucosidase 1 [Mus musculus]	10	72	10.2	834	91831	9	MmNaOH-MM_liver_CNBrTi_211.2050.2050.2	2	3.3731	0.3667	1406.56	1406.5	1	75	1	K.SISGHTSELGDFR.L	228	2	*
20	ENSG00000115275:ENSMUSG00000030036:ENSRNOG00000008648	GCS1	gi|31981106|ref|NP_065644.2|	gi|31981106|ref|NP_065644.2|	glucosidase 1 [Mus musculus]	10	72	10.2	834	91831	9	MmNaOH-MM_liver_CNBrTi_107.4120.4120.2	2	4.7027	0.2593	1981.85	1979.2	1	52.941177	10	R.EALGHWLGLLNADGWIGR.E	466	2	*
20	ENSG00000115275:ENSMUSG00000030036:ENSRNOG00000008648	GCS1	gi|31981106|ref|NP_065644.2|	gi|31981106|ref|NP_065644.2|	glucosidase 1 [Mus musculus]	10	72	10.2	834	91831	9	MmNaOH-MM_liver_CNBrTi_212.1935.1935.2	2	3.5919	0.3355	1313.58	1312.6	1	65	1	R.ARVPPEFLVQR.A	493	2	*
20	ENSG00000115275:ENSMUSG00000030036:ENSRNOG00000008648	GCS1	gi|31981106|ref|NP_065644.2|	gi|31981106|ref|NP_065644.2|	glucosidase 1 [Mus musculus]	10	72	10.2	834	91831	9	MmNaOH-MM_liver_CNBrTi_106.4122.4122.3	3	4.7196	0.2479	1978.89	1979.2	1	42.647057	1	R.EALGHWLGLLNADGWIGR.E	466	2	*
20	ENSG00000115275:ENSMUSG00000030036:ENSRNOG00000008648	GCS1	gi|31981106|ref|NP_065644.2|	gi|31981106|ref|NP_065644.2|	glucosidase 1 [Mus musculus]	10	72	10.2	834	91831	9	MmNaOH-MM_liver_CNBrTi_105.3002.3002.2	2	5.0644	0.4318	1830.96	1832.1	1	75	9	R.GFLWDEGFHQLVVQR.W	444	2	*
20	ENSG00000115275:ENSMUSG00000030036:ENSRNOG00000008648	GCS1	gi|31981106|ref|NP_065644.2|	gi|31981106|ref|NP_065644.2|	glucosidase 1 [Mus musculus]	10	72	10.2	834	91831	9	MmNaOH-MM_liver_CNBrTi_105.1611.1611.2	2	3.1263	0.133	1313.58	1312.6	1	75	1	R.ARVPPEFLVQR.A	493	2	*
20	ENSG00000115275:ENSMUSG00000030036:ENSRNOG00000008648	GCS1	gi|31981106|ref|NP_065644.2|	gi|31981106|ref|NP_065644.2|	glucosidase 1 [Mus musculus]	10	72	10.2	834	91831	9	MmNaOH-MM_liver_CNBrTi_204.1644.1644.2	2	2.0861	0.1144	1085.57	1085.3	2	75	2	R.VPPEFLVQR.A	495	2	*
21	ENSG00000181035:ENSMUSG00000002346:ENSRNOG00000020345	SLC25A42	gi|56090652|ref|NP_001007571.1|	gi|56090652|ref|NP_001007571.1|	solute carrier family 25, member 42 [Mus musculus]	2	36	6.9	318	35241	10.1	MmNaOH-MM_liver_CNBrTi_211.3542.3542.2	2	4.4737	0.4475	2189.4	2188.6	1	54.761906	30	R.LLAGALAGTTAASLTYPLDLVR.A	135	2	*
21	ENSG00000181035:ENSMUSG00000002346:ENSRNOG00000020345	SLC25A42	gi|56090652|ref|NP_001007571.1|	gi|56090652|ref|NP_001007571.1|	solute carrier family 25, member 42 [Mus musculus]	2	36	6.9	318	35241	10.1	MmNaOH-MM_liver_CNBrTi_101.3886.3886.2	2	3.0758	0.3028	2189.15	2188.6	9	30.952381	2	R.LLAGALAGTTAASLTYPLDLVR.A	135	2	*
21	ENSG00000181035:ENSMUSG00000002346:ENSRNOG00000020345	SLC25A42	gi|56090652|ref|NP_001007571.1|	gi|56090652|ref|NP_001007571.1|	solute carrier family 25, member 42 [Mus musculus]	2	36	6.9	318	35241	10.1	MmNaOH-MM_liver_CNBrTi_212.2765.2765.3	3	4.5404	0.3741	2188.76	2188.6	2	33.333336	4	R.LLAGALAGTTAASLTYPLDLVR.A	135	2	*
22	ENSG00000170439:ENSMUSG00000025347:ENSRNOG00000007927	METTL7B	gi|27229118|ref|NP_082129.2|	gi|27229118|ref|NP_082129.2|	methyltransferase like 7B [Mus musculus]	3	16	15.2	244	28049	8.6	MmNaOH-MM_liver_CNBrTi_101.2655.2655.2	2	3.4193	0.1253	1960.14	1960.2	2	50	3	R.AQFSEVQLEWQPPPFR.W	215	2	*
22	ENSG00000170439:ENSMUSG00000025347:ENSRNOG00000007927	METTL7B	gi|27229118|ref|NP_082129.2|	gi|27229118|ref|NP_082129.2|	methyltransferase like 7B [Mus musculus]	3	16	15.2	244	28049	8.6	MmNaOH-MM_liver_CNBrTi_211.2935.2935.2	2	3.6221	0.241	1960.7	1960.2	1	60.000004	8	R.AQFSEVQLEWQPPPFR.W	215	2	*
22	ENSG00000170439:ENSMUSG00000025347:ENSRNOG00000007927	METTL7B	gi|27229118|ref|NP_082129.2|	gi|27229118|ref|NP_082129.2|	methyltransferase like 7B [Mus musculus]	3	16	15.2	244	28049	8.6	MmNaOH-MM_liver_CNBrTi_110.3430.3430.3	3	4.5109	0.2487	2396.84	2396.8	2	33.75	2	R.VLRPGGLLFFWEHVAEPQGSR.A	163	2	*
22	ENSG00000170439:ENSMUSG00000025347:ENSRNOG00000007927	METTL7B	gi|27229118|ref|NP_082129.2|	gi|27229118|ref|NP_082129.2|	methyltransferase like 7B [Mus musculus]	3	16	15.2	244	28049	8.6	MmNaOH-MM_liver_CNBrTi_110.3418.3418.2	2	4.1457	0.325	2397.28	2396.8	1	40	3	R.VLRPGGLLFFWEHVAEPQGSR.A	163	2	*
23	NA:NA:ENSRNOG00000028419	FTL2	gi|130485277|ref|NP_032075.2|	gi|130485277|ref|NP_032075.2|;gi|149264343|ref|XP_001478	ferritin light chain 2 [Mus musculus]	5	12	20.2	183	20738	6	MmNaOH-MM_liver_CNBrTi_208.2111.2111.3	3	3.8896	0.2846	2375.14	2374.6	1	31.818182	4	R.VAGPQPAQTGAPQGSLGEYLFER.L	155	2	
23	NA:NA:ENSRNOG00000028419	FTL2	gi|130485277|ref|NP_032075.2|	gi|130485277|ref|NP_032075.2|;gi|149264343|ref|XP_001478	ferritin light chain 2 [Mus musculus]	5	12	20.2	183	20738	6	MmNaOH-MM_liver_CNBrTi_101.1315.1315.2	2	2.6109	0.0987	1483.9	1481.6	5	50	1	R.QNYSTEVEAAVNR.L	7	2	
23	NA:NA:ENSRNOG00000028419	FTL2	gi|130485277|ref|NP_032075.2|	gi|130485277|ref|NP_032075.2|;gi|149264343|ref|XP_001478	ferritin light chain 2 [Mus musculus]	5	12	20.2	183	20738	6	MmNaOH-MM_liver_CNBrTi_209.2050.2050.2	2	5.2973	0.4071	2374.46	2374.6	1	59.090908	2	R.VAGPQPAQTGAPQGSLGEYLFER.L	155	2	
23	NA:NA:ENSRNOG00000028419	FTL2	gi|130485277|ref|NP_032075.2|	gi|130485277|ref|NP_032075.2|;gi|149264343|ref|XP_001478	ferritin light chain 2 [Mus musculus]	5	12	20.2	183	20738	6	MmNaOH-MM_liver_CNBrTi_108.2202.2202.3	3	4.4741	0.3594	2530.58	2530.8	1	40.217392	3	R.RVAGPQPAQTGAPQGSLGEYLFER.L	154	2	
23	NA:NA:ENSRNOG00000028419	FTL2	gi|130485277|ref|NP_032075.2|	gi|130485277|ref|NP_032075.2|;gi|149264343|ref|XP_001478	ferritin light chain 2 [Mus musculus]	5	12	20.2	183	20738	6	MmNaOH-MM_liver_CNBrTi_108.2203.2203.2	2	4.8027	0.4493	2530.97	2530.8	1	39.130436	2	R.RVAGPQPAQTGAPQGSLGEYLFER.L	154	2	
24	NA:ENSMUSG00000078688:ENSRNOG00000033208	Q78E17	gi|113930714|ref|NP_001039015.1|	gi|113930714|ref|NP_001039015.1|;gi|13654245|ref|NP_1124	major urinary protein 2 [Mus musculus]	3	11	25	180	20648	5	MmNaOH-MM_liver_CNBrTi_202.2511.2511.2	2	3.3524	0.244	2011.43	2011.2	1	52.941177	1	K.AGEYSVTYDGFNTFTIPK.T	95	2	
24	NA:ENSMUSG00000078688:ENSRNOG00000033208	Q78E17	gi|113930714|ref|NP_001039015.1|	gi|113930714|ref|NP_001039015.1|;gi|13654245|ref|NP_1124	major urinary protein 2 [Mus musculus]	3	11	25	180	20648	5	MmNaOH-MM_liver_CNBrTi_201.0839.0839.2	2	3.5164	0.1474	1259.26	1259.4	1	80	5	R.ENIIDLSNANR.C	164	2	
24	NA:ENSMUSG00000078688:ENSRNOG00000033208	Q78E17	gi|113930714|ref|NP_001039015.1|	gi|113930714|ref|NP_001039015.1|;gi|13654245|ref|NP_1124	major urinary protein 2 [Mus musculus]	3	11	25	180	20648	5	MmNaOH-MM_liver_CNBrTi_104.4223.4223.2	2	2.6806	0.1376	1898.01	1896.3	2	43.333332	1	R.LFLEQIHVLENSLVLK.F	58	2	
24	NA:ENSMUSG00000078688:ENSRNOG00000033208	Q78E17	gi|113930714|ref|NP_001039015.1|	gi|113930714|ref|NP_001039015.1|;gi|13654245|ref|NP_1124	major urinary protein 2 [Mus musculus]	3	11	25	180	20648	5	MmNaOH-MM_liver_CNBrTi_101.0462.0462.2	2	3.4339	0.2282	1259.44	1259.4	5	75	4	R.ENIIDLSNANR.C	164	2	
25	ENSG00000110628:ENSMUSG00000000154:ENSRNOG00000020562	SLC22A18	gi|112363088|ref|NP_032793.2|	gi|112363088|ref|NP_032793.2|	solute carrier family 22 (organic cation transporter), member 18 [M	1	36	2.9	410	43375	9.1	MmNaOH-MM_liver_CNBrTi_101.2070.2070.2	2	3.1764	0.3232	1261.05	1261.5	1	77.27273	1	R.TLGPTLGGLLYR.S	364	2	*
25	ENSG00000110628:ENSMUSG00000000154:ENSRNOG00000020562	SLC22A18	gi|112363088|ref|NP_032793.2|	gi|112363088|ref|NP_032793.2|	solute carrier family 22 (organic cation transporter), member 18 [M	1	36	2.9	410	43375	9.1	MmNaOH-MM_liver_CNBrTi_209.2029.2029.2	2	3.4258	0.4247	1261.49	1261.5	1	68.181816	35	R.TLGPTLGGLLYR.S	364	2	*
26	ENSG00000115255:ENSMUSG00000035504:NA	REEP6	gi|21314830|ref|NP_647453.1|	gi|21314830|ref|NP_647453.1|	polyposis locus protein 1-like 1 [Mus musculus]	1	12	5	201	22204	7.3	MmNaOH-MM_liver_CNBrTi_101.0151.0151.2	2	3.4895	0.2562	1002.34	1001.2	1	88.88889	4	R.ALDLAAGITR.D	162	2	*
26	ENSG00000115255:ENSMUSG00000035504:NA	REEP6	gi|21314830|ref|NP_647453.1|	gi|21314830|ref|NP_647453.1|	polyposis locus protein 1-like 1 [Mus musculus]	1	12	5	201	22204	7.3	MmNaOH-MM_liver_CNBrTi_201.0902.0902.2	2	3.534	0.247	1001.29	1001.2	1	83.33333	8	R.ALDLAAGITR.D	162	2	*
27	ENSG00000189043:ENSMUSG00000029632:ENSRNOG00000005512	NDUFA4	gi|33563266|ref|NP_035016.1|	gi|33563266|ref|NP_035016.1|	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4 [Mus m	1	5	14.6	82	9327	9.5	MmNaOH-MM_liver_CNBrTi_205.2318.2318.2	2	3.3036	0.2328	1433.07	1433.6	2	72.72727	4	R.LALFNPDVSWDR.K	36	2	*
27	ENSG00000189043:ENSMUSG00000029632:ENSRNOG00000005512	NDUFA4	gi|33563266|ref|NP_035016.1|	gi|33563266|ref|NP_035016.1|	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4 [Mus m	1	5	14.6	82	9327	9.5	MmNaOH-MM_liver_CNBrTi_101.2395.2395.2	2	3.3628	0.2129	1433.72	1433.6	1	68.181816	1	R.LALFNPDVSWDR.K	36	2	*
28	ENSG00000204128:ENSMUSG00000026227:ENSRNOG00000017557	C2orf72	gi|82881070|ref|XP_910782.1|	gi|82881070|ref|XP_910782.1|	PREDICTED: hypothetical protein LOC72792 [Mus musculus]	5	12	24	287	30391	6.1	MmNaOH-MM_liver_CNBrTi_211.2894.2894.2	2	3.4661	0.4268	1866.82	1866.1	1	52.77778	5	R.PASPAEPPFQALVEAAGGR.G	12	2	*
28	ENSG00000204128:ENSMUSG00000026227:ENSRNOG00000017557	C2orf72	gi|82881070|ref|XP_910782.1|	gi|82881070|ref|XP_910782.1|	PREDICTED: hypothetical protein LOC72792 [Mus musculus]	5	12	24	287	30391	6.1	MmNaOH-MM_liver_CNBrTi_104.3612.3612.3	3	3.3723	0.3154	2960.97	2962.3	1	27.67857	3	M.ESELEALAPRPASPAEPPFQALVEAAGGR.G	2	1	*
28	ENSG00000204128:ENSMUSG00000026227:ENSRNOG00000017557	C2orf72	gi|82881070|ref|XP_910782.1|	gi|82881070|ref|XP_910782.1|	PREDICTED: hypothetical protein LOC72792 [Mus musculus]	5	12	24	287	30391	6.1	MmNaOH-MM_liver_CNBrTi_105.1848.1848.3	3	3.3419	0.2091	2858.28	2857.1	1	28.703705	1	R.QVGGPVQAAAFRPGCPASSLAVQEAACR.A	166	2	*
28	ENSG00000204128:ENSMUSG00000026227:ENSRNOG00000017557	C2orf72	gi|82881070|ref|XP_910782.1|	gi|82881070|ref|XP_910782.1|	PREDICTED: hypothetical protein LOC72792 [Mus musculus]	5	12	24	287	30391	6.1	MmNaOH-MM_liver_CNBrTi_101.3688.3688.2	2	3.8887	0.317	1395.84	1396.7	1	81.818184	2	R.APELQLLETLLR.T	149	2	*
28	ENSG00000204128:ENSMUSG00000026227:ENSRNOG00000017557	C2orf72	gi|82881070|ref|XP_910782.1|	gi|82881070|ref|XP_910782.1|	PREDICTED: hypothetical protein LOC72792 [Mus musculus]	5	12	24	287	30391	6.1	MmNaOH-MM_liver_CNBrTi_101.3696.3696.1	1	1.9391	0.1099	1395.75	1396.7	5	54.545456	1	R.APELQLLETLLR.T	149	2	*
29	ENSG00000075624:ENSMUSG00000029580:ENSRNOG00000034254	ACTB	gi|6671509|ref|NP_031419.1|	gi|6671509|ref|NP_031419.1|;gi|6752954|ref|NP_033739.1|	actin, beta, cytoplasmic [Mus musculus]	5	12	21.3	375	41737	5.5	MmNaOH-MM_liver_CNBrTi_104.1658.1658.2	2	2.6257	0.2474	1199.26	1199.4	1	65	2	R.AVFPSIVGRPR.H	29	2	
29	ENSG00000075624:ENSMUSG00000029580:ENSRNOG00000034254	ACTB	gi|6671509|ref|NP_031419.1|	gi|6671509|ref|NP_031419.1|;gi|6752954|ref|NP_033739.1|	actin, beta, cytoplasmic [Mus musculus]	5	12	21.3	375	41737	5.5	MmNaOH-MM_liver_CNBrTi_103.2838.2838.3	3	5.4017	0.3914	2582.78	2582.9	1	31.52174	7	M.DSGDGVTHTVPIYEGYALPHAILR.L	154	1	
29	ENSG00000075624:ENSMUSG00000029580:ENSRNOG00000034254	ACTB	gi|6671509|ref|NP_031419.1|	gi|6671509|ref|NP_031419.1|;gi|6752954|ref|NP_033739.1|	actin, beta, cytoplasmic [Mus musculus]	5	12	21.3	375	41737	5.5	MmNaOH-MM_liver_CNBrTi_101.1626.1626.2	2	3.4411	0.2363	1954.87	1955.3	1	52.941177	1	R.VAPEEHPVLLTEAPLNPK.A	96	2	
29	ENSG00000075624:ENSMUSG00000029580:ENSRNOG00000034254	ACTB	gi|6671509|ref|NP_031419.1|	gi|6671509|ref|NP_031419.1|;gi|6752954|ref|NP_033739.1|	actin, beta, cytoplasmic [Mus musculus]	5	12	21.3	375	41737	5.5	MmNaOH-MM_liver_CNBrTi_109.2216.2216.2	2	2.9394	0.2573	1516.39	1516.7	1	75	1	K.IWHHTFYNELR.V	85	2	
29	ENSG00000075624:ENSMUSG00000029580:ENSRNOG00000034254	ACTB	gi|6671509|ref|NP_031419.1|	gi|6671509|ref|NP_031419.1|;gi|6752954|ref|NP_033739.1|	actin, beta, cytoplasmic [Mus musculus]	5	12	21.3	375	41737	5.5	MmNaOH-MM_liver_CNBrTi_202.2100.2100.2	2	3.2093	0.3331	1791.68	1792	1	56.666668	1	K.SYELPDGQVITIGNER.F	239	2	
30	ENSG00000172817:ENSMUSG00000039519:ENSRNOG00000009730	CYP7B1	gi|75677410|ref|NP_031851.2|	gi|75677410|ref|NP_031851.2|	cytochrome P450, family 7, subfamily b, polypeptide 1 [Mus muscu	5	16	13.8	507	58490	8.9	MmNaOH-MM_liver_CNBrTi_203.2094.2094.2	2	2.6511	0.19	1703.53	1706	1	64.28571	1	R.MFLGIQHPDSAVSFR.Y	485	2	*
30	ENSG00000172817:ENSMUSG00000039519:ENSRNOG00000009730	CYP7B1	gi|75677410|ref|NP_031851.2|	gi|75677410|ref|NP_031851.2|	cytochrome P450, family 7, subfamily b, polypeptide 1 [Mus muscu	5	16	13.8	507	58490	8.9	MmNaOH-MM_liver_CNBrTi_103.0067.0067.2	2	4.3427	0.3122	2119.24	2118.4	1	52.941177	10	R.EQLDSLVCLESTILEVLR.L	342	2	*
30	ENSG00000172817:ENSMUSG00000039519:ENSRNOG00000009730	CYP7B1	gi|75677410|ref|NP_031851.2|	gi|75677410|ref|NP_031851.2|	cytochrome P450, family 7, subfamily b, polypeptide 1 [Mus muscu	5	16	13.8	507	58490	8.9	MmNaOH-MM_liver_CNBrTi_107.3588.3588.3	3	4.3534	0.1942	2583.16	2582	1	31.818182	1	R.KGDFVALFPPLIHNDPEIFDAPK.E	387	2	*
30	ENSG00000172817:ENSMUSG00000039519:ENSRNOG00000009730	CYP7B1	gi|75677410|ref|NP_031851.2|	gi|75677410|ref|NP_031851.2|	cytochrome P450, family 7, subfamily b, polypeptide 1 [Mus muscu	5	16	13.8	507	58490	8.9	MmNaOH-MM_liver_CNBrTi_101.3878.3878.2	2	3.5548	0.2298	1674.64	1675	1	69.230774	2	M.FPYLVSDIPIQLLR.N	221	1	*
30	ENSG00000172817:ENSMUSG00000039519:ENSRNOG00000009730	CYP7B1	gi|75677410|ref|NP_031851.2|	gi|75677410|ref|NP_031851.2|	cytochrome P450, family 7, subfamily b, polypeptide 1 [Mus muscu	5	16	13.8	507	58490	8.9	MmNaOH-MM_liver_CNBrTi_103.1994.1994.2	2	3.2132	0.2683	1574.49	1574.8	1	61.538464	2	M.FLGIQHPDSAVSFR.Y	486	1	*
31	NA:ENSMUSG00000054630:ENSRNOG00000029973	UGT2B	gi|6678501|ref|NP_033493.1|	gi|6678501|ref|NP_033493.1|	UDP glucuronosyltransferase 2 family, polypeptide B5 [Mus muscu	8	24	13.2	530	60856	7.9	MmNaOH-MM_liver_CNBrTi_209.3735.3735.2	2	4.7566	0.302	1981.83	1981.2	1	59.375	5	K.SDVLNALEEVIENPFYK.K	424	2	
31	NA:ENSMUSG00000054630:ENSRNOG00000029973	UGT2B	gi|6678501|ref|NP_033493.1|	gi|6678501|ref|NP_033493.1|	UDP glucuronosyltransferase 2 family, polypeptide B5 [Mus muscu	8	24	13.2	530	60856	7.9	MmNaOH-MM_liver_CNBrTi_207.2704.2704.3	3	4.5	0.1622	1494.94	1495.8	1	53.846157	1	K.ANAIAWALAQIPQK.V	322	2	
31	NA:ENSMUSG00000054630:ENSRNOG00000029973	UGT2B	gi|6678501|ref|NP_033493.1|	gi|6678501|ref|NP_033493.1|	UDP glucuronosyltransferase 2 family, polypeptide B5 [Mus muscu	8	24	13.2	530	60856	7.9	MmNaOH-MM_liver_CNBrTi_208.2689.2689.2	2	4.1506	0.3238	1496.41	1495.8	1	73.07692	6	K.ANAIAWALAQIPQK.V	322	2	
31	NA:ENSMUSG00000054630:ENSRNOG00000029973	UGT2B	gi|6678501|ref|NP_033493.1|	gi|6678501|ref|NP_033493.1|	UDP glucuronosyltransferase 2 family, polypeptide B5 [Mus muscu	8	24	13.2	530	60856	7.9	MmNaOH-MM_liver_CNBrTi_209.0490.0490.2	2	2.9322	0.0923	1067.96	1068.2	2	77.77778	1	K.TPATLGHNTR.V	344	2	
31	NA:ENSMUSG00000054630:ENSRNOG00000029973	UGT2B	gi|6678501|ref|NP_033493.1|	gi|6678501|ref|NP_033493.1|	UDP glucuronosyltransferase 2 family, polypeptide B5 [Mus muscu	8	24	13.2	530	60856	7.9	MmNaOH-MM_liver_CNBrTi_101.1971.1971.1	1	2.1183	0.1395	1098.79	1099.3	4	75	1	K.IILDELVQR.G	41	2	
31	NA:ENSMUSG00000054630:ENSRNOG00000029973	UGT2B	gi|6678501|ref|NP_033493.1|	gi|6678501|ref|NP_033493.1|	UDP glucuronosyltransferase 2 family, polypeptide B5 [Mus muscu	8	24	13.2	530	60856	7.9	MmNaOH-MM_liver_CNBrTi_108.1922.1922.2	2	3.1454	0.1034	2044.88	2045.3	1	50	4	R.GHEVTVLRPSAYYVLDPK.K	50	2	
31	NA:ENSMUSG00000054630:ENSRNOG00000029973	UGT2B	gi|6678501|ref|NP_033493.1|	gi|6678501|ref|NP_033493.1|	UDP glucuronosyltransferase 2 family, polypeptide B5 [Mus muscu	8	24	13.2	530	60856	7.9	MmNaOH-MM_liver_CNBrTi_107.1926.1926.3	3	3.868	0.2959	2045.93	2045.3	1	38.235294	2	R.GHEVTVLRPSAYYVLDPK.K	50	2	
31	NA:ENSMUSG00000054630:ENSRNOG00000029973	UGT2B	gi|6678501|ref|NP_033493.1|	gi|6678501|ref|NP_033493.1|	UDP glucuronosyltransferase 2 family, polypeptide B5 [Mus muscu	8	24	13.2	530	60856	7.9	MmNaOH-MM_liver_CNBrTi_101.4108.4108.2	2	3.8149	0.2074	2196.89	2196.5	1	50	2	M.SKSDVLNALEEVIENPFYK.K	422	1	*
31	NA:ENSMUSG00000054630:ENSRNOG00000029973	UGT2B	gi|6678501|ref|NP_033493.1|	gi|6678501|ref|NP_033493.1|	UDP glucuronosyltransferase 2 family, polypeptide B5 [Mus muscu	8	24	13.2	530	60856	7.9	MmNaOH-MM_liver_CNBrTi_101.4907.4907.2	2	4.5183	0.3486	1981.75	1981.2	1	56.25	2	K.SDVLNALEEVIENPFYK.K	424	2	
32	ENSG00000100243:ENSMUSG00000018042:ENSRNOG00000009592	CYB5R3	gi|19745150|ref|NP_084063.1|	gi|19745150|ref|NP_084063.1|	diaphorase 1 [Mus musculus]	4	10	14.3	301	34128	8.4	MmNaOH-MM_liver_CNBrTi_110.3182.3182.3	3	5.2787	0.3569	2560.5	2560	1	40.909092	4	R.FALPSPQHILGLPIGQHIYLSTR.I	62	2	*
32	ENSG00000100243:ENSMUSG00000018042:ENSRNOG00000009592	CYB5R3	gi|19745150|ref|NP_084063.1|	gi|19745150|ref|NP_084063.1|	diaphorase 1 [Mus musculus]	4	10	14.3	301	34128	8.4	MmNaOH-MM_liver_CNBrTi_110.3226.3226.2	2	4.7518	0.3323	2559.24	2560	1	47.727272	4	R.FALPSPQHILGLPIGQHIYLSTR.I	62	2	*
32	ENSG00000100243:ENSMUSG00000018042:ENSRNOG00000009592	CYB5R3	gi|19745150|ref|NP_084063.1|	gi|19745150|ref|NP_084063.1|	diaphorase 1 [Mus musculus]	4	10	14.3	301	34128	8.4	MmNaOH-MM_liver_CNBrTi_210.1362.1362.2	2	2.6068	0.2224	1079.38	1079.2	1	81.25	1	M.KIGDTIEFR.G	135	1	*
32	ENSG00000100243:ENSMUSG00000018042:ENSRNOG00000009592	CYB5R3	gi|19745150|ref|NP_084063.1|	gi|19745150|ref|NP_084063.1|	diaphorase 1 [Mus musculus]	4	10	14.3	301	34128	8.4	MmNaOH-MM_liver_CNBrTi_203.1990.1990.2	2	2.4944	0.195	1361.64	1361.5	1	75	1	M.IQFACLPNLER.V	280	1	*
33	ENSG00000136986:ENSMUSG00000022365:ENSRNOG00000005551	DERL1	gi|13195638|ref|NP_077169.1|	gi|13195638|ref|NP_077169.1|	Der1-like domain family, member 1 [Mus musculus]	2	13	7.6	251	28835	9.5	MmNaOH-MM_liver_CNBrTi_106.1323.1323.2	2	2.5398	0.102	1002.47	1002.1	2	85.71429	3	R.HNWGQGFR.L	240	2	*
33	ENSG00000136986:ENSMUSG00000022365:ENSRNOG00000005551	DERL1	gi|13195638|ref|NP_077169.1|	gi|13195638|ref|NP_077169.1|	Der1-like domain family, member 1 [Mus musculus]	2	13	7.6	251	28835	9.5	MmNaOH-MM_liver_CNBrTi_204.2915.2915.2	2	3.317	0.0872	1386.56	1386.6	1	75	10	R.NFLSTPQFLYR.W	198	2	*
34	ENSG00000131781:ENSMUSG00000028088:ENSRNOG00000018076	FMO5	gi|149251662|ref|XP_001475872.1|	gi|149251662|ref|XP_001475872.1|	PREDICTED: similar to Flavin containing monooxygenase 5 isofor	7	24	15.4	533	60001	8.7	MmNaOH-MM_liver_CNBrTi_205.1808.1808.2	2	3.6072	0.2801	1419.51	1417.7	1	72.72727	6	R.LLLGPCTPVQYR.L	463	2	
34	ENSG00000131781:ENSMUSG00000028088:ENSRNOG00000018076	FMO5	gi|149251662|ref|XP_001475872.1|	gi|149251662|ref|XP_001475872.1|	PREDICTED: similar to Flavin containing monooxygenase 5 isofor	7	24	15.4	533	60001	8.7	MmNaOH-MM_liver_CNBrTi_104.4162.4162.3	3	4.0629	0.2251	2465.91	2464.9	1	32.142857	5	M.EEIADLVGVRPNILPLVFTDPR.L	437	1	
34	ENSG00000131781:ENSMUSG00000028088:ENSRNOG00000018076	FMO5	gi|149251662|ref|XP_001475872.1|	gi|149251662|ref|XP_001475872.1|	PREDICTED: similar to Flavin containing monooxygenase 5 isofor	7	24	15.4	533	60001	8.7	MmNaOH-MM_liver_CNBrTi_101.1779.1779.2	2	2.6561	0.1476	1431.23	1431.7	3	57.14286	1	R.IAVIGAGASGLTCIK.C	6	2	
34	ENSG00000131781:ENSMUSG00000028088:ENSRNOG00000018076	FMO5	gi|149251662|ref|XP_001475872.1|	gi|149251662|ref|XP_001475872.1|	PREDICTED: similar to Flavin containing monooxygenase 5 isofor	7	24	15.4	533	60001	8.7	MmNaOH-MM_liver_CNBrTi_203.1686.1686.2	2	2.8357	0.2314	962.16	961.07	6	87.5	2	R.SGDIGGLWR.F	35	2	
34	ENSG00000131781:ENSMUSG00000028088:ENSRNOG00000018076	FMO5	gi|149251662|ref|XP_001475872.1|	gi|149251662|ref|XP_001475872.1|	PREDICTED: similar to Flavin containing monooxygenase 5 isofor	7	24	15.4	533	60001	8.7	MmNaOH-MM_liver_CNBrTi_211.2833.2833.2	2	2.5421	0.2135	1382.46	1382.6	2	63.636364	1	R.PNILPLVFTDPR.L	447	2	
34	ENSG00000131781:ENSMUSG00000028088:ENSRNOG00000018076	FMO5	gi|149251662|ref|XP_001475872.1|	gi|149251662|ref|XP_001475872.1|	PREDICTED: similar to Flavin containing monooxygenase 5 isofor	7	24	15.4	533	60001	8.7	MmNaOH-MM_liver_CNBrTi_206.0656.0656.2	2	2.8134	0.147	1078.16	1077.2	1	81.25	1	R.KTILTTEDR.V	486	2	
34	ENSG00000131781:ENSMUSG00000028088:ENSRNOG00000018076	FMO5	gi|149251662|ref|XP_001475872.1|	gi|149251662|ref|XP_001475872.1|	PREDICTED: similar to Flavin containing monooxygenase 5 isofor	7	24	15.4	533	60001	8.7	MmNaOH-MM_liver_CNBrTi_101.1720.1720.2	2	2.8835	0.2289	1418.76	1417.7	2	63.636364	2	R.LLLGPCTPVQYR.L	463	2	
34	ENSG00000131781:ENSMUSG00000028088:ENSRNOG00000018076	FMO5	gi|149251662|ref|XP_001475872.1|	gi|149251662|ref|XP_001475872.1|	PREDICTED: similar to Flavin containing monooxygenase 5 isofor	7	24	15.4	533	60001	8.7	MmNaOH-MM_liver_CNBrTi_211.1902.1902.2	2	4.1957	0.3956	1677.56	1677.8	1	60.714287	6	R.ALSQHPTVNDDLPNR.I	278	2	*
35	NA:NA:ENSRNOG00000000790	LOC676837	gi|149269220|ref|XP_001473590.1|	gi|149269220|ref|XP_001473590.1|;gi|149269222|ref|XP_001	PREDICTED: similar to MHC H2-K 24 polypeptide isoform 1 [Mus	3	11	7.5	385	43242	7.3	MmNaOH-MM_liver_CNBrTi_101.0282.0282.2	2	3.6896	0.4023	1650.12	1649.9	1	60.714287	4	R.YFVTAVSRPGLGEPR.F	45	2	
35	NA:NA:ENSRNOG00000000790	LOC676837	gi|149269220|ref|XP_001473590.1|	gi|149269220|ref|XP_001473590.1|;gi|149269222|ref|XP_001	PREDICTED: similar to MHC H2-K 24 polypeptide isoform 1 [Mus	3	11	7.5	385	43242	7.3	MmNaOH-MM_liver_CNBrTi_206.2152.2152.2	2	4.3233	0.3878	1630.55	1630.8	1	73.07692	2	R.FIAVGYVDDTQFVR.F	60	2	
35	NA:NA:ENSRNOG00000000790	LOC676837	gi|149269220|ref|XP_001473590.1|	gi|149269220|ref|XP_001473590.1|;gi|149269222|ref|XP_001	PREDICTED: similar to MHC H2-K 24 polypeptide isoform 1 [Mus	3	11	7.5	385	43242	7.3	MmNaOH-MM_liver_CNBrTi_101.0259.0259.3	3	3.5457	0.1559	1650.7	1649.9	1	50	5	R.YFVTAVSRPGLGEPR.F	45	2	
36	ENSG00000148248:ENSMUSG00000014867:ENSRNOG00000005247	SURF4	gi|6755698|ref|NP_035642.1|	gi|6755698|ref|NP_035642.1|	surfeit gene 4 [Mus musculus]	3	9	11.2	269	30381	7.8	MmNaOH-MM_liver_CNBrTi_110.3547.3547.2	2	4.0192	0.4258	1767.2	1767.1	1	65.625	2	M.RNLALGGGLLLLLAESR.S	119	1	*
36	ENSG00000148248:ENSMUSG00000014867:ENSRNOG00000005247	SURF4	gi|6755698|ref|NP_035642.1|	gi|6755698|ref|NP_035642.1|	surfeit gene 4 [Mus musculus]	3	9	11.2	269	30381	7.8	MmNaOH-MM_liver_CNBrTi_101.3287.3287.2	2	3.5266	0.1559	1537.78	1537.8	1	75	2	R.LCLISTFLEDGIR.M	31	2	*
36	ENSG00000148248:ENSMUSG00000014867:ENSRNOG00000005247	SURF4	gi|6755698|ref|NP_035642.1|	gi|6755698|ref|NP_035642.1|	surfeit gene 4 [Mus musculus]	3	9	11.2	269	30381	7.8	MmNaOH-MM_liver_CNBrTi_210.2775.2775.2	2	4.1615	0.3032	1537.53	1537.8	1	79.16667	4	R.LCLISTFLEDGIR.M	31	2	*
36	ENSG00000148248:ENSMUSG00000014867:ENSRNOG00000005247	SURF4	gi|6755698|ref|NP_035642.1|	gi|6755698|ref|NP_035642.1|	surfeit gene 4 [Mus musculus]	3	9	11.2	269	30381	7.8	MmNaOH-MM_liver_CNBrTi_102.4879.4879.2	2	4.5878	0.4029	1611.07	1610.9	1	73.333336	1	R.NLALGGGLLLLLAESR.S	120	2	*
37	ENSG00000151726:ENSMUSG00000018796:ENSRNOG00000010633	ACSL1	gi|31560705|ref|NP_032007.2|	gi|31560705|ref|NP_032007.2|	acyl-CoA synthetase long-chain family member 1 [Mus musculus]	5	40	5.3	699	77952	7.1	MmNaOH-MM_liver_CNBrTi_101.2004.2004.2	2	3.1494	0.1477	1366.94	1366.7	5	68.181816	1	K.VLQPTIFPVVPR.L	358	2	*
37	ENSG00000151726:ENSMUSG00000018796:ENSRNOG00000010633	ACSL1	gi|31560705|ref|NP_032007.2|	gi|31560705|ref|NP_032007.2|	acyl-CoA synthetase long-chain family member 1 [Mus musculus]	5	40	5.3	699	77952	7.1	MmNaOH-MM_liver_CNBrTi_101.1642.1642.2	2	3.2617	0.2784	1053.05	1053.2	1	93.75	1	K.IGFFQGDIR.L	342	2	
37	ENSG00000151726:ENSMUSG00000018796:ENSRNOG00000010633	ACSL1	gi|31560705|ref|NP_032007.2|	gi|31560705|ref|NP_032007.2|	acyl-CoA synthetase long-chain family member 1 [Mus musculus]	5	40	5.3	699	77952	7.1	MmNaOH-MM_liver_CNBrTi_203.2614.2614.2	2	3.5886	0.3828	1618.24	1617.9	1	63.333332	3	M.ITGAAPVSATVLTFLR.T	433	1	*
37	ENSG00000151726:ENSMUSG00000018796:ENSRNOG00000010633	ACSL1	gi|31560705|ref|NP_032007.2|	gi|31560705|ref|NP_032007.2|	acyl-CoA synthetase long-chain family member 1 [Mus musculus]	5	40	5.3	699	77952	7.1	MmNaOH-MM_liver_CNBrTi_206.2012.2012.1	1	2.7744	0.0977	1366.9	1366.7	4	54.545456	1	K.VLQPTIFPVVPR.L	358	2	*
37	ENSG00000151726:ENSMUSG00000018796:ENSRNOG00000010633	ACSL1	gi|31560705|ref|NP_032007.2|	gi|31560705|ref|NP_032007.2|	acyl-CoA synthetase long-chain family member 1 [Mus musculus]	5	40	5.3	699	77952	7.1	MmNaOH-MM_liver_CNBrTi_206.1995.1995.2	2	3.6398	0.1398	1365.95	1366.7	1	77.27273	20	K.VLQPTIFPVVPR.L	358	2	*
37	ENSG00000151726:ENSMUSG00000018796:ENSRNOG00000010633	ACSL1	gi|31560705|ref|NP_032007.2|	gi|31560705|ref|NP_032007.2|	acyl-CoA synthetase long-chain family member 1 [Mus musculus]	5	40	5.3	699	77952	7.1	MmNaOH-MM_liver_CNBrTi_203.1821.1821.2	2	3.195	0.2627	1053.32	1053.2	1	81.25	13	K.IGFFQGDIR.L	342	2	
37	ENSG00000151726:ENSMUSG00000018796:ENSRNOG00000010633	ACSL1	gi|31560705|ref|NP_032007.2|	gi|31560705|ref|NP_032007.2|	acyl-CoA synthetase long-chain family member 1 [Mus musculus]	5	40	5.3	699	77952	7.1	MmNaOH-MM_liver_CNBrTi_205.1831.1831.1	1	2.0135	0.15	1052.66	1053.2	2	68.75	1	K.IGFFQGDIR.L	342	2	
38	ENSG00000138115:ENSMUSG00000062624:ENSRNOG00000036595	CYP2C8	gi|67010061|ref|NP_001019890.1|	gi|67010061|ref|NP_001019890.1|	hypothetical protein LOC545288 [Mus musculus]	2	19	4.3	491	56145	7.4	MmNaOH-MM_liver_CNBrTi_201.0642.0642.2	2	2.6281	0.1417	1272.17	1272.4	2	75	3	K.VQEEIDNVIGR.H	323	2	
38	ENSG00000138115:ENSMUSG00000062624:ENSRNOG00000036595	CYP2C8	gi|67010061|ref|NP_001019890.1|	gi|67010061|ref|NP_001019890.1|	hypothetical protein LOC545288 [Mus musculus]	2	19	4.3	491	56145	7.4	MmNaOH-MM_liver_CNBrTi_205.3149.3149.2	2	4.0192	0.3353	1330.32	1330.5	1	83.33333	11	R.DFIDYFLIQR.C	262	2	
38	ENSG00000138115:ENSMUSG00000062624:ENSRNOG00000036595	CYP2C8	gi|67010061|ref|NP_001019890.1|	gi|67010061|ref|NP_001019890.1|	hypothetical protein LOC545288 [Mus musculus]	2	19	4.3	491	56145	7.4	MmNaOH-MM_liver_CNBrTi_101.1048.1048.2	2	3.9384	0.2661	1274.12	1272.4	2	85	5	K.VQEEIDNVIGR.H	323	2	
39	ENSG00000083807:ENSMUSG00000030382:ENSRNOG00000019626	SLC27A5	gi|6678011|ref|NP_033538.1|	gi|6678011|ref|NP_033538.1|	solute carrier family 27 (fatty acid transporter), member 5 [Mus mu	4	21	10.4	689	76186	8.4	MmNaOH-MM_liver_CNBrTi_101.4583.4583.2	2	3.4684	0.3507	1993.2	1993.3	1	52.941177	1	R.EGFDVGIIADPLYILDNK.A	650	2	*
39	ENSG00000083807:ENSMUSG00000030382:ENSRNOG00000019626	SLC27A5	gi|6678011|ref|NP_033538.1|	gi|6678011|ref|NP_033538.1|	solute carrier family 27 (fatty acid transporter), member 5 [Mus mu	4	21	10.4	689	76186	8.4	MmNaOH-MM_liver_CNBrTi_104.2554.2554.2	2	3.3995	0.2402	1559.48	1559.8	1	70.83333	8	R.SWLPAYATPHFIR.I	617	2	*
39	ENSG00000083807:ENSMUSG00000030382:ENSRNOG00000019626	SLC27A5	gi|6678011|ref|NP_033538.1|	gi|6678011|ref|NP_033538.1|	solute carrier family 27 (fatty acid transporter), member 5 [Mus mu	4	21	10.4	689	76186	8.4	MmNaOH-MM_liver_CNBrTi_203.3365.3365.2	2	4.2154	0.281	2452.83	2453.7	1	47.727272	2	R.SSGASVLIVDPDLQENLEEVLPK.L	218	2	*
39	ENSG00000083807:ENSMUSG00000030382:ENSRNOG00000019626	SLC27A5	gi|6678011|ref|NP_033538.1|	gi|6678011|ref|NP_033538.1|	solute carrier family 27 (fatty acid transporter), member 5 [Mus mu	4	21	10.4	689	76186	8.4	MmNaOH-MM_liver_CNBrTi_203.3943.3943.2	2	5.1166	0.2914	1994.94	1993.3	1	61.764706	9	R.EGFDVGIIADPLYILDNK.A	650	2	*
39	ENSG00000083807:ENSMUSG00000030382:ENSRNOG00000019626	SLC27A5	gi|6678011|ref|NP_033538.1|	gi|6678011|ref|NP_033538.1|	solute carrier family 27 (fatty acid transporter), member 5 [Mus mu	4	21	10.4	689	76186	8.4	MmNaOH-MM_liver_CNBrTi_101.4559.4559.2	2	3.4264	0.2281	2118.49	2119.4	1	58.823532	1	M.LTPFELVQFDIETAEPLR.D	460	1	*
40	ENSG00000135220:ENSMUSG00000035780:ENSRNOG00000001975	UGT2A3	gi|13386284|ref|NP_082370.1|	gi|13386284|ref|NP_082370.1|	UDP glucuronosyltransferase 2 family, polypeptide A3 [Mus muscu	4	16	8.6	534	61133	7.6	MmNaOH-MM_liver_CNBrTi_107.4234.4234.2	2	4.7815	0.3084	2412.84	2412.7	1	55.263157	2	R.IPLHFENIPLLYEIETAENR.L	69	2	*
40	ENSG00000135220:ENSMUSG00000035780:ENSRNOG00000001975	UGT2A3	gi|13386284|ref|NP_082370.1|	gi|13386284|ref|NP_082370.1|	UDP glucuronosyltransferase 2 family, polypeptide A3 [Mus muscu	4	16	8.6	534	61133	7.6	MmNaOH-MM_liver_CNBrTi_108.4226.4226.3	3	4.6532	0.3004	2413.71	2412.7	1	39.473686	3	R.IPLHFENIPLLYEIETAENR.L	69	2	*
40	ENSG00000135220:ENSMUSG00000035780:ENSRNOG00000001975	UGT2A3	gi|13386284|ref|NP_082370.1|	gi|13386284|ref|NP_082370.1|	UDP glucuronosyltransferase 2 family, polypeptide A3 [Mus muscu	4	16	8.6	534	61133	7.6	MmNaOH-MM_liver_CNBrTi_109.1457.1457.2	2	3.0211	0.1862	1455.64	1455.7	3	59.090908	5	R.IHHDQPVKPLDR.A	448	2	
40	ENSG00000135220:ENSMUSG00000035780:ENSRNOG00000001975	UGT2A3	gi|13386284|ref|NP_082370.1|	gi|13386284|ref|NP_082370.1|	UDP glucuronosyltransferase 2 family, polypeptide A3 [Mus muscu	4	16	8.6	534	61133	7.6	MmNaOH-MM_liver_CNBrTi_206.2795.2795.2	2	4.0383	0.2294	1466.36	1466.8	1	73.07692	6	K.ANLIASVLAQIPQK.V	321	2	*
41	ENSG00000162365:ENSMUSG00000066071:ENSRNOG00000029919	CYP4A22	gi|86198312|ref|NP_803125.2|	gi|86198312|ref|NP_803125.2|	cytochrome P450, family 4, subfamily a, polypeptide 12 [Mus musc	8	26	16.5	508	58350	9.1	MmNaOH-MM_liver_CNBrTi_209.1943.1943.2	2	2.8505	0.1531	960.33	960.17	6	100	5	R.FLAPWIGR.G	120	2	
41	ENSG00000162365:ENSMUSG00000066071:ENSRNOG00000029919	CYP4A22	gi|86198312|ref|NP_803125.2|	gi|86198312|ref|NP_803125.2|	cytochrome P450, family 4, subfamily a, polypeptide 12 [Mus musc	8	26	16.5	508	58350	9.1	MmNaOH-MM_liver_CNBrTi_109.3136.3136.3	3	3.9161	0.2791	2713.34	2711	1	31.818182	1	M.LSFYGLHHNPTVWPNPEVFDPSR.F	411	1	
41	ENSG00000162365:ENSMUSG00000066071:ENSRNOG00000029919	CYP4A22	gi|86198312|ref|NP_803125.2|	gi|86198312|ref|NP_803125.2|	cytochrome P450, family 4, subfamily a, polypeptide 12 [Mus musc	8	26	16.5	508	58350	9.1	MmNaOH-MM_liver_CNBrTi_203.1733.1733.2	2	3.1809	0.3856	1305.29	1305.4	1	72.72727	4	R.ELSSPVTFPDGR.S	390	2	

rk	ORTHO_GROUPS	GENE_NAME	Locus	Proteins In Group	Description	Sequence Count	Spectrum Count	Coverage	Length	MW	pI	MatchID	Z	XCorr	DeltCN	M+H+	CalcM +H+	SpRk	Ion Proportion	Count	Sequence	Sequence Position	Tryptic	Unique
41	ENSG00000162365:ENSMUSG00000066071:ENSRNOG00000029919	CYP4A22	gi|86198312|ref|NP_803125.2|	gi|86198312|ref|NP_803125.2|	cytochrome P450, family 4, subfamily a, polypeptide 12 [Mus musc	8	26	16.5	508	58350	9.1	MmNaOH-MM_liver_CNBrTi_109.2252.2252.2	2	3.2183	0.2035	1400.78	1400.5	1	70.83333	1	R.HSHSFLPFSGGAR.N	441	2	
41	ENSG00000162365:ENSMUSG00000066071:ENSRNOG00000029919	CYP4A22	gi|86198312|ref|NP_803125.2|	gi|86198312|ref|NP_803125.2|	cytochrome P450, family 4, subfamily a, polypeptide 12 [Mus musc	8	26	16.5	508	58350	9.1	MmNaOH-MM_liver_CNBrTi_109.2253.2253.1	1	2.568	0.3183	1399.66	1400.5	1	62.5	1	R.HSHSFLPFSGGAR.N	441	2	
41	ENSG00000162365:ENSMUSG00000066071:ENSRNOG00000029919	CYP4A22	gi|86198312|ref|NP_803125.2|	gi|86198312|ref|NP_803125.2|	cytochrome P450, family 4, subfamily a, polypeptide 12 [Mus musc	8	26	16.5	508	58350	9.1	MmNaOH-MM_liver_CNBrTi_101.3935.3935.2	2	2.7	0.2633	1869.94	1870.1	8	43.333332	1	K.SYIQAVEDLNDLVFSR.V	214	2	*
41	ENSG00000162365:ENSMUSG00000066071:ENSRNOG00000029919	CYP4A22	gi|86198312|ref|NP_803125.2|	gi|86198312|ref|NP_803125.2|	cytochrome P450, family 4, subfamily a, polypeptide 12 [Mus musc	8	26	16.5	508	58350	9.1	MmNaOH-MM_liver_CNBrTi_109.4921.4921.2	2	4.1461	0.3193	1492.84	1492.8	1	72.72727	1	R.RLDFLDILLFAR.M	286	2	
41	ENSG00000162365:ENSMUSG00000066071:ENSRNOG00000029919	CYP4A22	gi|86198312|ref|NP_803125.2|	gi|86198312|ref|NP_803125.2|	cytochrome P450, family 4, subfamily a, polypeptide 12 [Mus musc	8	26	16.5	508	58350	9.1	MmNaOH-MM_liver_CNBrTi_101.1740.1740.1	1	2.6617	0.1141	1306.85	1305.4	6	59.090908	1	R.ELSSPVTFPDGR.S	390	2	
41	ENSG00000162365:ENSMUSG00000066071:ENSRNOG00000029919	CYP4A22	gi|86198312|ref|NP_803125.2|	gi|86198312|ref|NP_803125.2|	cytochrome P450, family 4, subfamily a, polypeptide 12 [Mus musc	8	26	16.5	508	58350	9.1	MmNaOH-MM_liver_CNBrTi_208.3319.3319.2	2	5.0485	0.4986	1870.2	1870.1	1	63.333332	11	K.SYIQAVEDLNDLVFSR.V	214	2	*
42	ENSG00000074695:ENSMUSG00000041891:ENSRNOG00000024470	LMAN1	gi|21312570|ref|NP_081676.1|	gi|21312570|ref|NP_081676.1|	lectin, mannose-binding, 1 [Mus musculus]	1	11	2.1	517	57789	6.3	MmNaOH-MM_liver_CNBrTi_101.0446.0446.2	2	3.8436	0.3029	1284.07	1284.4	2	80	8	R.YVSSLTEEISR.R	370	2	*
42	ENSG00000074695:ENSMUSG00000041891:ENSRNOG00000024470	LMAN1	gi|21312570|ref|NP_081676.1|	gi|21312570|ref|NP_081676.1|	lectin, mannose-binding, 1 [Mus musculus]	1	11	2.1	517	57789	6.3	MmNaOH-MM_liver_CNBrTi_201.0864.0864.2	2	2.9451	0.2376	1283.97	1284.4	1	75	3	R.YVSSLTEEISR.R	370	2	*
43	ENSG00000180432:ENSMUSG00000050445:ENSRNOG00000019481	CYP8B1	gi|31981808|ref|NP_034142.2|	gi|31981808|ref|NP_034142.2|	cytochrome P450, family 8, subfamily b, polypeptide 1 [Mus muscu	5	16	8	500	57706	8.8	MmNaOH-MM_liver_CNBrTi_206.2033.2033.2	2	3.7102	0.3285	1542.52	1543.8	1	73.07692	10	K.LVDPDIPVPPIDPR.R	464	2	*
43	ENSG00000180432:ENSMUSG00000050445:ENSRNOG00000019481	CYP8B1	gi|31981808|ref|NP_034142.2|	gi|31981808|ref|NP_034142.2|	cytochrome P450, family 8, subfamily b, polypeptide 1 [Mus muscu	5	16	8	500	57706	8.8	MmNaOH-MM_liver_CNBrTi_210.1275.1275.2	2	2.4747	0.2311	1379.92	1380.5	1	68.181816	2	K.VFGYQSVDGDHR.M	109	2	*
43	ENSG00000180432:ENSMUSG00000050445:ENSRNOG00000019481	CYP8B1	gi|31981808|ref|NP_034142.2|	gi|31981808|ref|NP_034142.2|	cytochrome P450, family 8, subfamily b, polypeptide 1 [Mus muscu	5	16	8	500	57706	8.8	MmNaOH-MM_liver_CNBrTi_211.2057.2057.2	2	3.5033	0.2817	1487.89	1488.6	1	66.66667	1	R.WGFGTSQPSHEVR.F	479	2	*
43	ENSG00000180432:ENSMUSG00000050445:ENSRNOG00000019481	CYP8B1	gi|31981808|ref|NP_034142.2|	gi|31981808|ref|NP_034142.2|	cytochrome P450, family 8, subfamily b, polypeptide 1 [Mus muscu	5	16	8	500	57706	8.8	MmNaOH-MM_liver_CNBrTi_109.2096.2096.2	2	4.0337	0.4143	1643.7	1644.8	1	65.38461	1	R.RWGFGTSQPSHEVR.F	478	2	*
43	ENSG00000180432:ENSMUSG00000050445:ENSRNOG00000019481	CYP8B1	gi|31981808|ref|NP_034142.2|	gi|31981808|ref|NP_034142.2|	cytochrome P450, family 8, subfamily b, polypeptide 1 [Mus muscu	5	16	8	500	57706	8.8	MmNaOH-MM_liver_CNBrTi_109.2100.2100.3	3	3.364	0.2309	1644.98	1644.8	1	48.076923	1	R.RWGFGTSQPSHEVR.F	478	2	*
43	ENSG00000180432:ENSMUSG00000050445:ENSRNOG00000019481	CYP8B1	gi|31981808|ref|NP_034142.2|	gi|31981808|ref|NP_034142.2|	cytochrome P450, family 8, subfamily b, polypeptide 1 [Mus muscu	5	16	8	500	57706	8.8	MmNaOH-MM_liver_CNBrTi_101.2146.2146.2	2	3.0676	0.2381	1543.66	1543.8	1	61.538464	1	K.LVDPDIPVPPIDPR.R	464	2	*
44	ENSG00000140505:ENSMUSG00000032310:ENSRNOG00000016173	CYP1A2	gi|6753566|ref|NP_034123.1|	gi|6753566|ref|NP_034123.1|	cytochrome P450, family 1, subfamily a, polypeptide 2 [Mus muscu	8	12	23.2	513	58184	8.8	MmNaOH-MM_liver_CNBrTi_101.4350.4350.3	3	3.5982	0.1378	3508.95	3506	1	20.967741	2	M.AEVGHFEPVSQVVESVANVIGAMCFGKNFPRK.S	180	1	*
44	ENSG00000140505:ENSMUSG00000032310:ENSRNOG00000016173	CYP1A2	gi|6753566|ref|NP_034123.1|	gi|6753566|ref|NP_034123.1|	cytochrome P450, family 1, subfamily a, polypeptide 2 [Mus muscu	8	12	23.2	513	58184	8.8	MmNaOH-MM_liver_CNBrTi_101.1748.1748.2	2	3.6552	0.2478	1422.71	1420.6	1	77.27273	1	R.LSQQYGDVLQIR.I	67	2	
44	ENSG00000140505:ENSMUSG00000032310:ENSRNOG00000016173	CYP1A2	gi|6753566|ref|NP_034123.1|	gi|6753566|ref|NP_034123.1|	cytochrome P450, family 1, subfamily a, polypeptide 2 [Mus muscu	8	12	23.2	513	58184	8.8	MmNaOH-MM_liver_CNBrTi_102.1343.1343.2	2	3.9584	0.3529	1438.22	1438.6	1	68.181816	2	K.PGTCEHVQAWPR.F	499	2	*
44	ENSG00000140505:ENSMUSG00000032310:ENSRNOG00000016173	CYP1A2	gi|6753566|ref|NP_034123.1|	gi|6753566|ref|NP_034123.1|	cytochrome P450, family 1, subfamily a, polypeptide 2 [Mus muscu	8	12	23.2	513	58184	8.8	MmNaOH-MM_liver_CNBrTi_103.1239.1239.3	3	3.3653	0.1544	1438.54	1438.6	1	52.272724	1	K.PGTCEHVQAWPR.F	499	2	*
44	ENSG00000140505:ENSMUSG00000032310:ENSRNOG00000016173	CYP1A2	gi|6753566|ref|NP_034123.1|	gi|6753566|ref|NP_034123.1|	cytochrome P450, family 1, subfamily a, polypeptide 2 [Mus muscu	8	12	23.2	513	58184	8.8	MmNaOH-MM_liver_CNBrTi_202.2171.2171.2	2	2.8149	0.2482	1598.41	1598.9	1	46.666668	1	R.IGSTPVVVLSGLNTIK.Q	79	2	
44	ENSG00000140505:ENSMUSG00000032310:ENSRNOG00000016173	CYP1A2	gi|6753566|ref|NP_034123.1|	gi|6753566|ref|NP_034123.1|	cytochrome P450, family 1, subfamily a, polypeptide 2 [Mus muscu	8	12	23.2	513	58184	8.8	MmNaOH-MM_liver_CNBrTi_203.3514.3514.2	2	4.6589	0.5034	2126.81	2127.4	1	66.66667	2	K.DFVENVTSGNAVDFFPVLR.Y	224	2	*
44	ENSG00000140505:ENSMUSG00000032310:ENSRNOG00000016173	CYP1A2	gi|6753566|ref|NP_034123.1|	gi|6753566|ref|NP_034123.1|	cytochrome P450, family 1, subfamily a, polypeptide 2 [Mus muscu	8	12	23.2	513	58184	8.8	MmNaOH-MM_liver_CNBrTi_202.2684.2684.2	2	3.107	0.222	1336.99	1337.5	1	72.72727	1	K.NSIQDITSALFK.H	277	2	*
44	ENSG00000140505:ENSMUSG00000032310:ENSRNOG00000016173	CYP1A2	gi|6753566|ref|NP_034123.1|	gi|6753566|ref|NP_034123.1|	cytochrome P450, family 1, subfamily a, polypeptide 2 [Mus muscu	8	12	23.2	513	58184	8.8	MmNaOH-MM_liver_CNBrTi_204.1296.1296.2	2	3.696	0.229	1811.63	1811	1	66.66667	1	R.FLTNNNSAIDKTQSEK.V	430	2	*
44	ENSG00000140505:ENSMUSG00000032310:ENSRNOG00000016173	CYP1A2	gi|6753566|ref|NP_034123.1|	gi|6753566|ref|NP_034123.1|	cytochrome P450, family 1, subfamily a, polypeptide 2 [Mus muscu	8	12	23.2	513	58184	8.8	MmNaOH-MM_liver_CNBrTi_201.1766.1766.2	2	3.5805	0.3344	1420.73	1420.6	1	72.72727	1	R.LSQQYGDVLQIR.I	67	2	
45	ENSG00000213908:ENSMUSG00000005547:ENSRNOG00000028900	CYP2A7P1	gi|75832129|ref|NP_031838.2|	gi|75832129|ref|NP_031838.2|	cytochrome P450, family 2, subfamily a, polypeptide 5 [Mus muscu	4	18	6.7	494	56713	9.2	MmNaOH-MM_liver_CNBrTi_212.2313.2313.2	2	2.4767	0.2803	1385.84	1383.6	1	68.181816	1	R.YGPVFTIYLGPR.R	65	2	*
45	ENSG00000213908:ENSMUSG00000005547:ENSRNOG00000028900	CYP2A7P1	gi|75832129|ref|NP_031838.2|	gi|75832129|ref|NP_031838.2|	cytochrome P450, family 2, subfamily a, polypeptide 5 [Mus muscu	4	18	6.7	494	56713	9.2	MmNaOH-MM_liver_CNBrTi_205.2861.2861.2	2	3.499	0.1721	1125.95	1126.3	1	87.5	14	R.DFIDSFLIR.M	266	2	
45	ENSG00000213908:ENSMUSG00000005547:ENSRNOG00000028900	CYP2A7P1	gi|75832129|ref|NP_031838.2|	gi|75832129|ref|NP_031838.2|	cytochrome P450, family 2, subfamily a, polypeptide 5 [Mus muscu	4	18	6.7	494	56713	9.2	MmNaOH-MM_liver_CNBrTi_202.2908.2908.1	1	2.2618	0.101	1126.71	1126.3	5	68.75	1	R.DFIDSFLIR.M	266	2	
45	ENSG00000213908:ENSMUSG00000005547:ENSRNOG00000028900	CYP2A7P1	gi|75832129|ref|NP_031838.2|	gi|75832129|ref|NP_031838.2|	cytochrome P450, family 2, subfamily a, polypeptide 5 [Mus muscu	4	18	6.7	494	56713	9.2	MmNaOH-MM_liver_CNBrTi_101.3211.3211.2	2	3.1286	0.2334	1126.28	1126.3	4	87.5	1	R.DFIDSFLIR.M	266	2	
45	ENSG00000213908:ENSMUSG00000005547:ENSRNOG00000028900	CYP2A7P1	gi|75832129|ref|NP_031838.2|	gi|75832129|ref|NP_031838.2|	cytochrome P450, family 2, subfamily a, polypeptide 5 [Mus muscu	4	18	6.7	494	56713	9.2	MmNaOH-MM_liver_CNBrTi_212.1960.1960.2	2	3.7432	0.3433	1456.59	1456.6	1	77.27273	1	M.PYTEAVIHEIQR.F	350	1	
46	ENSG00000167165:ENSMUSG00000054545:ENSRNOG00000018740	UGT1A9	gi|47059133|ref|NP_958812.1|	gi|47059133|ref|NP_958812.1|	UDP glucuronosyltransferase 1 family, polypeptide A6B [Mus musc	7	68	15.1	531	60435	8.7	MmNaOH-MM_liver_CNBrTi_203.5853.5853.2	2	3.0751	0.2046	1013.35	1013.2	1	92.85714	57	R.IPQTVLWR.Y	327	2	
46	ENSG00000167165:ENSMUSG00000054545:ENSRNOG00000018740	UGT1A9	gi|47059133|ref|NP_958812.1|	gi|47059133|ref|NP_958812.1|	UDP glucuronosyltransferase 1 family, polypeptide A6B [Mus musc	7	68	15.1	531	60435	8.7	MmNaOH-MM_liver_CNBrTi_105.5076.5076.2	2	5.3294	0.3908	2224.89	2225.6	1	63.88889	3	M.PCGVILAEYLNLPSVYLFR.G	154	1	
46	ENSG00000167165:ENSMUSG00000054545:ENSRNOG00000018740	UGT1A9	gi|47059133|ref|NP_958812.1|	gi|47059133|ref|NP_958812.1|	UDP glucuronosyltransferase 1 family, polypeptide A6B [Mus musc	7	68	15.1	531	60435	8.7	MmNaOH-MM_liver_CNBrTi_204.2472.2472.2	2	2.5751	0.2247	1682.95	1682.9	4	46.153847	1	K.IFSVPYSLEELQTR.F	77	2	
46	ENSG00000167165:ENSMUSG00000054545:ENSRNOG00000018740	UGT1A9	gi|47059133|ref|NP_958812.1|	gi|47059133|ref|NP_958812.1|	UDP glucuronosyltransferase 1 family, polypeptide A6B [Mus musc	7	68	15.1	531	60435	8.7	MmNaOH-MM_liver_CNBrTi_105.3871.3871.2	2	3.5042	0.3862	2031.97	2032.4	1	50	1	R.GHDIVVLVPEVNLLLGESK.Y	53	2	
46	ENSG00000167165:ENSMUSG00000054545:ENSRNOG00000018740	UGT1A9	gi|47059133|ref|NP_958812.1|	gi|47059133|ref|NP_958812.1|	UDP glucuronosyltransferase 1 family, polypeptide A6B [Mus musc	7	68	15.1	531	60435	8.7	MmNaOH-MM_liver_CNBrTi_204.1766.1766.1	1	2.3725	0.1664	1012.57	1013.2	3	78.57143	2	R.IPQTVLWR.Y	327	2	
46	ENSG00000167165:ENSMUSG00000054545:ENSRNOG00000018740	UGT1A9	gi|47059133|ref|NP_958812.1|	gi|47059133|ref|NP_958812.1|	UDP glucuronosyltransferase 1 family, polypeptide A6B [Mus musc	7	68	15.1	531	60435	8.7	MmNaOH-MM_liver_CNBrTi_209.0878.0878.2	2	2.6761	0.2241	1112.16	1112.2	1	81.25	3	K.EIVEHLSER.G	44	2	
46	ENSG00000167165:ENSMUSG00000054545:ENSRNOG00000018740	UGT1A9	gi|47059133|ref|NP_958812.1|	gi|47059133|ref|NP_958812.1|	UDP glucuronosyltransferase 1 family, polypeptide A6B [Mus musc	7	68	15.1	531	60435	8.7	MmNaOH-MM_liver_CNBrTi_207.0602.0602.2	2	2.7701	0.2575	1208	1208.4	1	70	1	R.YTGTRPSNLAK.N	335	2	
47	ENSG00000197142:ENSMUSG00000024981:ENSRNOG00000016265	ACSL5	gi|58218988|ref|NP_082252.1|	gi|58218988|ref|NP_082252.1|	acyl-CoA synthetase long-chain family member 5 [Mus musculus]	3	33	3.7	683	76206	7.1	MmNaOH-MM_liver_CNBrTi_205.1831.1831.1	1	2.0135	0.15	1052.66	1053.2	2	68.75	1	K.IGFFQGDIR.L	326	2	
47	ENSG00000197142:ENSMUSG00000024981:ENSRNOG00000016265	ACSL5	gi|58218988|ref|NP_082252.1|	gi|58218988|ref|NP_082252.1|	acyl-CoA synthetase long-chain family member 5 [Mus musculus]	3	33	3.7	683	76206	7.1	MmNaOH-MM_liver_CNBrTi_206.2651.2651.2	2	3.8082	0.3462	1691.98	1692	1	63.333332	17	M.ITGAAPISTPVLTFFR.A	417	1	*
47	ENSG00000197142:ENSMUSG00000024981:ENSRNOG00000016265	ACSL5	gi|58218988|ref|NP_082252.1|	gi|58218988|ref|NP_082252.1|	acyl-CoA synthetase long-chain family member 5 [Mus musculus]	3	33	3.7	683	76206	7.1	MmNaOH-MM_liver_CNBrTi_203.1821.1821.2	2	3.195	0.2627	1053.32	1053.2	1	81.25	13	K.IGFFQGDIR.L	326	2	
47	ENSG00000197142:ENSMUSG00000024981:ENSRNOG00000016265	ACSL5	gi|58218988|ref|NP_082252.1|	gi|58218988|ref|NP_082252.1|	acyl-CoA synthetase long-chain family member 5 [Mus musculus]	3	33	3.7	683	76206	7.1	MmNaOH-MM_liver_CNBrTi_101.2810.2810.2	2	3.4307	0.2579	1692.71	1692	1	56.666668	1	M.ITGAAPISTPVLTFFR.A	417	1	*
47	ENSG00000197142:ENSMUSG00000024981:ENSRNOG00000016265	ACSL5	gi|58218988|ref|NP_082252.1|	gi|58218988|ref|NP_082252.1|	acyl-CoA synthetase long-chain family member 5 [Mus musculus]	3	33	3.7	683	76206	7.1	MmNaOH-MM_liver_CNBrTi_101.1642.1642.2	2	3.2617	0.2784	1053.05	1053.2	1	93.75	1	K.IGFFQGDIR.L	326	2	
48	ENSG00000138115:ENSMUSG00000074882:ENSRNOG00000036595	CYP2C8	gi|88319958|ref|NP_001034644.1|	gi|88319958|ref|NP_001034644.1|	cytochrome P450 2C40 family [Mus musculus]	2	14	4.3	491	55969	7.2	MmNaOH-MM_liver_CNBrTi_101.1048.1048.2	2	3.9384	0.2661	1274.12	1272.4	2	85	5	K.VQEEIDNVIGR.H	323	2	
48	ENSG00000138115:ENSMUSG00000074882:ENSRNOG00000036595	CYP2C8	gi|88319958|ref|NP_001034644.1|	gi|88319958|ref|NP_001034644.1|	cytochrome P450 2C40 family [Mus musculus]	2	14	4.3	491	55969	7.2	MmNaOH-MM_liver_CNBrTi_208.2807.2807.2	2	3.8694	0.1829	1316.49	1316.5	1	83.33333	6	R.DFVDYFLIQR.C	262	2	*
48	ENSG00000138115:ENSMUSG00000074882:ENSRNOG00000036595	CYP2C8	gi|88319958|ref|NP_001034644.1|	gi|88319958|ref|NP_001034644.1|	cytochrome P450 2C40 family [Mus musculus]	2	14	4.3	491	55969	7.2	MmNaOH-MM_liver_CNBrTi_201.0642.0642.2	2	2.6281	0.1417	1272.17	1272.4	2	75	3	K.VQEEIDNVIGR.H	323	2	
49	ENSG00000134716:ENSMUSG00000052520:NA	CYP2J2	gi|6753586|ref|NP_034137.1|	gi|6753586|ref|NP_034137.1|	cytochrome P450, family 2, subfamily j, polypeptide 5 [Mus muscul	4	10	10.8	501	57784	8.7	MmNaOH-MM_liver_CNBrTi_105.1438.1438.2	2	4.1122	0.2595	1576.33	1575.8	1	79.16667	3	R.IQEETHHLVEAIR.E	159	2	*
49	ENSG00000134716:ENSMUSG00000052520:NA	CYP2J2	gi|6753586|ref|NP_034137.1|	gi|6753586|ref|NP_034137.1|	cytochrome P450, family 2, subfamily j, polypeptide 5 [Mus muscul	4	10	10.8	501	57784	8.7	MmNaOH-MM_liver_CNBrTi_212.1869.1869.2	2	3.3898	0.2579	1575.77	1575.8	1	62.5	1	R.IQEETHHLVEAIR.E	159	2	*
49	ENSG00000134716:ENSMUSG00000052520:NA	CYP2J2	gi|6753586|ref|NP_034137.1|	gi|6753586|ref|NP_034137.1|	cytochrome P450, family 2, subfamily j, polypeptide 5 [Mus muscul	4	10	10.8	501	57784	8.7	MmNaOH-MM_liver_CNBrTi_209.1365.1365.3	3	3.3945	0.0946	1428.01	1427.6	1	52.272724	1	M.PYTNAVIHEVQR.F	359	1	
49	ENSG00000134716:ENSMUSG00000052520:NA	CYP2J2	gi|6753586|ref|NP_034137.1|	gi|6753586|ref|NP_034137.1|	cytochrome P450, family 2, subfamily j, polypeptide 5 [Mus muscul	4	10	10.8	501	57784	8.7	MmNaOH-MM_liver_CNBrTi_103.0006.0006.3	3	4.2122	0.2862	3150.85	3150.4	1	22.321428	1	R.TTSFNEENLISTTLDLFLGGTETTSSTLR.W	292	2	*
49	ENSG00000134716:ENSMUSG00000052520:NA	CYP2J2	gi|6753586|ref|NP_034137.1|	gi|6753586|ref|NP_034137.1|	cytochrome P450, family 2, subfamily j, polypeptide 5 [Mus muscul	4	10	10.8	501	57784	8.7	MmNaOH-MM_liver_CNBrTi_102.0262.0262.2	2	3.67	0.387	3148.7	3150.4	1	33.92857	2	R.TTSFNEENLISTTLDLFLGGTETTSSTLR.W	292	2	*
49	ENSG00000134716:ENSMUSG00000052520:NA	CYP2J2	gi|6753586|ref|NP_034137.1|	gi|6753586|ref|NP_034137.1|	cytochrome P450, family 2, subfamily j, polypeptide 5 [Mus muscul	4	10	10.8	501	57784	8.7	MmNaOH-MM_liver_CNBrTi_212.3656.3656.2	2	4.4432	0.3982	3150.52	3150.4	1	37.5	2	R.TTSFNEENLISTTLDLFLGGTETTSSTLR.W	292	2	*
50	ENSG00000215021:ENSMUSG00000004264:ENSRNOG00000012999	PHB2	gi|126723336|ref|NP_031557.2|	gi|126723336|ref|NP_031557.2|	B-cell receptor-associated protein 37 [Mus musculus]	3	6	14.4	299	33296	9.8	MmNaOH-MM_liver_CNBrTi_102.4310.4310.2	2	3.6746	0.3385	1724.47	1725	1	66.66667	3	R.IPWFQYPIIYDIR.A	72	2	*
50	ENSG00000215021:ENSMUSG00000004264:ENSRNOG00000012999	PHB2	gi|126723336|ref|NP_031557.2|	gi|126723336|ref|NP_031557.2|	B-cell receptor-associated protein 37 [Mus musculus]	3	6	14.4	299	33296	9.8	MmNaOH-MM_liver_CNBrTi_205.3049.3049.2	2	5.3456	0.4278	2226.05	2226.5	1	61.11111	2	R.IYLTADNLVLNLQDESFTR.G	271	2	*
50	ENSG00000215021:ENSMUSG00000004264:ENSRNOG00000012999	PHB2	gi|126723336|ref|NP_031557.2|	gi|126723336|ref|NP_031557.2|	B-cell receptor-associated protein 37 [Mus musculus]	3	6	14.4	299	33296	9.8	MmNaOH-MM_liver_CNBrTi_206.1072.1072.2	2	2.369	0.3135	1217.67	1218.3	2	60.000004	1	R.ESVFTVEGGHR.A	38	2	*
51	ENSG00000106638:ENSMUSG00000005374:NA	TBL2	gi|31543845|ref|NP_038791.2|	gi|31543845|ref|NP_038791.2|	transducin (beta)-like 2 [Mus musculus]	3	8	8.1	442	49584	9	MmNaOH-MM_liver_CNBrTi_108.3216.3216.2	2	5.446	0.4118	2576.69	2577	1	54.347824	1	R.LALSPDTHVLALATGTNIHLFNTR.R	332	2	*
51	ENSG00000106638:ENSMUSG00000005374:NA	TBL2	gi|31543845|ref|NP_038791.2|	gi|31543845|ref|NP_038791.2|	transducin (beta)-like 2 [Mus musculus]	3	8	8.1	442	49584	9	MmNaOH-MM_liver_CNBrTi_108.3230.3230.3	3	5.4208	0.3809	2576.93	2577	1	43.47826	4	R.LALSPDTHVLALATGTNIHLFNTR.R	332	2	*
51	ENSG00000106638:ENSMUSG00000005374:NA	TBL2	gi|31543845|ref|NP_038791.2|	gi|31543845|ref|NP_038791.2|	transducin (beta)-like 2 [Mus musculus]	3	8	8.1	442	49584	9	MmNaOH-MM_liver_CNBrTi_207.1454.1454.2	2	3.6886	0.3846	1338.25	1338.5	2	81.818184	3	R.ANVELDHATLVR.F	128	2	*
52	ENSG00000060971:ENSMUSG00000010651:ENSRNOG00000030287	ACAA1	gi|22122797|ref|NP_666342.1|	gi|22122797|ref|NP_666342.1|	acetyl-Coenzyme A acyltransferase 1B [Mus musculus]	1	11	4.5	424	43995	8.5	MmNaOH-MM_liver_CNBrTi_203.2501.2501.2	2	4.4139	0.2963	2043.72	2043.4	1	55.555557	10	R.IAQFLSGIPETVPLSTVNR.Q	103	2	
52	ENSG00000060971:ENSMUSG00000010651:ENSRNOG00000030287	ACAA1	gi|22122797|ref|NP_666342.1|	gi|22122797|ref|NP_666342.1|	acetyl-Coenzyme A acyltransferase 1B [Mus musculus]	1	11	4.5	424	43995	8.5	MmNaOH-MM_liver_CNBrTi_101.2590.2590.2	2	2.9766	0.2157	2042.43	2043.4	6	41.666664	1	R.IAQFLSGIPETVPLSTVNR.Q	103	2	
53	ENSG00000127948:ENSMUSG00000005514:ENSRNOG00000001442	POR	gi|6679421|ref|NP_032924.1|	gi|6679421|ref|NP_032924.1|	cytochrome P450 reductase [Mus musculus]	5	15	10.9	678	77044	5.5	MmNaOH-MM_liver_CNBrTi_110.3542.3542.3	3	5.2746	0.3399	2981.49	2981.5	1	37.5	2	R.HILAILQDYPSLRPPIDHLCELLPR.L	426	2	*
53	ENSG00000127948:ENSMUSG00000005514:ENSRNOG00000001442	POR	gi|6679421|ref|NP_032924.1|	gi|6679421|ref|NP_032924.1|	cytochrome P450 reductase [Mus musculus]	5	15	10.9	678	77044	5.5	MmNaOH-MM_liver_CNBrTi_202.2307.2307.2	2	3.9183	0.3633	1638.79	1638.9	1	61.538464	9	R.TALTYYLDITNPPR.T	369	2	*
53	ENSG00000127948:ENSMUSG00000005514:ENSRNOG00000001442	POR	gi|6679421|ref|NP_032924.1|	gi|6679421|ref|NP_032924.1|	cytochrome P450 reductase [Mus musculus]	5	15	10.9	678	77044	5.5	MmNaOH-MM_liver_CNBrTi_202.2347.2347.3	3	4.1407	0.2483	1638.73	1638.9	8	46.153847	1	R.TALTYYLDITNPPR.T	369	2	*
53	ENSG00000127948:ENSMUSG00000005514:ENSRNOG00000001442	POR	gi|6679421|ref|NP_032924.1|	gi|6679421|ref|NP_032924.1|	cytochrome P450 reductase [Mus musculus]	5	15	10.9	678	77044	5.5	MmNaOH-MM_liver_CNBrTi_204.2194.2194.2	2	4.7588	0.5434	2117.87	2118.3	1	63.88889	2	R.NIIVFYGSQTGTAEEFANR.L	79	2	*
53	ENSG00000127948:ENSMUSG00000005514:ENSRNOG00000001442	POR	gi|6679421|ref|NP_032924.1|	gi|6679421|ref|NP_032924.1|	cytochrome P450 reductase [Mus musculus]	5	15	10.9	678	77044	5.5	MmNaOH-MM_liver_CNBrTi_106.1400.1400.2	2	4.1191	0.4421	1768.7	1768.9	1	66.66667	1	K.LIHEGGAHIYVCGDAR.N	619	2	*
54	ENSG00000138115:ENSMUSG00000003053:ENSRNOG00000013241	CYP2C8	gi|116268125|ref|NP_031841.3|	gi|116268125|ref|NP_031841.3|	cytochrome P450, family 2, subfamily c, polypeptide 29 [Mus musc	6	10	10.6	490	55716	8.3	MmNaOH-MM_liver_CNBrTi_202.2604.2604.2	2	2.8027	0.1985	1190.77	1190.4	1	81.25	1	R.DFIDYYLIK.Q	262	2	
54	ENSG00000138115:ENSMUSG00000003053:ENSRNOG00000013241	CYP2C8	gi|116268125|ref|NP_031841.3|	gi|116268125|ref|NP_031841.3|	cytochrome P450, family 2, subfamily c, polypeptide 29 [Mus musc	6	10	10.6	490	55716	8.3	MmNaOH-MM_liver_CNBrTi_101.2476.2476.2	2	3.4406	0.1771	2042.85	2041.4	1	61.764706	2	R.FIDLLPTSLPHAVTCDIK.F	358	2	*
54	ENSG00000138115:ENSMUSG00000003053:ENSRNOG00000013241	CYP2C8	gi|116268125|ref|NP_031841.3|	gi|116268125|ref|NP_031841.3|	cytochrome P450, family 2, subfamily c, polypeptide 29 [Mus musc	6	10	10.6	490	55716	8.3	MmNaOH-MM_liver_CNBrTi_101.1708.1708.2	2	3.2762	0.1761	1731.73	1731.9	1	57.692307	1	R.VQEEAQCLVEELRK.T	145	2	
54	ENSG00000138115:ENSMUSG00000003053:ENSRNOG00000013241	CYP2C8	gi|116268125|ref|NP_031841.3|	gi|116268125|ref|NP_031841.3|	cytochrome P450, family 2, subfamily c, polypeptide 29 [Mus musc	6	10	10.6	490	55716	8.3	MmNaOH-MM_liver_CNBrTi_202.1951.1951.2	2	4.4813	0.3644	1604.31	1603.7	1	79.16667	2	R.VQEEAQCLVEELR.K	145	2	
54	ENSG00000138115:ENSMUSG00000003053:ENSRNOG00000013241	CYP2C8	gi|116268125|ref|NP_031841.3|	gi|116268125|ref|NP_031841.3|	cytochrome P450, family 2, subfamily c, polypeptide 29 [Mus musc	6	10	10.6	490	55716	8.3	MmNaOH-MM_liver_CNBrTi_211.1977.1977.2	2	2.9136	0.2115	1300.39	1300.5	6	70	1	R.VQEEIDRVVGR.S	323	2	
54	ENSG00000138115:ENSMUSG00000003053:ENSRNOG00000013241	CYP2C8	gi|116268125|ref|NP_031841.3|	gi|116268125|ref|NP_031841.3|	cytochrome P450, family 2, subfamily c, polypeptide 29 [Mus musc	6	10	10.6	490	55716	8.3	MmNaOH-MM_liver_CNBrTi_202.2599.2599.1	1	2.4194	0.223	1189.52	1190.4	1	75	1	R.DFIDYYLIK.Q	262	2	
54	ENSG00000138115:ENSMUSG00000003053:ENSRNOG00000013241	CYP2C8	gi|116268125|ref|NP_031841.3|	gi|116268125|ref|NP_031841.3|	cytochrome P450, family 2, subfamily c, polypeptide 29 [Mus musc	6	10	10.6	490	55716	8.3	MmNaOH-MM_liver_CNBrTi_101.1930.1930.2	2	4.88	0.3012	1603.6	1603.7	1	87.5	2	R.VQEEAQCLVEELR.K	145	2	
55	ENSG00000101974:ENSMUSG00000062949:ENSRNOG00000003472	ATP11C	gi|49355804|ref|NP_001001798.1|	gi|49355804|ref|NP_001001798.1|;gi|83745137|ref|NP_00103	Atpase, class VI, type 11C isoform b [Mus musculus]	5	15	3.8	1116	127809	7	MmNaOH-MM_liver_CNBrTi_101.1587.1587.3	3	3.0879	0.1223	2087.05	2087.3	9	33.333336	1	R.TVFVGNHPISGTEPYIAQR.F	21	2	
55	ENSG00000101974:ENSMUSG00000062949:ENSRNOG00000003472	ATP11C	gi|49355804|ref|NP_001001798.1|	gi|49355804|ref|NP_001001798.1|;gi|83745137|ref|NP_00103	Atpase, class VI, type 11C isoform b [Mus musculus]	5	15	3.8	1116	127809	7	MmNaOH-MM_liver_CNBrTi_105.1747.1747.1	1	2.674	0.264	1185.6	1186.4	8	68.75	1	R.LHELLIEYR.K	715	2	
55	ENSG00000101974:ENSMUSG00000062949:ENSRNOG00000003472	ATP11C	gi|49355804|ref|NP_001001798.1|	gi|49355804|ref|NP_001001798.1|;gi|83745137|ref|NP_00103	Atpase, class VI, type 11C isoform b [Mus musculus]	5	15	3.8	1116	127809	7	MmNaOH-MM_liver_CNBrTi_104.1750.1750.2	2	3.5644	0.2464	1186.56	1186.4	1	87.5	5	R.LHELLIEYR.K	715	2	
55	ENSG00000101974:ENSMUSG00000062949:ENSRNOG00000003472	ATP11C	gi|49355804|ref|NP_001001798.1|	gi|49355804|ref|NP_001001798.1|;gi|83745137|ref|NP_00103	Atpase, class VI, type 11C isoform b [Mus musculus]	5	15	3.8	1116	127809	7	MmNaOH-MM_liver_CNBrTi_101.1592.1592.2	2	3.8551	0.3495	2087.14	2087.3	1	52.77778	1	R.TVFVGNHPISGTEPYIAQR.F	21	2	
55	ENSG00000101974:ENSMUSG00000062949:ENSRNOG00000003472	ATP11C	gi|49355804|ref|NP_001001798.1|	gi|49355804|ref|NP_001001798.1|;gi|83745137|ref|NP_00103	Atpase, class VI, type 11C isoform b [Mus musculus]	5	15	3.8	1116	127809	7	MmNaOH-MM_liver_CNBrTi_207.2590.2590.2	2	2.804	0.0955	1635.61	1634.8	1	76.92308	5	R.FGFTFLGNQNGYIR.V	508	2	
55	ENSG00000101974:ENSMUSG00000062949:ENSRNOG00000003472	ATP11C	gi|49355804|ref|NP_001001798.1|	gi|49355804|ref|NP_001001798.1|;gi|83745137|ref|NP_00103	Atpase, class VI, type 11C isoform b [Mus musculus]	5	15	3.8	1116	127809	7	MmNaOH-MM_liver_CNBrTi_101.2815.2815.2	2	2.3639	0.1951	1635.5	1634.8	1	57.692307	2	R.FGFTFLGNQNGYIR.V	508	2	
56	ENSG00000146648:ENSMUSG00000020122:ENSRNOG00000004332	EGFR	gi|46560582|ref|NP_997538.1|	gi|46560582|ref|NP_997538.1|;gi|6681283|ref|NP_031938.1|	epidermal growth factor receptor isoform 1 [Mus musculus]	5	25	4	1210	134853	6.9	MmNaOH-MM_liver_CNBrTi_101.2276.2276.2	2	4.5213	0.4468	1906.26	1906.1	1	66.66667	3	R.LTQLGTFEDHFLSLQR.M	38	2	
56	ENSG00000146648:ENSMUSG00000020122:ENSRNOG00000004332	EGFR	gi|46560582|ref|NP_997538.1|	gi|46560582|ref|NP_997538.1|;gi|6681283|ref|NP_031938.1|	epidermal growth factor receptor isoform 1 [Mus musculus]	5	25	4	1210	134853	6.9	MmNaOH-MM_liver_CNBrTi_101.1978.1978.2	2	2.5388	0.1994	1209.46	1209.5	1	83.33333	1	R.IPLENLQIIR.G	99	2	
56	ENSG00000146648:ENSMUSG00000020122:ENSRNOG00000004332	EGFR	gi|46560582|ref|NP_997538.1|	gi|46560582|ref|NP_997538.1|;gi|6681283|ref|NP_031938.1|	epidermal growth factor receptor isoform 1 [Mus musculus]	5	25	4	1210	134853	6.9	MmNaOH-MM_liver_CNBrTi_203.1975.1975.1	1	2.9712	0.0991	1208.72	1209.5	1	66.66667	1	R.IPLENLQIIR.G	99	2	
56	ENSG00000146648:ENSMUSG00000020122:ENSRNOG00000004332	EGFR	gi|46560582|ref|NP_997538.1|	gi|46560582|ref|NP_997538.1|;gi|6681283|ref|NP_031938.1|	epidermal growth factor receptor isoform 1 [Mus musculus]	5	25	4	1210	134853	6.9	MmNaOH-MM_liver_CNBrTi_203.1966.1966.2	2	3.382	0.1909	1209.46	1209.5	1	94.44444	5	R.IPLENLQIIR.G	99	2	
56	ENSG00000146648:ENSMUSG00000020122:ENSRNOG00000004332	EGFR	gi|46560582|ref|NP_997538.1|	gi|46560582|ref|NP_997538.1|;gi|6681283|ref|NP_031938.1|	epidermal growth factor receptor isoform 1 [Mus musculus]	5	25	4	1210	134853	6.9	MmNaOH-MM_liver_CNBrTi_205.0795.0795.2	2	2.9984	0.2549	1407.52	1407.5	1	68.181816	2	R.NYVVTDHGSCVR.A	298	2	
56	ENSG00000146648:ENSMUSG00000020122:ENSRNOG00000004332	EGFR	gi|46560582|ref|NP_997538.1|	gi|46560582|ref|NP_997538.1|;gi|6681283|ref|NP_031938.1|	epidermal growth factor receptor isoform 1 [Mus musculus]	5	25	4	1210	134853	6.9	MmNaOH-MM_liver_CNBrTi_205.2263.2263.2	2	4.4688	0.2416	1226.53	1226.5	1	90	13	R.NLQEILIGAVR.F	139	2	
57	ENSG00000010932:ENSMUSG00000040181:ENSRNOG00000034191	FMO1	gi|6753890|ref|NP_034361.1|	gi|6753890|ref|NP_034361.1|	flavin containing monooxygenase 1 [Mus musculus]	2	9	6.2	532	59915	8.5	MmNaOH-MM_liver_CNBrTi_104.5278.5278.3	3	4.0695	0.3313	2754.02	2754.1	1	25	3	K.ALQTDYITYIDDLLTSINAKPDLR.A	427	2	*
57	ENSG00000010932:ENSMUSG00000040181:ENSRNOG00000034191	FMO1	gi|6753890|ref|NP_034361.1|	gi|6753890|ref|NP_034361.1|	flavin containing monooxygenase 1 [Mus musculus]	2	9	6.2	532	59915	8.5	MmNaOH-MM_liver_CNBrTi_208.0469.0469.2	2	2.9153	0.2847	1103.98	1104.2	1	87.5	6	R.FTEHVEEGR.A	43	2	*
58	NA:ENSMUSG00000062284:ENSRNOG00000010189	EG547267	gi|149267539|ref|XP_001481149.1|	gi|149267539|ref|XP_001481149.1|;gi|149267855|ref|XP_001	PREDICTED: hypothetical protein [Mus musculus]	2	2	14.5	145	16565	10.9	MmNaOH-MM_liver_CNBrTi_102.3902.3902.2	2	2.9544	0.2992	1399.51	1399.6	1	72.72727	1	K.TTPDVIFVFGFR.T	62	2	
58	NA:ENSMUSG00000062284:ENSRNOG00000010189	EG547267	gi|149267539|ref|XP_001481149.1|	gi|149267539|ref|XP_001481149.1|;gi|149267855|ref|XP_001	PREDICTED: hypothetical protein [Mus musculus]	2	2	14.5	145	16565	10.9	MmNaOH-MM_liver_CNBrTi_208.1230.1230.2	2	2.8217	0.2559	978.31	978.18	1	93.75	1	M.VIDVLHPGK.A	36	1	
59	ENSG00000169223:ENSMUSG00000021484:ENSRNOG00000016161	LMAN2	gi|34328278|ref|NP_080104.2|	gi|34328278|ref|NP_080104.2|	lectin, mannose-binding 2 [Mus musculus]	3	4	3.1	358	40430	7	MmNaOH-MM_liver_CNBrTi_210.1302.1302.2	2	2.6239	0.3407	1074.1	1074.2	1	75	1	R.DHDTFLAVR.Y	212	2	*
59	ENSG00000169223:ENSMUSG00000021484:ENSRNOG00000016161	LMAN2	gi|34328278|ref|NP_080104.2|	gi|34328278|ref|NP_080104.2|	lectin, mannose-binding 2 [Mus musculus]	3	4	3.1	358	40430	7	MmNaOH-MM_liver_CNBrTi_105.1418.1418.3	3	3.6109	0.21	1345.75	1344.5	5	50	2	R.NRDHDTFLAVR.Y	210	2	*
59	ENSG00000169223:ENSMUSG00000021484:ENSRNOG00000016161	LMAN2	gi|34328278|ref|NP_080104.2|	gi|34328278|ref|NP_080104.2|	lectin, mannose-binding 2 [Mus musculus]	3	4	3.1	358	40430	7	MmNaOH-MM_liver_CNBrTi_104.1411.1411.2	2	2.7964	0.2144	1344.3	1344.5	9	65	1	R.NRDHDTFLAVR.Y	210	2	*
60	ENSG00000101474:ENSMUSG00000033096:ENSRNOG00000006795	C20orf3	gi|21313668|ref|NP_082253.1|	gi|21313668|ref|NP_082253.1|	RIKEN cDNA 2310001A20 [Mus musculus]	4	6	17.8	415	46434	6.3	MmNaOH-MM_liver_CNBrTi_109.2148.2148.3	3	3.3119	0.1204	2035.5	2034.3	1	35.294117	1	R.RPLRPQVVTDDGQVPEVK.E	11	2	*
60	ENSG00000101474:ENSMUSG00000033096:ENSRNOG00000006795	C20orf3	gi|21313668|ref|NP_082253.1|	gi|21313668|ref|NP_082253.1|	RIKEN cDNA 2310001A20 [Mus musculus]	4	6	17.8	415	46434	6.3	MmNaOH-MM_liver_CNBrTi_206.3851.3851.3	3	3.3731	0.2581	2850.5	2851.1	4	25.961538	1	R.LFENQLSGPESIVNIGDVLFTGTADGR.V	93	2	*
60	ENSG00000101474:ENSMUSG00000033096:ENSRNOG00000006795	C20orf3	gi|21313668|ref|NP_082253.1|	gi|21313668|ref|NP_082253.1|	RIKEN cDNA 2310001A20 [Mus musculus]	4	6	17.8	415	46434	6.3	MmNaOH-MM_liver_CNBrTi_107.2714.2714.3	3	3.859	0.1849	3295.01	3293.5	1	25.892857	1	R.SLHDPDGQVVTYVSEAHEHDGYLYLGSFR.S	375	2	
60	ENSG00000101474:ENSMUSG00000033096:ENSRNOG00000006795	C20orf3	gi|21313668|ref|NP_082253.1|	gi|21313668|ref|NP_082253.1|	RIKEN cDNA 2310001A20 [Mus musculus]	4	6	17.8	415	46434	6.3	MmNaOH-MM_liver_CNBrTi_206.3817.3817.2	2	4.6427	0.4024	2850.46	2851.1	1	42.307693	3	R.LFENQLSGPESIVNIGDVLFTGTADGR.V	93	2	*
61	NA:ENSMUSG00000034450:ENSRNOG00000016648	GULO	gi|30520195|ref|NP_848862.1|	gi|30520195|ref|NP_848862.1|	gulonolactone (L-) oxidase [Mus musculus]	2	6	5.7	440	50478	8.2	MmNaOH-MM_liver_CNBrTi_102.2215.2215.2	2	3.2743	0.2944	1826.87	1826	4	57.14286	2	R.FTRGDDILLSPCFQR.D	343	2	*
61	NA:ENSMUSG00000034450:ENSRNOG00000016648	GULO	gi|30520195|ref|NP_848862.1|	gi|30520195|ref|NP_848862.1|	gulonolactone (L-) oxidase [Mus musculus]	2	6	5.7	440	50478	8.2	MmNaOH-MM_liver_CNBrTi_210.1114.1114.2	2	3.2441	0.2183	1169.55	1169.4	1	94.44444	4	K.VVAHYPVEVR.F	333	2	*
62	ENSG00000145626:ENSMUSG00000072664:ENSRNOG00000025010	UGT3A1	gi|46402181|ref|NP_997099.1|	gi|46402181|ref|NP_997099.1|	UDP glycosyltransferases 3 family, polypeptide A1 [Mus musculus]	3	6	7.8	523	59742	7.2	MmNaOH-MM_liver_CNBrTi_102.3644.3644.2	2	2.9065	0.2943	1774.75	1775.1	1	53.571426	3	M.DWLPQIDLLAHPSIR.L	350	1	*
62	ENSG00000145626:ENSMUSG00000072664:ENSRNOG00000025010	UGT3A1	gi|46402181|ref|NP_997099.1|	gi|46402181|ref|NP_997099.1|	UDP glycosyltransferases 3 family, polypeptide A1 [Mus musculus]	3	6	7.8	523	59742	7.2	MmNaOH-MM_liver_CNBrTi_207.2054.2054.2	2	3.4642	0.2809	1396.12	1395.6	1	86.36364	2	K.LLYEGGDIPDFR.K	56	2	*
62	ENSG00000145626:ENSMUSG00000072664:ENSRNOG00000025010	UGT3A1	gi|46402181|ref|NP_997099.1|	gi|46402181|ref|NP_997099.1|	UDP glycosyltransferases 3 family, polypeptide A1 [Mus musculus]	3	6	7.8	523	59742	7.2	MmNaOH-MM_liver_CNBrTi_207.1400.1400.2	2	3.1559	0.1441	1451.03	1451.7	4	61.538464	1	R.VSQILQGGGHDVIK.L	42	2	*
63	ENSG00000110955:ENSMUSG00000025393:ENSRNOG00000002840	ATP5B	gi|31980648|ref|NP_058054.2|	gi|31980648|ref|NP_058054.2|	ATP synthase, H+ transporting mitochondrial F1 complex, beta sub	3	7	8.9	529	56301	5.3	MmNaOH-MM_liver_CNBrTi_202.2510.2510.2	2	3.2748	0.2216	1988.47	1989.2	7	41.666664	1	R.AIAELGIYPAVDPLDSTSR.I	388	2	*
63	ENSG00000110955:ENSMUSG00000025393:ENSRNOG00000002840	ATP5B	gi|31980648|ref|NP_058054.2|	gi|31980648|ref|NP_058054.2|	ATP synthase, H+ transporting mitochondrial F1 complex, beta sub	3	7	8.9	529	56301	5.3	MmNaOH-MM_liver_CNBrTi_206.2477.2477.2	2	4.4205	0.4451	1440.26	1440.7	1	79.16667	4	R.VALTGLTVAEYFR.D	282	2	*
63	ENSG00000110955:ENSMUSG00000025393:ENSRNOG00000002840	ATP5B	gi|31980648|ref|NP_058054.2|	gi|31980648|ref|NP_058054.2|	ATP synthase, H+ transporting mitochondrial F1 complex, beta sub	3	7	8.9	529	56301	5.3	MmNaOH-MM_liver_CNBrTi_101.1852.1852.2	2	3.1048	0.462	1650.78	1651.9	1	64.28571	2	R.LVLEVAQHLGESTVR.T	95	2	*
64	ENSG00000105699:ENSMUSG00000001247:ENSRNOG00000021053	LSR	gi|30794490|ref|NP_059101.1|	gi|30794490|ref|NP_059101.1|	lipolysis stimulated lipoprotein receptor [Mus musculus]	3	8	9.4	594	66108	6.5	MmNaOH-MM_liver_CNBrTi_206.1648.1648.2	2	3.2955	0.1385	1284.02	1284.4	1	75	2	R.PPYGYPGDFDR.T	295	2	*
64	ENSG00000105699:ENSMUSG00000001247:ENSRNOG00000021053	LSR	gi|30794490|ref|NP_059101.1|	gi|30794490|ref|NP_059101.1|	lipolysis stimulated lipoprotein receptor [Mus musculus]	3	8	9.4	594	66108	6.5	MmNaOH-MM_liver_CNBrTi_104.1434.1434.3	3	5.1049	0.3445	3508.23	3509.6	1	26.724138	2	R.VYREEEEEEEEGHYPPAPPPYSETDSQASR.E	548	2	*
64	ENSG00000105699:ENSMUSG00000001247:ENSRNOG00000021053	LSR	gi|30794490|ref|NP_059101.1|	gi|30794490|ref|NP_059101.1|	lipolysis stimulated lipoprotein receptor [Mus musculus]	3	8	9.4	594	66108	6.5	MmNaOH-MM_liver_CNBrTi_209.1321.1321.2	2	4.436	0.3624	1525.62	1525.7	1	67.85714	4	R.TSSVGGHSSQVPLLR.E	306	2	*
65	ENSG00000163399:ENSMUSG00000033161:ENSRNOG00000030019	ATP1A1	gi|21450277|ref|NP_659149.1|	gi|21450277|ref|NP_659149.1|	Na+/K+ -ATPase alpha 1 subunit [Mus musculus]	5	14	4.8	1023	112982	5.5	MmNaOH-MM_liver_CNBrTi_203.1577.1577.2	2	3.3515	0.1379	1264.53	1264.5	1	75	6	R.LNIPVNQVNPR.D	648	2	*
65	ENSG00000163399:ENSMUSG00000033161:ENSRNOG00000030019	ATP1A1	gi|21450277|ref|NP_659149.1|	gi|21450277|ref|NP_659149.1|	Na+/K+ -ATPase alpha 1 subunit [Mus musculus]	5	14	4.8	1023	112982	5.5	MmNaOH-MM_liver_CNBrTi_203.2719.2719.2	2	4.4614	0.3502	1753.65	1753.9	1	66.66667	2	K.DAFQNAYLELGGLGER.V	536	2	*
65	ENSG00000163399:ENSMUSG00000033161:ENSRNOG00000030019	ATP1A1	gi|21450277|ref|NP_659149.1|	gi|21450277|ref|NP_659149.1|	Na+/K+ -ATPase alpha 1 subunit [Mus musculus]	5	14	4.8	1023	112982	5.5	MmNaOH-MM_liver_CNBrTi_101.1719.1719.2	2	3.5329	0.4452	1519.91	1520.6	1	66.66667	1	R.SPDFTNENPLETR.N	228	2	*
65	ENSG00000163399:ENSMUSG00000033161:ENSRNOG00000030019	ATP1A1	gi|21450277|ref|NP_659149.1|	gi|21450277|ref|NP_659149.1|	Na+/K+ -ATPase alpha 1 subunit [Mus musculus]	5	14	4.8	1023	112982	5.5	MmNaOH-MM_liver_CNBrTi_211.2067.2067.1	1	2.5525	0.2204	1135.56	1136.3	5	68.75	2	R.YHTEIVFAR.T	684	2	*
65	ENSG00000163399:ENSMUSG00000033161:ENSRNOG00000030019	ATP1A1	gi|21450277|ref|NP_659149.1|	gi|21450277|ref|NP_659149.1|	Na+/K+ -ATPase alpha 1 subunit [Mus musculus]	5	14	4.8	1023	112982	5.5	MmNaOH-MM_liver_CNBrTi_211.2069.2069.2	2	2.3965	0.2532	1136.4	1136.3	7	81.25	1	R.YHTEIVFAR.T	684	2	*
65	ENSG00000163399:ENSMUSG00000033161:ENSRNOG00000030019	ATP1A1	gi|21450277|ref|NP_659149.1|	gi|21450277|ref|NP_659149.1|	Na+/K+ -ATPase alpha 1 subunit [Mus musculus]	5	14	4.8	1023	112982	5.5	MmNaOH-MM_liver_CNBrTi_103.1531.1531.1	1	2.2976	0.1444	1135.58	1136.3	4	62.5	2	R.YHTEIVFAR.T	684	2	*
66	ENSG00000198277:ENSMUSG00000029260:ENSRNOG00000029007	UGT2B	gi|23956406|ref|NP_705826.1|	gi|23956406|ref|NP_705826.1|	UDP glucuronosyltransferase 2 family, polypeptide B34 [Mus musc	4	8	8.6	532	60877	7.9	MmNaOH-MM_liver_CNBrTi_109.4508.4508.3	3	3.7317	0.1857	2933.88	2932.3	3	28.260868	1	R.TYWDLEFPHPVLPNFDFIGGLHCR.P	263	2	*
66	ENSG00000198277:ENSMUSG00000029260:ENSRNOG00000029007	UGT2B	gi|23956406|ref|NP_705826.1|	gi|23956406|ref|NP_705826.1|	UDP glucuronosyltransferase 2 family, polypeptide B34 [Mus musc	4	8	8.6	532	60877	7.9	MmNaOH-MM_liver_CNBrTi_204.0731.0731.2	2	2.4676	0.1996	1073.15	1073.2	8	72.22222	1	M.SSTDLHTALK.T	424	1	*
66	ENSG00000198277:ENSMUSG00000029260:ENSRNOG00000029007	UGT2B	gi|23956406|ref|NP_705826.1|	gi|23956406|ref|NP_705826.1|	UDP glucuronosyltransferase 2 family, polypeptide B34 [Mus musc	4	8	8.6	532	60877	7.9	MmNaOH-MM_liver_CNBrTi_109.4528.4528.2	2	2.9476	0.2204	2930.81	2932.3	1	32.608696	1	R.TYWDLEFPHPVLPNFDFIGGLHCR.P	263	2	*
66	ENSG00000198277:ENSMUSG00000029260:ENSRNOG00000029007	UGT2B	gi|23956406|ref|NP_705826.1|	gi|23956406|ref|NP_705826.1|	UDP glucuronosyltransferase 2 family, polypeptide B34 [Mus musc	4	8	8.6	532	60877	7.9	MmNaOH-MM_liver_CNBrTi_109.1457.1457.2	2	3.0211	0.1862	1455.64	1455.7	3	59.090908	5	R.IHHDQPVKPLDR.A	451	2	
67	ENSG00000115486:ENSMUSG00000053460:ENSRNOG00000012975	GGCX	gi|9790009|ref|NP_062776.1|	gi|9790009|ref|NP_062776.1|	gamma-glutamyl carboxylase [Mus musculus]	2	10	4.2	757	87195	8	MmNaOH-MM_liver_CNBrTi_101.2967.2967.2	2	2.951	0.2272	1546.91	1545.8	1	62.5	1	R.VDIVQAVWSPFQR.T	486	2	*
67	ENSG00000115486:ENSMUSG00000053460:ENSRNOG00000012975	GGCX	gi|9790009|ref|NP_062776.1|	gi|9790009|ref|NP_062776.1|	gamma-glutamyl carboxylase [Mus musculus]	2	10	4.2	757	87195	8	MmNaOH-MM_liver_CNBrTi_206.2643.2643.2	2	3.662	0.3632	1545.05	1545.8	1	62.5	4	R.VDIVQAVWSPFQR.T	486	2	*
67	ENSG00000115486:ENSMUSG00000053460:ENSRNOG00000012975	GGCX	gi|9790009|ref|NP_062776.1|	gi|9790009|ref|NP_062776.1|	gamma-glutamyl carboxylase [Mus musculus]	2	10	4.2	757	87195	8	MmNaOH-MM_liver_CNBrTi_202.2962.2962.2	2	4.6218	0.3813	2025.55	2025.2	1	63.88889	4	R.DGLTGELGYLNPGVFTQSR.R	417	2	*
67	ENSG00000115486:ENSMUSG00000053460:ENSRNOG00000012975	GGCX	gi|9790009|ref|NP_062776.1|	gi|9790009|ref|NP_062776.1|	gamma-glutamyl carboxylase [Mus musculus]	2	10	4.2	757	87195	8	MmNaOH-MM_liver_CNBrTi_101.3130.3130.2	2	3.5106	0.4099	2024.18	2025.2	1	47.22222	1	R.DGLTGELGYLNPGVFTQSR.R	417	2	*
68	ENSG00000107581:ENSMUSG00000024991:ENSRNOG00000010117	EIF3A	gi|46575903|ref|NP_034253.2|	gi|46575903|ref|NP_034253.2|	eukaryotic translation initiation factor 3, subunit 10 (theta) [Mus mu	5	13	5.1	1344	161950	6.8	MmNaOH-MM_liver_CNBrTi_101.3638.3638.2	2	2.1974	0.1806	1735.47	1736	6	50	1	R.LTSLVPFVDAFQLER.A	455	2	*
68	ENSG00000107581:ENSMUSG00000024991:ENSRNOG00000010117	EIF3A	gi|46575903|ref|NP_034253.2|	gi|46575903|ref|NP_034253.2|	eukaryotic translation initiation factor 3, subunit 10 (theta) [Mus mu	5	13	5.1	1344	161950	6.8	MmNaOH-MM_liver_CNBrTi_107.1980.1980.2	2	2.2671	0.1831	1507.5	1507.8	2	53.846157	1	R.RLATLLGLQAPPTR.I	354	2	*
68	ENSG00000107581:ENSMUSG00000024991:ENSRNOG00000010117	EIF3A	gi|46575903|ref|NP_034253.2|	gi|46575903|ref|NP_034253.2|	eukaryotic translation initiation factor 3, subunit 10 (theta) [Mus mu	5	13	5.1	1344	161950	6.8	MmNaOH-MM_liver_CNBrTi_101.3300.3300.2	2	2.7231	0.0982	1925.81	1924.2	2	50	1	R.LLQQVAQIYQSIEFSR.L	439	2	*
68	ENSG00000107581:ENSMUSG00000024991:ENSRNOG00000010117	EIF3A	gi|46575903|ref|NP_034253.2|	gi|46575903|ref|NP_034253.2|	eukaryotic translation initiation factor 3, subunit 10 (theta) [Mus mu	5	13	5.1	1344	161950	6.8	MmNaOH-MM_liver_CNBrTi_108.1027.1027.2	2	2.572	0.0826	993.46	993.2	5	81.25	3	R.RVPPPALSR.D	1293	2	*
68	ENSG00000107581:ENSMUSG00000024991:ENSRNOG00000010117	EIF3A	gi|46575903|ref|NP_034253.2|	gi|46575903|ref|NP_034253.2|	eukaryotic translation initiation factor 3, subunit 10 (theta) [Mus mu	5	13	5.1	1344	161950	6.8	MmNaOH-MM_liver_CNBrTi_203.2370.2370.2	2	2.7976	0.1601	1523.58	1523.9	5	53.846157	1	R.VLLATLSIPITPER.T	322	2	*
68	ENSG00000107581:ENSMUSG00000024991:ENSRNOG00000010117	EIF3A	gi|46575903|ref|NP_034253.2|	gi|46575903|ref|NP_034253.2|	eukaryotic translation initiation factor 3, subunit 10 (theta) [Mus mu	5	13	5.1	1344	161950	6.8	MmNaOH-MM_liver_CNBrTi_206.4707.4707.2	2	3.2018	0.2312	1737.63	1736	1	57.14286	6	R.LTSLVPFVDAFQLER.A	455	2	*
69	ENSG00000073060:ENSMUSG00000037936:ENSRNOG00000000981	SCARB1	gi|14389423|ref|NP_058021.1|	gi|14389423|ref|NP_058021.1|	scavenger receptor class B, member 1 [Mus musculus]	2	5	7.9	509	56754	8.1	MmNaOH-MM_liver_CNBrTi_101.0480.0480.2	2	2.2486	0.0849	1082.48	1082.2	4	81.25	1	R.VFEGIPTYR.F	292	2	*
69	ENSG00000073060:ENSMUSG00000037936:ENSRNOG00000000981	SCARB1	gi|14389423|ref|NP_058021.1|	gi|14389423|ref|NP_058021.1|	scavenger receptor class B, member 1 [Mus musculus]	2	5	7.9	509	56754	8.1	MmNaOH-MM_liver_CNBrTi_201.1576.1576.2	2	2.6971	0.2344	1082.03	1082.2	1	87.5	3	R.VFEGIPTYR.F	292	2	*
69	ENSG00000073060:ENSMUSG00000037936:ENSRNOG00000000981	SCARB1	gi|14389423|ref|NP_058021.1|	gi|14389423|ref|NP_058021.1|	scavenger receptor class B, member 1 [Mus musculus]	2	5	7.9	509	56754	8.1	MmNaOH-MM_liver_CNBrTi_109.3992.3992.3	3	3.7422	0.1356	3362.88	3363.8	1	21.666666	1	R.FGAPLFLSHPHFYNADPVLSEAVLGLNPNPK.E	336	2	*
70	ENSG00000147383:ENSMUSG00000031349:ENSRNOG00000017099	NSDHL	gi|31982437|ref|NP_035071.3|	gi|31982437|ref|NP_035071.3|	NAD(P) dependent steroid dehydrogenase-like [Mus musculus]	3	4	10.5	362	40686	7.9	MmNaOH-MM_liver_CNBrTi_207.2420.2420.2	2	2.2964	0.1973	1810.59	1810.2	9	40	1	M.VVSPLIQIQPTFTPIR.V	302	1	*
70	ENSG00000147383:ENSMUSG00000031349:ENSRNOG00000017099	NSDHL	gi|31982437|ref|NP_035071.3|	gi|31982437|ref|NP_035071.3|	NAD(P) dependent steroid dehydrogenase-like [Mus musculus]	3	4	10.5	362	40686	7.9	MmNaOH-MM_liver_CNBrTi_212.1467.1467.2	2	2.7398	0.1097	1125.45	1125.3	1	81.25	1	R.TVQSFHHLR.K	351	2	*
70	ENSG00000147383:ENSMUSG00000031349:ENSRNOG00000017099	NSDHL	gi|31982437|ref|NP_035071.3|	gi|31982437|ref|NP_035071.3|	NAD(P) dependent steroid dehydrogenase-like [Mus musculus]	3	4	10.5	362	40686	7.9	MmNaOH-MM_liver_CNBrTi_202.2614.2614.2	2	2.9823	0.1272	1422.54	1421.7	5	66.66667	1	R.DPQLVPILIDAAR.K	197	2	*
70	ENSG00000147383:ENSMUSG00000031349:ENSRNOG00000017099	NSDHL	gi|31982437|ref|NP_035071.3|	gi|31982437|ref|NP_035071.3|	NAD(P) dependent steroid dehydrogenase-like [Mus musculus]	3	4	10.5	362	40686	7.9	MmNaOH-MM_liver_CNBrTi_109.1848.1848.2	2	2.543	0.15	1125.15	1125.3	5	75	1	R.TVQSFHHLR.K	351	2	*
71	ENSG00000137414:ENSMUSG00000069237:ENSRNOG00000026120	FAM8A1	gi|85701696|ref|NP_001028364.1|	gi|85701696|ref|NP_001028364.1|	Autosomal Highly Conserved Protein [Mus musculus]	2	3	11.3	399	42295	6.7	MmNaOH-MM_liver_CNBrTi_103.1418.1418.3	3	4.9116	0.325	3428.57	3428.6	1	23.529411	2	R.SRPPEQDGSGGDHEPVPSEPGSPTTTVAATAAAPR.S	10	2	*
71	ENSG00000137414:ENSMUSG00000069237:ENSRNOG00000026120	FAM8A1	gi|85701696|ref|NP_001028364.1|	gi|85701696|ref|NP_001028364.1|	Autosomal Highly Conserved Protein [Mus musculus]	2	3	11.3	399	42295	6.7	MmNaOH-MM_liver_CNBrTi_211.2135.2135.2	2	2.2908	0.1695	1185.45	1185.4	5	72.22222	1	R.EYVIPSLAHR.F	226	2	*
72	ENSG00000118298:ENSMUSG00000038526:ENSRNOG00000023162	CA14	gi|6753264|ref|NP_035927.1|	gi|6753264|ref|NP_035927.1|	carbonic anhydrase 14 [Mus musculus]	1	3	3.6	337	37505	6.4	MmNaOH-MM_liver_CNBrTi_211.3435.3435.2	2	2.7597	0.1609	1582.63	1582.8	1	63.636364	2	R.ELFPQQLEQFFR.Y	200	2	*
72	ENSG00000118298:ENSMUSG00000038526:ENSRNOG00000023162	CA14	gi|6753264|ref|NP_035927.1|	gi|6753264|ref|NP_035927.1|	carbonic anhydrase 14 [Mus musculus]	1	3	3.6	337	37505	6.4	MmNaOH-MM_liver_CNBrTi_101.3556.3556.2	2	3.2201	0.2781	1584.07	1582.8	1	59.090908	1	R.ELFPQQLEQFFR.Y	200	2	*
73	ENSG00000145626:ENSMUSG00000049152:ENSRNOG00000025010	UGT3A1	gi|21450243|ref|NP_659094.1|	gi|21450243|ref|NP_659094.1|	UDP glycosyltransferases 3 family, polypeptide A2 [Mus musculus]	2	4	4.4	523	59673	7.5	MmNaOH-MM_liver_CNBrTi_108.1370.1370.2	2	3.0493	0.2455	1374.89	1375.5	1	70	2	R.HRLTEEITYGR.S	93	2	*
73	ENSG00000145626:ENSMUSG00000049152:ENSRNOG00000025010	UGT3A1	gi|21450243|ref|NP_659094.1|	gi|21450243|ref|NP_659094.1|	UDP glycosyltransferases 3 family, polypeptide A2 [Mus musculus]	2	4	4.4	523	59673	7.5	MmNaOH-MM_liver_CNBrTi_207.2040.2040.2	2	3.7408	0.2456	1439.67	1438.6	1	81.818184	2	K.LLYESANIPDFR.K	56	2	*
74	ENSG00000186205:ENSMUSG00000026621:ENSRNOG00000004101	MOSC1	gi|124486921|ref|NP_001074830.1|	gi|124486921|ref|NP_001074830.1|;gi|149246564|ref|XP_001	MOCO sulphurase C-terminal domain containing 1 [Mus musculus]	2	3	11.1	342	38126	8.5	MmNaOH-MM_liver_CNBrTi_105.4288.4288.3	3	3.5884	0.2787	3298.57	3299.7	1	24.107143	1	R.LCDPSEQALYGKLPIFGQYFALENPGTIR.V	304	2	
74	ENSG00000186205:ENSMUSG00000026621:ENSRNOG00000004101	MOSC1	gi|124486921|ref|NP_001074830.1|	gi|124486921|ref|NP_001074830.1|;gi|149246564|ref|XP_001	MOCO sulphurase C-terminal domain containing 1 [Mus musculus]	2	3	11.1	342	38126	8.5	MmNaOH-MM_liver_CNBrTi_210.0823.0823.2	2	2.4229	0.0934	1008.51	1009.2	1	93.75	2	R.VHGLEIQGR.D	154	2	
75	NA:ENSMUSG00000043716:ENSRNOG00000031912	LOC367195	gi|31981515|ref|NP_035421.2|	gi|31981515|ref|NP_035421.2|;gi|82957963|ref|XP_924795.1|	ribosomal protein L7 [Mus musculus]	3	3	11.5	270	31420	10.9	MmNaOH-MM_liver_CNBrTi_106.1192.1192.2	2	2.6016	0.093	2244.18	2245.4	2	36.842106	1	K.KTTHFVEGGDAGNREDQINR.L	245	2	
75	NA:ENSMUSG00000043716:ENSRNOG00000031912	LOC367195	gi|31981515|ref|NP_035421.2|	gi|31981515|ref|NP_035421.2|;gi|82957963|ref|XP_924795.1|	ribosomal protein L7 [Mus musculus]	3	3	11.5	270	31420	10.9	MmNaOH-MM_liver_CNBrTi_211.1165.1165.2	2	3.2147	0.124	2118.64	2117.2	1	47.22222	1	K.TTHFVEGGDAGNREDQINR.L	246	2	

rk	ORTHO_GROUPS	GENE_NAME	Locus	Proteins In Group	Description	Sequence Count	Spectrum Count	Coverage	Length	MW	pI	MatchID	Z	XCorr	DeltCN	M+H+	CalcM +H+	SpRk	Ion Proportion	Count	Sequence	Sequence Position	Tryptic	Unique
75	NA:ENSMUSG00000043716:ENSRNOG00000031912	LOC367195	gi|31981515|ref|NP_035421.2|	gi|31981515|ref|NP_035421.2|;gi|82957963|ref|XP_924795.1|	ribosomal protein L7 [Mus musculus]	3	3	11.5	270	31420	10.9	MmNaOH-MM_liver_CNBrTi_201.1668.1668.2	2	2.215	0.0915	1186.93	1187.4	2	65	1	R.IALTDNSLIAR.S	189	2	
76	ENSG00000162365:ENSMUSG00000028715:ENSRNOG00000030154	CYP4A22	gi|6681121|ref|NP_031848.1|	gi|6681121|ref|NP_031848.1|	cytochrome P450, family 4, subfamily a, polypeptide 14 [Mus musc	5	9	11.6	507	58720	8.8	MmNaOH-MM_liver_CNBrTi_202.2303.2303.2	2	3.2539	0.2478	1440.14	1439.6	1	77.27273	2	K.AVEDLNNLTFFR.L	217	2	*
76	ENSG00000162365:ENSMUSG00000028715:ENSRNOG00000030154	CYP4A22	gi|6681121|ref|NP_031848.1|	gi|6681121|ref|NP_031848.1|	cytochrome P450, family 4, subfamily a, polypeptide 14 [Mus musc	5	9	11.6	507	58720	8.8	MmNaOH-MM_liver_CNBrTi_101.1740.1740.1	1	2.6617	0.1141	1306.85	1305.4	6	59.090908	1	R.ELSSPVTFPDGR.S	389	2	
76	ENSG00000162365:ENSMUSG00000028715:ENSRNOG00000030154	CYP4A22	gi|6681121|ref|NP_031848.1|	gi|6681121|ref|NP_031848.1|	cytochrome P450, family 4, subfamily a, polypeptide 14 [Mus musc	5	9	11.6	507	58720	8.8	MmNaOH-MM_liver_CNBrTi_109.2190.2190.2	2	3.7723	0.3595	2158.15	2158.3	1	42.105263	1	R.FAPDSSHHSHAYLPFSGGSR.N	433	2	*
76	ENSG00000162365:ENSMUSG00000028715:ENSRNOG00000030154	CYP4A22	gi|6681121|ref|NP_031848.1|	gi|6681121|ref|NP_031848.1|	cytochrome P450, family 4, subfamily a, polypeptide 14 [Mus musc	5	9	11.6	507	58720	8.8	MmNaOH-MM_liver_CNBrTi_203.1733.1733.2	2	3.1809	0.3856	1305.29	1305.4	1	72.72727	4	R.ELSSPVTFPDGR.S	389	2	
76	ENSG00000162365:ENSMUSG00000028715:ENSRNOG00000030154	CYP4A22	gi|6681121|ref|NP_031848.1|	gi|6681121|ref|NP_031848.1|	cytochrome P450, family 4, subfamily a, polypeptide 14 [Mus musc	5	9	11.6	507	58720	8.8	MmNaOH-MM_liver_CNBrTi_108.2254.2254.2	2	3.6668	0.3408	1806.77	1806.2	1	64.28571	1	M.LTPAFHYDILKPYVK.N	143	1	
77	ENSG00000198848:ENSMUSG00000056973:ENSRNOG00000015519	CES3	gi|117553604|ref|NP_444430.2|	gi|117553604|ref|NP_444430.2|	carboxylesterase 3 [Mus musculus]	2	4	6.5	565	61788	6.6	MmNaOH-MM_liver_CNBrTi_203.3245.3245.2	2	2.6166	0.2992	1875.14	1875.2	7	43.75	2	K.ESYPFLPTVIDGVVLPK.A	313	2	*
77	ENSG00000198848:ENSMUSG00000056973:ENSRNOG00000015519	CES3	gi|117553604|ref|NP_444430.2|	gi|117553604|ref|NP_444430.2|	carboxylesterase 3 [Mus musculus]	2	4	6.5	565	61788	6.6	MmNaOH-MM_liver_CNBrTi_101.3360.3360.2	2	4.2208	0.382	2135.67	2136.4	1	57.894737	2	K.AVIGDHGDEIFSVFGSPFLK.D	461	2	*
78	ENSG00000205702:ENSMUSG00000061740:ENSRNOG00000032261	CYP2D7P1	gi|31981029|ref|NP_062797.2|	gi|31981029|ref|NP_062797.2|	cytochrome P450, family 2, subfamily d, polypeptide 22 [Mus musc	6	6	15.8	500	56494	6.9	MmNaOH-MM_liver_CNBrTi_202.2591.2591.2	2	3.7769	0.1794	1273.23	1273.5	2	80	1	R.DIELQGFLIPK.G	384	2	*
78	ENSG00000205702:ENSMUSG00000061740:ENSRNOG00000032261	CYP2D7P1	gi|31981029|ref|NP_062797.2|	gi|31981029|ref|NP_062797.2|	cytochrome P450, family 2, subfamily d, polypeptide 22 [Mus musc	6	6	15.8	500	56494	6.9	MmNaOH-MM_liver_CNBrTi_209.1365.1365.3	3	3.3945	0.0946	1428.01	1427.6	1	52.272724	1	M.PYTNAVIHEVQR.F	357	1	
78	ENSG00000205702:ENSMUSG00000061740:ENSRNOG00000032261	CYP2D7P1	gi|31981029|ref|NP_062797.2|	gi|31981029|ref|NP_062797.2|	cytochrome P450, family 2, subfamily d, polypeptide 22 [Mus musc	6	6	15.8	500	56494	6.9	MmNaOH-MM_liver_CNBrTi_209.0933.0933.2	2	2.689	0.0808	1159.5	1159.3	1	83.33333	1	R.RSCLGEPLAR.M	444	2	
78	ENSG00000205702:ENSMUSG00000061740:ENSRNOG00000032261	CYP2D7P1	gi|31981029|ref|NP_062797.2|	gi|31981029|ref|NP_062797.2|	cytochrome P450, family 2, subfamily d, polypeptide 22 [Mus musc	6	6	15.8	500	56494	6.9	MmNaOH-MM_liver_CNBrTi_101.1892.1892.2	2	2.3457	0.2252	1760.88	1762	5	46.42857	1	R.ALTTPCPYQLCALPR.-	486	2	*
78	ENSG00000205702:ENSMUSG00000061740:ENSRNOG00000032261	CYP2D7P1	gi|31981029|ref|NP_062797.2|	gi|31981029|ref|NP_062797.2|	cytochrome P450, family 2, subfamily d, polypeptide 22 [Mus musc	6	6	15.8	500	56494	6.9	MmNaOH-MM_liver_CNBrTi_101.1878.1878.2	2	3.3859	0.3859	2071.15	2071.3	1	52.77778	1	R.FSISVPDGQPQPSDHGVFR.A	467	2	*
78	ENSG00000205702:ENSMUSG00000061740:ENSRNOG00000032261	CYP2D7P1	gi|31981029|ref|NP_062797.2|	gi|31981029|ref|NP_062797.2|	cytochrome P450, family 2, subfamily d, polypeptide 22 [Mus musc	6	6	15.8	500	56494	6.9	MmNaOH-MM_liver_CNBrTi_101.3027.3027.2	2	4.1509	0.3634	1350.53	1351.5	1	86.36364	1	R.DLTDAFLAEVEK.A	273	2	
79	ENSG00000004864:ENSMUSG00000015112:ENSRNOG00000009957	SLC25A13	gi|7657583|ref|NP_056644.1|	gi|7657583|ref|NP_056644.1|	solute carrier family 25 (mitochondrial carrier, adenine nucleotide tr	1	6	3.3	676	74467	8.6	MmNaOH-MM_liver_CNBrTi_209.3215.3215.2	2	3.7585	0.4498	2120.05	2120.5	1	42.857143	5	R.FGLGSIAGAVGATAVYPIDLVK.T	333	2	*
79	ENSG00000004864:ENSMUSG00000015112:ENSRNOG00000009957	SLC25A13	gi|7657583|ref|NP_056644.1|	gi|7657583|ref|NP_056644.1|	solute carrier family 25 (mitochondrial carrier, adenine nucleotide tr	1	6	3.3	676	74467	8.6	MmNaOH-MM_liver_CNBrTi_101.4023.4023.2	2	4.0815	0.3521	2120.33	2120.5	1	45.238094	1	R.FGLGSIAGAVGATAVYPIDLVK.T	333	2	*
80	ENSG00000163902:ENSMUSG00000030062:NA	RPN1	gi|31543605|ref|NP_598694.2|	gi|31543605|ref|NP_598694.2|	ribophorin I [Mus musculus]	3	5	4.9	608	68527	6.5	MmNaOH-MM_liver_CNBrTi_202.2418.2418.2	2	3.4914	0.2248	1650.81	1648.9	4	57.14286	1	R.ASSFVLALEPELESR.L	67	2	*
80	ENSG00000163902:ENSMUSG00000030062:NA	RPN1	gi|31543605|ref|NP_598694.2|	gi|31543605|ref|NP_598694.2|	ribophorin I [Mus musculus]	3	5	4.9	608	68527	6.5	MmNaOH-MM_liver_CNBrTi_208.1492.1492.2	2	3.1531	0.3321	1785.39	1785.9	1	57.14286	2	R.YDYQRQPDSGISSIR.S	265	2	*
80	ENSG00000163902:ENSMUSG00000030062:NA	RPN1	gi|31543605|ref|NP_598694.2|	gi|31543605|ref|NP_598694.2|	ribophorin I [Mus musculus]	3	5	4.9	608	68527	6.5	MmNaOH-MM_liver_CNBrTi_101.2463.2463.2	2	2.949	0.2401	1649.64	1648.9	1	53.571426	1	R.ASSFVLALEPELESR.L	67	2	*
80	ENSG00000163902:ENSMUSG00000030062:NA	RPN1	gi|31543605|ref|NP_598694.2|	gi|31543605|ref|NP_598694.2|	ribophorin I [Mus musculus]	3	5	4.9	608	68527	6.5	MmNaOH-MM_liver_CNBrTi_209.1450.1450.3	3	3.2657	0.2491	1787.03	1785.9	2	41.07143	1	R.YDYQRQPDSGISSIR.S	265	2	*
81	ENSG00000174444:ENSMUSG00000032399:ENSRNOG00000033834	RPL4	gi|30794450|ref|NP_077174.1|	gi|30794450|ref|NP_077174.1|	ribosomal protein L4 [Mus musculus]	2	3	8.1	419	47154	11	MmNaOH-MM_liver_CNBrTi_101.1672.1672.2	2	4.1097	0.3472	2334.65	2333.5	1	40.476192	1	R.QPYAVSELAGHQTSAESWGTGR.A	50	2	*
81	ENSG00000174444:ENSMUSG00000032399:ENSRNOG00000033834	RPL4	gi|30794450|ref|NP_077174.1|	gi|30794450|ref|NP_077174.1|	ribosomal protein L4 [Mus musculus]	2	3	8.1	419	47154	11	MmNaOH-MM_liver_CNBrTi_207.1162.1162.2	2	3.6883	0.3473	1190.34	1188.4	1	81.818184	2	K.KLEAAATALATK.S	353	2	*
82	ENSG00000186115:ENSMUSG00000024055:ENSRNOG00000034157	CYP4F2	gi|20373155|ref|NP_570952.1|	gi|20373155|ref|NP_570952.1|	cytochrome P450, family 4, subfamily f, polypeptide 13 [Mus musc	2	4	6.3	523	59823	7.7	MmNaOH-MM_liver_CNBrTi_108.4822.4822.2	2	3.0614	0.1561	2224.3	2224.5	2	36.842106	1	M.FGGHDTTTSALSWILYNLAR.H	326	1	*
82	ENSG00000186115:ENSMUSG00000024055:ENSRNOG00000034157	CYP4F2	gi|20373155|ref|NP_570952.1|	gi|20373155|ref|NP_570952.1|	cytochrome P450, family 4, subfamily f, polypeptide 13 [Mus musc	2	4	6.3	523	59823	7.7	MmNaOH-MM_liver_CNBrTi_209.2117.2117.2	2	3.327	0.1969	1364.23	1364.6	1	66.66667	3	R.SPLAFIPFSAGTR.N	453	2	*
83	ENSG00000117791:ENSMUSG00000073481:ENSRNOG00000037850	MOSC2	gi|19526848|ref|NP_598445.1|	gi|19526848|ref|NP_598445.1|	MOCO sulphurase C-terminal domain containing 2 [Mus musculus]	2	2	12.7	338	38194	8.7	MmNaOH-MM_liver_CNBrTi_103.4148.4148.3	3	3.9879	0.3159	4046.32	4045.4	1	22.058825	1	K.LYPSESYLQNYEVAYPDCSPVHLISEASLVDLNTR.L	194	2	*
83	ENSG00000117791:ENSMUSG00000073481:ENSRNOG00000037850	MOSC2	gi|19526848|ref|NP_598445.1|	gi|19526848|ref|NP_598445.1|	MOCO sulphurase C-terminal domain containing 2 [Mus musculus]	2	2	12.7	338	38194	8.7	MmNaOH-MM_liver_CNBrTi_205.1118.1118.2	2	2.4406	0.1185	838.05	838	9	92.85714	1	R.LGLPGQPR.S	12	2	*
84	ENSG00000107897:ENSMUSG00000026781:ENSRNOG00000017642	ACBD5	gi|27229192|ref|NP_083069.1|	gi|27229192|ref|NP_083069.1|	acyl-Coenzyme A binding domain containing 5 [Mus musculus]	2	3	4.7	473	52469	5.3	MmNaOH-MM_liver_CNBrTi_109.2042.2042.2	2	2.8859	0.1652	1404.65	1404.6	4	58.333332	1	R.VGNRIPHLSEGPK.G	352	2	*
84	ENSG00000107897:ENSMUSG00000026781:ENSRNOG00000017642	ACBD5	gi|27229192|ref|NP_083069.1|	gi|27229192|ref|NP_083069.1|	acyl-Coenzyme A binding domain containing 5 [Mus musculus]	2	3	4.7	473	52469	5.3	MmNaOH-MM_liver_CNBrTi_209.1885.1885.2	2	3.1608	0.3494	1044.97	1045.2	9	81.25	2	R.PGFWDPIGR.Y	55	2	
85	ENSG00000198277:ENSMUSG00000035836:ENSRNOG00000001990	UGT2B	gi|22779901|ref|NP_690024.1|	gi|22779901|ref|NP_690024.1|	UDP glucuronosyltransferase 2 family, polypeptide B1 [Mus muscu	4	4	8.5	529	60157	8.4	MmNaOH-MM_liver_CNBrTi_206.2352.2352.2	2	2.5633	0.247	1472.27	1472.6	9	59.090908	1	K.SWNQFYSDVLGR.P	232	2	*
85	ENSG00000198277:ENSMUSG00000035836:ENSRNOG00000001990	UGT2B	gi|22779901|ref|NP_690024.1|	gi|22779901|ref|NP_690024.1|	UDP glucuronosyltransferase 2 family, polypeptide B1 [Mus muscu	4	4	8.5	529	60157	8.4	MmNaOH-MM_liver_CNBrTi_101.1971.1971.1	1	2.1183	0.1395	1098.79	1099.3	4	75	1	K.IILDELVQR.G	41	2	
85	ENSG00000198277:ENSMUSG00000035836:ENSRNOG00000001990	UGT2B	gi|22779901|ref|NP_690024.1|	gi|22779901|ref|NP_690024.1|	UDP glucuronosyltransferase 2 family, polypeptide B1 [Mus muscu	4	4	8.5	529	60157	8.4	MmNaOH-MM_liver_CNBrTi_108.3559.3559.2	2	2.3408	0.1014	1315.94	1314.6	5	66.66667	1	R.AVFWIEYVMR.N	461	2	*
85	ENSG00000198277:ENSMUSG00000035836:ENSRNOG00000001990	UGT2B	gi|22779901|ref|NP_690024.1|	gi|22779901|ref|NP_690024.1|	UDP glucuronosyltransferase 2 family, polypeptide B1 [Mus muscu	4	4	8.5	529	60157	8.4	MmNaOH-MM_liver_CNBrTi_201.1940.1940.2	2	3.0527	0.156	1410.55	1410.7	2	69.230774	1	K.ANVVASALAQIPQK.V	322	2	*
86	ENSG00000204267:ENSMUSG00000024339:ENSRNOG00000000455	TAP2	gi|46399206|ref|NP_035660.2|	gi|46399206|ref|NP_035660.2|	transporter 2, ATP-binding cassette, sub-family B [Mus musculus]	2	3	4.4	702	77464	7.4	MmNaOH-MM_liver_CNBrTi_211.2177.2177.2	2	4.1094	0.3385	1529.57	1529.7	1	79.16667	1	R.DGQDVYAHLVQQR.L	687	2	*
86	ENSG00000204267:ENSMUSG00000024339:ENSRNOG00000000455	TAP2	gi|46399206|ref|NP_035660.2|	gi|46399206|ref|NP_035660.2|	transporter 2, ATP-binding cassette, sub-family B [Mus musculus]	2	3	4.4	702	77464	7.4	MmNaOH-MM_liver_CNBrTi_101.0464.0464.2	2	2.7519	0.1665	1529.46	1529.7	1	62.5	1	R.DGQDVYAHLVQQR.L	687	2	*
86	ENSG00000204267:ENSMUSG00000024339:ENSRNOG00000000455	TAP2	gi|46399206|ref|NP_035660.2|	gi|46399206|ref|NP_035660.2|	transporter 2, ATP-binding cassette, sub-family B [Mus musculus]	2	3	4.4	702	77464	7.4	MmNaOH-MM_liver_CNBrTi_102.4550.4550.2	2	3.7459	0.4212	2072.37	2072.4	1	52.941177	1	R.GGLLSFLLYQEEVGQYVR.N	406	2	*
87	ENSG00000152234:ENSMUSG00000025428:ENSRNOG00000017032	ATP5A1	gi|6680748|ref|NP_031531.1|	gi|6680748|ref|NP_031531.1|	ATP synthase, H+ transporting, mitochondrial F1 complex, alpha s	2	3	4	553	59753	9.2	MmNaOH-MM_liver_CNBrTi_205.3739.3739.3	3	4.7617	0.3242	2339.21	2339.6	2	35.714287	1	R.EVAAFAQFGSDLDAATQQLLSR.G	442	2	*
87	ENSG00000152234:ENSMUSG00000025428:ENSRNOG00000017032	ATP5A1	gi|6680748|ref|NP_031531.1|	gi|6680748|ref|NP_031531.1|	ATP synthase, H+ transporting, mitochondrial F1 complex, alpha s	2	3	4	553	59753	9.2	MmNaOH-MM_liver_CNBrTi_205.3738.3738.2	2	5.8389	0.4897	2339.67	2339.6	1	64.28571	1	R.EVAAFAQFGSDLDAATQQLLSR.G	442	2	*
87	ENSG00000152234:ENSMUSG00000025428:ENSRNOG00000017032	ATP5A1	gi|6680748|ref|NP_031531.1|	gi|6680748|ref|NP_031531.1|	ATP synthase, H+ transporting, mitochondrial F1 complex, alpha s	2	3	4	553	59753	9.2	MmNaOH-MM_liver_CNBrTi_101.4562.4562.2	2	5.7397	0.4279	2338.75	2339.6	1	54.761906	1	R.EVAAFAQFGSDLDAATQQLLSR.G	442	2	*
88	ENSG00000175003:ENSMUSG00000023829:ENSRNOG00000016337	SLC22A1	gi|31982010|ref|NP_033228.2|	gi|31982010|ref|NP_033228.2|	solute carrier family 22 member 1 [Mus musculus]	2	3	4.5	556	61521	6.7	MmNaOH-MM_liver_CNBrTi_101.2300.2300.2	2	2.6953	0.2109	1700.3	1698.9	1	56.666668	1	K.GVALPETIEEAENLGR.R	519	2	*
88	ENSG00000175003:ENSMUSG00000023829:ENSRNOG00000016337	SLC22A1	gi|31982010|ref|NP_033228.2|	gi|31982010|ref|NP_033228.2|	solute carrier family 22 member 1 [Mus musculus]	2	3	4.5	556	61521	6.7	MmNaOH-MM_liver_CNBrTi_203.2145.2145.2	2	3.1495	0.2595	1040.31	1040.2	1	93.75	2	R.SPSFADLFR.T	332	2	*
89	ENSG00000134824:ENSMUSG00000024665:ENSRNOG00000020440	FADS2	gi|9790071|ref|NP_062673.1|	gi|9790071|ref|NP_062673.1|	fatty acid desaturase 2 [Mus musculus]	1	2	3.4	444	52387	8.8	MmNaOH-MM_liver_CNBrTi_101.0015.0015.2	2	3.8786	0.3855	1638.43	1638.7	1	67.85714	1	R.VIGHYSGEDATDAFR.A	59	2	*
89	ENSG00000134824:ENSMUSG00000024665:ENSRNOG00000020440	FADS2	gi|9790071|ref|NP_062673.1|	gi|9790071|ref|NP_062673.1|	fatty acid desaturase 2 [Mus musculus]	1	2	3.4	444	52387	8.8	MmNaOH-MM_liver_CNBrTi_212.1932.1932.2	2	3.5322	0.3749	1639.66	1638.7	1	67.85714	1	R.VIGHYSGEDATDAFR.A	59	2	*
90	ENSG00000060566:ENSMUSG00000035041:ENSRNOG00000032202	CREB3L3	gi|21703728|ref|NP_663340.1|	gi|21703728|ref|NP_663340.1|	cAMP responsive element binding protein 3-like 3 [Mus musculus]	1	2	3.5	479	52145	5.1	MmNaOH-MM_liver_CNBrTi_101.4050.4050.2	2	3.595	0.2525	1826.69	1826.1	1	46.875	1	R.ATLLDWVASEPLLSPGR.V	433	2	*
90	ENSG00000060566:ENSMUSG00000035041:ENSRNOG00000032202	CREB3L3	gi|21703728|ref|NP_663340.1|	gi|21703728|ref|NP_663340.1|	cAMP responsive element binding protein 3-like 3 [Mus musculus]	1	2	3.5	479	52145	5.1	MmNaOH-MM_liver_CNBrTi_207.3360.3360.2	2	3.8415	0.2733	1825.5	1826.1	1	50	1	R.ATLLDWVASEPLLSPGR.V	433	2	*
91	ENSG00000110719:ENSMUSG00000001750:ENSRNOG00000017220	TCIRG1	gi|31980624|ref|NP_058617.2|	gi|31980624|ref|NP_058617.2|	T-cell, immune regulator 1 [Mus musculus]	2	3	5.6	834	93448	6.3	MmNaOH-MM_liver_CNBrTi_209.1793.1793.2	2	2.597	0.1486	1756.5	1756.1	2	44.11765	1	R.AGLTLAPPEGTLPAPPPR.D	75	2	*
91	ENSG00000110719:ENSMUSG00000001750:ENSRNOG00000017220	TCIRG1	gi|31980624|ref|NP_058617.2|	gi|31980624|ref|NP_058617.2|	T-cell, immune regulator 1 [Mus musculus]	2	3	5.6	834	93448	6.3	MmNaOH-MM_liver_CNBrTi_106.0302.0302.3	3	4.7355	0.3438	3373.66	3373.7	1	26.785713	2	R.TLQQLQQQSQELQEVLGETDRFLSQVLGR.V	257	2	*
92	ENSG00000185000:ENSMUSG00000022555:ENSRNOG00000028711	LOC727765	gi|6753632|ref|NP_034176.1|	gi|6753632|ref|NP_034176.1|	diacylglycerol O-acyltransferase 1 [Mus musculus]	2	2	9	498	56790	9.4	MmNaOH-MM_liver_CNBrTi_109.4352.4352.2	2	3.6606	0.3327	2285.57	2284.7	1	39.473686	1	R.TGVFLTSAFFHEYLVSVPLR.M	416	2	*
92	ENSG00000185000:ENSMUSG00000022555:ENSRNOG00000028711	LOC727765	gi|6753632|ref|NP_034176.1|	gi|6753632|ref|NP_034176.1|	diacylglycerol O-acyltransferase 1 [Mus musculus]	2	2	9	498	56790	9.4	MmNaOH-MM_liver_CNBrTi_208.1456.1456.2	2	5.3525	0.4557	2284	2283.5	1	52.083332	1	R.DAAVSPDLGAGGDAPAPAPAPAHTR.D	36	2	*
93	ENSG00000091262:ENSMUSG00000030834:ENSRNOG00000028781	ABCC6	gi|9055156|ref|NP_061265.1|	gi|9055156|ref|NP_061265.1|	ATP-binding cassette, sub-family C, member 6 [Mus musculus]	2	8	2.1	1498	164787	8.2	MmNaOH-MM_liver_CNBrTi_109.2288.2288.2	2	2.9595	0.2682	1713.07	1714	5	46.42857	1	R.ILVTHTLHVLPQADR.I	806	2	*
93	ENSG00000091262:ENSMUSG00000030834:ENSRNOG00000028781	ABCC6	gi|9055156|ref|NP_061265.1|	gi|9055156|ref|NP_061265.1|	ATP-binding cassette, sub-family C, member 6 [Mus musculus]	2	8	2.1	1498	164787	8.2	MmNaOH-MM_liver_CNBrTi_208.2605.2605.2	2	3.2691	0.2076	1767.69	1767.1	1	56.666668	7	R.ITIIPQDPVLFPGSLR.M	1337	2	*
94	ENSG00000184743:ENSMUSG00000024759:ENSRNOG00000021203	ATLA3	gi|31559920|ref|NP_666203.2|	gi|31559920|ref|NP_666203.2|	hypothetical protein LOC109168 [Mus musculus]	2	2	4.3	541	60515	6.1	MmNaOH-MM_liver_CNBrTi_101.1303.1303.2	2	2.2747	0.1552	1336.08	1336.6	5	54.545456	1	R.ALASVLLQDHIR.D	45	2	*
94	ENSG00000184743:ENSMUSG00000024759:ENSRNOG00000021203	ATLA3	gi|31559920|ref|NP_666203.2|	gi|31559920|ref|NP_666203.2|	hypothetical protein LOC109168 [Mus musculus]	2	2	4.3	541	60515	6.1	MmNaOH-MM_liver_CNBrTi_207.1218.1218.2	2	2.5154	0.1643	1296.08	1297.5	2	75	1	K.IYQGEDLPHPK.S	331	2	
95	ENSG00000147649:ENSMUSG00000022255:ENSRNOG00000006870	MTDH	gi|31982233|ref|NP_080278.3|	gi|31982233|ref|NP_080278.3|	LYRIC [Mus musculus]	2	2	2.2	579	63846	9.3	MmNaOH-MM_liver_CNBrTi_208.2621.2621.2	2	2.6033	0.2617	1206.12	1204.5	3	65	1	R.ELLSVGLGFLR.T	23	2	*
95	ENSG00000147649:ENSMUSG00000022255:ENSRNOG00000006870	MTDH	gi|31982233|ref|NP_080278.3|	gi|31982233|ref|NP_080278.3|	LYRIC [Mus musculus]	2	2	2.2	579	63846	9.3	MmNaOH-MM_liver_CNBrTi_108.3374.3374.2	2	3.0334	0.2287	1474.56	1473.8	1	66.66667	1	R.LRELLSVGLGFLR.T	21	2	*
96	ENSG00000023839:ENSMUSG00000025194:NA	ABCC2	gi|116063566|ref|NP_038834.2|	gi|116063566|ref|NP_038834.2|	ATP-binding cassette, sub-family C, member 2 [Mus musculus]	2	5	2.7	1543	173670	8.6	MmNaOH-MM_liver_CNBrTi_105.5547.5547.3	3	4.2052	0.3207	2591.56	2591	1	34.375	2	R.ILESAGGQIIIDGIDIASIGLHDLR.G	1348	2	*
96	ENSG00000023839:ENSMUSG00000025194:NA	ABCC2	gi|116063566|ref|NP_038834.2|	gi|116063566|ref|NP_038834.2|	ATP-binding cassette, sub-family C, member 2 [Mus musculus]	2	5	2.7	1543	173670	8.6	MmNaOH-MM_liver_CNBrTi_206.2700.2700.2	2	2.717	0.3628	1797.57	1798.1	1	56.666668	3	R.LTIIPQDPILFSGNLR.M	1375	2	*
97	ENSG00000204319:ENSMUSG00000073418:ENSRNOG00000000443	C4A	gi|149269273|ref|XP_001475202.1|	gi|149269273|ref|XP_001475202.1|;gi|6753226|ref|NP_03391	PREDICTED: similar to complement C4 [Mus musculus]	3	3	4.2	1539	170382	7.5	MmNaOH-MM_liver_CNBrTi_110.6150.6150.3	3	4.5683	0.3145	3003.44	3002.5	4	24.038462	1	R.SPTEPVPQAPALWIETTAYALLHLLLR.E	1245	2	
97	ENSG00000204319:ENSMUSG00000073418:ENSRNOG00000000443	C4A	gi|149269273|ref|XP_001475202.1|	gi|149269273|ref|XP_001475202.1|;gi|6753226|ref|NP_03391	PREDICTED: similar to complement C4 [Mus musculus]	3	3	4.2	1539	170382	7.5	MmNaOH-MM_liver_CNBrTi_202.2842.2842.2	2	2.9655	0.2698	2416.48	2416.6	1	40.909092	1	R.TLEIPGSSDPNIVPDGDFSSLVR.V	953	2	
97	ENSG00000204319:ENSMUSG00000073418:ENSRNOG00000000443	C4A	gi|149269273|ref|XP_001475202.1|	gi|149269273|ref|XP_001475202.1|;gi|6753226|ref|NP_03391	PREDICTED: similar to complement C4 [Mus musculus]	3	3	4.2	1539	170382	7.5	MmNaOH-MM_liver_CNBrTi_110.2426.2426.2	2	3.3482	0.2404	1773.8	1773.1	1	50	1	R.RAPHIQLVAQSPWLR.N	102	2	
98	ENSG00000035403:ENSMUSG00000021823:ENSRNOG00000010765	VCL	gi|31543942|ref|NP_033528.3|	gi|31543942|ref|NP_033528.3|	vinculin [Mus musculus]	1	2	2	1066	116717	6	MmNaOH-MM_liver_CNBrTi_101.5219.5219.2	2	3.3158	0.4705	2077.61	2077.4	1	52.499996	1	K.AIPDLTAPVAAVQAAVSNLVR.V	36	2	*
98	ENSG00000035403:ENSMUSG00000021823:ENSRNOG00000010765	VCL	gi|31543942|ref|NP_033528.3|	gi|31543942|ref|NP_033528.3|	vinculin [Mus musculus]	1	2	2	1066	116717	6	MmNaOH-MM_liver_CNBrTi_207.3976.3976.2	2	4.0737	0.384	2078.14	2077.4	1	55	1	K.AIPDLTAPVAAVQAAVSNLVR.V	36	2	*
99	ENSG00000196576:ENSMUSG00000036606:ENSRNOG00000007133	PLXNB2	gi|94398834|ref|XP_001003435.1|	gi|94398834|ref|XP_001003435.1|	PREDICTED: plexin B2 isoform 14 [Mus musculus]	2	3	2.1	1842	206229	5.9	MmNaOH-MM_liver_CNBrTi_105.4403.4403.3	3	3.1352	0.1083	3078.02	3078.4	2	23.148148	1	R.LSVSPLPTLTEDDELLCLFGDSPPHPAR.V	541	2	*
99	ENSG00000196576:ENSMUSG00000036606:ENSRNOG00000007133	PLXNB2	gi|94398834|ref|XP_001003435.1|	gi|94398834|ref|XP_001003435.1|	PREDICTED: plexin B2 isoform 14 [Mus musculus]	2	3	2.1	1842	206229	5.9	MmNaOH-MM_liver_CNBrTi_211.2145.2145.2	2	3.7383	0.2993	1152.18	1152.3	1	85	2	R.DGLVATAVLHR.G	379	2	*
100	NA:ENSMUSG00000041828:ENSRNOG00000004147	ABCA8A	gi|23346593|ref|NP_694785.1|	gi|23346593|ref|NP_694785.1|	ATP-binding cassette, sub-family A (ABC1), member 8a [Mus mus	2	2	2.7	1620	184110	7.2	MmNaOH-MM_liver_CNBrTi_206.3049.3049.2	2	3.279	0.0827	1576.45	1575.8	2	76.92308	1	R.FAEVEQLVSLLNGR.C	816	2	*
100	NA:ENSMUSG00000041828:ENSRNOG00000004147	ABCA8A	gi|23346593|ref|NP_694785.1|	gi|23346593|ref|NP_694785.1|	ATP-binding cassette, sub-family A (ABC1), member 8a [Mus mus	2	2	2.7	1620	184110	7.2	MmNaOH-MM_liver_CNBrTi_107.5768.5768.3	3	3.4358	0.1691	3167.9	3168.6	5	25	1	R.LNCFPVLVDIVSNGLLGLFAPSAHIQTDR.S	977	2	*
101	ENSG00000123384:ENSMUSG00000040249:ENSRNOG00000025053	LRP1	gi|124494256|ref|NP_032538.2|	gi|124494256|ref|NP_032538.2|	low density lipoprotein receptor-related protein 1 [Mus musculus]	3	3	0.7	4545	504775	5.4	MmNaOH-MM_liver_CNBrTi_210.1379.1379.2	2	2.7403	0.144	1323.2	1323.5	1	68.181816	1	R.TTLLAGDIEHPR.A	1380	2	*
101	ENSG00000123384:ENSMUSG00000040249:ENSRNOG00000025053	LRP1	gi|124494256|ref|NP_032538.2|	gi|124494256|ref|NP_032538.2|	low density lipoprotein receptor-related protein 1 [Mus musculus]	3	3	0.7	4545	504775	5.4	MmNaOH-MM_liver_CNBrTi_108.1694.1694.3	3	3.5227	0.25	2490.12	2490.7	3	30.952381	1	R.SLFPGHPHSAYEQTFQGDESVR.I	3881	2	*
101	ENSG00000123384:ENSMUSG00000040249:ENSRNOG00000025053	LRP1	gi|124494256|ref|NP_032538.2|	gi|124494256|ref|NP_032538.2|	low density lipoprotein receptor-related protein 1 [Mus musculus]	3	3	0.7	4545	504775	5.4	MmNaOH-MM_liver_CNBrTi_108.1696.1696.2	2	3.2786	0.3176	2489.89	2490.7	1	42.857143	1	R.SLFPGHPHSAYEQTFQGDESVR.I	3881	2	*
102	ENSG00000103018:ENSMUSG00000031924:ENSRNOG00000011142	CYB5B	gi|149275191|ref|XP_001473825.1|	gi|149275191|ref|XP_001473825.1|;gi|31542438|ref|NP_0798	PREDICTED: hypothetical protein [Mus musculus]	1	65	23.3	146	16329	4.9	MmNaOH-MM_liver_CNBrTi_104.3030.3030.3	3	6.8805	0.4969	3597.42	3598.8	1	31.818182	65	R.FLSEHPGGEEVLLEQAGADATESFEDVGHSPDAR.E	51	2	
103	ENSG00000138760:ENSMUSG00000029426:ENSRNOG00000002225	SCARB2	gi|6680878|ref|NP_031670.1|	gi|6680878|ref|NP_031670.1|	scavenger receptor class B, member 2 [Mus musculus]	3	24	7.9	478	54044	5.1	MmNaOH-MM_liver_CNBrTi_105.0166.0166.2	2	5.6236	0.4372	2110.01	2107.6	1	66.66667	16	R.TINIPLLTVVDLAQLTLLR.E	135	2	*
103	ENSG00000138760:ENSMUSG00000029426:ENSRNOG00000002225	SCARB2	gi|6680878|ref|NP_031670.1|	gi|6680878|ref|NP_031670.1|	scavenger receptor class B, member 2 [Mus musculus]	3	24	7.9	478	54044	5.1	MmNaOH-MM_liver_CNBrTi_105.0264.0264.3	3	5.387	0.3601	2107.83	2107.6	1	45.833336	6	R.TINIPLLTVVDLAQLTLLR.E	135	2	*
103	ENSG00000138760:ENSMUSG00000029426:ENSRNOG00000002225	SCARB2	gi|6680878|ref|NP_031670.1|	gi|6680878|ref|NP_031670.1|	scavenger receptor class B, member 2 [Mus musculus]	3	24	7.9	478	54044	5.1	MmNaOH-MM_liver_CNBrTi_105.3259.3259.2	2	4.0673	0.4269	2137.68	2138.4	1	55.555557	2	R.SVHITFSSFENVEGLPAFR.Y	276	2	*
104	ENSG00000099797:ENSMUSG00000031708:ENSRNOG00000018935	GPSN2	gi|19923070|ref|NP_598879.1|	gi|19923070|ref|NP_598879.1|	glycoprotein, synaptic 2 [Mus musculus]	1	15	2.9	308	36090	9.6	MmNaOH-MM_liver_CNBrTi_101.0802.0802.2	2	3.4349	0.2636	1128.43	1128.4	3	87.5	15	R.LLETLFVHR.F	142	2	*
105	ENSG00000162365:ENSMUSG00000078597:ENSRNOG00000029919	CYP4A22	gi|86198314|ref|NP_758510.2|	gi|86198314|ref|NP_758510.2|	cytochrome P450, family 4, subfamily a family [Mus musculus]	8	28	16.1	508	58309	8.9	MmNaOH-MM_liver_CNBrTi_109.3136.3136.3	3	3.9161	0.2791	2713.34	2711	1	31.818182	1	M.LSFYGLHHNPTVWPNPEVFDPSR.F	411	1	
105	ENSG00000162365:ENSMUSG00000078597:ENSRNOG00000029919	CYP4A22	gi|86198314|ref|NP_758510.2|	gi|86198314|ref|NP_758510.2|	cytochrome P450, family 4, subfamily a family [Mus musculus]	8	28	16.1	508	58309	8.9	MmNaOH-MM_liver_CNBrTi_103.3482.3482.2	2	4.5746	0.327	1684.76	1684.9	1	80.769226	14	R.GLLLLDGQTWFQHR.R	128	2	*
105	ENSG00000162365:ENSMUSG00000078597:ENSRNOG00000029919	CYP4A22	gi|86198314|ref|NP_758510.2|	gi|86198314|ref|NP_758510.2|	cytochrome P450, family 4, subfamily a family [Mus musculus]	8	28	16.1	508	58309	8.9	MmNaOH-MM_liver_CNBrTi_101.1740.1740.1	1	2.6617	0.1141	1306.85	1305.4	6	59.090908	1	R.ELSSPVTFPDGR.S	390	2	
105	ENSG00000162365:ENSMUSG00000078597:ENSRNOG00000029919	CYP4A22	gi|86198314|ref|NP_758510.2|	gi|86198314|ref|NP_758510.2|	cytochrome P450, family 4, subfamily a family [Mus musculus]	8	28	16.1	508	58309	8.9	MmNaOH-MM_liver_CNBrTi_203.1733.1733.2	2	3.1809	0.3856	1305.29	1305.4	1	72.72727	4	R.ELSSPVTFPDGR.S	390	2	
105	ENSG00000162365:ENSMUSG00000078597:ENSRNOG00000029919	CYP4A22	gi|86198314|ref|NP_758510.2|	gi|86198314|ref|NP_758510.2|	cytochrome P450, family 4, subfamily a family [Mus musculus]	8	28	16.1	508	58309	8.9	MmNaOH-MM_liver_CNBrTi_109.2253.2253.1	1	2.568	0.3183	1399.66	1400.5	1	62.5	1	R.HSHSFLPFSGGAR.N	441	2	
105	ENSG00000162365:ENSMUSG00000078597:ENSRNOG00000029919	CYP4A22	gi|86198314|ref|NP_758510.2|	gi|86198314|ref|NP_758510.2|	cytochrome P450, family 4, subfamily a family [Mus musculus]	8	28	16.1	508	58309	8.9	MmNaOH-MM_liver_CNBrTi_109.2252.2252.2	2	3.2183	0.2035	1400.78	1400.5	1	70.83333	1	R.HSHSFLPFSGGAR.N	441	2	
105	ENSG00000162365:ENSMUSG00000078597:ENSRNOG00000029919	CYP4A22	gi|86198314|ref|NP_758510.2|	gi|86198314|ref|NP_758510.2|	cytochrome P450, family 4, subfamily a family [Mus musculus]	8	28	16.1	508	58309	8.9	MmNaOH-MM_liver_CNBrTi_209.1943.1943.2	2	2.8505	0.1531	960.33	960.17	6	100	5	R.FLAPWIGR.G	120	2	
105	ENSG00000162365:ENSMUSG00000078597:ENSRNOG00000029919	CYP4A22	gi|86198314|ref|NP_758510.2|	gi|86198314|ref|NP_758510.2|	cytochrome P450, family 4, subfamily a family [Mus musculus]	8	28	16.1	508	58309	8.9	MmNaOH-MM_liver_CNBrTi_109.4921.4921.2	2	4.1461	0.3193	1492.84	1492.8	1	72.72727	1	R.RLDFLDILLFAR.M	286	2	
106	ENSG00000179091:ENSMUSG00000022551:ENSRNOG00000012457	CYC1	gi|13385006|ref|NP_079843.1|	gi|13385006|ref|NP_079843.1|	cytochrome c-1 [Mus musculus]	2	10	11.1	325	35328	9.2	MmNaOH-MM_liver_CNBrTi_101.1206.1206.2	2	3.2223	0.2858	1299.48	1299.5	1	72.72727	8	R.GLLSSLDHTSIR.R	100	2	*
106	ENSG00000179091:ENSMUSG00000022551:ENSRNOG00000012457	CYC1	gi|13385006|ref|NP_079843.1|	gi|13385006|ref|NP_079843.1|	cytochrome c-1 [Mus musculus]	2	10	11.1	325	35328	9.2	MmNaOH-MM_liver_CNBrTi_106.3690.3690.2	2	4.888	0.4013	2655.02	2655.9	1	45.652176	2	R.HGGEDYVFSLLTGYCEPPTGVSLR.E	205	2	*
107	ENSG00000187446:ENSMUSG00000014077:ENSRNOG00000008946	CHP	gi|149249669|ref|XP_001480493.1|	gi|149249669|ref|XP_001480493.1|;gi|149267344|ref|XP_205	PREDICTED: similar to EF-hand Ca2+ binding protein p22 [Mus m	2	10	14.4	195	22432	5.1	MmNaOH-MM_liver_CNBrTi_208.1958.1958.2	2	3.3054	0.148	1309.91	1308.5	2	72.72727	5	R.IPELAINPLGDR.I	54	2	
107	ENSG00000187446:ENSMUSG00000014077:ENSRNOG00000008946	CHP	gi|149249669|ref|XP_001480493.1|	gi|149249669|ref|XP_001480493.1|;gi|149267344|ref|XP_205	PREDICTED: similar to EF-hand Ca2+ binding protein p22 [Mus m	2	10	14.4	195	22432	5.1	MmNaOH-MM_liver_CNBrTi_206.2253.2253.2	2	3.5037	0.4164	1886.8	1887.1	1	53.333336	5	R.IINAFFSEGEDQVNFR.G	66	2	
108	ENSG00000221842:ENSMUSG00000052305:ENSRNOG00000025510	HBB	gi|17647499|ref|NP_058652.1|	gi|17647499|ref|NP_058652.1|	hemoglobin, beta adult minor chain [Mus musculus]	2	7	15	147	15878	8.1	MmNaOH-MM_liver_CNBrTi_208.1201.1201.2	2	3.5197	0.3145	1137.13	1137.4	1	81.818184	3	K.VVAGVATALAHK.Y	134	2	*
108	ENSG00000221842:ENSMUSG00000052305:ENSRNOG00000025510	HBB	gi|17647499|ref|NP_058652.1|	gi|17647499|ref|NP_058652.1|	hemoglobin, beta adult minor chain [Mus musculus]	2	7	15	147	15878	8.1	MmNaOH-MM_liver_CNBrTi_204.2122.2122.2	2	2.9556	0.109	1275.53	1275.5	1	77.77778	4	R.LLVVYPWTQR.Y	32	2	
109	ENSG00000138115:ENSMUSG00000067225:NA	CYP2C8	gi|149270669|ref|XP_920372.2|	gi|149270669|ref|XP_920372.2|;gi|45504402|ref|NP_996260.1	PREDICTED: similar to cytochrome P450 [Mus musculus]	1	14	4	302	34345	8.2	MmNaOH-MM_liver_CNBrTi_209.2137.2137.2	2	3.8574	0.4995	1401.51	1401.6	1	86.36364	14	R.VYGPVYTLYLGR.K	73	2	
110	ENSG00000127022:ENSMUSG00000020368:ENSRNOG00000003343	CANX	gi|6671664|ref|NP_031623.1|	gi|6671664|ref|NP_031623.1|	calnexin [Mus musculus]	1	26	2.7	591	67278	4.6	MmNaOH-MM_liver_CNBrTi_207.2106.2106.2	2	4.3064	0.4669	1771.27	1771.9	1	73.333336	26	K.APVPTGEVYFADSFDR.G	63	2	*
111	ENSG00000084453:ENSMUSG00000041698:ENSRNOG00000036984	SLCO1A2	gi|7305497|ref|NP_038825.1|	gi|7305497|ref|NP_038825.1|	solute carrier organic anion transporter family, member 1a1 [Mus m	3	12	4.2	670	74396	8.2	MmNaOH-MM_liver_CNBrTi_102.2063.2063.2	2	3.4915	0.313	1210.1	1210.5	1	90	9	R.HIYLGLPAAVR.G	599	2	*
111	ENSG00000084453:ENSMUSG00000041698:ENSRNOG00000036984	SLCO1A2	gi|7305497|ref|NP_038825.1|	gi|7305497|ref|NP_038825.1|	solute carrier organic anion transporter family, member 1a1 [Mus m	3	12	4.2	670	74396	8.2	MmNaOH-MM_liver_CNBrTi_101.3700.3700.2	2	2.7163	0.2637	1786.39	1787.2	5	46.875	2	R.LLAGIPAPVYFGALIDR.T	557	2	*
111	ENSG00000084453:ENSMUSG00000041698:ENSRNOG00000036984	SLCO1A2	gi|7305497|ref|NP_038825.1|	gi|7305497|ref|NP_038825.1|	solute carrier organic anion transporter family, member 1a1 [Mus m	3	12	4.2	670	74396	8.2	MmNaOH-MM_liver_CNBrTi_105.1866.1866.1	1	2.3139	0.1664	1209.69	1210.5	5	60.000004	1	R.HIYLGLPAAVR.G	599	2	*
112	ENSG00000111775:ENSMUSG00000041697:ENSRNOG00000001170	COX6A1	gi|6680988|ref|NP_031774.1|	gi|6680988|ref|NP_031774.1|	cytochrome c oxidase, subunit VI a, polypeptide 1 [Mus musculus]	2	2	14.3	112	12483	10	MmNaOH-MM_liver_CNBrTi_110.2182.2182.3	3	4.4604	0.4002	2015.95	2015.2	1	51.666664	1	R.HEEHERPPFVAYPHLR.I	66	2	*
112	ENSG00000111775:ENSMUSG00000041697:ENSRNOG00000001170	COX6A1	gi|6680988|ref|NP_031774.1|	gi|6680988|ref|NP_031774.1|	cytochrome c oxidase, subunit VI a, polypeptide 1 [Mus musculus]	2	2	14.3	112	12483	10	MmNaOH-MM_liver_CNBrTi_110.2178.2178.2	2	2.8656	0.1087	2014.79	2015.2	1	50	1	R.HEEHERPPFVAYPHLR.I	66	2	*
113	ENSG00000112081:ENSMUSG00000078134:ENSRNOG00000000520	SFRS3	gi|149251831|ref|XP_001479236.1|	gi|149251831|ref|XP_001479236.1|;gi|149266876|ref|XP_001	PREDICTED: similar to MGC89287 protein [Mus musculus]	2	6	14.7	156	18374	11.5	MmNaOH-MM_liver_CNBrTi_202.1775.1775.2	2	2.5897	0.3208	1044.01	1044.2	2	75	5	R.AFGYYGPLR.S	29	2	
113	ENSG00000112081:ENSMUSG00000078134:ENSRNOG00000000520	SFRS3	gi|149251831|ref|XP_001479236.1|	gi|149251831|ref|XP_001479236.1|;gi|149266876|ref|XP_001	PREDICTED: similar to MGC89287 protein [Mus musculus]	2	6	14.7	156	18374	11.5	MmNaOH-MM_liver_CNBrTi_212.2280.2280.2	2	2.8395	0.2815	1621.97	1622.8	1	61.538464	1	R.NPPGFAFVEFEDPR.D	44	2	
114	ENSG00000112473:ENSMUSG00000024327:ENSRNOG00000000465	SLC39A7	gi|118150670|ref|NP_032228.2|	gi|118150670|ref|NP_032228.2|	solute carrier family 39, member 7 [Mus musculus]	2	7	5.5	476	50657	6.9	MmNaOH-MM_liver_CNBrTi_104.5367.5367.2	2	5.4602	0.3968	2694.15	2695	1	50	3	R.VSGYLNLAADLAHNFTDGLAIGASFR.G	324	2	*
114	ENSG00000112473:ENSMUSG00000024327:ENSRNOG00000000465	SLC39A7	gi|118150670|ref|NP_032228.2|	gi|118150670|ref|NP_032228.2|	solute carrier family 39, member 7 [Mus musculus]	2	7	5.5	476	50657	6.9	MmNaOH-MM_liver_CNBrTi_103.5358.5358.3	3	4.0883	0.3804	2696.2	2695	1	31	4	R.VSGYLNLAADLAHNFTDGLAIGASFR.G	324	2	*
115	ENSG00000183048:ENSMUSG00000025792:ENSRNOG00000036693	SLC25A10	gi|7305501|ref|NP_038798.1|	gi|7305501|ref|NP_038798.1|	solute carrier family 25 (mitochondrial carrier, dicarboxylate transpo	2	9	8.4	287	31727	9.3	MmNaOH-MM_liver_CNBrTi_212.2761.2761.2	2	5.2845	0.5091	2312.43	2313.7	1	47.826088	8	K.VLLGGISGLTGGFVGTPADLVNVR.M	102	2	*
115	ENSG00000183048:ENSMUSG00000025792:ENSRNOG00000036693	SLC25A10	gi|7305501|ref|NP_038798.1|	gi|7305501|ref|NP_038798.1|	solute carrier family 25 (mitochondrial carrier, dicarboxylate transpo	2	9	8.4	287	31727	9.3	MmNaOH-MM_liver_CNBrTi_210.3032.3032.3	3	3.4574	0.1973	2313.69	2313.7	1	26.086956	1	K.VLLGGISGLTGGFVGTPADLVNVR.M	102	2	*
116	NA:ENSMUSG00000003429:ENSRNOG00000023237	RPS11	gi|21426889|ref|NP_038753.1|	gi|21426889|ref|NP_038753.1|	ribosomal protein S11 [Mus musculus]	1	2	5.1	158	18431	10.3	MmNaOH-MM_liver_CNBrTi_108.1486.1486.2	2	3.4075	0.2325	1136.15	1136.3	1	92.85714	2	R.RDYLHYIR.K	90	2	*
117	ENSG00000042445:ENSMUSG00000056666:ENSRNOG00000014090	RETSAT	gi|52627143|ref|NP_080435.3|	gi|52627143|ref|NP_080435.3|	all-trans-13,14-dihydroretinol saturase [Mus musculus]	2	18	4.8	609	67335	9	MmNaOH-MM_liver_CNBrTi_206.0720.0720.2	2	3.4655	0.2911	1247.04	1247.3	1	63.636364	16	R.GATYGADHDLAR.L	531	2	*
117	ENSG00000042445:ENSMUSG00000056666:ENSRNOG00000014090	RETSAT	gi|52627143|ref|NP_080435.3|	gi|52627143|ref|NP_080435.3|	all-trans-13,14-dihydroretinol saturase [Mus musculus]	2	18	4.8	609	67335	9	MmNaOH-MM_liver_CNBrTi_203.2647.2647.2	2	4.2752	0.3402	1761.04	1760	1	62.5	2	R.ASTQSLAEVLQQLGASR.E	236	2	*
118	ENSG00000086696:ENSMUSG00000031844:ENSRNOG00000013982	HSD17B2	gi|123173870|ref|NP_032316.2|	gi|123173870|ref|NP_032316.2|	hydroxysteroid (17-beta) dehydrogenase 2 [Mus musculus]	3	11	8.9	381	41836	8.6	MmNaOH-MM_liver_CNBrTi_202.1539.1539.2	2	2.4636	0.1989	1189.58	1188.3	3	61.11111	2	R.NPSSFYYPGR.M	334	2	*
118	ENSG00000086696:ENSMUSG00000031844:ENSRNOG00000013982	HSD17B2	gi|123173870|ref|NP_032316.2|	gi|123173870|ref|NP_032316.2|	hydroxysteroid (17-beta) dehydrogenase 2 [Mus musculus]	3	11	8.9	381	41836	8.6	MmNaOH-MM_liver_CNBrTi_205.0891.0891.2	2	3.2185	0.1678	1010.92	1011.1	1	87.5	7	R.DIQHAISAR.N	325	2	*
118	ENSG00000086696:ENSMUSG00000031844:ENSRNOG00000013982	HSD17B2	gi|123173870|ref|NP_032316.2|	gi|123173870|ref|NP_032316.2|	hydroxysteroid (17-beta) dehydrogenase 2 [Mus musculus]	3	11	8.9	381	41836	8.6	MmNaOH-MM_liver_CNBrTi_206.1500.1500.2	2	4.1618	0.3863	1838.66	1838.9	1	67.85714	2	K.DIQENYGQDYVHTQK.L	291	2	*
119	ENSG00000150527:ENSMUSG00000021000:ENSRNOG00000005101	CTAGE5	gi|119372290|ref|NP_666146.2|	gi|119372290|ref|NP_666146.2|	CTAGE family, member 5 [Mus musculus]	2	22	4	777	87490	5.1	MmNaOH-MM_liver_CNBrTi_211.2917.2917.2	2	3.8372	0.34	1511.54	1511.8	1	80.769226	21	R.AFLSPPTLLEGPLR.L	509	2	*
119	ENSG00000150527:ENSMUSG00000021000:ENSRNOG00000005101	CTAGE5	gi|119372290|ref|NP_666146.2|	gi|119372290|ref|NP_666146.2|	CTAGE family, member 5 [Mus musculus]	2	22	4	777	87490	5.1	MmNaOH-MM_liver_CNBrTi_212.2064.2064.2	2	2.4533	0.1362	1709.07	1709	2	50	1	R.GPSFPPPPPGSIYAAPR.D	690	2	*
120	ENSG00000161016:ENSMUSG00000003970:NA	RPL8	gi|6755358|ref|NP_036183.1|	gi|6755358|ref|NP_036183.1|	ribosomal protein L8 [Mus musculus]	2	7	9.3	257	28025	11	MmNaOH-MM_liver_CNBrTi_206.1235.1235.2	2	3.9953	0.3823	1690.67	1689.8	1	56.666668	4	R.ASGNYATVISHNPETK.K	129	2	*
120	ENSG00000161016:ENSMUSG00000003970:NA	RPL8	gi|6755358|ref|NP_036183.1|	gi|6755358|ref|NP_036183.1|	ribosomal protein L8 [Mus musculus]	2	7	9.3	257	28025	11	MmNaOH-MM_liver_CNBrTi_210.0750.0750.2	2	2.699	0.1395	827.95	828.05	2	92.85714	3	R.KVGLIAAR.R	234	2	*
121	ENSG00000075785:NA:NA	RAB7A	gi|6679599|ref|NP_033031.1|	gi|6679599|ref|NP_033031.1|	RAB7, member RAS oncogene family [Mus musculus]	3	5	17.9	207	23559	7.6	MmNaOH-MM_liver_CNBrTi_203.1894.1894.2	2	3.064	0.2239	1188.18	1188.4	1	77.77778	3	R.FQSLGVAFYR.G	70	2	*
121	ENSG00000075785:NA:NA	RAB7A	gi|6679599|ref|NP_033031.1|	gi|6679599|ref|NP_033031.1|	RAB7, member RAS oncogene family [Mus musculus]	3	5	17.9	207	23559	7.6	MmNaOH-MM_liver_CNBrTi_202.2360.2360.2	2	2.9575	0.2608	1590.38	1590.8	1	57.692307	1	K.EAINVEQAFQTIAR.N	158	2	*
121	ENSG00000075785:NA:NA	RAB7A	gi|6679599|ref|NP_033031.1|	gi|6679599|ref|NP_033031.1|	RAB7, member RAS oncogene family [Mus musculus]	3	5	17.9	207	23559	7.6	MmNaOH-MM_liver_CNBrTi_202.2430.2430.2	2	3.7782	0.3064	1477.76	1476.7	1	66.66667	1	R.DPENFPFVVLGNK.I	114	2	*
122	ENSG00000145425:ENSMUSG00000062611:ENSRNOG00000011893	RPS3A	gi|149265827|ref|XP_001480995.1|	gi|149265827|ref|XP_001480995.1|;gi|31980669|ref|NP_0586	PREDICTED: similar to ribosomal protein S3a [Mus musculus]	1	6	6.4	264	29825	9.7	MmNaOH-MM_liver_CNBrTi_207.2842.2842.2	2	3.9452	0.4984	1952.64	1953.2	1	59.375	6	R.VFEVSLADLQNDEVAFR.K	66	2	
123	ENSG00000130203:ENSMUSG00000002985:ENSRNOG00000018454	APOE	gi|6753102|ref|NP_033826.1|	gi|6753102|ref|NP_033826.1|	apolipoprotein E [Mus musculus]	2	7	6.4	311	35853	5.7	MmNaOH-MM_liver_CNBrTi_202.0927.0927.2	2	2.4949	0.2465	969.46	969.13	1	87.5	3	R.LGPLVEQGR.Q	191	2	*
123	ENSG00000130203:ENSMUSG00000002985:ENSRNOG00000018454	APOE	gi|6753102|ref|NP_033826.1|	gi|6753102|ref|NP_033826.1|	apolipoprotein E [Mus musculus]	2	7	6.4	311	35853	5.7	MmNaOH-MM_liver_CNBrTi_208.0684.0684.2	2	3.9931	0.1628	1229.03	1229.3	1	85	4	R.GRLEEVGNQAR.D	226	2	*
124	ENSG00000184752:ENSMUSG00000020022:ENSRNOG00000007407	NDUFA12	gi|27228985|ref|NP_079827.2|	gi|27228985|ref|NP_079827.2|	13kDa differentiation-associated protein [Mus musculus]	1	3	8.1	149	17633	9.5	MmNaOH-MM_liver_CNBrTi_208.0721.0721.2	2	2.6049	0.2808	1208.3	1209.4	1	68.181816	3	R.GVQQVTGHGGLR.G	14	2	*
125	ENSG00000072849:ENSMUSG00000018442:ENSRNOG00000007244	DERL2	gi|15808990|ref|NP_291040.1|	gi|15808990|ref|NP_291040.1|	Der1-like domain family, member 2 [Mus musculus]	1	2	12.6	239	27640	7.3	MmNaOH-MM_liver_CNBrTi_102.2935.2935.3	3	3.3307	0.2287	3405.66	3406.6	1	26.724138	2	R.TIFDTPDEDPNYNPLPEERPGGFAWGEGQR.L	207	2	*
126	ENSG00000164344:ENSMUSG00000031640:ENSRNOG00000014118	KLKB1	gi|19527190|ref|NP_598730.1|	gi|19527190|ref|NP_598730.1|	family 4 cytochrome P450 [Mus musculus]	1	10	1.9	525	60939	8.5	MmNaOH-MM_liver_CNBrTi_204.5348.5348.2	2	2.4629	0.2369	1134.24	1133.4	2	72.22222	10	R.VFPSVPLFAR.S	391	2	*
127	ENSG00000162877:ENSMUSG00000042251:ENSRNOG00000039745	PM20D1	gi|113374119|ref|NP_835180.1|	gi|113374119|ref|NP_835180.1|	hypothetical protein LOC212933 [Mus musculus]	1	4	2.2	503	55591	6.5	MmNaOH-MM_liver_CNBrTi_106.2839.2839.2	2	3.3326	0.2994	1382.48	1382.7	1	80	4	R.NLWLFHPIVSR.I	313	2	*
128	ENSG00000116133:ENSMUSG00000034926:ENSRNOG00000006787	DHCR24	gi|114155129|ref|NP_444502.2|	gi|114155129|ref|NP_444502.2|	24-dehydrocholesterol reductase precursor [Mus musculus]	1	4	3.7	516	60112	8.2	MmNaOH-MM_liver_CNBrTi_104.5642.5642.2	2	3.5703	0.1976	2310.1	2307.7	1	55.555557	4	R.SIFWELQDIIPFGNNPIFR.Y	334	2	*
129	ENSG00000117528:ENSMUSG00000028127:ENSRNOG00000011929	ABCD3	gi|60218877|ref|NP_033017.2|	gi|60218877|ref|NP_033017.2|	ATP-binding cassette, sub-family D, member 3 [Mus musculus]	3	5	5.2	659	75475	9.3	MmNaOH-MM_liver_CNBrTi_101.3282.3282.2	2	3.5194	0.1248	1343.87	1344.6	1	77.27273	2	R.VLGELWPLFGGR.L	485	2	*
129	ENSG00000117528:ENSMUSG00000028127:ENSRNOG00000011929	ABCD3	gi|60218877|ref|NP_033017.2|	gi|60218877|ref|NP_033017.2|	ATP-binding cassette, sub-family D, member 3 [Mus musculus]	3	5	5.2	659	75475	9.3	MmNaOH-MM_liver_CNBrTi_101.2079.2079.2	2	3.0537	0.2478	1699.17	1699.9	1	53.846157	1	K.EYLDNVQLGHILER.E	544	2	*
129	ENSG00000117528:ENSMUSG00000028127:ENSRNOG00000011929	ABCD3	gi|60218877|ref|NP_033017.2|	gi|60218877|ref|NP_033017.2|	ATP-binding cassette, sub-family D, member 3 [Mus musculus]	3	5	5.2	659	75475	9.3	MmNaOH-MM_liver_CNBrTi_105.3867.3867.3	3	4.8143	0.3181	2541.07	2540.9	1	35.714287	2	R.GISDQVLKEYLDNVQLGHILER.E	536	2	*
130	ENSG00000160868:ENSMUSG00000056035:ENSRNOG00000000978	CYP3A4	gi|6681113|ref|NP_031844.1|	gi|6681113|ref|NP_031844.1|	cytochrome P450, family 3, subfamily a, polypeptide 11 [Mus musc	4	9	10.9	504	57855	8.8	MmNaOH-MM_liver_CNBrTi_204.3412.3412.2	2	4.7623	0.3735	2305.26	2303.6	1	57.5	1	K.TWGLFDGQTPLLAVTDPETIK.N	71	2	*
130	ENSG00000160868:ENSMUSG00000056035:ENSRNOG00000000978	CYP3A4	gi|6681113|ref|NP_031844.1|	gi|6681113|ref|NP_031844.1|	cytochrome P450, family 3, subfamily a, polypeptide 11 [Mus musc	4	9	10.9	504	57855	8.8	MmNaOH-MM_liver_CNBrTi_207.1515.1515.2	2	2.2306	0.1084	1014.47	1014.2	7	85.71429	1	K.DSIEFFKK.F	244	2	
130	ENSG00000160868:ENSMUSG00000056035:ENSRNOG00000000978	CYP3A4	gi|6681113|ref|NP_031844.1|	gi|6681113|ref|NP_031844.1|	cytochrome P450, family 3, subfamily a, polypeptide 11 [Mus musc	4	9	10.9	504	57855	8.8	MmNaOH-MM_liver_CNBrTi_212.1904.1904.2	2	2.1743	0.111	1245.68	1245.5	9	72.22222	1	R.LYPIANRLER.V	367	2	*
130	ENSG00000160868:ENSMUSG00000056035:ENSRNOG00000000978	CYP3A4	gi|6681113|ref|NP_031844.1|	gi|6681113|ref|NP_031844.1|	cytochrome P450, family 3, subfamily a, polypeptide 11 [Mus musc	4	9	10.9	504	57855	8.8	MmNaOH-MM_liver_CNBrTi_204.3223.3223.2	2	2.9823	0.1241	1754.42	1753	1	60.000004	6	K.GSIDPYVYLPFGNGPR.N	426	2	
131	ENSG00000124222:ENSMUSG00000027522:ENSRNOG00000005281	STX16	gi|29789393|ref|NP_766263.1|	gi|29789393|ref|NP_766263.1|	syntaxin 16 [Mus musculus]	2	2	6.6	273	31148	5.7	MmNaOH-MM_liver_CNBrTi_101.5978.5978.2	2	4.0813	0.272	1935.68	1935.2	1	52.941177	1	R.NVVASLAQALQELSTSFR.H	108	2	*
131	ENSG00000124222:ENSMUSG00000027522:ENSRNOG00000005281	STX16	gi|29789393|ref|NP_766263.1|	gi|29789393|ref|NP_766263.1|	syntaxin 16 [Mus musculus]	2	2	6.6	273	31148	5.7	MmNaOH-MM_liver_CNBrTi_101.5982.5982.3	3	4.3429	0.3479	1935.62	1935.2	3	41.17647	1	R.NVVASLAQALQELSTSFR.H	108	2	*
132	ENSG00000137824:ENSMUSG00000070730:ENSRNOG00000011690	FAM82C	gi|85701644|ref|NP_001028308.1|	gi|85701644|ref|NP_001028308.1|	hypothetical protein LOC67809 [Mus musculus]	2	8	7.9	470	52029	5.2	MmNaOH-MM_liver_CNBrTi_208.4372.4372.2	2	5.376	0.4022	2440.64	2439.8	1	54.545456	1	K.TATALFESPLSATVQDALQSFLK.A	387	2	*
132	ENSG00000137824:ENSMUSG00000070730:ENSRNOG00000011690	FAM82C	gi|85701644|ref|NP_001028308.1|	gi|85701644|ref|NP_001028308.1|	hypothetical protein LOC67809 [Mus musculus]	2	8	7.9	470	52029	5.2	MmNaOH-MM_liver_CNBrTi_203.2437.2437.2	2	4.3934	0.3339	1428.58	1428.6	1	80.769226	7	R.SLQGLAGEIVGEVR.S	114	2	*
133	ENSG00000168028:ENSMUSG00000047676:ENSRNOG00000018645	RPSA	gi|149252001|ref|XP_001475568.1|	gi|149252001|ref|XP_001475568.1|;gi|149270876|ref|XP_001	PREDICTED: hypothetical protein [Mus musculus]	2	5	7.8	295	32838	4.9	MmNaOH-MM_liver_CNBrTi_209.2267.2267.2	2	3.0311	0.4167	1699.95	1699.9	1	53.571426	4	R.FTPGTFTNQIQAAFR.E	103	2	
133	ENSG00000168028:ENSMUSG00000047676:ENSRNOG00000018645	RPSA	gi|149252001|ref|XP_001475568.1|	gi|149252001|ref|XP_001475568.1|;gi|149270876|ref|XP_001	PREDICTED: hypothetical protein [Mus musculus]	2	5	7.8	295	32838	4.9	MmNaOH-MM_liver_CNBrTi_203.1421.1421.2	2	2.5341	0.1466	913.17	913.11	7	78.57143	1	R.LLVVTDPR.A	121	2	
134	ENSG00000103496:ENSMUSG00000030805:ENSRNOG00000019302	STX4	gi|6678177|ref|NP_033320.1|	gi|6678177|ref|NP_033320.1|	syntaxin 4A (placental) [Mus musculus]	1	5	3.7	298	34165	6.1	MmNaOH-MM_liver_CNBrTi_209.0745.0745.2	2	3.2823	0.2412	1080.29	1080.3	1	80	5	R.VALVVHSGAAR.L	23	2	*
135	NA:ENSMUSG00000073702:ENSRNOG00000000050	RPL31	gi|149267081|ref|XP_996461.2|	gi|149267081|ref|XP_996461.2|;gi|149267765|ref|XP_915749	PREDICTED: hypothetical protein [Mus musculus]	1	2	11.2	125	14463	10.5	MmNaOH-MM_liver_CNBrTi_202.2514.2514.2	2	3.3832	0.1579	1646.23	1646	1	65.38461	2	K.LYTLVTYVPVTTFK.N	102	2	
136	ENSG00000063177:ENSMUSG00000059070:ENSRNOG00000021035	RPL18	gi|83699424|ref|NP_033103.2|	gi|83699424|ref|NP_033103.2|	ribosomal protein L18 [Mus musculus]	2	3	12.2	188	21645	11.8	MmNaOH-MM_liver_CNBrTi_211.1793.1793.2	2	2.2497	0.2274	1141.44	1141.3	3	66.66667	1	R.TNRPPLSLSR.M	56	2	
136	ENSG00000063177:ENSMUSG00000059070:ENSRNOG00000021035	RPL18	gi|83699424|ref|NP_033103.2|	gi|83699424|ref|NP_033103.2|	ribosomal protein L18 [Mus musculus]	2	3	12.2	188	21645	11.8	MmNaOH-MM_liver_CNBrTi_202.2239.2239.2	2	4.2596	0.3192	1475.31	1475.7	1	79.16667	2	K.ILTFDQLALESPK.G	120	2	*
137	ENSG00000109919:ENSMUSG00000027282:ENSRNOG00000008682	MTCH2	gi|9790055|ref|NP_062732.1|	gi|9790055|ref|NP_062732.1|	mitochondrial carrier homolog 2 [Mus musculus]	2	2	5.3	303	33499	8.3	MmNaOH-MM_liver_CNBrTi_109.2708.2708.3	3	3.3873	0.2466	1777.85	1778.1	1	43.333332	1	R.SAATLITHPFHVITLR.S	132	2	*
137	ENSG00000109919:ENSMUSG00000027282:ENSRNOG00000008682	MTCH2	gi|9790055|ref|NP_062732.1|	gi|9790055|ref|NP_062732.1|	mitochondrial carrier homolog 2 [Mus musculus]	2	2	5.3	303	33499	8.3	MmNaOH-MM_liver_CNBrTi_109.2702.2702.2	2	2.8544	0.279	1778.64	1778.1	1	43.333332	1	R.SAATLITHPFHVITLR.S	132	2	*

rk	ORTHO_GROUPS	GENE_NAME	Locus	Proteins In Group	Description	Sequence Count	Spectrum Count	Coverage	Length	MW	pI	MatchID	Z	XCorr	DeltCN	M+H+	CalcM +H+	SpRk	Ion Proportion	Count	Sequence	Sequence Position	Tryptic	Unique
138	ENSG00000212870:ENSMUSG00000064367:ENSRNOG00000029971	MT-ND5	gi|34538608|ref|NP_904338.1|	gi|34538608|ref|NP_904338.1|	NADH dehydrogenase subunit 5 [Mus musculus]	1	4	3.3	607	68475	9	MmNaOH-MM_liver_CNBrTi_109.5100.5100.2	2	3.8687	0.3264	2254.68	2255.6	1	44.736843	4	K.ANPYSSFSTLLGFFPSIIHR.I	516	2	*
139	ENSG00000084733:ENSMUSG00000020671:NA	RAB10	gi|7710086|ref|NP_057885.1|	gi|7710086|ref|NP_057885.1|	RAB10, member RAS oncogene family [Mus musculus]	1	3	5.5	200	22541	8.4	MmNaOH-MM_liver_CNBrTi_208.2853.2853.2	2	3.4901	0.2429	1261.65	1262.5	1	85	3	K.AFLTLAEDILR.K	162	2	*
140	ENSG00000103415:ENSMUSG00000004070:ENSRNOG00000003773	HMOX2	gi|6754214|ref|NP_034573.1|	gi|6754214|ref|NP_034573.1|	heme oxygenase (decycling) 2 [Mus musculus]	2	2	6	315	35659	5.7	MmNaOH-MM_liver_CNBrTi_108.1870.1870.3	3	4.1534	0.3454	2210.6	2211.5	1	37.5	1	R.IHYVGQNEPELLVAHAYTR.Y	137	2	*
140	ENSG00000103415:ENSMUSG00000004070:ENSRNOG00000003773	HMOX2	gi|6754214|ref|NP_034573.1|	gi|6754214|ref|NP_034573.1|	heme oxygenase (decycling) 2 [Mus musculus]	2	2	6	315	35659	5.7	MmNaOH-MM_liver_CNBrTi_108.1874.1874.2	2	5.9979	0.4893	2210.95	2211.5	1	75	1	R.IHYVGQNEPELLVAHAYTR.Y	137	2	*
141	ENSG00000106327:ENSMUSG00000029716:ENSRNOG00000001407	TFR2	gi|113204630|ref|NP_056614.3|	gi|113204630|ref|NP_056614.3|	transferrin receptor 2 [Mus musculus]	3	5	2.5	798	88402	6.1	MmNaOH-MM_liver_CNBrTi_109.5982.5982.3	3	3.3488	0.1599	2074.29	2074.5	1	38.157894	1	R.GRLPAVVQAVAQLAGQLLIR.L	608	2	*
141	ENSG00000106327:ENSMUSG00000029716:ENSRNOG00000001407	TFR2	gi|113204630|ref|NP_056614.3|	gi|113204630|ref|NP_056614.3|	transferrin receptor 2 [Mus musculus]	3	5	2.5	798	88402	6.1	MmNaOH-MM_liver_CNBrTi_109.5998.5998.2	2	4.0931	0.4879	2072.28	2074.5	1	52.63158	3	R.GRLPAVVQAVAQLAGQLLIR.L	608	2	*
141	ENSG00000106327:ENSMUSG00000029716:ENSRNOG00000001407	TFR2	gi|113204630|ref|NP_056614.3|	gi|113204630|ref|NP_056614.3|	transferrin receptor 2 [Mus musculus]	3	5	2.5	798	88402	6.1	MmNaOH-MM_liver_CNBrTi_104.0287.0287.2	2	3.6259	0.3534	1861.21	1861.3	1	64.70589	1	R.LPAVVQAVAQLAGQLLIR.L	610	2	*
142	ENSG00000138073:ENSMUSG00000045302:ENSRNOG00000007141	PREB	gi|7710084|ref|NP_057912.1|	gi|7710084|ref|NP_057912.1|	prolactin regulatory element binding protein [Mus musculus]	1	6	2.2	416	45380	8.8	MmNaOH-MM_liver_CNBrTi_208.1925.1925.2	2	2.3674	0.3186	1048.33	1048.3	5	75	6	R.APFPLYALR.I	12	2	*
143	ENSG00000009765:ENSMUSG00000019762:ENSRNOG00000016286	IYD	gi|21312562|ref|NP_081667.1|	gi|21312562|ref|NP_081667.1|	iodotyrosine dehalogenase 1 protein [Mus musculus]	1	4	4.2	285	32814	6.4	MmNaOH-MM_liver_CNBrTi_210.2128.2128.2	2	3.0736	0.1181	1327.1	1327.7	2	72.72727	4	K.LLVLLPVGYPSR.D	255	2	*
144	ENSG00000074696:ENSMUSG00000033629:ENSRNOG00000030232	PTPLAD1	gi|28916663|ref|NP_067320.1|	gi|28916663|ref|NP_067320.1|;gi|7705459|ref|NP_057479.1|	protein tyrosine phosphatase-like A domain containing 1 [Mus mus	1	5	2.8	362	43145	9.1	MmNaOH-MM_liver_CNBrTi_209.3810.3810.2	2	3.0506	0.0896	1192.57	1191.4	3	72.22222	5	R.PLFLAPDFDR.W	100	2	
145	ENSG00000113621:ENSMUSG00000021497:ENSRNOG00000005316	TXNDC15	gi|52693935|ref|NP_780359.2|	gi|52693935|ref|NP_780359.2|	disulfide isomerase [Mus musculus]	1	2	6.1	344	38146	4.8	MmNaOH-MM_liver_CNBrTi_102.3583.3583.2	2	4.2955	0.4801	2220.3	2220.5	1	45	2	R.AFPTLGFLALDASQHSSLSTR.F	220	2	*
146	NA:ENSMUSG00000060264:NA	LOC433745	gi|149252852|ref|XP_001475783.1|	gi|149252852|ref|XP_001475783.1|;gi|149255712|ref|XP_001	PREDICTED: similar to ribosomal protein L3 [Mus musculus]	1	2	2.5	354	39964	10.1	MmNaOH-MM_liver_CNBrTi_104.1603.1603.2	2	3.0355	0.2252	983.78	984.15	1	93.75	2	R.HGSLGFLPR.K	11	2	
147	ENSG00000140612:ENSMUSG00000025724:ENSRNOG00000011029	SEC11A	gi|9910550|ref|NP_064335.1|	gi|9910550|ref|NP_064335.1|	Sec11-like 1 [Mus musculus]	1	1	4.5	179	20626	9.3	MmNaOH-MM_liver_CNBrTi_102.1872.1872.2	2	2.5211	0.1036	920.13	919.11	1	92.85714	1	R.VGEIVVFR.I	79	2	*
148	ENSG00000156052:ENSMUSG00000024639:ENSRNOG00000014183	GNAQ	gi|84662745|ref|NP_032165.3|	gi|84662745|ref|NP_032165.3|	guanine nucleotide binding protein, alpha q polypeptide [Mus musc	2	2	5.8	359	42158	5.7	MmNaOH-MM_liver_CNBrTi_108.4279.4279.2	2	2.6825	0.2936	2451.51	2451.9	1	37.5	1	R.VRVPTTGIIEYPFDLQSVIFR.M	182	2	*
148	ENSG00000156052:ENSMUSG00000024639:ENSRNOG00000014183	GNAQ	gi|84662745|ref|NP_032165.3|	gi|84662745|ref|NP_032165.3|	guanine nucleotide binding protein, alpha q polypeptide [Mus musc	2	2	5.8	359	42158	5.7	MmNaOH-MM_liver_CNBrTi_108.4275.4275.3	3	5.2687	0.3309	2451.72	2451.9	1	41.25	1	R.VRVPTTGIIEYPFDLQSVIFR.M	182	2	*
149	ENSG00000182327:ENSMUSG00000046811:ENSRNOG00000026488	GLTPD2	gi|149252026|ref|XP_001471857.1|	gi|149252026|ref|XP_001471857.1|	PREDICTED: hypothetical protein [Mus musculus]	4	4	9.7	321	34453	9.2	MmNaOH-MM_liver_CNBrTi_212.1683.1683.2	2	4.0243	0.3495	2079.85	2080.2	2	38.095238	1	R.GAGLLQRPGTEPGHSAGSSGSR.T	190	2	*
149	ENSG00000182327:ENSMUSG00000046811:ENSRNOG00000026488	GLTPD2	gi|149252026|ref|XP_001471857.1|	gi|149252026|ref|XP_001471857.1|	PREDICTED: hypothetical protein [Mus musculus]	4	4	9.7	321	34453	9.2	MmNaOH-MM_liver_CNBrTi_212.1680.1680.3	3	3.0488	0.1635	2080.04	2080.2	1	32.142857	1	R.GAGLLQRPGTEPGHSAGSSGSR.T	190	2	*
149	ENSG00000182327:ENSMUSG00000046811:ENSRNOG00000026488	GLTPD2	gi|149252026|ref|XP_001471857.1|	gi|149252026|ref|XP_001471857.1|	PREDICTED: hypothetical protein [Mus musculus]	4	4	9.7	321	34453	9.2	MmNaOH-MM_liver_CNBrTi_212.1680.1680.2	2	2.0783	0.1734	1387.08	1384.4	9	50	1	R.PGTEPGHSAGSSGSR.T	197	2	*
149	ENSG00000182327:ENSMUSG00000046811:ENSRNOG00000026488	GLTPD2	gi|149252026|ref|XP_001471857.1|	gi|149252026|ref|XP_001471857.1|	PREDICTED: hypothetical protein [Mus musculus]	4	4	9.7	321	34453	9.2	MmNaOH-MM_liver_CNBrTi_202.1887.1887.2	2	2.8627	0.1021	954.26	954.2	1	87.5	1	R.LAILALPSR.G	266	2	*
150	ENSG00000167315:ENSMUSG00000036880:ENSRNOG00000013766	ACAA2	gi|29126205|ref|NP_803421.1|	gi|29126205|ref|NP_803421.1|	acetyl-Coenzyme A acyltransferase 2 (mitochondrial 3-oxoacyl-Co	1	2	2.5	397	41830	8.1	MmNaOH-MM_liver_CNBrTi_107.1370.1370.2	2	3.2663	0.1831	1189.47	1189.4	1	83.33333	2	R.ITAHLVHELR.R	361	2	*
151	ENSG00000164209:ENSMUSG00000024259:ENSRNOG00000017091	SLC25A46	gi|13385672|ref|NP_080441.1|	gi|13385672|ref|NP_080441.1|	solute carrier family 25, member 46 [Mus musculus]	1	2	6	418	46224	7.6	MmNaOH-MM_liver_CNBrTi_109.5477.5477.3	3	3.9898	0.3957	2703.58	2704.2	1	31.25	2	R.FAGFGIGLASLFTENVLAHPCIVLR.R	100	2	*
152	ENSG00000120063:ENSMUSG00000020611:ENSRNOG00000036745	GNA13	gi|89001109|ref|NP_034433.3|	gi|89001109|ref|NP_034433.3|	guanine nucleotide binding protein, alpha 13 [Mus musculus]	1	4	2.7	377	44055	8.2	MmNaOH-MM_liver_CNBrTi_206.2227.2227.2	2	3.36	0.1549	1221.78	1220.5	1	88.88889	4	R.VFLQYLPAIR.A	141	2	*
153	ENSG00000140688:ENSMUSG00000030780:ENSRNOG00000020144	C16orf58	gi|21704184|ref|NP_663565.1|	gi|21704184|ref|NP_663565.1|	hypothetical protein LOC233913 [Mus musculus]	1	2	5.4	466	50469	7.1	MmNaOH-MM_liver_CNBrTi_105.3446.3446.3	3	4.498	0.3146	2542.33	2542.9	1	34.375	2	R.AATHGLILGALQEDGPLPGELAELR.H	379	2	*
154	ENSG00000162236:ENSMUSG00000010110:ENSRNOG00000018847	STX5	gi|34328465|ref|NP_062803.3|	gi|34328465|ref|NP_062803.3|	syntaxin 5 [Mus musculus]	1	3	8.3	301	34087	8.7	MmNaOH-MM_liver_CNBrTi_211.3058.3058.3	3	3.4235	0.1614	2385.71	2385.8	1	30.208334	3	R.APVSALPLAPNNLGGGPIILGAESR.A	160	2	*
155	ENSG00000125505:ENSMUSG00000035596:ENSRNOG00000038794	LENG4	gi|31542014|ref|NP_084210.2|	gi|31542014|ref|NP_084210.2|	leukocyte receptor cluster (LRC) member 4 [Mus musculus]	1	2	4.7	473	53436	8.7	MmNaOH-MM_liver_CNBrTi_108.4546.4546.3	3	4.281	0.4238	2641.59	2642.1	1	36.904762	2	R.TYLDWLEQPFFPEAVPSLRPLLR.R	172	2	*
156	ENSG00000058262:ENSMUSG00000030082:ENSRNOG00000013743	SEC61A1	gi|8394252|ref|NP_058602.1|	gi|8394252|ref|NP_058602.1|	Sec61 alpha subunit homolog [Mus musculus]	1	2	4.8	476	52265	8.1	MmNaOH-MM_liver_CNBrTi_102.4954.4954.2	2	3.4145	0.1883	2324.5	2323.6	2	34.090908	2	R.FSGNLLVSLLGTWSDTSSGGPAR.A	312	2	*
157	ENSG00000144959:ENSMUSG00000027698:ENSRNOG00000013313	AADACL1	gi|30520239|ref|NP_848887.1|	gi|30520239|ref|NP_848887.1|	arylacetamide deacetylase-like 1 [Mus musculus]	1	4	6.9	408	45740	7	MmNaOH-MM_liver_CNBrTi_211.4581.4581.3	3	3.8028	0.2727	2999.96	3000.5	1	28.703705	4	R.IVQEIPQLLDAAASPLIAEQEVLEALPK.T	312	2	*
158	NA:ENSMUSG00000046879:ENSRNOG00000031138	IRGM	gi|6680351|ref|NP_032352.1|	gi|6680351|ref|NP_032352.1|	immunity-related GTPase family, M [Mus musculus]	1	4	3.9	409	46552	8.3	MmNaOH-MM_liver_CNBrTi_210.1102.1102.2	2	4.3868	0.4302	1623.55	1623.8	1	63.333332	4	R.VIGHDEDASAPTGVVR.T	98	2	*
159	ENSG00000198327:ENSMUSG00000060639:ENSRNOG00000030142	HIST2H4B	gi|149263932|ref|XP_001476113.1|	gi|149263932|ref|XP_001476113.1|;gi|94378251|ref|XP_9814	PREDICTED: similar to histone H4 [Mus musculus]	1	1	11.7	103	11367	11.4	MmNaOH-MM_liver_CNBrTi_207.1380.1380.2	2	2.9283	0.1724	1327.18	1326.5	1	77.27273	1	R.DNIQGITKPAIR.R	25	2	
160	ENSG00000124587:ENSMUSG00000002763:ENSRNOG00000026481	PEX6	gi|21703962|ref|NP_663463.1|	gi|21703962|ref|NP_663463.1|	peroxisomal biogenesis factor 6 [Mus musculus]	1	4	2.4	981	104548	7.3	MmNaOH-MM_liver_CNBrTi_108.4934.4934.3	3	5.1376	0.4278	2596.73	2597.1	1	34.782608	4	R.LSILQALTAHLPLGQEVNLPQLAR.R	603	2	*
161	ENSG00000197408:ENSMUSG00000030483:ENSRNOG00000033680	CYP2B6	gi|50080153|ref|NP_034129.1|	gi|50080153|ref|NP_034129.1|;gi|6753576|ref|NP_034128.1|	cytochrome P450, family 2, subfamily b, polypeptide 10 isoform 2 [	2	2	2.4	491	55871	7.8	MmNaOH-MM_liver_CNBrTi_101.1792.1792.2	2	2.8591	0.2966	1351.63	1351.6	1	68.181816	1	R.FSDLIPIGVPHR.V	359	2	
161	ENSG00000197408:ENSMUSG00000030483:ENSRNOG00000033680	CYP2B6	gi|50080153|ref|NP_034129.1|	gi|50080153|ref|NP_034129.1|;gi|6753576|ref|NP_034128.1|	cytochrome P450, family 2, subfamily b, polypeptide 10 isoform 2 [	2	2	2.4	491	55871	7.8	MmNaOH-MM_liver_CNBrTi_102.2342.2342.3	3	4.0362	0.2671	1352.16	1351.6	1	54.545456	1	R.FSDLIPIGVPHR.V	359	2	
162	ENSG00000187630:ENSMUSG00000022210:ENSRNOG00000018239	DHRS4L2	gi|13507612|ref|NP_109611.1|	gi|13507612|ref|NP_109611.1|;gi|83816905|ref|NP_00103302	NADPH-dependent retinol dehydrogenase/reductase isoform 2 [Mu	1	2	6	216	23178	9.9	MmNaOH-MM_liver_CNBrTi_205.0920.0920.2	2	3.4652	0.3701	1339.72	1340.5	1	70.83333	2	R.LAEDGAHVVVSSR.K	53	2	
163	ENSG00000092295:ENSMUSG00000022218:ENSRNOG00000020136	TGM1	gi|31982705|ref|NP_064368.2|	gi|31982705|ref|NP_064368.2|	transglutaminase 1, K polypeptide [Mus musculus]	2	3	4.2	815	89826	6.5	MmNaOH-MM_liver_CNBrTi_105.0231.0231.2	2	3.8764	0.3751	2065.55	2063.4	1	58.333332	2	R.GTNPSAWVGSVEILLSYLR.T	348	2	*
163	ENSG00000092295:ENSMUSG00000022218:ENSRNOG00000020136	TGM1	gi|31982705|ref|NP_064368.2|	gi|31982705|ref|NP_064368.2|	transglutaminase 1, K polypeptide [Mus musculus]	2	3	4.2	815	89826	6.5	MmNaOH-MM_liver_CNBrTi_104.1950.1950.2	2	2.9192	0.259	1932.61	1933	1	50	1	R.EHHTDEFEYDELIVR.R	127	2	*
164	ENSG00000116521:ENSMUSG00000028049:ENSRNOG00000020504	SCAMP3	gi|118601011|ref|NP_036016.2|	gi|118601011|ref|NP_036016.2|	secretory carrier membrane protein 3 [Mus musculus]	1	3	3.7	349	38458	7.6	MmNaOH-MM_liver_CNBrTi_207.1047.1047.2	2	3.2356	0.3732	1309.29	1309.5	1	66.66667	3	R.ELQHVALGGAGTR.Q	121	2	*
165	ENSG00000141699:ENSMUSG00000017802:ENSRNOG00000020056	FAM134C	gi|21312666|ref|NP_080777.1|	gi|21312666|ref|NP_080777.1|	hypothetical protein LOC67998 isoform 1 [Mus musculus]	1	4	3.2	466	51638	5	MmNaOH-MM_liver_CNBrTi_205.2834.2834.2	2	3.3995	0.2066	1687.67	1687	1	57.14286	4	R.TLVEVLGPYEPLLSR.V	41	2	*
166	ENSG00000105701:ENSMUSG00000019428:ENSRNOG00000019944	FKBP8	gi|6857787|ref|NP_034353.1|	gi|6857787|ref|NP_034353.1|	FK506 binding protein 8 [Mus musculus]	1	3	8.2	355	38615	7	MmNaOH-MM_liver_CNBrTi_209.3929.3929.3	3	4.0701	0.2161	3120.13	3118.5	7	23.214285	3	R.EFLAATEPEPAPAPAPEEWLDILGNGLLR.M	18	2	*
167	ENSG00000168958:ENSMUSG00000026150:ENSRNOG00000025358	C2orf33	gi|40254163|ref|NP_083685.2|	gi|40254163|ref|NP_083685.2|;gi|82881738|ref|XP_918666.1|	hypothetical protein LOC75734 [Mus musculus]	1	1	9.3	291	32931	6.8	MmNaOH-MM_liver_CNBrTi_105.3450.3450.3	3	3.2084	0.1217	3139.66	3139.5	3	22.115383	1	R.VLTLSERPLDFLDLERPLPTPQSEESR.A	93	2	
168	ENSG00000144224:ENSMUSG00000026353:ENSRNOG00000003625	UBXD2	gi|85861252|ref|NP_080666.2|	gi|85861252|ref|NP_080666.2|	UBX domain containing 2 [Mus musculus]	2	4	7.9	506	56460	6.6	MmNaOH-MM_liver_CNBrTi_207.2970.2970.2	2	2.8917	0.099	1934.9	1935.3	1	47.22222	3	R.LLDLELAPSASVVLLPAGR.P	378	2	*
168	ENSG00000144224:ENSMUSG00000026353:ENSRNOG00000003625	UBXD2	gi|85861252|ref|NP_080666.2|	gi|85861252|ref|NP_080666.2|	UBX domain containing 2 [Mus musculus]	2	4	7.9	506	56460	6.6	MmNaOH-MM_liver_CNBrTi_202.2140.2140.2	2	3.9869	0.3045	2279.77	2279.4	1	42.5	1	R.LPDGSSFTNQFPSDAPLEEAR.Q	324	2	*
169	ENSG00000162365:ENSMUSG00000066072:ENSRNOG00000009597	CYP4A22	gi|47059035|ref|NP_034141.2|	gi|47059035|ref|NP_034141.2|	cytochrome P450, family 4, subfamily a, polypeptide 10 [Mus musc	5	5	11	509	58339	8.6	MmNaOH-MM_liver_CNBrTi_108.2254.2254.2	2	3.6668	0.3408	1806.77	1806.2	1	64.28571	1	M.LTPAFHYDILKPYVK.N	145	1	
169	ENSG00000162365:ENSMUSG00000066072:ENSRNOG00000009597	CYP4A22	gi|47059035|ref|NP_034141.2|	gi|47059035|ref|NP_034141.2|	cytochrome P450, family 4, subfamily a, polypeptide 10 [Mus musc	5	5	11	509	58339	8.6	MmNaOH-MM_liver_CNBrTi_101.2843.2843.2	2	3.1867	0.2877	1862.24	1863.1	2	53.333336	1	R.TYLQAIGDLNNLFHSR.V	215	2	
169	ENSG00000162365:ENSMUSG00000066072:ENSRNOG00000009597	CYP4A22	gi|47059035|ref|NP_034141.2|	gi|47059035|ref|NP_034141.2|	cytochrome P450, family 4, subfamily a, polypeptide 10 [Mus musc	5	5	11	509	58339	8.6	MmNaOH-MM_liver_CNBrTi_109.4921.4921.2	2	4.1461	0.3193	1492.84	1492.8	1	72.72727	1	R.RLDFLDILLFAR.M	287	2	
169	ENSG00000162365:ENSMUSG00000066072:ENSRNOG00000009597	CYP4A22	gi|47059035|ref|NP_034141.2|	gi|47059035|ref|NP_034141.2|	cytochrome P450, family 4, subfamily a, polypeptide 10 [Mus musc	5	5	11	509	58339	8.6	MmNaOH-MM_liver_CNBrTi_109.2253.2253.1	1	2.568	0.3183	1399.66	1400.5	1	62.5	1	R.HSHSFLPFSGGAR.N	442	2	
169	ENSG00000162365:ENSMUSG00000066072:ENSRNOG00000009597	CYP4A22	gi|47059035|ref|NP_034141.2|	gi|47059035|ref|NP_034141.2|	cytochrome P450, family 4, subfamily a, polypeptide 10 [Mus musc	5	5	11	509	58339	8.6	MmNaOH-MM_liver_CNBrTi_109.2252.2252.2	2	3.2183	0.2035	1400.78	1400.5	1	70.83333	1	R.HSHSFLPFSGGAR.N	442	2	
170	ENSG00000121691:ENSMUSG00000027187:ENSRNOG00000008364	CAT	gi|6753272|ref|NP_033934.1|	gi|6753272|ref|NP_033934.1|	catalase [Mus musculus]	2	4	4.6	527	59734	8.1	MmNaOH-MM_liver_CNBrTi_206.2049.2049.2	2	3.3791	0.2679	1804.44	1805.1	1	60.714287	1	R.LGPNYLQIPVNCPYR.A	366	2	*
170	ENSG00000121691:ENSMUSG00000027187:ENSRNOG00000008364	CAT	gi|6753272|ref|NP_033934.1|	gi|6753272|ref|NP_033934.1|	catalase [Mus musculus]	2	4	4.6	527	59734	8.1	MmNaOH-MM_liver_CNBrTi_208.1344.1344.2	2	2.5984	0.2452	1119.5	1120.3	2	81.25	3	R.LFAYPDTHR.H	355	2	*
171	ENSG00000163686:ENSMUSG00000025277:ENSRNOG00000008167	ABHD6	gi|31560264|ref|NP_079617.2|	gi|31560264|ref|NP_079617.2|	abhydrolase domain containing 6 [Mus musculus]	1	1	4.2	336	38205	8.5	MmNaOH-MM_liver_CNBrTi_107.1707.1707.2	2	2.7886	0.1794	1923.74	1924	2	50	1	R.YAHHEDYQFCYSFR.G	52	2	*
172	ENSG00000117480:ENSMUSG00000034171:ENSRNOG00000011019	FAAH	gi|31542795|ref|NP_034303.2|	gi|31542795|ref|NP_034303.2|	fatty acid amide hydrolase [Mus musculus]	3	4	6.9	579	63191	7.9	MmNaOH-MM_liver_CNBrTi_212.3305.3305.3	3	3.6484	0.2379	2432.58	2432.9	4	35.714287	1	R.LQNPDLDSEALLALPLLQLVQK.L	64	2	*
172	ENSG00000117480:ENSMUSG00000034171:ENSRNOG00000011019	FAAH	gi|31542795|ref|NP_034303.2|	gi|31542795|ref|NP_034303.2|	fatty acid amide hydrolase [Mus musculus]	3	4	6.9	579	63191	7.9	MmNaOH-MM_liver_CNBrTi_212.3324.3324.2	2	4.0934	0.2485	2434.97	2432.9	1	45.238094	2	R.LQNPDLDSEALLALPLLQLVQK.L	64	2	*
172	ENSG00000117480:ENSMUSG00000034171:ENSRNOG00000011019	FAAH	gi|31542795|ref|NP_034303.2|	gi|31542795|ref|NP_034303.2|	fatty acid amide hydrolase [Mus musculus]	3	4	6.9	579	63191	7.9	MmNaOH-MM_liver_CNBrTi_206.3371.3371.2	2	2.9214	0.3644	1952.65	1953.2	1	47.058823	1	K.LQSGELSPEAVLFTYLGK.A	86	2	*
173	ENSG00000117594:ENSMUSG00000016194:NA	HSD11B1	gi|113680741|ref|NP_032314.2|	gi|113680741|ref|NP_032314.2|	hydroxysteroid 11-beta dehydrogenase 1 [Mus musculus]	1	2	4.5	292	32364	8.5	MmNaOH-MM_liver_CNBrTi_208.1857.1857.2	2	3.4391	0.3829	1335.64	1335.6	1	66.66667	2	K.SPLTPILLGNPGR.K	261	2	*
174	ENSG00000117242:ENSMUSG00000028757:ENSRNOG00000015079	DDOST	gi|46195798|ref|NP_031864.2|	gi|46195798|ref|NP_031864.2|	dolichyl-di-phosphooligosaccharide-protein glycotransferase [Mus	3	3	4.3	441	49028	5.8	MmNaOH-MM_liver_CNBrTi_211.2157.2157.2	2	2.1529	0.1265	1023.38	1023.1	3	78.57143	1	R.DTHSLFFR.S	43	2	*
174	ENSG00000117242:ENSMUSG00000028757:ENSRNOG00000015079	DDOST	gi|46195798|ref|NP_031864.2|	gi|46195798|ref|NP_031864.2|	dolichyl-di-phosphooligosaccharide-protein glycotransferase [Mus	3	3	4.3	441	49028	5.8	MmNaOH-MM_liver_CNBrTi_211.2159.2159.1	1	2.1701	0.2827	1022.46	1023.1	1	78.57143	1	R.DTHSLFFR.S	43	2	*
174	ENSG00000117242:ENSMUSG00000028757:ENSRNOG00000015079	DDOST	gi|46195798|ref|NP_031864.2|	gi|46195798|ref|NP_031864.2|	dolichyl-di-phosphooligosaccharide-protein glycotransferase [Mus	3	3	4.3	441	49028	5.8	MmNaOH-MM_liver_CNBrTi_202.2148.2148.2	2	4.0117	0.3287	1270.48	1270.5	1	85	1	R.TLVLLDNLNVR.D	32	2	*
175	ENSG00000105854:ENSMUSG00000032667:ENSRNOG00000009112	PON2	gi|34303979|ref|NP_899131.1|	gi|34303979|ref|NP_899131.1|	paraoxonase 2 [Mus musculus]	1	1	4.5	354	39617	5.8	MmNaOH-MM_liver_CNBrTi_109.2261.2261.2	2	3.5423	0.4163	1876.39	1877.2	1	63.333332	1	R.LFVYHPNHPPASEVLR.I	290	2	*
176	ENSG00000156049:ENSMUSG00000024697:ENSRNOG00000014840	GNA14	gi|31542895|ref|NP_032163.2|	gi|31542895|ref|NP_032163.2|;gi|6754004|ref|NP_034431.1|	guanine nucleotide binding protein, alpha 14 [Mus musculus]	1	1	5.9	355	41469	6.1	MmNaOH-MM_liver_CNBrTi_108.4778.4778.3	3	4.4669	0.3233	2493.75	2493.9	1	37.5	1	R.VRVPTTGIIEYPFDLENIIFR.M	178	2	
177	ENSG00000198171:ENSMUSG00000068290:ENSRNOG00000021232	C20orf116	gi|110350660|ref|NP_084108.1|	gi|110350660|ref|NP_084108.1|	hypothetical protein LOC77006 [Mus musculus]	1	2	5.4	315	35977	5.3	MmNaOH-MM_liver_CNBrTi_202.2551.2551.2	2	3.9752	0.4546	1859.5	1860.1	1	62.5	2	R.IQDLLTEGTLTGVIDDR.G	250	2	*
178	ENSG00000174640:ENSMUSG00000032548:ENSRNOG00000009005	SLCO2A1	gi|110625831|ref|NP_201571.2|	gi|110625831|ref|NP_201571.2|	solute carrier organic anion transporter family, member 2a1 [Mus m	1	4	1.6	643	70147	8.7	MmNaOH-MM_liver_CNBrTi_209.2101.2101.2	2	2.7586	0.2178	1219.45	1218.5	1	72.22222	4	R.FVFPLQTIPR.V	389	2	*
179	NA:ENSMUSG00000025197:ENSRNOG00000013291	CYP2C23	gi|48374085|ref|NP_001001446.2|	gi|48374085|ref|NP_001001446.2|	cytochrome P450, family 2, subfamily c, polypeptide 44 [Mus musc	1	3	3.2	494	56456	8.5	MmNaOH-MM_liver_CNBrTi_208.3407.3407.2	2	3.7684	0.3153	1736.81	1737	1	63.333332	3	K.GTAVFPFLSSILLDQK.E	388	2	*
180	ENSG00000115307:ENSMUSG00000068328:ENSRNOG00000007842	AUP1	gi|90403601|ref|NP_031543.2|	gi|90403601|ref|NP_031543.2|	ancient ubiquitous protein [Mus musculus]	1	1	6.4	439	49351	9.2	MmNaOH-MM_liver_CNBrTi_109.2516.2516.3	3	3.1918	0.1811	3020.6	3021.4	1	26.85185	1	R.LRPQSVQSSFPSPPSPSSDVQLTTLAHR.V	305	2	*
181	ENSG00000142655:ENSMUSG00000028975:ENSRNOG00000013498	PEX14	gi|9790153|ref|NP_062755.1|	gi|9790153|ref|NP_062755.1|	peroxisomal biogenesis factor 14 [Mus musculus]	2	2	5.9	376	41208	5.1	MmNaOH-MM_liver_CNBrTi_209.2393.2393.2	2	2.7224	0.2056	1114.99	1115.4	2	83.33333	1	R.YLLPLILGGR.E	130	2	*
181	ENSG00000142655:ENSMUSG00000028975:ENSRNOG00000013498	PEX14	gi|9790153|ref|NP_062755.1|	gi|9790153|ref|NP_062755.1|	peroxisomal biogenesis factor 14 [Mus musculus]	2	2	5.9	376	41208	5.1	MmNaOH-MM_liver_CNBrTi_207.1302.1302.2	2	3.2337	0.1728	1309.7	1310.5	2	72.72727	1	K.VQELAHELATAK.A	184	2	*
182	ENSG00000167536:ENSMUSG00000020834:ENSRNOG00000009673	DHRS13	gi|117647267|ref|NP_899109.2|	gi|117647267|ref|NP_899109.2|	dehydrogenase/reductase (SDR family) member 13 [Mus musculu	1	2	2.7	376	40745	7.9	MmNaOH-MM_liver_CNBrTi_207.0696.0696.2	2	2.3476	0.1797	1039.42	1039.2	1	77.77778	2	R.VVIVSSAAHR.R	165	2	*
183	ENSG00000167165:ENSMUSG00000054545:ENSRNOG00000018740	UGT1A9	gi|47059131|ref|NP_964006.1|	gi|47059131|ref|NP_964006.1|	UDP glucuronosyltransferase 1 family, polypeptide A9 [Mus muscu	4	61	5.7	528	59934	8.4	MmNaOH-MM_liver_CNBrTi_203.5853.5853.2	2	3.0751	0.2046	1013.35	1013.2	1	92.85714	57	R.IPQTVLWR.Y	324	2	
183	ENSG00000167165:ENSMUSG00000054545:ENSRNOG00000018740	UGT1A9	gi|47059131|ref|NP_964006.1|	gi|47059131|ref|NP_964006.1|	UDP glucuronosyltransferase 1 family, polypeptide A9 [Mus muscu	4	61	5.7	528	59934	8.4	MmNaOH-MM_liver_CNBrTi_207.2636.2636.2	2	2.1342	0.197	1300.39	1300.5	5	60.000004	1	K.YFSLPSVIFAR.G	158	2	*
183	ENSG00000167165:ENSMUSG00000054545:ENSRNOG00000018740	UGT1A9	gi|47059131|ref|NP_964006.1|	gi|47059131|ref|NP_964006.1|	UDP glucuronosyltransferase 1 family, polypeptide A9 [Mus muscu	4	61	5.7	528	59934	8.4	MmNaOH-MM_liver_CNBrTi_204.1766.1766.1	1	2.3725	0.1664	1012.57	1013.2	3	78.57143	2	R.IPQTVLWR.Y	324	2	
183	ENSG00000167165:ENSMUSG00000054545:ENSRNOG00000018740	UGT1A9	gi|47059131|ref|NP_964006.1|	gi|47059131|ref|NP_964006.1|	UDP glucuronosyltransferase 1 family, polypeptide A9 [Mus muscu	4	61	5.7	528	59934	8.4	MmNaOH-MM_liver_CNBrTi_207.0602.0602.2	2	2.7701	0.2575	1208	1208.4	1	70	1	R.YTGTRPSNLAK.N	332	2	
184	ENSG00000143870:ENSMUSG00000020571:NA	PDIA6	gi|149262992|ref|XP_001476035.1|	gi|149262992|ref|XP_001476035.1|;gi|58037267|ref|NP_0822	PREDICTED: similar to Protein disulfide isomerase associated 6 [	1	2	3.6	391	42858	6.7	MmNaOH-MM_liver_CNBrTi_202.2838.2838.2	2	4.2823	0.2745	1388.22	1387.6	1	76.92308	2	R.TGEAIVDAALSALR.Q	124	2	
185	ENSG00000211456:ENSMUSG00000025240:ENSRNOG00000005149	SACM1L	gi|13507622|ref|NP_109617.1|	gi|13507622|ref|NP_109617.1|	SAC1 (supressor of actin mutations 1, homolog)-like [Mus musculu	2	3	3.4	587	66944	7.3	MmNaOH-MM_liver_CNBrTi_202.2067.2067.2	2	3.1452	0.12	1115.43	1115.3	4	83.33333	1	R.TNVIQSLLAR.R	396	2	*
185	ENSG00000211456:ENSMUSG00000025240:ENSRNOG00000005149	SACM1L	gi|13507622|ref|NP_109617.1|	gi|13507622|ref|NP_109617.1|	SAC1 (supressor of actin mutations 1, homolog)-like [Mus musculu	2	3	3.4	587	66944	7.3	MmNaOH-MM_liver_CNBrTi_205.0631.0631.2	2	2.5397	0.1079	1165.78	1166.3	4	72.22222	2	R.ELSAQPEVHR.F	175	2	*
186	ENSG00000148343:ENSMUSG00000026858:ENSRNOG00000017513	FAM73B	gi|30425102|ref|NP_780601.1|	gi|30425102|ref|NP_780601.1|	hypothetical protein LOC108958 [Mus musculus]	2	3	6.7	593	65548	5.4	MmNaOH-MM_liver_CNBrTi_211.3671.3671.2	2	2.5501	0.1094	2397.99	2395.8	1	36.95652	1	R.SEILLGYLGAPVASSIGLNGPLPR.E	561	2	*
186	ENSG00000148343:ENSMUSG00000026858:ENSRNOG00000017513	FAM73B	gi|30425102|ref|NP_780601.1|	gi|30425102|ref|NP_780601.1|	hypothetical protein LOC108958 [Mus musculus]	2	3	6.7	593	65548	5.4	MmNaOH-MM_liver_CNBrTi_205.3330.3330.2	2	3.2893	0.2791	1776.96	1777	3	50	2	R.YTSVPALAEDILQLSR.R	543	2	*
187	ENSG00000119688:ENSMUSG00000021240:ENSRNOG00000011964	ABCD4	gi|6680614|ref|NP_033018.1|	gi|6680614|ref|NP_033018.1|	ATP-binding cassette, sub-family D, member 4 [Mus musculus]	2	3	5.6	606	68549	6.4	MmNaOH-MM_liver_CNBrTi_203.3439.3439.2	2	5.539	0.5205	2360.71	2361.5	1	55	1	K.YAVLDEATSALTEEAESELYR.I	544	2	*
187	ENSG00000119688:ENSMUSG00000021240:ENSRNOG00000011964	ABCD4	gi|6680614|ref|NP_033018.1|	gi|6680614|ref|NP_033018.1|	ATP-binding cassette, sub-family D, member 4 [Mus musculus]	2	3	5.6	606	68549	6.4	MmNaOH-MM_liver_CNBrTi_207.2694.2694.2	2	4.502	0.2271	1376.78	1376.6	1	83.33333	2	R.FLELAGLSSLVAR.T	496	2	*
188	ENSG00000185187:ENSMUSG00000025494:ENSRNOG00000015593	SIGIRR	gi|110625701|ref|NP_075546.2|	gi|110625701|ref|NP_075546.2|	single Ig IL-1 receptor related protein [Mus musculus]	1	2	3.7	409	46159	5.7	MmNaOH-MM_liver_CNBrTi_204.1790.1790.2	2	4.1222	0.3526	1624.86	1625.8	1	71.42857	2	R.GPVFGEPPTPLQETR.I	359	2	*
189	ENSG00000172482:ENSMUSG00000026272:ENSRNOG00000023856	AGXT	gi|111038130|ref|NP_057911.2|	gi|111038130|ref|NP_057911.2|	alanine-glyoxylate aminotransferase [Mus musculus]	1	2	3.1	414	45912	8.2	MmNaOH-MM_liver_CNBrTi_207.1754.1754.2	2	2.9206	0.2793	1305.43	1305.6	1	75	2	R.LLLGPGPSNLAPR.V	46	2	*
190	ENSG00000127463:ENSMUSG00000078517:ENSRNOG00000018097	KIAA0090	gi|31542273|ref|NP_666269.2|	gi|31542273|ref|NP_666269.2|;gi|85861260|ref|NP_00103428	hypothetical protein LOC230866 isoform 1 [Mus musculus]	2	2	3.6	997	111605	7.4	MmNaOH-MM_liver_CNBrTi_108.4392.4392.3	3	4.0251	0.3088	2334.68	2334.6	1	32.894737	1	R.QLHELAPSIFFYLVDAEQGR.L	665	2	
190	ENSG00000127463:ENSMUSG00000078517:ENSRNOG00000018097	KIAA0090	gi|31542273|ref|NP_666269.2|	gi|31542273|ref|NP_666269.2|;gi|85861260|ref|NP_00103428	hypothetical protein LOC230866 isoform 1 [Mus musculus]	2	2	3.6	997	111605	7.4	MmNaOH-MM_liver_CNBrTi_108.3304.3304.2	2	2.6847	0.3174	1630.43	1630	1	46.666668	1	R.HLLIGLPSGAILSLPK.A	864	2	
191	ENSG00000167114:ENSMUSG00000059316:ENSRNOG00000014369	SLC27A4	gi|45597453|ref|NP_036119.1|	gi|45597453|ref|NP_036119.1|	solute carrier family 27 (fatty acid transporter), member 4 [Mus mu	1	3	1.4	643	72319	8.6	MmNaOH-MM_liver_CNBrTi_204.2130.2130.2	2	3.1642	0.1851	1109.03	1108.4	7	75	3	R.ILSFVYPIR.L	409	2	*
192	ENSG00000188338:ENSMUSG00000010064:ENSRNOG00000016827	SLC38A3	gi|34328322|ref|NP_076294.2|	gi|34328322|ref|NP_076294.2|	N system amino acids transporter NAT-1 [Mus musculus]	1	1	3.4	505	55592	7.1	MmNaOH-MM_liver_CNBrTi_102.2183.2183.2	2	3.5168	0.3384	1833.13	1834.1	2	46.875	1	K.HLEGLLPVGVPTTDTQR.T	18	2	*
193	ENSG00000164040:ENSMUSG00000049940:ENSRNOG00000014051	PGRMC2	gi|82889417|ref|XP_130859.7|	gi|82889417|ref|XP_130859.7|	PREDICTED: progesterone receptor membrane component 2 isof	1	1	6.5	217	23334	5.1	MmNaOH-MM_liver_CNBrTi_211.2622.2622.2	2	3.0792	0.3959	1473.82	1473.7	1	65.38461	1	K.FYGPAGPYGIFAGR.D	130	2	*
194	ENSG00000142973:ENSMUSG00000028713:ENSRNOG00000009741	CYP4B1	gi|6681123|ref|NP_031849.1|	gi|6681123|ref|NP_031849.1|	cytochrome P450, family 4, subfamily b, polypeptide 1 [Mus muscu	1	1	2.3	511	58900	8.4	MmNaOH-MM_liver_CNBrTi_106.4492.4492.2	2	4.3911	0.3609	1383.65	1383.6	1	86.36364	1	R.HLDFLDILLGAR.D	282	2	*
195	ENSG00000139641:ENSMUSG00000025366:ENSRNOG00000003909	FAM62A	gi|33859650|ref|NP_035973.1|	gi|33859650|ref|NP_035973.1|	extended synaptotagmin-like protein 1 [Mus musculus]	2	5	2.7	1092	121553	6	MmNaOH-MM_liver_CNBrTi_205.2571.2571.2	2	3.4226	0.3141	1310.3	1310.6	1	75	4	R.ALTLGALTLPLAR.L	541	2	
195	ENSG00000139641:ENSMUSG00000025366:ENSRNOG00000003909	FAM62A	gi|33859650|ref|NP_035973.1|	gi|33859650|ref|NP_035973.1|	extended synaptotagmin-like protein 1 [Mus musculus]	2	5	2.7	1092	121553	6	MmNaOH-MM_liver_CNBrTi_211.3501.3501.2	2	2.5598	0.1783	1788.93	1790.2	7	43.333332	1	R.LLVPLVPDLQDVAQLR.S	298	2	
196	ENSG00000149485:ENSMUSG00000010663:ENSRNOG00000020480	FADS1	gi|22164784|ref|NP_666206.1|	gi|22164784|ref|NP_666206.1|	delta-5 desaturase [Mus musculus]	2	2	5.8	447	52323	9.3	MmNaOH-MM_liver_CNBrTi_202.1968.1968.2	2	3.018	0.3121	1329.33	1329.5	1	83.33333	1	R.YFTWEEVAQR.S	21	2	*
196	ENSG00000149485:ENSMUSG00000010663:ENSRNOG00000020480	FADS1	gi|22164784|ref|NP_666206.1|	gi|22164784|ref|NP_666206.1|	delta-5 desaturase [Mus musculus]	2	2	5.8	447	52323	9.3	MmNaOH-MM_liver_CNBrTi_205.1563.1563.2	2	2.912	0.2209	1574.59	1574.8	3	53.333336	1	M.APDPVPTPGPASAQLR.Q	2	1	*
197	ENSG00000119777:ENSMUSG00000038828:ENSRNOG00000008812	TMEM214	gi|31559970|ref|NP_653108.2|	gi|31559970|ref|NP_653108.2|	hypothetical protein LOC68796 [Mus musculus]	1	3	1.7	687	76430	9.3	MmNaOH-MM_liver_CNBrTi_207.2371.2371.2	2	2.7892	0.222	1337.47	1337.6	1	68.181816	3	K.ALSPFAIAYLDR.L	289	2	*
198	ENSG00000125912:ENSMUSG00000020238:ENSRNOG00000004793	NCLN	gi|33469043|ref|NP_598770.1|	gi|33469043|ref|NP_598770.1|;gi|51873031|ref|NP_064555.2|	nicalin homolog [Mus musculus]	1	1	2.5	563	62908	6.5	MmNaOH-MM_liver_CNBrTi_110.2262.2262.3	3	4.552	0.3373	1665.35	1664.9	1	51.923077	1	R.RLPAFTLSHLESHR.A	379	2	
200	ENSG00000086848:ENSMUSG00000032059:ENSRNOG00000010877	ALG9	gi|19527202|ref|NP_598742.1|	gi|19527202|ref|NP_598742.1|	alpha-1,2-mannosyltransferase ALG9 [Mus musculus]	1	1	3.4	611	69561	8.9	MmNaOH-MM_liver_CNBrTi_102.5047.5047.2	2	2.8253	0.2666	2570.19	2569.9	4	35	1	R.FPSSFLLPDNWQLQFIPSEFR.G	475	2	
201	ENSG00000204221:ENSMUSG00000024312:ENSRNOG00000029500	WDR46	gi|10181122|ref|NP_065628.1|	gi|10181122|ref|NP_065628.1|	WD repeat domain 46 [Mus musculus]	1	1	4	622	69048	9.8	MmNaOH-MM_liver_CNBrTi_107.0111.0111.2	2	2.2716	0.1388	2537.74	2535.8	1	31.25	1	R.GGVRAVAVDSTGTYMATSGLDHQLK.I	359	2	*
202	ENSG00000196620:ENSMUSG00000070704:ENSRNOG00000001980	UGT2B15	gi|71274184|ref|NP_001025038.1|	gi|71274184|ref|NP_001025038.1|	UDP glucuronosyltransferase 2 family, polypeptide B36 [Mus musc	3	8	4.5	530	61041	8.3	MmNaOH-MM_liver_CNBrTi_208.2689.2689.2	2	4.1506	0.3238	1496.41	1495.8	1	73.07692	6	K.ANAIAWALAQIPQK.V	322	2	
202	ENSG00000196620:ENSMUSG00000070704:ENSRNOG00000001980	UGT2B15	gi|71274184|ref|NP_001025038.1|	gi|71274184|ref|NP_001025038.1|	UDP glucuronosyltransferase 2 family, polypeptide B36 [Mus musc	3	8	4.5	530	61041	8.3	MmNaOH-MM_liver_CNBrTi_202.0567.0567.2	2	2.3979	0.1805	1027.94	1028.2	2	72.22222	1	K.TPATLGPNTR.I	344	2	*
202	ENSG00000196620:ENSMUSG00000070704:ENSRNOG00000001980	UGT2B15	gi|71274184|ref|NP_001025038.1|	gi|71274184|ref|NP_001025038.1|	UDP glucuronosyltransferase 2 family, polypeptide B36 [Mus musc	3	8	4.5	530	61041	8.3	MmNaOH-MM_liver_CNBrTi_207.2704.2704.3	3	4.5	0.1622	1494.94	1495.8	1	53.846157	1	K.ANAIAWALAQIPQK.V	322	2	
203	ENSG00000109971:ENSMUSG00000015656:ENSRNOG00000030228	HSPA8	gi|31981690|ref|NP_112442.2|	gi|31981690|ref|NP_112442.2|	heat shock protein 8 [Mus musculus]	1	1	2	646	70871	5.5	MmNaOH-MM_liver_CNBrTi_101.0564.0564.2	2	2.6062	0.2078	1488.37	1488.6	6	62.5	1	R.TTPSYVAFTDTER.L	37	2	
204	NA:NA:ENSRNOG00000000790	LOC676837	gi|149269298|ref|XP_001003707.2|	gi|149269298|ref|XP_001003707.2|;gi|149274805|ref|XP_001	PREDICTED: similar to MHC class I antigen isoform 2 [Mus muscu	1	2	2.2	552	61771	8.1	MmNaOH-MM_liver_CNBrTi_207.1938.1938.2	2	3.7883	0.2549	1622.47	1622.7	1	86.36364	2	R.WIEQEGPEYWER.N	242	2	
205	ENSG00000103227:ENSMUSG00000002279:ENSRNOG00000000230	TMEM112	gi|31981342|ref|NP_083900.2|	gi|31981342|ref|NP_083900.2|	hypothetical protein LOC76483 [Mus musculus]	1	2	1.6	567	65094	9.3	MmNaOH-MM_liver_CNBrTi_207.1835.1835.2	2	2.7539	0.2077	1060.1	1060.3	5	81.25	2	R.IGPYFPPLR.Q	535	2	*
206	ENSG00000065361:ENSMUSG00000018166:ENSRNOG00000004964	ERBB3	gi|61098019|ref|NP_034283.1|	gi|61098019|ref|NP_034283.1|	v-erb-b2 erythroblastic leukemia viral oncogene homolog 3 [Mus m	1	2	2	1339	147613	6.6	MmNaOH-MM_liver_CNBrTi_108.5603.5603.3	3	4.109	0.3292	2951.06	2951.4	1	31.730768	2	R.LLGLCPGSSLQLVTQYLPLGSLLDHVR.Q	772	2	*
207	ENSG00000108829:ENSMUSG00000020869:ENSRNOG00000003524	LRRC59	gi|19527026|ref|NP_598568.1|	gi|19527026|ref|NP_598568.1|;gi|56605670|ref|NP_00100828	leucine rich repeat containing 59 [Mus musculus]	1	1	3.9	307	34877	9.5	MmNaOH-MM_liver_CNBrTi_202.2302.2302.2	2	2.8979	0.2241	1316.35	1316.6	2	63.636364	1	R.LVTLPVSFAQLK.N	97	2	
208	ENSG00000153707:ENSMUSG00000028399:ENSRNOG00000005711	PTPRD	gi|62177150|ref|NP_001014310.1|	gi|62177150|ref|NP_001014310.1|;gi|90403603|ref|NP_03534	protein tyrosine phosphatase, receptor type, D isoform A [Mus mus	2	4	2.8	1254	141640	6.5	MmNaOH-MM_liver_CNBrTi_205.3085.3085.2	2	3.5953	0.3287	2599.51	2600.9	1	45.652176	1	R.VLLSAIEGIPGSDYVNANYIDGYR.K	739	2	
208	ENSG00000153707:ENSMUSG00000028399:ENSRNOG00000005711	PTPRD	gi|62177150|ref|NP_001014310.1|	gi|62177150|ref|NP_001014310.1|;gi|90403603|ref|NP_03534	protein tyrosine phosphatase, receptor type, D isoform A [Mus mus	2	4	2.8	1254	141640	6.5	MmNaOH-MM_liver_CNBrTi_206.1231.1231.2	2	3.4828	0.2925	1309	1309.4	2	80	3	R.YANVIAYDHSR.V	728	2	
209	ENSG00000130714:ENSMUSG00000039254:ENSRNOG00000010477	POMT1	gi|21553107|ref|NP_660127.1|	gi|21553107|ref|NP_660127.1|	protein-O-mannosyltransferase 1 [Mus musculus]	1	1	1.7	746	85234	8.3	MmNaOH-MM_liver_CNBrTi_110.1986.1986.2	2	2.7047	0.1758	1526.03	1526.8	4	58.333332	1	R.HQLVVNNPPRPVR.H	384	2	*
210	ENSG00000197635:ENSMUSG00000035000:ENSRNOG00000030763	DPP4	gi|6753674|ref|NP_034204.1|	gi|6753674|ref|NP_034204.1|	dipeptidylpeptidase 4 [Mus musculus]	1	1	2.8	760	87437	6.4	MmNaOH-MM_liver_CNBrTi_107.5747.5747.2	2	3.0925	0.277	2344.08	2342.6	2	40	1	R.LNWATYLASTENIIVASFDGR.G	555	2	*
211	ENSG00000168036:ENSMUSG00000006932:ENSRNOG00000019139	CTNNB1	gi|6671684|ref|NP_031640.1|	gi|6671684|ref|NP_031640.1|	catenin (cadherin associated protein), beta 1, 88kDa [Mus musculu	1	1	2.7	781	85471	5.9	MmNaOH-MM_liver_CNBrTi_101.6250.6250.2	2	2.4464	0.1262	2429.8	2429.9	1	35	1	R.GLNTIPLFVQLLYSPIENIQR.V	592	2	*
212	ENSG00000072274:ENSMUSG00000022797:ENSRNOG00000001766	TFRC	gi|11596855|ref|NP_035768.1|	gi|11596855|ref|NP_035768.1|	transferrin receptor [Mus musculus]	1	2	2.1	763	85731	6.6	MmNaOH-MM_liver_CNBrTi_206.2475.2475.2	2	3.2899	0.325	1746.52	1746.9	1	56.666668	2	R.SAFSNLFGGEPLSYTR.F	7	2	*
213	ENSG00000004939:ENSMUSG00000006574:ENSRNOG00000020951	SLC4A1	gi|6755560|ref|NP_035533.1|	gi|6755560|ref|NP_035533.1|	solute carrier family 4 (anion exchanger), member 1 [Mus musculu	1	1	1.2	929	103135	5.4	MmNaOH-MM_liver_CNBrTi_107.2431.2431.2	2	2.3841	0.2261	1311.91	1311.6	1	70	1	R.GWVIHPLGLYR.L	665	2	*
214	ENSG00000205702:ENSMUSG00000068085:ENSRNOG00000029128	CYP2D7P1	gi|82958348|ref|XP_910862.1|	gi|149266772|ref|XP_001479975.1|;gi|82958348|ref|XP_9108	PREDICTED: similar to Cytochrome P450 2D11 (CYPIID11) (P450	7	66	13.9	504	57002	6.5	MmNaOH-MM_liver_CNBrTi_101.2919.2919.1	1	2.7825	0.2275	1363.75	1364.5	1	68.181816	1	R.NLTDAFLAEIEK.V	273	2	
214	ENSG00000205702:ENSMUSG00000068085:ENSRNOG00000029128	CYP2D7P1	gi|82958348|ref|XP_910862.1|	gi|149266772|ref|XP_001479975.1|;gi|82958348|ref|XP_9108	PREDICTED: similar to Cytochrome P450 2D11 (CYPIID11) (P450	7	66	13.9	504	57002	6.5	MmNaOH-MM_liver_CNBrTi_106.1418.1418.2	2	2.6953	0.1275	965.99	966.13	1	100	1	R.RFSVSTLR.N	136	2	
214	ENSG00000205702:ENSMUSG00000068085:ENSRNOG00000029128	CYP2D7P1	gi|82958348|ref|XP_910862.1|	gi|149266772|ref|XP_001479975.1|;gi|82958348|ref|XP_9108	PREDICTED: similar to Cytochrome P450 2D11 (CYPIID11) (P450	7	66	13.9	504	57002	6.5	MmNaOH-MM_liver_CNBrTi_104.2438.2438.3	3	4.155	0.299	1485.52	1485.7	1	60.000004	5	R.RFEYEDPFLIR.M	197	2	
214	ENSG00000205702:ENSMUSG00000068085:ENSRNOG00000029128	CYP2D7P1	gi|82958348|ref|XP_910862.1|	gi|149266772|ref|XP_001479975.1|;gi|82958348|ref|XP_9108	PREDICTED: similar to Cytochrome P450 2D11 (CYPIID11) (P450	7	66	13.9	504	57002	6.5	MmNaOH-MM_liver_CNBrTi_110.4854.4854.3	3	4.1092	0.2543	3020.93	3023.5	6	25.961538	1	R.IPGLADMVFQGQKSFMAILDNLLTENR.T	236	2	
214	ENSG00000205702:ENSMUSG00000068085:ENSRNOG00000029128	CYP2D7P1	gi|82958348|ref|XP_910862.1|	gi|149266772|ref|XP_001479975.1|;gi|82958348|ref|XP_9108	PREDICTED: similar to Cytochrome P450 2D11 (CYPIID11) (P450	7	66	13.9	504	57002	6.5	MmNaOH-MM_liver_CNBrTi_211.1929.1929.2	2	2.5817	0.1741	965.69	966.13	1	85.71429	1	R.RFSVSTLR.N	136	2	
214	ENSG00000205702:ENSMUSG00000068085:ENSRNOG00000029128	CYP2D7P1	gi|82958348|ref|XP_910862.1|	gi|149266772|ref|XP_001479975.1|;gi|82958348|ref|XP_9108	PREDICTED: similar to Cytochrome P450 2D11 (CYPIID11) (P450	7	66	13.9	504	57002	6.5	MmNaOH-MM_liver_CNBrTi_209.1365.1365.3	3	3.3945	0.0946	1428.01	1427.6	1	52.272724	1	M.PYTNAVIHEVQR.F	357	1	
214	ENSG00000205702:ENSMUSG00000068085:ENSRNOG00000029128	CYP2D7P1	gi|82958348|ref|XP_910862.1|	gi|149266772|ref|XP_001479975.1|;gi|82958348|ref|XP_9108	PREDICTED: similar to Cytochrome P450 2D11 (CYPIID11) (P450	7	66	13.9	504	57002	6.5	MmNaOH-MM_liver_CNBrTi_203.2749.2749.2	2	4.4631	0.2852	1364.38	1364.5	1	86.36364	50	R.NLTDAFLAEIEK.V	273	2	
214	ENSG00000205702:ENSMUSG00000068085:ENSRNOG00000029128	CYP2D7P1	gi|82958348|ref|XP_910862.1|	gi|149266772|ref|XP_001479975.1|;gi|82958348|ref|XP_9108	PREDICTED: similar to Cytochrome P450 2D11 (CYPIID11) (P450	7	66	13.9	504	57002	6.5	MmNaOH-MM_liver_CNBrTi_102.2694.2694.2	2	3.1936	0.2709	1485.56	1485.7	1	70	5	R.RFEYEDPFLIR.M	197	2	
214	ENSG00000205702:ENSMUSG00000068085:ENSRNOG00000029128	CYP2D7P1	gi|82958348|ref|XP_910862.1|	gi|149266772|ref|XP_001479975.1|;gi|82958348|ref|XP_9108	PREDICTED: similar to Cytochrome P450 2D11 (CYPIID11) (P450	7	66	13.9	504	57002	6.5	MmNaOH-MM_liver_CNBrTi_101.2930.2930.2	2	4.2944	0.2241	1364.85	1364.5	1	81.818184	1	R.NLTDAFLAEIEK.V	273	2	
215	ENSG00000205702:ENSMUSG00000068085:ENSRNOG00000029128	CYP2D7P1	gi|149266772|ref|XP_001479975.1|	gi|149266772|ref|XP_001479975.1|;gi|82958348|ref|XP_9108	PREDICTED: similar to P45016a-ms2 [Mus musculus]	9	70	17.1	504	56988	6.3	MmNaOH-MM_liver_CNBrTi_106.1418.1418.2	2	2.6953	0.1275	965.99	966.13	1	100	1	R.RFSVSTLR.N	136	2	
215	ENSG00000205702:ENSMUSG00000068085:ENSRNOG00000029128	CYP2D7P1	gi|149266772|ref|XP_001479975.1|	gi|149266772|ref|XP_001479975.1|;gi|82958348|ref|XP_9108	PREDICTED: similar to P45016a-ms2 [Mus musculus]	9	70	17.1	504	56988	6.3	MmNaOH-MM_liver_CNBrTi_104.1894.1894.2	2	3.2706	0.1653	1500.74	1501.7	1	80	5	R.RFEYEDPYLIR.M	197	2	
215	ENSG00000205702:ENSMUSG00000068085:ENSRNOG00000029128	CYP2D7P1	gi|149266772|ref|XP_001479975.1|	gi|149266772|ref|XP_001479975.1|;gi|82958348|ref|XP_9108	PREDICTED: similar to P45016a-ms2 [Mus musculus]	9	70	17.1	504	56988	6.3	MmNaOH-MM_liver_CNBrTi_101.1700.1700.1	1	2.17	0.0907	1500.75	1501.7	2	55	2	R.RFEYEDPYLIR.M	197	2	
215	ENSG00000205702:ENSMUSG00000068085:ENSRNOG00000029128	CYP2D7P1	gi|149266772|ref|XP_001479975.1|	gi|149266772|ref|XP_001479975.1|;gi|82958348|ref|XP_9108	PREDICTED: similar to P45016a-ms2 [Mus musculus]	9	70	17.1	504	56988	6.3	MmNaOH-MM_liver_CNBrTi_102.2012.2012.3	3	4.0934	0.1859	1502.42	1501.7	1	57.5	6	R.RFEYEDPYLIR.M	197	2	
215	ENSG00000205702:ENSMUSG00000068085:ENSRNOG00000029128	CYP2D7P1	gi|149266772|ref|XP_001479975.1|	gi|149266772|ref|XP_001479975.1|;gi|82958348|ref|XP_9108	PREDICTED: similar to P45016a-ms2 [Mus musculus]	9	70	17.1	504	56988	6.3	MmNaOH-MM_liver_CNBrTi_101.2930.2930.2	2	4.2944	0.2241	1364.85	1364.5	1	81.818184	1	R.NLTDAFLAEIEK.V	273	2	
215	ENSG00000205702:ENSMUSG00000068085:ENSRNOG00000029128	CYP2D7P1	gi|149266772|ref|XP_001479975.1|	gi|149266772|ref|XP_001479975.1|;gi|82958348|ref|XP_9108	PREDICTED: similar to P45016a-ms2 [Mus musculus]	9	70	17.1	504	56988	6.3	MmNaOH-MM_liver_CNBrTi_209.1365.1365.3	3	3.3945	0.0946	1428.01	1427.6	1	52.272724	1	M.PYTNAVIHEVQR.F	357	1	
215	ENSG00000205702:ENSMUSG00000068085:ENSRNOG00000029128	CYP2D7P1	gi|149266772|ref|XP_001479975.1|	gi|149266772|ref|XP_001479975.1|;gi|82958348|ref|XP_9108	PREDICTED: similar to P45016a-ms2 [Mus musculus]	9	70	17.1	504	56988	6.3	MmNaOH-MM_liver_CNBrTi_101.2919.2919.1	1	2.7825	0.2275	1363.75	1364.5	1	68.181816	1	R.NLTDAFLAEIEK.V	273	2	
215	ENSG00000205702:ENSMUSG00000068085:ENSRNOG00000029128	CYP2D7P1	gi|149266772|ref|XP_001479975.1|	gi|149266772|ref|XP_001479975.1|;gi|82958348|ref|XP_9108	PREDICTED: similar to P45016a-ms2 [Mus musculus]	9	70	17.1	504	56988	6.3	MmNaOH-MM_liver_CNBrTi_101.4840.4840.2	2	2.5707	0.1714	1776.66	1776.1	6	43.333332	1	M.LNNAVCNVIASLIFAR.R	181	1	
215	ENSG00000205702:ENSMUSG00000068085:ENSRNOG00000029128	CYP2D7P1	gi|149266772|ref|XP_001479975.1|	gi|149266772|ref|XP_001479975.1|;gi|82958348|ref|XP_9108	PREDICTED: similar to P45016a-ms2 [Mus musculus]	9	70	17.1	504	56988	6.3	MmNaOH-MM_liver_CNBrTi_211.1929.1929.2	2	2.5817	0.1741	965.69	966.13	1	85.71429	1	R.RFSVSTLR.N	136	2	
215	ENSG00000205702:ENSMUSG00000068085:ENSRNOG00000029128	CYP2D7P1	gi|149266772|ref|XP_001479975.1|	gi|149266772|ref|XP_001479975.1|;gi|82958348|ref|XP_9108	PREDICTED: similar to P45016a-ms2 [Mus musculus]	9	70	17.1	504	56988	6.3	MmNaOH-MM_liver_CNBrTi_110.4854.4854.3	3	4.1092	0.2543	3020.93	3023.5	6	25.961538	1	R.IPGLADMVFQGQKSFMAILDNLLTENR.T	236	2	
215	ENSG00000205702:ENSMUSG00000068085:ENSRNOG00000029128	CYP2D7P1	gi|149266772|ref|XP_001479975.1|	gi|149266772|ref|XP_001479975.1|;gi|82958348|ref|XP_9108	PREDICTED: similar to P45016a-ms2 [Mus musculus]	9	70	17.1	504	56988	6.3	MmNaOH-MM_liver_CNBrTi_203.2749.2749.2	2	4.4631	0.2852	1364.38	1364.5	1	86.36364	50	R.NLTDAFLAEIEK.V	273	2	
216	ENSG00000101290:ENSMUSG00000058793:ENSRNOG00000021265	CDS2	gi|20149726|ref|NP_619592.1|	gi|20149726|ref|NP_619592.1|	phosphatidate cytidylyltransferase 2 [Mus musculus]	1	1	3.8	444	51314	7	MmNaOH-MM_liver_CNBrTi_207.3047.3047.2	2	2.7343	0.2615	1916.95	1917.2	1	50	1	R.LQEYNIPGVIQSAIGWK.T	311	2	*
217	ENSG00000198561:ENSMUSG00000034101:ENSRNOG00000030790	CTNND1	gi|83745122|ref|NP_031641.2|	gi|83745122|ref|NP_031641.2|	catenin, delta 1 isoform 1 [Mus musculus]	2	2	2.3	938	104925	6.9	MmNaOH-MM_liver_CNBrTi_205.0643.0643.2	2	2.4882	0.2177	1027.14	1027.1	3	72.22222	1	R.VGGSSVDLHR.F	265	2	*
217	ENSG00000198561:ENSMUSG00000034101:ENSRNOG00000030790	CTNND1	gi|83745122|ref|NP_031641.2|	gi|83745122|ref|NP_031641.2|	catenin, delta 1 isoform 1 [Mus musculus]	2	2	2.3	938	104925	6.9	MmNaOH-MM_liver_CNBrTi_202.2218.2218.2	2	3.3771	0.3792	1450.22	1450.7	1	68.181816	1	R.GYELLFQPEVVR.I	655	2	*
218	ENSG00000046604:ENSMUSG00000044393:ENSRNOG00000016526	DSG2	gi|22779879|ref|NP_031909.1|	gi|22779879|ref|NP_031909.1|	desmoglein 2 [Mus musculus]	1	1	1.1	1122	122397	5.3	MmNaOH-MM_liver_CNBrTi_109.2009.2009.2	2	2.5792	0.2204	1263.44	1263.4	2	68.181816	1	R.SLLTAGATHHVR.T	729	2	*
219	ENSG00000087111:ENSMUSG00000041958:ENSRNOG00000011366	PIGS	gi|41351529|ref|NP_958808.1|	gi|41351529|ref|NP_958808.1|	phosphatidylinositol glycan anchor biosynthesis, class S [Mus mus	1	1	3.1	555	61711	6.9	MmNaOH-MM_liver_CNBrTi_212.2695.2695.2	2	2.828	0.145	1814.09	1814.1	1	50	1	R.APLPYSDISGLNALLLR.L	44	2	*
220	ENSG00000167930:ENSMUSG00000024187:ENSRNOG00000028241	ITFG3	gi|46402185|ref|NP_997100.1|	gi|46402185|ref|NP_997100.1|	integrin alpha FG-GAP repeat containing 3 [Mus musculus]	1	1	2.9	555	60576	5.7	MmNaOH-MM_liver_CNBrTi_211.1987.1987.2	2	4.1041	0.4774	1684.6	1684.8	1	66.66667	1	R.VIHLGEGSSDSDQAIR.D	528	2	*
221	ENSG00000033867:ENSMUSG00000021733:ENSRNOG00000005957	SLC4A7	gi|117320529|ref|NP_001028442.2|	gi|117320529|ref|NP_001028442.2|	solute carrier family 4, sodium bicarbonate cotransporter, member	1	2	1.6	1131	127221	6.4	MmNaOH-MM_liver_CNBrTi_211.3227.3227.2	2	3.1494	0.2235	1834.21	1834.2	1	50	2	R.LAPAVLLSGLTEVPVPTR.F	330	2	*
222	ENSG00000179087:ENSMUSG00000068587:ENSRNOG00000026177	MGAM	gi|149255014|ref|XP_001481364.1|	gi|149255014|ref|XP_001481364.1|;gi|149255059|ref|XP_001	PREDICTED: similar to maltase-glucoamylase [Mus musculus]	1	6	0.3	3629	414322	5.7	MmNaOH-MM_liver_CNBrTi_206.2499.2499.2	2	2.7124	0.141	1233.39	1233.4	3	72.22222	6	R.AYVAFPDFFR.D	1361	2	
223	ENSG00000118705:ENSMUSG00000027642:ENSRNOG00000007492	RPN2	gi|34996495|ref|NP_062616.2|	gi|34996495|ref|NP_062616.2|	ribophorin II [Mus musculus]	1	1	3.5	631	69063	5.8	MmNaOH-MM_liver_CNBrTi_207.3308.3308.2	2	3.8892	0.3692	2270.99	2271.4	1	45.238094	1	K.NFESLSEAFSVASAAAALSQNR.Y	245	2	*
224	ENSG00000091039:ENSMUSG00000020189:ENSRNOG00000026962	OSBPL8	gi|51243036|ref|NP_001003717.1|	gi|51243036|ref|NP_001003717.1|	oxysterol-binding protein-like protein 8 isoform b [Mus musculus]	1	1	1.3	847	96981	7.5	MmNaOH-MM_liver_CNBrTi_206.2376.2376.2	2	3.4913	0.3037	1284.57	1284.6	1	80	1	R.VVLPTFILEPR.S	381	2	
225	ENSG00000130402:ENSMUSG00000054808:ENSRNOG00000020433	ACTN4	gi|11230802|ref|NP_068695.1|	gi|11230802|ref|NP_068695.1|;gi|61097906|ref|NP_598917.1|	actinin alpha 4 [Mus musculus]	1	1	1.3	912	104977	5.4	MmNaOH-MM_liver_CNBrTi_212.2661.2661.2	2	3.6373	0.0962	1387.33	1387.6	1	77.27273	1	R.VGWEQLLTTIAR.T	735	2	
226	ENSG00000032444:ENSMUSG00000004565:ENSRNOG00000000977	PNPLA6	gi|7657401|ref|NP_056616.1|	gi|7657401|ref|NP_056616.1|	patatin-like phospholipase domain containing 6 [Mus musculus]	1	1	1.1	1327	146562	8	MmNaOH-MM_liver_CNBrTi_204.2499.2499.2	2	2.6891	0.311	1591.91	1591.8	3	53.571426	1	R.ALLGASALDSIQEFR.L	775	2	*
227	ENSG00000112851:ENSMUSG00000021709:NA	ERBB2IP	gi|54607112|ref|NP_067538.2|	gi|54607112|ref|NP_067538.2|;gi|54607114|ref|NP_00100586	Erbb2 interacting protein isoform 2 [Mus musculus]	1	1	0.9	1376	154327	5.6	MmNaOH-MM_liver_CNBrTi_212.2492.2492.2	2	3.2433	0.27	1321.54	1321.6	1	72.72727	1	R.LTFIPGFIGSLR.Q	219	2	

rk	ORTHO_GROUPS	GENE_NAME	Locus	Proteins In Group	Description	Sequence Count	Spectrum Count	Coverage	Length	MW	pI	MatchID	Z	XCorr	DeltCN	M+H+	CalcM +H+	SpRk	Ion Proportion	Count	Sequence	Sequence Position	Tryptic	Unique
228	ENSG00000075568:ENSMUSG00000026116:ENSRNOG00000017265	TMEM131	gi|119372306|ref|NP_061360.2|	gi|119372306|ref|NP_061360.2|;gi|149233754|ref|XP_001477	transmembrane protein 131 [Mus musculus]	1	1	0.7	1877	204650	8.5	MmNaOH-MM_liver_CNBrTi_212.1641.1641.2	2	2.114	0.1862	1540.44	1539.7	1	53.846157	1	R.LSPAPLTHPSHPER.A	1317	2	
229			Contaminant_GR78_HUMAN	Contaminant_GR78_HUMAN;Contaminant_GR78_MESAU;C	owl|P11021| 78 KD GLUCOSE REGULATED PROTEIN PRECUR	1	2	2.1	653	72116	5.1	MmNaOH-MM_liver_CNBrTi_201.1726.1726.2	2	2.9561	0.2783	1568.68	1567.7	1	57.692307	1	R.ITPSYVAFTPEGER.L	61	2	
229			Contaminant_GR78_HUMAN	Contaminant_GR78_HUMAN;Contaminant_GR78_MESAU;C	owl|P11021| 78 KD GLUCOSE REGULATED PROTEIN PRECUR	1	2	2.1	653	72116	5.1	MmNaOH-MM_liver_CNBrTi_101.1662.1662.2	2	3.177	0.3412	1567.52	1567.7	1	53.846157	1	R.ITPSYVAFTPEGER.L	61	2	
230			Contaminant_gi|7463016|pir||S77957	Contaminant_gi|7463016|pir||S77957	lysyl endopeptidase (EC 3.4.21.50) - Lysobacter enzymogenes	4	6	12.3	269	27961	6.7	MmNaOH-MM_liver_CNBrTi_212.1827.1827.2	2	4.5079	0.4506	1921.7	1921.1	1	58.823532	2	R.DQNFAGATAIHHPNVAEK.R	138	2	*
230			Contaminant_gi|7463016|pir||S77957	Contaminant_gi|7463016|pir||S77957	lysyl endopeptidase (EC 3.4.21.50) - Lysobacter enzymogenes	4	6	12.3	269	27961	6.7	MmNaOH-MM_liver_CNBrTi_108.1355.1355.3	3	3.3723	0.2224	2077.18	2077.3	1	37.5	1	R.DQNFAGATAIHHPNVAEKR.I	138	2	*
230			Contaminant_gi|7463016|pir||S77957	Contaminant_gi|7463016|pir||S77957	lysyl endopeptidase (EC 3.4.21.50) - Lysobacter enzymogenes	4	6	12.3	269	27961	6.7	MmNaOH-MM_liver_CNBrTi_201.0006.0006.2	2	3.8141	0.2849	1428.33	1428.5	1	76.92308	2	R.VFTSWTGGGTSATR.L	230	2	*
230			Contaminant_gi|7463016|pir||S77957	Contaminant_gi|7463016|pir||S77957	lysyl endopeptidase (EC 3.4.21.50) - Lysobacter enzymogenes	4	6	12.3	269	27961	6.7	MmNaOH-MM_liver_CNBrTi_108.1360.1360.2	2	4.6549	0.3542	2076.87	2077.3	1	52.77778	1	R.DQNFAGATAIHHPNVAEKR.I	138	2	*
231			Contaminant_TRYPSIN	Contaminant_TRYPSIN	no description	3	7	18.3	229	23993	7.9	MmNaOH-MM_liver_CNBrTi_202.2016.2016.2	2	4.3593	0.4201	2163.34	2164.3	1	42.105263	2	R.LGEDNINVVEGNEQFISASK.S	56	2	*
231			Contaminant_TRYPSIN	Contaminant_TRYPSIN	no description	3	7	18.3	229	23993	7.9	MmNaOH-MM_liver_CNBrTi_101.2039.2039.2	2	3.7573	0.2425	2163.84	2164.3	5	39.473686	1	R.LGEDNINVVEGNEQFISASK.S	56	2	*
231			Contaminant_TRYPSIN	Contaminant_TRYPSIN	no description	3	7	18.3	229	23993	7.9	MmNaOH-MM_liver_CNBrTi_108.2578.2578.3	3	4.0932	0.126	2514.53	2515.9	1	33.333336	3	K.SIVHPSYNSNTLNNDIMLIKLK.S	76	2	*
231			Contaminant_TRYPSIN	Contaminant_TRYPSIN	no description	3	7	18.3	229	23993	7.9	MmNaOH-MM_liver_CNBrTi_108.2555.2555.2	2	5.0282	0.3948	2516.12	2515.9	1	47.61905	1	K.SIVHPSYNSNTLNNDIMLIKLK.S	76	2	*
232			Contaminant_KERATIN03	Contaminant_KERATIN03	no description	1	1	1.5	593	59519	5.2	MmNaOH-MM_liver_CNBrTi_208.1370.1370.2	2	2.1177	0.1235	1064.53	1065.3	2	75	1	R.LASYLDKVR.A	157	2	
233			Contaminant_KERATIN13	Contaminant_KERATIN13	no description	1	1	1.9	643	65494	6.6	MmNaOH-MM_liver_CNBrTi_206.0713.0713.2	2	2.3277	0.1408	1341.76	1341.5	5	54.545456	1	K.SKAEAESLYQSK.Y	364	2	*
234			gi|114145561|ref|NP_112447.2|	gi|114145561|ref|NP_112447.2|	keratin complex 2, basic, gene 8 [Mus musculus]	1	2	2.4	490	54565	5.8	MmNaOH-MM_liver_CNBrTi_202.2454.2454.2	2	3.6766	0.3661	1420.6	1420.6	1	68.181816	2	R.LEGLTDEINFLR.Q	220	2	
SHUFFLED			SHUFFLED_gi|30425204|ref|NP_780675.1|		FALSE POSITIVE	1	2	1.7	705	81252	9.2	MmNaOH-MM_liver_CNBrTi_204.1955.1955.3	3	3.1744	0.1251	1560.9	1558.8	2	45.454548	2	K.WQVKPCILNFPR.S	183	2	*
SHUFFLED			SHUFFLED_gi|124486933|ref|NP_001074828.1		FALSE POSITIVE	1	2	0.3	2799	309095	5.8	MmNaOH-MM_liver_CNBrTi_202.1042.1042.2	2	2.1551	0.156	947.17	948.16	6	85.71429	2	R.RALAFLTR.T	1471	2	*

Table S3B. Detailed peptide and spectral counts for proteins detected by MudPIT analysis of Microsomal Membranes (MMs) isolated from Mouse Liver

Proteins are ranked by their frequency of detection in MMs and decreasing averaged dNSAFs values.
For each run (See details in Table S1A), the following parameters are specified for each protein:

columns ending with _P: peptide counts
columns ending with _S: total spectral counts
columns ending with _sS: spectral counts for peptides shared between protein isoforms
columns ending with _uDP: spectral counts for peptides uniquely matching the protein
columns ending with _uS: spectral counts for peptides uniquely matching the protein
columns ending with _dS: spectral counts distributed according to the spectral count contribution of peptides unique to each isoform
columns ending with _SC: sequence coverage
columns ending with _dNSAF: Normalized Spectral Abundance Factors, calculated based on distributed spectral counts and protein length.

The number of times a protein is detected across multiple analyses is listed in the "Detected # Out of" columns.
dNSAF are averaged across mulitple runs ("dNSAF AVG" columns).
Columns ending with PredHel and TMHMM_Topology list the number and position of transmembrane helices predicted for each protein by TMHMM.
The columns starting with "SIGNALP" are the output from SIGNALP HMM predictions on each protein for type of signal peptide sequences, their position (_POS) and probability (_SPROB).
Additional annotations are reported in the "NCBI_Region_Note" and "GO_" columns.

														MMs																							
rk	ORTHO_GROUP	GENE_NAME	Locus	Proteins In Group	Description	Length	MW	pI	PredHel	TMHMM_Topology	SIGNALP_HMM_TYPE (S= signal; A= Anchor; Q= none)	SIGNALP_HMM_POS	SIGNALP_HMM_SPROB	MmNaOH-MM_liver_CNBrTi_1_P	MmNaOH-MM_liver_CNBrTi_1_S	MmNaOH-MM_liver_CNBrTi_1_sS	MmNaOH-MM_liver_CNBrTi_1_uDP	MmNaOH-MM_liver_CNBrTi_1_uS	MmNaOH-MM_liver_CNBrTi_1_dS	MmNaOH-MM_liver_CNBrTi_1_SC	MmNaOH-MM_liver_CNBrTi_1_dNSAF	MmNaOH-MM_liver_CNBrTi_2_P	MmNaOH-MM_liver_CNBrTi_2_S	MmNaOH-MM_liver_CNBrTi_2_sS	MmNaOH-MM_liver_CNBrTi_2_uDP	MmNaOH-MM_liver_CNBrTi_2_uS	MmNaOH-MM_liver_CNBrTi_2_dS	MmNaOH-MM_liver_CNBrTi_2_SC	MmNaOH-MM_liver_CNBrTi_2_dNSAF	IMMs Detected # Out of 2	IMMs dNSAF AVG	IMMs dNSAF SDV	NCBI_Region_Note	GO_Component	GO_Function	Total_P	Total_S
1	ENSG00000205754:ENSMUSG00000030236:ENSRNOG00000030538	SLCO1B2	gi|14547899|ref|NP_06	gi|14547899|ref|NP_065241.1|;gi|30102937|ref|NP_839953.1|	solute carrier organic anion transporter fami	689	76729	8.7	12	i28-50o65-8	Q	43	0.041	2	7	0	0	7	7	5.37	0.00449	2	363	0	0	363	363	5.37	0.0984	2	0.051054	0.066407	S-100/ICaBP-like domain; S-100/intestinal calcium binding	extracellular space	calcium ion binding [pmid 2149559]; signal transducer	4	370
2	ENSG00000205702:ENSMUSG00000014372:ENSRNOG00000029128	NR_002570.2	gi|31981816|ref|NP_03	gi|31981816|ref|NP_034135.2|	cytochrome P450, family 2, subfamily d, pol	504	57233	6.6	2	o4-26i301-3	A	26	0.063	12	28	24	2	4	27.11	22.42	0.02378	11	186	57	2	129	185.2	18.25	0.06863	2	0.045796	0.031718	Ubiquitin-conjugating enzyme E2, catalytic (UBCc) domain;			23	214
3	ENSG00000008394:ENSMUSG00000008540:ENSRNOG00000007743	MGST1	gi|31981068|ref|NP_06	gi|31981068|ref|NP_064330.2|	microsomal glutathione S-transferase 1 [Mu	155	17552	9.7	2	i12-34o131	Q	36	0.005	2	30	0	2	30	30	18.06	0.08557	1	2	0	1	2	2	11.61	0.00241	2	0.043433	0.0588	Cytochrome P450. Cytochrome P450s are haem-thiolate	integral to membrane; membrane	heme binding; iron ion binding; isomerase activity; metal	3	32
4	ENSG00000093010:ENSMUSG00000000326:ENSRNOG00000001889	COMT	gi|6680982|ref|NP_031	gi|6680982|ref|NP_031770.1|	catechol-O-methyltransferase [Mus musculu	265	29496	5.8	1	i2-24o	S	26	1	3	28	0	3	28	28	21.89	0.04671	2	33	0	2	33	33	13.96	0.02326	2	0.034601	0.016583	GST_C family, Chloride Intracellular Channel (CLIC) subfamily;	brush border [pmid 10793131]; cytoplasm [pmid 10793131];	chloride ion binding; protein binding [pmid 14667819];	5	61
5	ENSG00000105518:ENSMUSG00000040883:ENSRNOG00000011747	NP_940938.1	gi|31982159|ref|NP_84	gi|31982159|ref|NP_848692.2|	hypothetical protein LOC235043 [Mus musc	189	21180	9.4	4	o15-37i57-7	A	25	0.075	1	1	0	1	1	1	8.99	0.00234	1	66	0	1	66	66	8.99	0.06522	2	0.033524	0.044467	The excision repair protein UvrA domain II; Nucleotide excision	apical plasma membrane; integral to plasma membrane;	ATPase activity, coupled to transmembrane movement of	2	67
6	ENSG00000197838:ENSMUSG00000060407:ENSRNOG00000020817	CYP2A13	gi|19526798|ref|NP_59	gi|19526798|ref|NP_598418.1|	cytochrome P450, family 2, subfamily a, pol	492	56179	9.2	1	i2-24o	S	26	0.977	1	1	0	1	1	1	2.24	0.0009	2	157	0	2	157	157	5.08	0.0596	2	0.030023	0.04151	Sulfotransferase domain; pfam00685	cytosol	aryl sulfotransferase activity; nucleotide binding;	3	158
7	ENSG00000143819:ENSMUSG00000038776:ENSRNOG00000003515	EPHX1	gi|6753762|ref|NP_034	gi|6753762|ref|NP_034275.1|	epoxide hydrolase 1, microsomal [Mus mus	455	52577	8.4	0	o	A	21	0.089	2	4	0	2	4	4	5.49	0.00389	3	127	0	3	127	127	7.03	0.05213	2	0.027792	0.034116	Eukaryotic porin; pfam01459	integral to plasma membrane; membrane; mitochondrial outer	voltage-gated anion channel porin activity [pmid	5	131
8	ENSG00000130649:ENSMUSG00000025479:ENSRNOG00000012458	CYP2E1	gi|11276065|ref|NP_06	gi|11276065|ref|NP_067257.1|	cytochrome P450, family 2, subfamily e, pol	493	56805	8.4	1	i2-23o	S	20	0.77	4	8	0	4	8	8	10.55	0.00717	3	101	0	3	101	101	7.1	0.03827	2	0.022531	0.021985	DnaJ central domain (4 repeats). The central cysteine-rich (CR)		low-density lipoprotein receptor binding; metal ion	7	109
9	ENSG00000005421:ENSMUSG00000002588:ENSRNOG00000008902	PON1	gi|7242183|ref|NP_035	gi|7242183|ref|NP_035264.1|	paraoxonase 1 [Mus musculus]	355	39531	5.2	0	o	S	16	0.994	1	1	0	1	1	1	4.79	0.00125	1	80	0	1	80	80	4.51	0.04209	2	0.021504	0.028882	Myosin tail. The myosin molecule is a multi-subunit complex			2	81
10	ENSG00000205702:ENSMUSG00000068086:ENSRNOG00000029128	NR_002570.2	gi|6753584|ref|NP_034	gi|6753584|ref|NP_034136.1|	cytochrome P450, family 2, subfamily d, pol	504	56949	6.3	0	o	A	29	0.215	8	28	18	3	10	27.26	17.66	0.02391	5	36	4	1	32	34.34	11.31	0.01273	2	0.01812	0.007912	GRIM-19 protein. This family consists of several eukaryotic	cytoplasm [pmid 10924506]; integral to membrane; membrane;	ATP binding [pmid 10924506]; NADH dehydrogenase	13	64
11	ENSG00000101856:ENSMUSG00000006373:ENSRNOG00000012786	PGRMC1	gi|31980806|ref|NP_05	gi|31980806|ref|NP_058063.2|;gi|5729875|ref|NP_006658.1|	progesterone receptor membrane compone	195	21694	4.7	1	o20-42i	Q	49	0.046	1	12	0	0	12	12	7.69	0.02721	2	9	0	0	9	9	11.79	0.00862	2	0.017707	0.013142	Cytochrome b5-like Heme/Steroid binding domain. This family	endoplasmic reticulum; integral to membrane; membrane;	lipid binding; receptor activity; steroid binding	3	21
12	ENSG00000197446:ENSMUSG00000052974:ENSRNOG00000032805	CYP2F1	gi|124001560|ref|NP_0	gi|124001560|ref|NP_031843.2|	cytochrome P450, family 2, subfamily f, poly	491	55949	7.9	1	i7-24o	S	24	0.994	5	33	0	5	33	33	15.48	0.02971	6	16	1	4	15	16	16.09	0.00609	2	0.017687	0.016706	WWE domain. The WWE domain is named after three of its	intracellular	thyroid hormone receptor binding; ubiquitin-protein ligase	11	49
13	NA:ENSMUSG00000060613:ENSRNOG00000021924	CYP2C22	gi|21703982|ref|NP_66	gi|21703982|ref|NP_663474.1|	cytochrome P450, family 2, subfamily c, pol	489	56068	8.2	1	i2-20o	S	28	0.975	1	2	0	1	2	2	2.25	0.00181	3	88	0	3	88	88	6.34	0.03361	2	0.017574	0.022489	Rab6 subfamily. Rab6 is involved in microtubule-dependent			4	90
14	ENSG00000166347:ENSMUSG00000024646:ENSRNOG00000015205	CYB5A	gi|13385268|ref|NP_08	gi|13385268|ref|NP_080073.1|	cytochrome b-5 [Mus musculus]	134	15241	5.1	1	i109-131o	Q	0	0	2	5	0	2	5	5	22.39	0.0165	4	13	0	4	13	13	41.04	0.01812	2	0.017135	0.001149	Cytochrome b5-like Heme/Steroid binding domain. This family	endoplasmic reticulum; membrane; microsome; mitochondrion	iron ion binding; metal ion binding; stearoyl-CoA 9-	6	18
15	ENSG00000205702:ENSMUSG00000022445:ENSRNOG00000008988	CYP2D7P1	gi|13386414|ref|NP_08	gi|13386414|ref|NP_083838.1|	cytochrome P450, family 2, subfamily d, pol	500	56950	6.6	2	o10-27i301	A	26	0.048	9	28	4	5	24	27.55	19.8	0.02436	5	29	3	2	26	26.44	13.4	0.00988	2	0.016928	0.010243	Transmembrane amino acid transporter protein. This	membrane	amino acid transporter activity; amino acid-polyamine	14	57
16	ENSG00000172828:ENSMUSG00000069922:ENSRNOG00000026731	CES3	gi|82919057|ref|XP_92	gi|82919057|ref|XP_920143.1|;gi|82919063|ref|XP_928645.1|;gi|94384283|ref|XP_001002887.1|	PREDICTED: similar to Es31 protein isofor	571	63318	6.1	1	i13-30o	S	32	0.876	5	10	0	0	10	10	14.19	0.00774	3	78	0	0	78	78	5.95	0.02551	2	0.016484	0.012567	short chain dehydrogenase; PRK08264	endoplasmic reticulum; integral to membrane; membrane;	11-beta-hydroxysteroid dehydrogenase activity;	8	88
17	ENSG00000167165:ENSMUSG00000054545:ENSRNOG00000018740	UGT1A9	gi|47059135|ref|NP_96	gi|47059135|ref|NP_964007.1|	UDP glucuronosyltransferase 1 family, poly	535	60066	8.7	2	i5-27o493-5	S	30	0.999	2	2	0	2	2	2	5.05	0.00165	4	89	60	2	29	80.18	10.65	0.02799	2	0.014707	0.018624	AAA-superfamily of ATPases associated with a wide variety of			6	91
18	ENSG00000212695:ENSMUSG00000045128:ENSRNOG00000018795	Q76N54	gi|149240702|ref|XP_0	gi|149240702|ref|XP_001476096.1|;gi|58037465|ref|NP_084027.1|	PREDICTED: hypothetical protein [Mus mus	176	20762	10.7	0	o	Q	25	0	1	9	0	0	9	9	7.39	0.02261	1	3	0	0	3	3	7.39	0.00318	2	0.012739	0.013734	Ribosomal L18ae protein family; pfam01775			2	12
19	ENSG00000140284:ENSMUSG00000027359:ENSRNOG00000010128	SLC27A2	gi|113374154|ref|NP_0	gi|113374154|ref|NP_036108.2|	solute carrier family 27 (fatty acid transporte	620	70423	8.9	2	o5-27i266-2	S	25	0.994	6	8	0	6	8	8	15.16	0.0057	4	62	0	4	62	62	9.68	0.01868	2	0.012085	0.009174	Soluble NSF (N-ethylmaleimide-sensitive fusion protein)-	cytoplasm [pmid 9587053]; Golgi apparatus [pmid 9587053];	protein transporter activity; t-SNARE activity [pmid	10	70
20	ENSG00000115275:ENSMUSG00000030036:ENSRNOG00000008648	GCS1	gi|31981106|ref|NP_06	gi|31981106|ref|NP_065644.2|	glucosidase 1 [Mus musculus]	834	91831	9	1	i40-62o	A	63	0.332	3	22	0	3	22	22	5.28	0.01166	5	50	0	5	50	50	6.24	0.0112	2	0.011314	0.000328	Mannosyl oligosaccharide glucosidase. This is a family of	endoplasmic reticulum; integral to membrane; membrane	hydrolase activity; hydrolase activity, acting on glycosyl	8	72
21	ENSG00000181035:ENSMUSG00000002346:ENSRNOG00000020345	SLC25A42	gi|56090652|ref|NP_00	gi|56090652|ref|NP_001007571.1|	solute carrier family 25, member 42 [Mus m	318	35241	10.1	1	i186-208o	Q	48	0.051	1	2	0	1	2	2	6.92	0.00278	1	34	0	1	34	34	6.92	0.01997	2	0.011283	0.012155	Mitochondrial carrier protein; pfam00153	integral to membrane; membrane; mitochondrial inner membrane	binding	2	36
22	ENSG00000170439:ENSMUSG00000025347:ENSRNOG00000007927	METTL7B	gi|27229118|ref|NP_08	gi|27229118|ref|NP_082129.2|	methyltransferase like 7B [Mus musculus]	244	28049	8.6	1	o5-27i	S	24	0.998	2	8	0	2	8	8	15.16	0.01449	1	8	0	1	8	8	6.56	0.00612	2	0.010194	0.005919	Homeodomain; DNA binding domains involved in the		metal ion binding	3	16
23	NA:NA:ENSRNOG00000028419	FTL2	gi|130485277|ref|NP_0	[illegible]	ferritin light chain 2 [Mus musculus]	183	20738	6	0	o	Q	0	0	2	6	0	0	6	6	20.22	0.01449	1	6	0	0	6	6	12.57	0.00612	2	0.010194	0.005919	Acyl CoA:acetate/3-ketoacid CoA transferase, alpha subunit	mitochondrion	3-oxoacid CoA-transferase activity [pmid 8751852];	3	12
24	NA:ENSMUSG00000078688:ENSRNOG00000033208	Q78E17	gi|113930714|ref|NP_0	gi|113930714|ref|NP_001039015.1|;gi|13654245|ref|NP_112465.1|;gi|149252769|ref|XP_001477261.1|	major urinary protein 2 [Mus musculus]	180	20648	5	0	o	S	19	1	2	5	0	0	5	5	15	0.01228	2	6	0	0	6	6	16.11	0.00623	2	0.009152	0.004281	Sep15/SelM redox domain. Sep15 and SelM are eukaryotic			4	11
25	ENSG00000110628:ENSMUSG00000000154:ENSRNOG00000020562	SLC22A18	gi|112363088|ref|NP_0	gi|112363088|ref|NP_032793.2|	solute carrier family 22 (organic cation trans	410	43375	9.1	10	i12-34o49-7	S	44	0.88	1	1	0	1	1	1	2.93	0.00108	1	35	0	1	35	35	2.93	0.01594	2	0.008445	0.010512	HMGB-UBF_HMG-box, class II and III members of the HMG-box			2	36
26	ENSG00000115255:ENSMUSG00000035504:NA	REEP6	gi|21314830|ref|NP_64	gi|21314830|ref|NP_647453.1|	polyposis locus protein 1-like 1 [Mus muscu	201	22204	7.3	3	i43-65o89-1	A	56	0.001	1	4	0	1	4	4	4.98	0.0088	1	8	0	1	8	8	4.98	0.00743	2	0.008032	0.000964	TB2/DP1, HVA22 family. This family includes members from a	membrane	protein binding	2	12
27	ENSG00000189043:ENSMUSG00000029632:ENSRNOG00000005512	NDUFA4	gi|33563266|ref|NP_03	gi|33563266|ref|NP_035016.1|	NADH dehydrogenase (ubiquinone) 1 alpha	82	9327	9.5	1	i12-34o	S	30	0.901	1	1	0	1	1	1	14.63	0.00539	1	4	0	1	4	4	14.63	0.00911	2	0.007183	0.00263		mitochondrial inner membrane; mitochondrion	NADH dehydrogenase (ubiquinone) activity;	2	5
28	ENSG00000204128:ENSMUSG00000026227:ENSRNOG00000017557	C2orf72	gi|82881070|ref|XP_91	gi|82881070|ref|XP_910782.1|	PREDICTED: hypothetical protein LOC7279	287	30391	6.1	0	o	Q	32	0.001	3	7	0	3	7	7	24.04	0.01078	1	5	0	1	5	5	6.62	0.00325	2	0.006937	0.005324				4	12
29	ENSG00000075624:ENSMUSG00000029580:ENSRNOG00000034254	ACTB	gi|6671509|ref|NP_031	gi|6671509|ref|NP_031419.1|;gi|6752954|ref|NP_033739.1|	actin, beta, cytoplasmic [Mus musculus]	375	41737	5.5	0	o	Q	20	0	4	11	0	0	11	11	17.07	0.01297	1	1	0	0	1	1	4.27	0.0005	2	0.006648	0.008818	Actin; An ubiquitous protein involved in the formation of	actin filament; cytoskeleton; cytosol; soluble fraction	ATP binding; nucleotide binding; protein binding;	5	12
30	ENSG00000172817:ENSMUSG00000039519:ENSRNOG00000009730	CYP7B1	gi|75677410|ref|NP_03	gi|75677410|ref|NP_031851.2|	cytochrome P450, family 7, subfamily b, pol	507	58490	8.9	3	o15-34i178	S	36	0.677	4	15	0	4	15	15	13.61	0.01308	1	1	0	1	1	1	2.96	0.00037	2	0.006639	0.008988	U1-like zinc finger; Family of C2H2-type zinc fingers, present in			5	16
31	NA:ENSMUSG00000054630:ENSRNOG00000029973	UGT2B	gi|6678501|ref|NP_033	gi|6678501|ref|NP_033493.1|	UDP glucuronosyltransferase 2 family, poly	530	60856	7.9	1	o495-517i	S	24	0.995	4	11	1	3	10	10.91	10.38	0.0091	3	13	7	2	6	12	10.38	0.00423	2	0.00659	0.003444	Glycosyltransferase family 28 C-terminal domain. The	endoplasmic reticulum; integral to membrane; membrane;	glucuronosyltransferase activity; transferase activity;	7	24
32	ENSG00000100243:ENSMUSG00000018042:ENSRNOG00000009592	CYB5R3	gi|19745150|ref|NP_08	gi|19745150|ref|NP_084063.1|	diaphorase 1 [Mus musculus]	301	34128	8.4	0	o	Q	22	0.275	1	8	0	1	8	8	7.64	0.01175	2	2	0	2	2	2	6.64	0.00124	2	0.006416	0.007431	RNA recognition motif; smart00360			3	10
33	ENSG00000136986:ENSMUSG00000022365:ENSRNOG00000005551	DERL1	gi|13195638|ref|NP_07	gi|13195638|ref|NP_077169.1|	Der1-like domain family, member 1 [Mus mu	251	28835	9.5	5	i20-42o57-7	Q	33	0.019	1	3	0	1	3	3	3.19	0.00528	1	10	0	1	10	10	4.38	0.00744	2	0.006301	0.001526	Der1-like family. The endoplasmic reticulum (ER) of the yeast	endoplasmic reticulum; integral to endoplasmic reticulum	MHC class I protein binding; protein binding; receptor	2	13
34	ENSG00000131781:ENSMUSG00000028088:ENSRNOG00000018076	FMO5	gi|149251662|ref|XP_0	gi|149251662|ref|XP_001475872.1|	PREDICTED: similar to Flavin containing m	533	60001	8.7	1	o510-532i	S	19	0.828	3	8	0	3	8	8	9.19	0.00664	5	16	0	5	16	16	10.69	0.00561	2	0.006058	0.000727				8	24
35	NA:NA:ENSRNOG00000000790	LOC676837	gi|149269220|ref|XP_0	gi|149269220|ref|XP_001473590.1|;gi|149269222|ref|XP_001473611.1|	PREDICTED: similar to MHC H2-K 24 polyp	385	43242	7.3	1	o322-344i	S	22	1	1	9	0	0	9	9	3.9	0.01033	1	2	0	0	2	2	3.64	0.00097	2	0.005583	0.006622	Myosin motor domain, type II myosins. Myosin II mediates	cytoskeleton		2	11
36	ENSG00000148248:ENSMUSG00000014867:ENSRNOG00000005247	SURF4	gi|6755698|ref|NP_035	gi|6755698|ref|NP_035642.1|	surfeit gene 4 [Mus musculus]	269	30381	7.8	5	o63-85i92-1	Q	0	0	3	5	0	3	5	5	11.15	0.00822	1	4	0	1	4	4	4.83	0.00278	2	0.005435	0.003847	SURF4 family; pfam02077	endoplasmic reticulum; integral to membrane; membrane		4	9
37	ENSG00000151726:ENSMUSG00000018796:ENSRNOG00000010633	ACSL1	gi|31560705|ref|NP_03	gi|31560705|ref|NP_032007.2|	acyl-CoA synthetase long-chain family mem	699	77952	7.1	1	i21-43o	A	46	0	2	2	1	1	1	1.5	4.29	0.00095	3	38	14	2	24	32.2	6.58	0.0086	2	0.004738	0.005412	Long-chain acyl-CoA synthetases (AMP-forming) [Lipid	integral to membrane; membrane; mitochondrion; peroxisome	catalytic activity; ligase activity; long-chain-fatty-acid-	5	40
38	ENSG00000138115:ENSMUSG00000062624:ENSRNOG00000036595	CYP2C8	gi|67010061|ref|NP_00	gi|67010061|ref|NP_001019890.1|	hypothetical protein LOC545288 [Mus musc	491	56145	7.4	0	o	S	26	0.996	1	5	0	0	5	5	2.24	0.0045	2	14	3	1	11	12.94	6.52	0.00492	2	0.004665	0.000298	Cytochrome P450. Cytochrome P450s are haem-thiolate	membrane	heme binding; iron ion binding; metal ion binding;	3	19
39	ENSG00000083807:ENSMUSG00000030382:ENSRNOG00000019626	SLC27A5	gi|6678011|ref|NP_033	gi|6678011|ref|NP_033538.1|	solute carrier family 27 (fatty acid transporte	689	76186	8.4	3	i7-24o29-51	S	21	1	3	10	0	3	10	10	7.11	0.00642	2	11	0	2	11	11	5.95	0.00298	2	0.004647	0.002429	Acyl-coenzyme A synthetases/AMP-(fatty) acid ligases [Lipid	endoplasmic reticulum; integral to membrane; membrane	ATP binding; cholate-CoA ligase activity; ligase activity;	5	21
40	ENSG00000135220:ENSMUSG00000035780:ENSRNOG00000001975	UGT2A3	gi|13386284|ref|NP_08	gi|13386284|ref|NP_082370.1|	UDP glucuronosyltransferase 2 family, poly	534	61133	7.6	2	i7-29o493-5	S	19	0.997	2	10	5	1	5	8.571	8.24	0.0071	1	6	0	1	6	6	2.62	0.0021	2	0.004544	0.003534	ELM2 domain. The ELM2 (Egl-27 and MTA1 homology 2)			3	16
41	ENSG00000162365:ENSMUSG00000066071:ENSRNOG00000029919	CYP4A22	gi|86198312|ref|NP_80	gi|86198312|ref|NP_803125.2|	cytochrome P450, family 4, subfamily a, pol	508	58350	9.1	0	o	S	38	0.822	5	6	5	1	1	1.317	19.49	0.00115	3	20	9	1	11	19.38	9.45	0.00713	2	0.004103	0.00423	Cytochrome P450. Cytochrome P450s are haem-thiolate		iron ion binding; metal ion binding; oxidoreductase	8	26
42	ENSG00000074695:ENSMUSG00000041891:ENSRNOG00000024470	LMAN1	gi|21312570|ref|NP_08	gi|21312570|ref|NP_081676.1|	lectin, mannose-binding, 1 [Mus musculus]	517	57789	6.3	1	o483-505i	S	33	0.999	1	8	0	1	8	8	2.13	0.00684	1	3	0	1	3	3	2.13	0.00108	2	0.003915	0.004071	Legume-like lectin family. Lectins are structurally diverse	endoplasmic reticulum; ER-Golgi intermediate compartment;	sugar binding	2	11
43	ENSG00000180432:ENSMUSG00000050445:ENSRNOG00000019481	CYP8B1	gi|31981808|ref|NP_03	gi|31981808|ref|NP_034142.2|	cytochrome P450, family 8, subfamily b, pol	500	57706	8.8	1	i7-24o	S	20	0.885	2	3	0	2	3	3	5.6	0.00265	3	13	0	3	13	13	7.8	0.00486	2	0.003719	0.001558	Cytochrome P450. Cytochrome P450s are haem-thiolate	endoplasmic reticulum; integral to membrane; membrane;	heme binding; iron ion binding; metal ion binding;	5	16
44	ENSG00000140505:ENSMUSG00000032310:ENSRNOG00000016173	CYP1A2	gi|6753566|ref|NP_034	gi|6753566|ref|NP_034123.1|	cytochrome P450, family 1, subfamily a, pol	513	58184	8.8	1	i7-29o	S	30	0.988	3	6	0	3	6	6	10.92	0.00517	5	6	0	5	6	6	14.62	0.00218	2	0.003636	0.002112	Cytochrome P450. Cytochrome P450s are haem-thiolate	endoplasmic reticulum; membrane; microsome	heme binding; iron ion binding; metal ion binding;	8	12
45	ENSG00000213908:ENSMUSG00000005547:ENSRNOG00000028900	CYP2A7P1	gi|75832129|ref|NP_03	gi|75832129|ref|NP_031838.2|	cytochrome P450, family 2, subfamily a, pol	494	56713	9.2	1	i5-24o	S	23	0.887	1	1	0	1	1	1	1.82	0.00089	3	17	0	3	17	17	6.68	0.00643	2	0.003632	0.003912	Cytochrome P450. Cytochrome P450s are haem-thiolate	endoplasmic reticulum; membrane; microsome	heme binding; iron ion binding; metal ion binding;	4	18
46	ENSG00000167165:ENSMUSG00000054545:ENSRNOG00000018740	UGT1A9	gi|47059133|ref|NP_95	gi|47059133|ref|NP_958812.1|	UDP glucuronosyltransferase 1 family, poly	531	60435	8.7	1	o489-511i	S	27	0.996	2	4	0	2	4	4	7.16	0.00333	4	64	60	2	4	11.06	9.98	0.00389	2	0.003574	0.000396	Glycosyltransferase family 28 C-terminal domain. The		transferase activity; transferase activity, transferring	6	68
47	ENSG00000197142:ENSMUSG00000024981:ENSRNOG00000016265	ACSL5	gi|58218988|ref|NP_08	gi|58218988|ref|NP_082252.1|	acyl-CoA synthetase long-chain family mem	683	76206	7.1	1	i7-29o	A	36	0.094	2	2	1	1	1	1.5	4.98	0.00097	2	31	14	1	17	22.8	4.98	0.00624	2	0.003574	0.003723	Long-chain acyl-CoA synthetases (AMP-forming) [Lipid	integral to membrane; membrane; mitochondrial inner membrane		4	33
48	ENSG00000138115:ENSMUSG00000074882:ENSRNOG00000036595	CYP2C8	gi|88319958|ref|NP_00	gi|88319958|ref|NP_001034644.1|	cytochrome P450 2C40 family [Mus muscul	491	55969	7.2	0	o	S	26	0.998	1	5	0	0	5	5	2.24	0.0045	2	9	3	1	6	7.059	6.52	0.00269	2	0.003555	0.001285	Cytochrome P450. Cytochrome P450s are haem-thiolate	membrane	heme binding; iron ion binding; metal ion binding;	3	14
49	ENSG00000134716:ENSMUSG00000052520:NA	CYP2J2	gi|6753586|ref|NP_034	gi|6753586|ref|NP_034137.1|	cytochrome P450, family 2, subfamily j, poly	501	57784	8.7	1	i13-35o	S	38	0.743	2	6	0	2	6	6	8.38	0.00529	4	4	1	2	3	3.016	13.17	0.00112	2	0.003171	0.002949	Cytochrome P450. Cytochrome P450s are haem-thiolate	endoplasmic reticulum; membrane; microsome	heme binding; iron ion binding; metal ion binding;	6	10
50	ENSG00000215021:ENSMUSG00000004264:ENSRNOG00000012999	PHB2	gi|126723336|ref|NP_0	gi|126723336|ref|NP_031557.2|	B-cell receptor-associated protein 37 [Mus	299	33296	9.8	0	o	S	34	0.583	1	3	0	1	3	3	4.35	0.00444	2	3	0	2	3	3	10.03	0.00187	2	0.00312	0.001811	Glycosyltransferase family 28 C-terminal domain. The			3	6
51	ENSG00000106638:ENSMUSG00000005374:NA	TBL2	gi|31543845|ref|NP_03	gi|31543845|ref|NP_038791.2|	transducin (beta)-like 2 [Mus musculus]	442	49584	9	1	i9-31o	S	29	0.97	1	5	0	1	5	5	5.43	0.005	1	3	0	1	3	3	2.71	0.00127	2	0.003098	0.00264	WD40 domain, found in a number of eukaryotic proteins that			2	8
52	ENSG00000060971:ENSMUSG00000010651:ENSRNOG00000030287	ACAA1	gi|22122797|ref|NP_66	gi|22122797|ref|NP_666342.1|	acetyl-Coenzyme A acyltransferase 1B [Mu	424	43995	8.5	0	o	S	36	0.761	1	1	0	1	1	1	4.48	0.00104	1	10	0	1	10	10	4.48	0.00441	2	0.002701	0.002378	Thiolase are ubiquitous enzymes that catalyze the reversible		acyltransferase activity; transferase activity	2	11
53	ENSG00000127948:ENSMUSG00000005514:ENSRNOG00000001442	POR	gi|6679421|ref|NP_032	gi|6679421|ref|NP_032924.1|	cytochrome P450 reductase [Mus musculus	678	77044	5.5	1	i20-42o	Q	40	0	2	3	0	2	3	3	6.05	0.00196	2	12	0	2	12	12	4.87	0.00331	2	0.002606	0.000954	Oxidoreductase NAD-binding domain. Xanthine	endoplasmic reticulum; membrane; microsome; soluble fraction	electron carrier activity; FMN binding; iron ion binding;	4	15
54	ENSG00000138115:ENSMUSG00000003053:ENSRNOG00000013241	CYP2C8	gi|116268125|ref|NP_0	gi|116268125|ref|NP_031841.3|	cytochrome P450, family 2, subfamily c, pol	490	55716	8.3	0	o	S	26	0.997	3	5	3	1	2	5	9.39	0.00451	3	5	5	0	0	2	9.39	0.00076	2	0.002605	0.002651	Cytochrome P450. Cytochrome P450s are haem-thiolate	endoplasmic reticulum; membrane; microsome	heme binding; iron ion binding; metal ion binding;	6	10
55	ENSG00000101974:ENSMUSG00000062949:ENSRNOG00000003472	ATP11C	gi|49355804|ref|NP_00	gi|49355804|ref|NP_001001798.1|;gi|83745137|ref|NP_001032952.1|	Atpase, class VI, type 11C isoform b [Mus n	1116	127809	7	8	i67-89o291	Q	32	0	3	10	0	0	10	10	3.76	0.00396	1	5	0	0	5	5	1.25	0.00084	2	0.002371	0.002209	GRIM-19 protein. This family consists of several eukaryotic			4	15
56	ENSG00000146648:ENSMUSG00000020122:ENSRNOG00000004332	EGFR	gi|46560582|ref|NP_99	gi|46560582|ref|NP_997538.1|;gi|6681283|ref|NP_031938.1|	epidermal growth factor receptor isoform 1 [	1210	134853	6.9	2	o648-670i7	S	25	0.995	2	4	0	0	4	4	2.15	0.00146	3	21	0	0	21	21	2.73	0.00324	2	0.00233	0.001259	Receptor L domain. The L domains from these receptors make	basolateral plasma membrane; endocytic vesicle; intracellular;	ATP binding; electron carrier activity; epidermal growth	5	25
57	ENSG00000010932:ENSMUSG00000040181:ENSRNOG00000034191	FMO1	gi|6753890|ref|NP_034	gi|6753890|ref|NP_034361.1|	flavin containing monooxygenase 1 [Mus mu	532	59915	8.5	1	o509-531i	S	18	0.722	1	3	0	1	3	3	4.51	0.00249	1	6	0	1	6	6	1.69	0.00211	2	0.002276	0.000273	Flavin-binding monooxygenase-like. This family includes FMO	endoplasmic reticulum; integral to membrane; intrinsic to	dimethylaniline monooxygenase (N-oxide-forming)	2	9
58	NA:ENSMUSG00000062284:ENSRNOG00000010189	EG547267	gi|149267539|ref|XP_0	[illegible]	PREDICTED: hypothetical protein [Mus mus	145	16565	10.9	0	o	Q	19	0.022	1	1	0	0	1	1	8.28	0.00305	1	1	0	0	1	1	6.21	0.00129	2	0.002144	0.001245	Ribosomal protein S24E [Translation, ribosomal structure and			2	2
59	ENSG00000169223:ENSMUSG00000021484:ENSRNOG00000016161	LMAN2	gi|34328278|ref|NP_08	gi|34328278|ref|NP_080104.2|	lectin, mannose-binding 2 [Mus musculus]	358	40430	7	1	o325-347i	S	47	0.999	1	3	0	1	3	3	3.07	0.0037	1	1	0	1	1	1	2.51	0.00052	2	0.002088	0.002251	EF-hand, calcium binding motif; A diverse superfamily of calcium	cytoskeleton; myosin	calcium ion binding; motor activity	2	4
60	ENSG00000101474:ENSMUSG00000033096:ENSRNOG00000006795	C20orf3	gi|21313668|ref|NP_08	gi|21313668|ref|NP_082253.1|	RIKEN cDNA 2310001A20 [Mus musculus]	415	46434	6.3	1	i37-59o	A	57	0.001	2	2	0	2	2	2	11.33	0.00213	1	4	0	1	4	4	6.51	0.0018	2	0.001945	0.000234	Strictosidine synthase. Strictosidine synthase (E.C. 4.3.3.2) is	integral to membrane; membrane	strictosidine synthase activity	3	6
61	NA:ENSMUSG00000034450:ENSRNOG00000016648	GULO	gi|30520195|ref|NP_84	gi|30520195|ref|NP_848862.1|	gulonolactone (L-) oxidase [Mus musculus]	440	50478	8.2	0	o	Q	19	0	1	2	0	1	2	2	3.41	0.00201	1	4	0	1	4	4	2.27	0.0017	2	0.001835	0.00022	D-arabinono-1,4-lactone oxidase. This domain is specific to D-	endoplasmic reticulum; integral to membrane; membrane;	D-arabinono-1,4-lactone oxidase activity; L-	2	6
62	ENSG00000145626:ENSMUSG00000072664:ENSRNOG00000025010	UGT3A1	gi|46402181|ref|NP_99	gi|46402181|ref|NP_997099.1|	UDP glycosyltransferases 3 family, polypep	523	59742	7.2	2	i7-29o488-5	S	23	1	1	3	0	1	3	3	2.87	0.00254	2	3	0	2	3	3	4.97	0.00107	2	0.001783	0.001036	Glycosyltransferase family 28 C-terminal domain. The		transferase activity; transferase activity, transferring	3	6
63	ENSG00000110955:ENSMUSG00000025393:ENSRNOG00000002840	ATP5B	gi|31980648|ref|NP_05	gi|31980648|ref|NP_058054.2|	ATP synthase, H+ transporting mitochondria	529	56301	5.3	0	o	S	43	0.939	1	2	0	1	2	2	2.84	0.00167	2	5	0	2	5	5	6.05	0.00177	2	0.001701	6.65E-05	F1 ATP synthase beta subunit, nucleotide-binding domain. The	hydrogen-translocating F-type ATPase complex; integral to	ATP binding; hydrogen ion transporter activity; hydrogen-	3	7
64	ENSG00000105699:ENSMUSG00000001247:ENSRNOG00000021053	LSR	gi|30794490|ref|NP_05	gi|30794490|ref|NP_059101.1|	lipolysis stimulated lipoprotein receptor [Mus	594	66108	6.5	1	o207-229i	S	37	0.986	1	2	0	1	2	2	5.05	0.00149	2	6	0	2	6	6	4.38	0.00189	2	0.001671	0.000282		cellular_component; chylomicron; integral to membrane;	lipid transporter activity	3	8
65	ENSG00000163399:ENSMUSG00000033161:ENSRNOG00000030019	ATP1A1	gi|21450277|ref|NP_65	gi|21450277|ref|NP_659149.1|	Na+/K+ -ATPase alpha 1 subunit [Mus mus	1023	112982	5.5	10	i95-117o13	Q	0	0	2	3	0	2	3	3	2.15	0.0013	3	11	0	3	11	11	3.52	0.00201	2	0.001637	0.000503	haloacid dehalogenase-like hydrolase. This family are	basolateral plasma membrane; microsome; plasma membrane;	4-nitrophenylphosphatase activity; catalytic activity;	5	14
66	ENSG00000198277:ENSMUSG00000029260:ENSRNOG00000029007	UGT2B	gi|23956406|ref|NP_70	gi|23956406|ref|NP_705826.1|	UDP glucuronosyltransferase 2 family, poly	532	60877	7.9	1	o489-511i	S	26	1	2	7	5	1	2	3.429	9.02	0.00285	1	1	0	1	1	1	1.88	0.00035	2	0.001581	0.001766	Glycosyltransferase family 28 C-terminal domain. The		transferase activity; transferase activity, transferring	3	8
67	ENSG00000115486:ENSMUSG00000053460:ENSRNOG00000012975	GGCX	gi|9790009|ref|NP_062	gi|9790009|ref|NP_062776.1|	gamma-glutamyl carboxylase [Mus musculu	757	87195	8	5	i123-145o1	Q	19	0.001	2	2	0	2	2	2	4.23	0.00117	2	8	0	2	8	8	4.23	0.00197	2	0.001556	0.00057	Vitamin K-dependent gamma-carboxylase. Using reduced	endoplasmic reticulum; membrane	gamma-glutamyl carboxylase activity; protein binding	4	10
68	ENSG00000107581:ENSMUSG00000024991:ENSRNOG00000010117	EIF3A	gi|46575903|ref|NP_03	gi|46575903|ref|NP_034253.2|	eukaryotic translation initiation factor 3, sub	1344	161950	6.8	0	o	Q	0	0	4	6	0	4	6	6	4.02	0.00197	2	7	0	2	7	7	2.16	0.00097	2	0.001457	0.000708	motif in proteasome subunits, Int-6, Nip-1 and TRIP-15; Also	nucleus	translation initiation factor activity	6	13
69	ENSG00000073060:ENSMUSG00000037936:ENSRNOG00000000981	SCARB1	gi|14389423|ref|NP_05	gi|14389423|ref|NP_058021.1|	scavenger receptor class B, member 1 [Mus	509	56754	8.1	2	i9-31o440-4	A	26	0.352	2	2	0	2	2	2	7.86	0.00174	1	3	0	1	3	3	1.77	0.0011	2	0.001404	0.00045	CD36 family. The CD36 family is thought to be a novel class of	caveolar membrane; integral to membrane of membrane fraction;	receptor activity	3	5
70	ENSG00000147383:ENSMUSG00000031349:ENSRNOG00000017099	NSDHL	gi|31982437|ref|NP_03	gi|31982437|ref|NP_035071.3|	NAD(P) dependent steroid dehydrogenase-	362	40686	7.9	1	o285-307i	Q	27	0	1	1	0	1	1	1	2.49	0.00122	3	3	0	3	3	3	10.5	0.00155	2	0.001371	0.000231	Male sterility protein. This family represents the C-terminal	membrane	3-beta-hydroxy-delta5-steroid dehydrogenase activity;	4	4
71	ENSG00000137414:ENSMUSG00000069237:ENSRNOG00000026120	FAM8A1	gi|85701696|ref|NP_00	gi|85701696|ref|NP_001028364.1|	Autosomal Highly Conserved Protein [Mus r	399	42295	6.7	3	o241-263i2	Q	50	0	1	2	0	1	2	2	8.77	0.00222	1	1	0	1	1	1	2.51	0.00047	2	0.001326	0.001236	RDD family. This family of proteins contain three highly			2	3
72	ENSG00000118298:ENSMUSG00000038526:ENSRNOG00000023162	CA14	gi|6753264|ref|NP_035	gi|6753264|ref|NP_035927.1|	carbonic anhydrase 14 [Mus musculus]	337	37505	6.4	1	o290-312i	S	16	0.981	1	1	0	1	1	1	3.56	0.00131	1	2	0	1	2	2	3.56	0.00111	2	0.001198	0.000144	Type I phosphodiesterase / nucleotide pyrophosphatase. This	endoplasmic reticulum; endosome; extracellular space; Golgi	calcium ion binding; hydrolase activity; steryl-sulfatase	2	3
73	ENSG00000145626:ENSMUSG00000049152:ENSRNOG00000025010	UGT3A1	gi|21450243|ref|NP_65	gi|21450243|ref|NP_659094.1|	UDP glycosyltransferases 3 family, polypep	523	59673	7.5	1	o488-510i	S	23	0.999	1	2	0	1	2	2	2.1	0.00169	1	2	0	1	2	2	2.29	0.00071	2	0.001189	0.00069	Glycosyltransferase family 28 C-terminal domain. The		transferase activity; transferase activity, transferring	2	4
74	ENSG00000186205:ENSMUSG00000026621:ENSRNOG00000004101	MOSC1	gi|124486921|ref|NP_0	[illegible]	MOCO sulphurase C-terminal domain conta	342	38126	8.5	1	o25-44i	S	41	0.955	1	1	0	0	1	1	8.48	0.00129	1	2	0	0	2	2	2.63	0.00109	2	0.00118	0.000142	MOSC domain. The MOSC (MOCO sulfurase C-terminal)	mitochondrial inner membrane		2	3
75	NA:ENSMUSG00000043716:ENSRNOG00000031912	LOC367195	gi|31981515|ref|NP_03	gi|31981515|ref|NP_035421.2|;gi|82957963|ref|XP_924795.1|	ribosomal protein L7 [Mus musculus]	270	31420	10.9	0	o	Q	25	0	1	1	0	0	1	1	7.41	0.00164	2	2	1	1	1	1	11.11	0.00069	2	0.001152	0.000669	Uncharacterized conserved protein [Function unknown];			3	3
76	ENSG00000162365:ENSMUSG00000028715:ENSRNOG00000030154	CYP4A22	gi|6681121|ref|NP_031	gi|6681121|ref|NP_031848.1|	cytochrome P450, family 4, subfamily a, pol	507	58720	8.8	2	o15-32i113	A	37	0.164	3	3	2	1	1	1.563	12.23	0.00136	2	6	4	1	2	2.615	7.1	0.00096	2	0.001151	0.000282	Cytochrome P450. Cytochrome P450s are haem-thiolate	endoplasmic reticulum; membrane; microsome	alkane 1-monooxygenase activity; heme binding; iron ion	5	9
77	ENSG00000198848:ENSMUSG00000056973:ENSRNOG00000015519	CES3	gi|117553604|ref|NP_4	gi|117553604|ref|NP_444430.2|	carboxylesterase 3 [Mus musculus]	565	61788	6.6	0	o	S	19	0.999	1	2	0	1	2	2	3.54	0.00156	1	2	0	1	2	2	3.01	0.00066	2	0.001101	0.000639	Esterases and lipases (includes fungal lipases,		hydrolase activity	2	4
78	ENSG00000205702:ENSMUSG00000061740:ENSRNOG00000032261	CYP2D7P1	gi|31981029|ref|NP_06	gi|31981029|ref|NP_062797.2|	cytochrome P450, family 2, subfamily d, pol	500	56494	6.9	1	i9-28o	A	34	0.336	3	3	1	2	2	2.077	11.6	0.00184	3	3	2	1	1	1.012	9	0.00038	2	0.001094	0.001031	Cytochrome P450. Cytochrome P450s are haem-thiolate	cytoplasm	heme binding; iron ion binding; metal ion binding;	6	6
79	ENSG00000004864:ENSMUSG00000015112:ENSRNOG00000009957	SLC25A13	gi|7657583|ref|NP_056	gi|7657583|ref|NP_056644.1|	solute carrier family 25 (mitochondrial carrie	676	74467	8.6	0	o	Q	15	0	1	1	0	1	1	1	3.25	0.00065	1	5	0	1	5	5	3.25	0.00138	2	0.001008	0.000514	S-100/ICaBP-like domain; S-100/intestinal calcium binding	integral to membrane; membrane; mitochondrial inner membrane	binding; calcium ion binding; L-glutamate transporter	2	6
80	ENSG00000163902:ENSMUSG00000030062:NA	RPN1	gi|31543605|ref|NP_59	gi|31543605|ref|NP_598694.2|	ribophorin I [Mus musculus]	608	68527	6.5	1	o441-460i	S	26	1	1	1	0	1	1	1	2.47	0.00073	2	4	0	2	4	4	4.93	0.00123	2	0.000969	0.000355	Ribophorin I. Ribophorin I is an essential subunit of	endoplasmic reticulum membrane; membrane		3	5
81	ENSG00000174444:ENSMUSG00000032399:ENSRNOG00000033834	RPL4	gi|30794450|ref|NP_07	gi|30794450|ref|NP_077174.1|	ribosomal protein L4 [Mus musculus]	419	47154	11	0	o	Q	20	0.001	1	1	0	1	1	1	5.25	0.00106	1	2	0	1	2	2	2.86	0.00089	2	0.000963	0.000116	50S ribosomal protein L4P; PRK04042	intracellular; ribonucleoprotein complex; ribosome	protein binding; structural constituent of ribosome	2	3
82	ENSG00000186115:ENSMUSG00000024055:ENSRNOG00000034157	CYP4F2	gi|20373155|ref|NP_57	gi|20373155|ref|NP_570952.1|	cytochrome P450, family 4, subfamily f, poly	523	59823	7.7	1	i20-42o	S	37	0.995	1	1	0	1	1	1	3.82	0.00085	1	3	0	1	3	3	2.49	0.00107	2	0.000949	0.00016	Cytochrome P450. Cytochrome P450s are haem-thiolate		heme binding; iron ion binding; metal ion binding	2	4
83	ENSG00000117791:ENSMUSG00000073481:ENSRNOG00000037850	MOSC2	gi|19526848|ref|NP_59	gi|19526848|ref|NP_598445.1|	MOCO sulphurase C-terminal domain conta	338	38194	8.7	1	o20-39i	S	37	0.912	1	1	0	1	1	1	10.36	0.00131	1	1	0	1	1	1	2.37	0.00055	2	0.00092	0.000534	MOSC domain. The MOSC (MOCO sulfurase C-terminal)	mitochondrial inner membrane; mitochondrion		2	2
84	ENSG00000107897:ENSMUSG00000026781:ENSRNOG00000017642	ACBD5	gi|27229192|ref|NP_08	gi|27229192|ref|NP_083069.1|	acyl-Coenzyme A binding domain containin	473	52469	5.3	1	o443-465i	Q	0	0	1	1	0	1	1	1	2.75	0.00093	1	2	0	1	2	2	1.9	0.00079	2	0.000853	0.000102	Acyl CoA binding protein (ACBP) binds thiol esters of long fatty	cellular_component	acyl-CoA binding; molecular_function	2	3
85	ENSG00000198277:ENSMUSG00000035836:ENSRNOG00000001990	UGT2B	gi|22779901|ref|NP_69	gi|22779901|ref|NP_690024.1|	UDP glucuronosyltransferase 2 family, poly	529	60157	8.4	1	o494-516i	S	25	0.96	2	2	1	1	1	1.091	5.29	0.00091	2	2	0	2	2	2	4.91	0.00071	2	0.0008	0.000145	Glycosyltransferase family 28 C-terminal domain. The			4	4
86	ENSG00000204267:ENSMUSG00000024339:ENSRNOG00000000455	TAP2	gi|46399206|ref|NP_03	gi|46399206|ref|NP_035660.2|	transporter 2, ATP-binding cassette, sub-fa	702	77464	7.4	5	i55-77o97-1	S	29	0.997	2	2	0	2	2	2	4.42	0.00126	1	1	0	1	1	1	1.85	0.00027	2	0.000754	0.000702	TAP, the Transporter Associated with Antigen Processing; TAP	cytosol; endoplasmic reticulum; endoplasmic reticulum lumen;	ATP binding; ATPase activity; ATPase activity, coupled	3	3
87	ENSG00000152234:ENSMUSG00000025428:ENSRNOG00000017032	ATP5A1	gi|6680748|ref|NP_031	gi|6680748|ref|NP_031531.1|	ATP synthase, H+ transporting, mitochondri	553	59753	9.2	0	o	S	39	0.567	1	1	0	1	1	1	3.98	0.0008	1	2	0	1	2	2	3.98	0.00068	2	0.00073	8.76E-05	F1 ATP synthase alpha, central domain. The F-ATPase is found	mitochondrial inner membrane; mitochondrion; proton-	ATP binding; hydrogen ion transporter activity; hydrogen-	2	3
88	ENSG00000175003:ENSMUSG00000023829:ENSRNOG00000016337	SLC22A1	gi|31982010|ref|NP_03	gi|31982010|ref|NP_033228.2|	solute carrier family 22 member 1 [Mus mus	556	61521	6.7	12	i21-43o149	A	34	0.027	1	1	0	1	1	1	2.88	0.0008	1	2	0	1	2	2	1.62	0.00067	2	0.000726	8.72E-05	D-xylose transporter; PRK10077	integral to plasma membrane	ATP binding; nucleotide binding; organic cation	2	3
89	ENSG00000134824:ENSMUSG00000024665:ENSRNOG00000020440	FADS2	gi|9790071|ref|NP_062	gi|9790071|ref|NP_062673.1|	fatty acid desaturase 2 [Mus musculus]	444	52387	8.8	4	i124-143o1	Q	0	0	1	1	0	1	1	1	3.38	0.001	1	1	0	1	1	1	3.38	0.00042	2	0.0007	0.000407	The Delta6 Fatty Acid Desaturase (Delta6-FADS)-like CD	membrane; membrane fraction	heme binding; iron ion binding; metal ion binding;	2	2
90	ENSG00000060566:ENSMUSG00000035041:ENSRNOG00000032202	CREB3L3	gi|21703728|ref|NP_66	gi|21703728|ref|NP_663340.1|	cAMP responsive element binding protein 3	479	52145	5.1	0	o	Q	23	0.002	1	1	0	1	1	1	3.55	0.00092	1	1	0	1	1	1	3.55	0.00039	2	0.000649	0.000377	basic region leucin zipper; smart00338	nucleus	DNA binding; protein dimerization activity; sequence-	2	2
91	ENSG00000110719:ENSMUSG00000001750:ENSRNOG00000017220	TCIRG1	gi|31980624|ref|NP_05	gi|31980624|ref|NP_058617.2|	T-cell, immune regulator 1 [Mus musculus]	834	93448	6.3	8	o398-420i4	S	23	0.98	1	2	0	1	2	2	3.48	0.00106	1	1	0	1	1	1	2.16	0.00022	2	0.000634	0.000591	V-type ATPase 116kDa subunit family. This family consists of	plasma membrane		2	3
92	ENSG00000185000:ENSMUSG00000022555:ENSRNOG00000028711	LOC727765	gi|6753632|ref|NP_034	gi|6753632|ref|NP_034176.1|	diacylglycerol O-acyltransferase 1 [Mus mus	498	56790	9.4	8	o137-159i1	Q	28	0	1	1	0	1	1	1	4.02	0.00089	1	1	0	1	1	1	5.02	0.00038	2	0.000624	0.000363	Acyl-CoA cholesterol acyltransferase [Lipid metabolism];	endoplasmic reticulum; membrane; membrane fraction	2-acylglycerol O-acyltransferase activity;	2	2
93	ENSG00000091262:ENSMUSG00000030834:ENSRNOG00000028781	ABCC6	gi|9055156|ref|NP_061	gi|9055156|ref|NP_061265.1|	ATP-binding cassette, sub-family C, membe	1498	164787	8.2	14	o44-61i81-1	Q	44	0.031	1	1	0	1	1	1	1	0.0003	1	7	0	1	7	7	1.07	0.00087	2	0.000579	0.000408	ABC (ATP-binding cassette) transporter nucleotide-binding		ATP binding; ATPase activity; ATPase activity, coupled	2	8
94	ENSG00000184743:ENSMUSG00000024759:ENSRNOG00000021203	ATLA3	gi|31559920|ref|NP_66	gi|31559920|ref|NP_666203.2|	hypothetical protein LOC109168 [Mus musc	541	60515	6.1	2	i445-464o4	Q	19	0.005	1	1	0	1	1	1	2.22	0.00082	1	1	0	1	1	1	2.03	0.00035	2	0.000575	0.000334	Guanylate-binding protein (GBP), N-terminal domain. Guanylate-		GTP binding; GTPase activity	2	2
95	ENSG00000147649:ENSMUSG00000022255:ENSRNOG00000006870	MTDH	gi|31982233|ref|NP_08	gi|31982233|ref|NP_080278.3|	LYRIC [Mus musculus]	579	63846	9.3	1	i50-72o	A	0	0	1	1	0	1	1	1	2.25	0.00076	1	1	0	1	1	1	1.9	0.00032	2	0.000537	0.000312		endoplasmic reticulum; integral to membrane; membrane;		2	2
96	ENSG00000023839:ENSMUSG00000025194:NA	ABCC2	gi|116063566|ref|NP_0	gi|116063566|ref|NP_038834.2|	ATP-binding cassette, sub-family C, membe	1543	173670	8.6	16	o29-51i63-8	A	21	0	1	2	0	1	2	2	1.62	0.00057	1	3	0	1	3	3	1.04	0.00036	2	0.000463	0.000148	CcmA, the ATP-binding component of the bacterial CcmAB	apical plasma membrane; integral to membrane; integral to	ATP binding; ATPase activity; ATPase activity, coupled	2	5
97	ENSG00000204319:ENSMUSG00000073418:ENSRNOG00000000443	C4A	gi|149269273|ref|XP_0	[illegible]	PREDICTED: similar to complement C4 [Mu	1539	170382	7.5	0	o	S	20	0.999	2	2	0	0	2	2	2.73	0.00057	1	1	0	0	1	1	1.49	0.00012	2	0.000344	0.00032	Anaphylatoxin homologous domain; C3a, C4a and C5a			3	3
98	ENSG00000035403:ENSMUSG00000021823:ENSRNOG00000010765	VCL	gi|31543942|ref|NP_03	gi|31543942|ref|NP_033528.3|	vinculin [Mus musculus]	1066	116717	6	0	o	Q	19	0	1	1	0	1	1	1	1.97	0.00041	1	1	0	1	1	1	1.97	0.00018	2	0.000292	0.000169	Vinculin family; pfam01044	actin cytoskeleton; adherens junction; costamere; cytoskeleton;	actin binding; protein binding; structural molecule activity	2	2
99	ENSG00000196576:ENSMUSG00000036606:ENSRNOG00000007133	PLXNB2	gi|94398834|ref|XP_00	gi|94398834|ref|XP_001003435.1|	PREDICTED: plexin B2 isoform 14 [Mus mu	1842	206229	5.9	0	o	S	20	0.991	1	1	0	1	1	1	1.52	0.00024	1	2	0	1	2	2	0.6	0.0002	2	0.000219	2.63E-05	Sema domain. The Sema domain occurs in semaphorins, which			2	3
100	NA:ENSMUSG00000041828:ENSRNOG00000004147	ABCA8A	gi|23346593|ref|NP_69	gi|23346593|ref|NP_694785.1|	ATP-binding cassette, sub-family A (ABC1),	1620	184110	7.2	15	i31-53o222	A	51	0	1	1	0	1	1	1	1.79	0.00027	1	1	0	1	1	1	0.86	0.00012	2	0.000192	0.000111				2	2
101	ENSG00000123384:ENSMUSG00000040249:ENSRNOG00000025053	LRP1	gi|124494256|ref|NP_0	gi|124494256|ref|NP_032538.2|	low density lipoprotein receptor-related prot	4545	504775	5.4	1	o4423-4445	S	20	1	1	2	0	1	2	2	0.48	0.00019	1	1	0	1	1	1	0.26	4.1E-05	2	0.000116	0.000109	Low Density Lipoprotein Receptor Class A domain, a cysteine-	integral to membrane; membrane fraction	receptor activity	2	3
102	ENSG00000103018:ENSMUSG00000031924:ENSRNOG00000011142	CYB5B	gi|149275191|ref|XP_0	gi|149275191|ref|XP_001473825.1|;gi|31542438|ref|NP_079834.2|	PREDICTED: hypothetical protein [Mus mus	146	16329	4.9	1	i119-141o	Q	16	0	1	65	0	0	65	65	23.29	0.19682	X	X	X	X	X	X	X	0	1	0.194307	0.139174	Cytochrome b5-like Heme/Steroid binding domain. This family			1	65
103	ENSG00000138760:ENSMUSG00000029426:ENSRNOG00000002225	SCARB2	gi|6680878|ref|NP_031	gi|6680878|ref|NP_031670.1|	scavenger receptor class B, member 2 [Mus	478	54044	5.1	2	i7-29o434-4	S	27	0.864	2	24	0	2	24	24	7.95	0.0222	X	X	X	X	X	X	X	0	1	0.021914	0.015696	RPA3: A subfamily of OB folds similar to human RPA3 (also	DNA replication factor A complex [pmid 8454588]; nucleus	nucleic acid binding; single-stranded DNA binding [pmid	2	24
104	ENSG00000099797:ENSMUSG00000031708:ENSRNOG00000018935	GPSN2	gi|19923070|ref|NP_59	gi|19923070|ref|NP_598879.1|	glycoprotein, synaptic 2 [Mus musculus]	308	36090	9.6	4	i85-107o16	Q	0	0	1	15	0	1	15	15	2.92	0.02153	X	X	X	X	X	X	X	0	1	0.021255	0.015224	ROKNT (NUC014) domain. This presumed domain is found at	nucleus; ribonucleoprotein complex	DNA binding; nucleic acid binding; protein binding [pmid	1	15
105	ENSG00000162365:ENSMUSG00000078597:ENSRNOG00000029919	CYP4A22	gi|86198314|ref|NP_75	gi|86198314|ref|NP_758510.2|	cytochrome P450, family 4, subfamily a fam	508	58309	8.9	0	o	S	38	0.822	5	19	5	1	14	18.43	19.09	0.01604	2	9	9	0	0	0	3.94	0	1	0.015837	0.011343	motif in proteasome subunits, Int-6, Nip-1 and TRIP-15; Also	eukaryotic translation initiation factor 3 complex [pmid 9054404]	translation initiation factor activity	7	28
106	ENSG00000179091:ENSMUSG00000022551:ENSRNOG00000012457	CYC1	gi|13385006|ref|NP_07	gi|13385006|ref|NP_079843.1|	cytochrome c-1 [Mus musculus]	325	35328	9.2	1	i59-81o	S	35	0.909	2	10	0	2	10	10	11.08	0.0136	X	X	X	X	X	X	X	0	1	0.013429	0.009619	Non-repetitive/WGA-negative nucleoporin. This is a family of	nuclear pore; nucleus	nucleocytoplasmic transporter activity; structural	2	10
107	ENSG00000187446:ENSMUSG00000014077:ENSRNOG00000008946	CHP	gi|149249669|ref|XP_0	gi|149249669|ref|XP_001480493.1|;gi|149267344|ref|XP_205829.5|	PREDICTED: similar to EF-hand Ca2+ bind	195	22432	5.1	0	o	Q	0	0	X	X	X	X	X	X	X	0	2	10	0	0	10	10	14.36	0.00958	1	0.009507	0.006773	EF-hand, calcium binding motif; A diverse superfamily of calcium			2	10
108	ENSG00000221842:ENSMUSG00000052305:ENSRNOG00000025510	HBB	gi|17647499|ref|NP_05	gi|17647499|ref|NP_058652.1|	hemoglobin, beta adult minor chain [Mus mu	147	15878	8.1	0	o	Q	22	0.005	X	X	X	X	X	X	X	0	2	7	0	2	7	7	14.97	0.00889	1	0.008828	0.006289	WD40 domain, found in a number of eukaryotic proteins that			2	7
109	ENSG00000138115:ENSMUSG00000067225:NA	CYP2C8	gi|149270669|ref|XP_9	gi|149270669|ref|XP_920372.2|;gi|45504402|ref|NP_998260.1|;gi|6753580|ref|NP_034131.1|	PREDICTED: similar to cytochrome P450 [M	302	34345	8.2	1	i12-34o	A	37	0.201	X	X	X	X	X	X	X	0	1	14	0	0	14	14	3.97	0.00866	1	0.008594	0.006123	Cytochrome P450. Cytochrome P450s are haem-thiolate			1	14
110	ENSG00000127022:ENSMUSG00000020368:ENSRNOG00000003343	CANX	gi|6671664|ref|NP_031	gi|6671664|ref|NP_031623.1|	calnexin [Mus musculus]	591	67278	4.6	1	o484-506i	S	21	1	X	X	X	X	X	X	X	0	1	26	0	1	26	26	2.71	0.00822	1	0.008156	0.00581	Calreticulin family; pfam00262	endoplasmic reticulum; integral to membrane; membrane	calcium ion binding; sugar binding	1	26
111	ENSG00000084453:ENSMUSG00000041698:ENSRNOG00000036984	SLCO1A2	gi|7305497|ref|NP_038	gi|7305497|ref|NP_038825.1|	solute carrier organic anion transporter fami	670	74396	8.2	11	i21-43o58-8	Q	37	0.054	2	12	0	2	12	12	4.18	0.00792	X	X	X	X	X	X	X	0	1	0.007817	0.005599	The kazal-type serine protease inhibitor domain has been	basolateral plasma membrane; integral to membrane; integral to	organic anion transporter activity; transporter activity	2	12
112	ENSG00000111775:ENSMUSG00000041697:ENSRNOG00000001170	COX6A1	gi|6680988|ref|NP_031	gi|6680988|ref|NP_031774.1|	cytochrome c oxidase, subunit VI a, polype	112	12483	10	1	o43-62i	A	57	0.1	1	2	0	1	2	2	14.29	0.00789	X	X	X	X	X	X	X	0	1	0.007794	0.005582	Cytochrome c oxidase subunit VIa; cd00925	membrane; mitochondrial envelope; mitochondrion	cytochrome-c oxidase activity; oxidoreductase activity	1	2
113	ENSG00000112081:ENSMUSG00000078134:ENSRNOG00000000520	SFRS3	gi|149251831|ref|XP_0	[illegible]	PREDICTED: similar to MGC89287 protein	156	18374	11.5	0	o	Q	0	0	X	X	X	X	X	X	X	0	2	6	0	0	6	6	14.74	0.00718	1	0.00713	0.00508	RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain). The			2	6
114	ENSG00000112473:ENSMUSG00000024327:ENSRNOG00000000465	SLC39A7	gi|118150670|ref|NP_0	gi|118150670|ref|NP_032228.2|	solute carrier family 39, member 7 [Mus mu	476	50657	6.9	7	i7-26o142-1	S	28	0.977	1	7	0	1	7	7	5.46	0.0065	X	X	X	X	X	X	X	0	1	0.006418	0.004597	ZIP Zinc transporter. The ZIP family consists of zinc transport	membrane	metal ion transporter activity; zinc ion binding	1	7
115	ENSG00000183048:ENSMUSG00000025792:ENSRNOG00000036693	SLC25A10	gi|7305501|ref|NP_038	gi|7305501|ref|NP_038798.1|	solute carrier family 25 (mitochondrial carrie	287	31727	9.3	0	o	S	24	0.852	X	X	X	X	X	X	X	0	1	9	0	1	9	9	8.36	0.00586	1	0.005814	0.004142	Mitochondrial carrier protein; pfam00153	integral to membrane; membrane; mitochondrial inner membrane	binding; electrochemical potential-driven transporter	1	9

Korfali_S3B

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rk	ORTHO_GROUP	GENE_NAME	Locus	Proteins In Group	Description	Length	MW	pI	PredHel	TMHMM_Topology	SIGNALP_HMM_TYPE (S= signal; A= Anchor; Q= none)	SIGNALP_HMM_POS	SIGNALP_HMM_SPROB	MmNaOH-MM_liver_CNBrTi_1_P	MmNaOH-MM_liver_CNBrTi_1_S	MmNaOH-MM_liver_CNBrTi_1_sS	MmNaOH-MM_liver_CNBrTi_1_uDP	MmNaOH-MM_liver_CNBrTi_1_uS	MmNaOH-MM_liver_CNBrTi_1_dS	MmNaOH-MM_liver_CNBrTi_1_SC	MmNaOHMM_liver_CNBrTi_1_dNSAF	MmNaOH-MM_liver_CNBrTi_2_P	MmNaOH-MM_liver_CNBrTi_2_S	MmNaOH-MM_liver_CNBrTi_2_sS	MmNaOH-MM_liver_CNBrTi_2_uDP	MmNaOH-MM_liver_CNBrTi_2_uS	MmNaOH-MM_liver_CNBrTi_2_dS	MmNaOH-MM_liver_CNBrTi_2_SC	MmNaOH-MM_liver_CNBrTi_2_dNSAF	IMMs Detected # Out of 2	IMMs dNSAF AVG	IMMs dNSAF SDV	NCBI_Region_Note	GO_Component	GO_Function	Total_P	Total_S
116	NA:ENSMUSG00000003429:ENSRNOG00000023237	RPS11	gi|21426889|ref|NP_03	gi|21426889|ref|NP_038753.1|	ribosomal protein S11 [Mus musculus]	158	18431	10.3	0	o	Q	0	0	1	2	0	1	2	2	5.06	0.0056	X	X	X	X	X	X	X	0	1	0.005525	0.003957	Domain of unknown function (DUF382). This domain is specific			1	2
117	ENSG00000042445:ENSMUSG00000056666:ENSRNOG00000014090	RETSAT	gi|52627143|ref|NP_08	gi|52627143|ref|NP_080435.3|	all-trans-13,14-dihydroretinol saturase [Mus	609	67335	9	1	i5-27o	S	26	1	X	X	X	X	X	X	X	0	2	18	0	2	18	18	4.76	0.00552	1	0.00548	0.003904	MOSC domain. The MOSC (MOCO sulfurase C-terminal)	extracellular space; integral to membrane; mitochondrial inner		2	18
118	ENSG00000086696:ENSMUSG00000031844:ENSRNOG00000013982	HSD17B2	gi|123173870|ref|NP_0	gi|123173870|ref|NP_032316.2|	hydroxysteroid (17-beta) dehydrogenase 2 [	381	41836	8.6	2	o10-27i40-6	A	65	0.02	X	X	X	X	X	X	X	0	3	11	0	3	11	11	8.92	0.00539	1	0.005352	0.003813	short chain dehydrogenase; PRK06182	membrane	estradiol 17-beta-dehydrogenase activity;	3	11
119	ENSG00000150527:ENSMUSG00000021000:ENSRNOG00000005101	CTAGE5	gi|119372290|ref|NP_6	gi|119372290|ref|NP_666146.2|	CTAGE family, member 5 [Mus musculus]	777	87490	5.1	1	i9-31o	A	26	0.024	X	X	X	X	X	X	X	0	2	22	0	2	22	22	3.99	0.00529	1	0.005249	0.00374	Chromosome segregation ATPases [Cell division and	integral to membrane; membrane		2	22
120	ENSG00000161016:ENSMUSG00000003970:NA	RPL8	gi|6755358|ref|NP_036	gi|6755358|ref|NP_036183.1|	ribosomal protein L8 [Mus musculus]	257	28025	11	0	o	Q	27	0	X	X	X	X	X	X	X	0	2	7	0	2	7	7	9.34	0.00509	1	0.00505	0.003597	Ribosomal Proteins L2, RNA binding domain; pfam00181	ribonucleoprotein complex	rRNA binding	2	7
121	ENSG00000075785:NA:NA	RAB7A	gi|6679599|ref|NP_033	gi|6679599|ref|NP_033031.1|	RAB7, member RAS oncogene family [Mus	207	23559	7.6	0	o	Q	21	0.163	X	X	X	X	X	X	X	0	3	5	0	3	5	5	17.87	0.00451	1	0.004478	0.00319	Rab7 subfamily. Rab7 is a small Rab GTPase that regulates	Golgi apparatus; late endosome; lysosome; membrane	GTP binding; nucleotide binding	3	5
122	ENSG00000145425:ENSMUSG00000062611:ENSRNOG00000011893	RPS3A	gi|149265827|ref|XP_0	gi|149265827|ref|XP_001480995.1|;gi|31980669|ref|NP_058655.2|;gi|94395719|ref|XP_979863.1|	PREDICTED: similar to ribosomal protein S	264	29825	9.7	0	o	Q	0	0	X	X	X	X	X	X	X	0	1	6	0	0	6	6	6.44	0.00424	1	0.004213	0.003002	Ribosomal S3Ae family; pfam01015			1	6
123	ENSG00000130203:ENSMUSG00000002985:ENSRNOG00000018454	APOE	gi|6753102|ref|NP_033	gi|6753102|ref|NP_033826.1|	apolipoprotein E [Mus musculus]	311	35853	5.7	0	o	S	19	1	X	X	X	X	X	X	X	0	2	7	0	2	7	7	6.43	0.0042	1	0.004173	0.002973	Apolipoprotein A1/A4/E domain. These proteins contain several	chylomicron; cytoplasm; extracellular region	antioxidant activity; beta-amyloid binding; heparin	2	7
124	ENSG00000184752:ENSMUSG00000020022:ENSRNOG00000007407	NDUFA12	gi|27228985|ref|NP_07	gi|27228985|ref|NP_079827.2|	13kDa differentiation-associated protein [Mu	149	17633	9.5	0	o	Q	21	0	X	X	X	X	X	X	X	0	1	3	0	1	3	3	8.05	0.00376	1	0.003733	0.002659	NADH ubiquinone oxidoreductase subunit NDUFA12. This family	membrane	electron carrier activity	1	3
125	ENSG00000072849:ENSMUSG00000018442:ENSRNOG00000007244	DERL2	gi|15808990|ref|NP_29	gi|15808990|ref|NP_291040.1|	Der1-like domain family, member 2 [Mus mu	239	27640	7.3	4	i57-79o99-1	Q	34	0.039	1	2	0	1	2	2	12.55	0.0037	X	X	X	X	X	X	X	0	1	0.003652	0.002616	Der1-like family. The endoplasmic reticulum (ER) of the yeast	endoplasmic reticulum; integral to endoplasmic reticulum	molecular_function; protein binding	1	2
126	ENSG00000164344:ENSMUSG00000031640:ENSRNOG00000014118	KLKB1	gi|19527190|ref|NP_59	gi|19527190|ref|NP_598730.1|	family 4 cytochrome P450 [Mus musculus]	525	60939	8.5	1	i13-35o	S	28	0.889	X	X	X	X	X	X	X	0	1	10	0	1	10	10	1.9	0.00356	1	0.003531	0.002516	Cytochrome P450. Cytochrome P450s are haem-thiolate	cellular_component; endoplasmic reticulum; integral to	heme binding; iron ion binding; metal ion binding;	1	10
127	ENSG00000162877:ENSMUSG00000042251:ENSRNOG00000039745	PM20D1	gi|113374119|ref|NP_8	gi|113374119|ref|NP_835180.1|	hypothetical protein LOC212933 [Mus musc	503	55591	6.5	0	o	S	25	0.999	1	4	0	1	4	4	2.19	0.00352	X	X	X	X	X	X	X	0	1	0.003471	0.002486	Acetylornithine deacetylase/Succinyl-diaminopimelate		hydrolase activity; protein dimerization activity	1	4
128	ENSG00000116133:ENSMUSG00000034926:ENSRNOG00000006787	DHCR24	gi|114155129|ref|NP_4	gi|114155129|ref|NP_444502.2|	24-dehydrocholesterol reductase precursor	516	60112	8.2	2	o5-27i34-56	S	23	0.989	1	4	0	1	4	4	3.68	0.00343	X	X	X	X	X	X	X	0	1	0.003383	0.002423	FAD binding domain. This family consists of various enzymes		oxidoreductase activity, acting on the CH-CH group of	1	4
129	ENSG00000117528:ENSMUSG00000028127:ENSRNOG00000011929	ABCD3	gi|60218877|ref|NP_03	gi|60218877|ref|NP_033017.2|	ATP-binding cassette, sub-family D, membe	659	75475	9.3	1	o495-517i	S	18	0.991	3	5	0	3	5	5	5.16	0.00335	X	X	X	X	X	X	X	0	1	0.003311	0.002372	ABC transporter transmembrane region 2. This domain covers	integral to membrane; membrane; mitochondrial inner membrane	ATP binding; ATPase activity; ATPase activity, coupled	3	5
130	ENSG00000160868:ENSMUSG00000056035:ENSRNOG00000000978	CYP3A4	gi|6681113|ref|NP_031	gi|6681113|ref|NP_031844.1|	cytochrome P450, family 3, subfamily a, pol	504	57855	8.8	2	o4-26i219-2	S	23	0.681	X	X	X	X	X	X	X	0	4	9	0	4	9	9	10.91	0.00334	1	0.003311	0.002358	Cytochrome P450. Cytochrome P450s are haem-thiolate	endoplasmic reticulum; membrane; microsome	heme binding; iron ion binding; metal ion binding;	4	9
131	ENSG00000124222:ENSMUSG00000027522:ENSRNOG00000005281	STX16	gi|29789393|ref|NP_76	gi|29789393|ref|NP_766263.1|	syntaxin 16 [Mus musculus]	273	31148	5.7	1	o251-270i	Q	17	0.003	1	2	0	1	2	2	6.59	0.00324	X	X	X	X	X	X	X	0	1	0.003197	0.00229	Soluble NSF (N-ethylmaleimide-sensitive fusion protein)-			1	2
132	ENSG00000137824:ENSMUSG00000070730:ENSRNOG00000011690	FAM82C	gi|85701644|ref|NP_00	gi|85701644|ref|NP_001028308.1|	hypothetical protein LOC67809 [Mus muscu	470	52029	5.2	1	i13-35o	S	33	0.629	X	X	X	X	X	X	X	0	2	8	0	2	8	8	7.87	0.00318	1	0.003156	0.002248			binding	2	8
133	ENSG00000168028:ENSMUSG00000047676:ENSRNOG00000018645	RPSA	gi|149252001|ref|XP_0	[illegible]	PREDICTED: hypothetical protein [Mus mus	295	32838	4.9	0	o	Q	31	0	X	X	X	X	X	X	X	0	2	5	0	0	5	5	7.8	0.00317	1	0.003142	0.002239	PDZ domain found in a variety of Eumetazoan signaling	cytoplasm; membrane; nucleus; plasma membrane	protein binding	2	5
134	ENSG00000103496:ENSMUSG00000030805:ENSRNOG00000019302	STX4	gi|6678177|ref|NP_033	gi|6678177|ref|NP_033320.1|	syntaxin 4A (placental) [Mus musculus]	298	34165	6.1	1	i274-296o	Q	0	0	X	X	X	X	X	X	X	0	1	5	0	1	5	5	3.69	0.00313	1	0.003111	0.002216	Syntaxin N-terminus domain; syntaxins are nervous system-	cytoplasm; membrane; plasma membrane	protein binding; protein transporter activity	1	5
135	NA:ENSMUSG00000073702:ENSRNOG00000000050	RPL31	gi|149267081|ref|XP_9	[illegible]	PREDICTED: hypothetical protein [Mus mus	125	14463	10.5	0	o	Q	0	0	X	X	X	X	X	X	X	0	1	2	0	0	2	2	11.2	0.00299	1	0.002966	0.002113		ER-Golgi intermediate compartment [pmid 15308636]; Golgi		1	2
136	ENSG00000063177:ENSMUSG00000059070:ENSRNOG00000021035	RPL18	gi|83699424|ref|NP_03	gi|83699424|ref|NP_033103.2|	ribosomal protein L18 [Mus musculus]	188	21645	11.8	0	o	Q	0	0	X	X	X	X	X	X	X	0	2	3	0	2	3	3	12.23	0.00298	1	0.002958	0.002108	Ribosomal protein L18E [Translation, ribosomal structure and	intracellular; ribonucleoprotein complex; ribosome	structural constituent of ribosome	2	3
137	ENSG00000109919:ENSMUSG00000027282:ENSRNOG00000008682	MTCH2	gi|9790055|ref|NP_062	gi|9790055|ref|NP_062732.1|	mitochondrial carrier homolog 2 [Mus muscu	303	33499	8.3	0	o	Q	19	0.468	1	2	0	1	2	2	5.28	0.00292	X	X	X	X	X	X	X	0	1	0.002881	0.002063	Mitochondrial carrier protein; pfam00153	integral to membrane; membrane; mitochondrial inner membrane	binding	1	2
138	ENSG00000212870:ENSMUSG00000064367:ENSRNOG00000029971	MT-ND5	gi|34538608|ref|NP_90	gi|34538608|ref|NP_904338.1|	NADH dehydrogenase subunit 5 [Mus musc	607	68475	9	16	o5-27i34-56	S	25	0.906	1	4	0	1	4	4	3.29	0.00291	X	X	X	X	X	X	X	0	1	0.002876	0.00206	NADH-Ubiquinone/plastoquinone (complex I), various chains.			1	4
139	ENSG00000084733:ENSMUSG00000020671:NA	RAB10	gi|7710086|ref|NP_057	gi|7710086|ref|NP_057885.1|	RAB10, member RAS oncogene family [Mu	200	22541	8.4	0	o	Q	22	0.218	X	X	X	X	X	X	X	0	1	3	0	1	3	3	5.5	0.0028	1	0.002781	0.001981	Rab8/Sec4/Ypt2. Rab8/Sec4/Ypt2 are known or suspected to	Golgi apparatus; intracellular; membrane	GTP binding; nucleotide binding; protein binding	1	3
140	ENSG00000103415:ENSMUSG00000004070:ENSRNOG00000003773	HMOX2	gi|6754214|ref|NP_034	gi|6754214|ref|NP_034573.1|	heme oxygenase (decycling) 2 [Mus muscu	315	35659	5.7	1	o295-314i	Q	0	0	1	2	0	1	2	2	6.03	0.00281	X	X	X	X	X	X	X	0	1	0.002771	0.001985	Heme oxygenase catalyzes the rate limiting step in the	endoplasmic reticulum; microsome	heme oxygenase (decyclizing) activity; iron ion binding;	1	2
141	ENSG00000106327:ENSMUSG00000029716:ENSRNOG00000001407	TFR2	gi|113204630|ref|NP_0	gi|113204630|ref|NP_056614.3|	transferrin receptor 2 [Mus musculus]	798	88402	6.1	1	i80-102o	Q	22	0	2	5	0	2	5	5	2.51	0.00277	X	X	X	X	X	X	X	0	1	0.002735	0.001959	PA_TfR: Protease-associated domain containing proteins like	integral to membrane; membrane	ferrochelatase activity; peptidase activity; receptor	2	5
142	ENSG00000138073:ENSMUSG00000045302:ENSRNOG00000007141	PREB	gi|7710084|ref|NP_057	gi|7710084|ref|NP_057912.1|	prolactin regulatory element binding protein	416	45380	8.8	2	o312-331i3	Q	38	0.09	X	X	X	X	X	X	X	0	1	6	0	1	6	6	2.16	0.00269	1	0.002674	0.001905	K homology RNA-binding domain, type I. KH binds single-			1	6
143	ENSG00000009765:ENSMUSG00000019762:ENSRNOG00000016286	IYD	gi|21312562|ref|NP_08	gi|21312562|ref|NP_081667.1|	iodotyrosine dehalogenase 1 protein [Mus m	285	32814	6.4	1	i2-20o	A	24	0.25	X	X	X	X	X	X	X	0	1	4	0	1	4	4	4.21	0.00262	1	0.002602	0.001854	Iodotyrosine dehalogenase catalyzes the removal of iodine from	integral to membrane; membrane	oxidoreductase activity	1	4
144	ENSG00000074696:ENSMUSG00000033629:ENSRNOG00000030232	PTPLAD1	gi|28916663|ref|NP_06	gi|28916663|ref|NP_067320.1|;gi|7705459|ref|NP_057479.1|	protein tyrosine phosphatase-like A domain	362	43145	9.1	5	o153-175i2	Q	14	0	X	X	X	X	X	X	X	0	1	5	0	0	5	5	2.76	0.00258	1	0.002561	0.001824	homolog to co-chaperone p23; p23 binds heat shock protein		protein binding	1	5
145	ENSG00000113621:ENSMUSG00000021497:ENSRNOG00000005316	TXNDC15	gi|52693935|ref|NP_78	gi|52693935|ref|NP_780359.2|	disulfide isomerase [Mus musculus]	344	38146	4.8	1	o305-324i	S	21	1	1	2	0	1	2	2	6.1	0.00257	X	X	X	X	X	X	X	0	1	0.002537	0.001817	PDIa family, endoplasmic reticulum protein 44 (ERp44)-like		protein disulfide oxidoreductase activity	1	2
146	NA:ENSMUSG00000060264:NA	LOC433745	gi|149252852|ref|XP_0	[illegible]	PREDICTED: similar to ribosomal protein L3	354	39964	10.1	0	o	Q	24	0.002	1	2	0	0	2	2	2.54	0.0025	X	X	X	X	X	X	X	0	1	0.002466	0.001766	50S ribosomal protein L3P; PRK04231			1	2
147	ENSG00000140612:ENSMUSG00000025724:ENSRNOG00000011029	SEC11A	gi|9910550|ref|NP_064	gi|9910550|ref|NP_064335.1|	Sec11-like 1 [Mus musculus]	179	20626	9.3	1	i21-43o	Q	33	0	1	1	0	1	1	1	4.47	0.00247	X	X	X	X	X	X	X	0	1	0.002438	0.001746	Peptidase S24-like; pfam00717	endoplasmic reticulum; membrane; microsome	hydrolase activity; peptidase activity; serine-type	1	1
148	ENSG00000156052:ENSMUSG00000024639:ENSRNOG00000014183	GNAQ	gi|84662745|ref|NP_03	gi|84662745|ref|NP_032165.3|	guanine nucleotide binding protein, alpha q	359	42158	5.7	0	o	Q	19	0.005	1	2	0	1	2	2	5.85	0.00246	X	X	X	X	X	X	X	0	1	0.002431	0.001742	G-protein alpha subunit. G proteins couple receptors of	heterotrimeric G-protein complex	GTP binding; GTPase activity; guanyl nucleotide binding;	1	2
149	ENSG00000182327:ENSMUSG00000046811:ENSRNOG00000026488	GLTPD2	gi|149252026|ref|XP_0	gi|149252026|ref|XP_001471857.1|	PREDICTED: hypothetical protein [Mus mus	321	34453	9.2	1	o15-37i	A	46	0.149	X	X	X	X	X	X	X	0	3	4	0	3	4	4	9.66	0.00233	1	0.00231	0.001646	Glycolipid transfer protein (GLTP). GLTP is a cytosolic protein			3	4
150	ENSG00000167315:ENSMUSG00000036880:ENSRNOG00000013766	ACAA2	gi|29126205|ref|NP_80	gi|29126205|ref|NP_803421.1|	acetyl-Coenzyme A acyltransferase 2 (mito	397	41830	8.1	0	o	Q	22	0.067	1	2	0	1	2	2	2.52	0.00223	X	X	X	X	X	X	X	0	1	0.002199	0.001575	Thiolase are ubiquitous enzymes that catalyze the reversible	mitochondrial inner membrane; mitochondrion		1	2
151	ENSG00000164209:ENSMUSG00000024259:ENSRNOG00000017091	SLC25A46	gi|13385672|ref|NP_08	gi|13385672|ref|NP_080441.1|	solute carrier family 25, member 46 [Mus m	418	46224	7.6	2	o268-290i3	Q	35	0	1	2	0	1	2	2	5.98	0.00212	X	X	X	X	X	X	X	0	1	0.002088	0.001496	Mitochondrial carrier protein; pfam00153	integral to membrane; membrane	binding	1	2
152	ENSG00000120063:ENSMUSG00000020611:ENSRNOG00000036745	GNA13	gi|89001109|ref|NP_03	gi|89001109|ref|NP_034433.3|	guanine nucleotide binding protein, alpha 13	377	44055	8.2	0	o	S	26	0.813	X	X	X	X	X	X	X	0	1	4	0	1	4	4	2.65	0.00198	1	0.001967	0.001401	G-protein alpha subunit. G proteins couple receptors of	heterotrimeric G-protein complex; membrane	GTP binding; GTPase activity; guanyl nucleotide binding;	1	4
153	ENSG00000140688:ENSMUSG00000030780:ENSRNOG00000020144	C16orf58	gi|21704184|ref|NP_66	gi|21704184|ref|NP_663565.1|	hypothetical protein LOC233913 [Mus musc	466	50469	7.1	0	o	Q	27	0.071	1	2	0	1	2	2	5.36	0.0019	X	X	X	X	X	X	X	0	1	0.001873	0.001342	Protein of unknown function, DUF647; pfam04884			1	2
154	ENSG00000162236:ENSMUSG00000010110:ENSRNOG00000018847	STX5	gi|34328465|ref|NP_06	gi|34328465|ref|NP_062803.3|	syntaxin 5 [Mus musculus]	301	34087	8.7	1	i280-299o	Q	20	0	X	X	X	X	X	X	X	0	1	3	0	1	3	3	8.31	0.00186	1	0.001848	0.001316	Soluble NSF (N-ethylmaleimide-sensitive fusion protein)-	Golgi membrane		1	3
155	ENSG00000125505:ENSMUSG00000035596:ENSRNOG00000038794	LENG4	gi|31542014|ref|NP_08	gi|31542014|ref|NP_084210.2|	leukocyte receptor cluster (LRC) member 4	473	53436	8.7	5	o5-22i35-57	A	54	0.18	1	2	0	1	2	2	4.65	0.00187	X	X	X	X	X	X	X	0	1	0.001845	0.001322	Predicted membrane protein [Function unknown]; COG5202		receptor activity	1	2
156	ENSG00000058262:ENSMUSG00000030082:ENSRNOG00000013743	SEC61A1	gi|8394252|ref|NP_058	gi|8394252|ref|NP_058602.1|	Sec61 alpha subunit homolog [Mus musculu	476	52265	8.1	10	i33-55o75-9	A	47	0.001	1	2	0	1	2	2	4.83	0.00186	X	X	X	X	X	X	X	0	1	0.001834	0.001313	Preprotein translocase subunit SecY [Intracellular trafficking	endoplasmic reticulum; integral to membrane; membrane	protein translocase activity	1	2
157	ENSG00000144959:ENSMUSG00000027698:ENSRNOG00000013313	AADACL1	gi|30520239|ref|NP_84	gi|30520239|ref|NP_848887.1|	arylacetamide deacetylase-like 1 [Mus musc	408	45740	7	1	i5-27o	S	16	0.991	X	X	X	X	X	X	X	0	1	4	0	1	4	4	6.86	0.00183	1	0.001818	0.001295	alpha/beta hydrolase fold. This catalytic domain is found in a			1	4
158	NA:ENSMUSG00000046879:ENSRNOG00000031138	IRGM	gi|6680351|ref|NP_032	gi|6680351|ref|NP_032352.1|	immunity-related GTPase family, M [Mus mu	409	46552	8.3	0	o	Q	21	0.038	X	X	X	X	X	X	X	0	1	4	0	1	4	4	3.91	0.00183	1	0.001813	0.001292	p47 (47-kDa) family. The p47 GTPase family consists of	endoplasmic reticulum		1	4
159	ENSG00000198327:ENSMUSG00000060639:ENSRNOG00000030142	HIST2H4B	gi|149263932|ref|XP_0	gi|149263932|ref|XP_001476113.1|;gi|94378251|ref|XP_981474.1|	PREDICTED: similar to histone H4 [Mus mu	103	11367	11.4	0	o	Q	0	0	X	X	X	X	X	X	X	0	1	1	0	0	1	1	11.65	0.00181	1	0.0018	0.001282	Histone H4, one of the four histones, along with H2A, H2B and			1	1
160	ENSG00000124587:ENSMUSG00000002763:ENSRNOG00000026481	PEX6	gi|21703962|ref|NP_66	gi|21703962|ref|NP_663463.1|	peroxisomal biogenesis factor 6 [Mus musc	981	104548	7.3	0	o	Q	49	0.362	1	4	0	1	4	4	2.45	0.0018	X	X	X	X	X	X	X	0	1	0.00178	0.001275	NACHT domain. This NTPase domain is found in apoptosis	membrane; peroxisome	ATP binding; nucleoside-triphosphatase activity;	1	4
161	ENSG00000197408:ENSMUSG00000030483:ENSRNOG00000033680	CYP2B6	gi|50080153|ref|NP_03	gi|50080153|ref|NP_034129.1|;gi|6753576|ref|NP_034128.1|	cytochrome P450, family 2, subfamily b, pol	491	55871	7.8	1	i5-22o	S	23	0.999	1	2	0	0	2	2	2.44	0.0018	X	X	X	X	X	X	X	0	1	0.001778	0.001273	Cytochrome P450. Cytochrome P450s are haem-thiolate	endoplasmic reticulum; membrane; microsome	heme binding; iron ion binding; metal ion binding;	1	2
162	ENSG00000187630:ENSMUSG00000022210:ENSRNOG00000018239	DHRS4L2	gi|13507612|ref|NP_10	gi|13507612|ref|NP_109611.1|;gi|83816905|ref|NP_001033027.1|	NADPH-dependent retinol dehydrogenase/r	216	23178	9.9	0	o	S	24	0.61	X	X	X	X	X	X	X	0	1	2	0	0	2	2	6.02	0.00173	1	0.001717	0.001223	short chain dehydrogenase; PRK07035	mitochondrion; peroxisome	retinal dehydrogenase activity	1	2
163	ENSG00000092295:ENSMUSG00000022218:ENSRNOG00000020136	TGM1	gi|31982705|ref|NP_06	gi|31982705|ref|NP_064368.2|	transglutaminase 1, K polypeptide [Mus mus	815	89826	6.5	0	o	Q	61	0	2	3	0	2	3	3	4.17	0.00163	X	X	X	X	X	X	X	0	1	0.001607	0.001151	Transglutaminase-like superfamily. This family includes animal	cell-cell adherens junction	metal ion binding	2	3
164	ENSG00000116521:ENSMUSG00000028049:ENSRNOG00000020504	SCAMP3	gi|118601011|ref|NP_0	gi|118601011|ref|NP_036016.2|	secretory carrier membrane protein 3 [Mus	349	38458	7.6	4	i171-193o1	Q	0	0	X	X	X	X	X	X	X	0	1	3	0	1	3	3	3.72	0.00161	1	0.001594	0.001135	SCAMP family; pfam04144	Golgi membrane; membrane		1	3
165	ENSG00000141699:ENSMUSG00000017802:ENSRNOG00000020056	FAM134C	gi|21312666|ref|NP_08	gi|21312666|ref|NP_080777.1|	hypothetical protein LOC67998 isoform 1 [M	466	51638	5	2	o79-101i18	Q	19	0.006	X	X	X	X	X	X	X	0	1	4	0	1	4	4	3.22	0.0016	1	0.001591	0.001134				1	4
166	ENSG00000105701:ENSMUSG00000019428:ENSRNOG00000019944	FKBP8	gi|6857787|ref|NP_034	gi|6857787|ref|NP_034353.1|	FK506 binding protein 8 [Mus musculus]	355	38615	7	1	o333-352i	Q	26	0	X	X	X	X	X	X	X	0	1	3	0	1	3	3	8.17	0.00158	1	0.001567	0.001116	Tetratricopeptide repeat domain; typically contains 34 amino	integral to endoplasmic reticulum membrane; mitochondrial	binding; isomerase activity; peptidyl-prolyl cis-trans	1	3
167	ENSG00000168958:ENSMUSG00000026150:ENSRNOG00000025358	C2orf33	gi|40254163|ref|NP_08	gi|40254163|ref|NP_083685.2|;gi|82881738|ref|XP_918666.1|	hypothetical protein LOC75734 [Mus muscu	291	32931	6.8	1	o272-289i	Q	0	0	1	1	0	0	1	1	9.28	0.00152	X	X	X	X	X	X	X	0	1	0.0015	0.001074	Protein of unknown function (DUF800). This family consists of			1	1
168	ENSG00000144224:ENSMUSG00000026353:ENSRNOG00000003625	UBXD2	gi|85861252|ref|NP_08	gi|85861252|ref|NP_080666.2|	UBX domain containing 2 [Mus musculus]	506	56460	6.6	0	o	S	29	0.699	X	X	X	X	X	X	X	0	2	4	0	2	4	4	7.91	0.00148	1	0.001466	0.001044	UAS family; UAS is a domain of unknown function. Most			2	4
169	ENSG00000162365:ENSMUSG00000066072:ENSRNOG00000009597	CYP4A22	gi|47059035|ref|NP_03	gi|47059035|ref|NP_034141.2|	cytochrome P450, family 4, subfamily a, pol	509	58339	8.6	2	o15-32i117	S	35	0.728	5	5	4	1	1	1.688	13.95	0.00147	X	X	X	X	X	X	X	0	1	0.001447	0.001036	Cytochrome P450. Cytochrome P450s are haem-thiolate	membrane; microsome	heme binding; iron ion binding; metal ion binding;	5	5
170	ENSG00000121691:ENSMUSG00000027187:ENSRNOG00000008364	CAT	gi|6753272|ref|NP_033	gi|6753272|ref|NP_033934.1|	catalase [Mus musculus]	527	59734	8.1	0	o	Q	0	0	X	X	X	X	X	X	X	0	2	4	0	2	4	4	4.55	0.00142	1	0.001407	0.001002	Catalase. Catalase is an ubiquitous enzyme found in both	mitochondrion; peroxisomal membrane; peroxisome	catalase activity; iron ion binding; metal ion binding;	2	4
171	ENSG00000163686:ENSMUSG00000025277:ENSRNOG00000008167	ABHD6	gi|31560264|ref|NP_07	gi|31560264|ref|NP_079617.2|	abhydrolase domain containing 6 [Mus mus	336	38205	8.5	1	i7-29o	A	18	0.085	1	1	0	1	1	1	4.17	0.00132	X	X	X	X	X	X	X	0	1	0.001299	0.00093	Pancreatic lipase-like enzymes. Lipases are esterases that can		epoxide hydrolase activity; hydrolase activity	1	1
172	ENSG00000117480:ENSMUSG00000034171:ENSRNOG00000011019	FAAH	gi|31542795|ref|NP_03	gi|31542795|ref|NP_034303.2|	fatty acid amide hydrolase [Mus musculus]	579	63191	7.9	1	i7-29o	S	26	0.973	X	X	X	X	X	X	X	0	2	4	0	2	4	4	6.91	0.00129	1	0.001281	0.000912	Asp-tRNAAsn/Glu-tRNAGln amidotransferase A subunit and	endoplasmic reticulum; integral to membrane; membrane	amidase activity; hydrolase activity	2	4
173	ENSG00000117594:ENSMUSG00000016194:NA	HSD11B1	gi|113680741|ref|NP_0	gi|113680741|ref|NP_032314.2|	hydroxysteroid 11-beta dehydrogenase 1 [M	292	32364	8.5	1	i7-24o	A	23	0.243	X	X	X	X	X	X	X	0	1	2	0	1	2	2	4.45	0.00128	1	0.00127	0.000905	short chain dehydrogenase; PRK06181	endoplasmic reticulum; integral to membrane; membrane;	11-beta-hydroxysteroid dehydrogenase activity;	1	2
174	ENSG00000117242:ENSMUSG00000028757:ENSRNOG00000015079	DDOST	gi|46195798|ref|NP_03	gi|46195798|ref|NP_031864.2|	dolichyl-di-phosphooligosaccharide-protein	441	49028	5.8	2	i7-29o410-4	S	28	0.994	X	X	X	X	X	X	X	0	2	3	0	2	3	3	4.31	0.00127	1	0.001261	0.000898	Dolichyl-diphosphooligosaccharide-protein glycosyltransferase	endoplasmic reticulum membrane; membrane; oligosaccharyl	dolichyl-diphosphooligosaccharide-protein	2	3
175	ENSG00000105854:ENSMUSG00000032667:ENSRNOG00000009112	PON2	gi|34303979|ref|NP_89	gi|34303979|ref|NP_899131.1|	paraoxonase 2 [Mus musculus]	354	39617	5.8	0	o	S	24	0.991	1	1	0	1	1	1	4.52	0.00125	X	X	X	X	X	X	X	0	1	0.001233	0.000883	Very long chain acyl-CoA dehydrogenase (VLCAD). VLCAD	mitochondrion [pmid 7668252]	FAD binding; long-chain-acyl-CoA dehydrogenase	1	1
176	ENSG00000156049:ENSMUSG00000024697:ENSRNOG00000014840	GNA14	gi|31542895|ref|NP_03	gi|31542895|ref|NP_032163.2|;gi|6754004|ref|NP_034431.1|	guanine nucleotide binding protein, alpha 14	355	41469	6.1	0	o	Q	15	0	1	1	0	0	1	1	5.92	0.00125	X	X	X	X	X	X	X	0	1	0.001229	0.000881	G-protein alpha subunit. G proteins couple receptors of	heterotrimeric G-protein complex	GTP binding; GTPase activity; guanyl nucleotide binding;	1	1
177	ENSG00000198171:ENSMUSG00000068290:ENSRNOG00000021232	C20orf116	gi|110350660|ref|NP_0	gi|110350660|ref|NP_084108.1|	hypothetical protein LOC77006 [Mus muscu	315	35977	5.3	1	o4-21i	S	31	0.98	X	X	X	X	X	X	X	0	1	2	0	1	2	2	5.4	0.00119	1	0.001177	0.000839				1	2
178	ENSG00000174640:ENSMUSG00000032548:ENSRNOG00000009005	SLCO2A1	gi|110625831|ref|NP_2	gi|110625831|ref|NP_201571.2|	solute carrier organic anion transporter fami	643	70147	8.7	11	o71-93i100	A	50	0.172	X	X	X	X	X	X	X	0	1	4	0	1	4	4	1.56	0.00116	1	0.001153	0.000822	The kazal-type serine protease inhibitor domain has been	integral to plasma membrane	prostaglandin transporter activity	1	4
179	NA:ENSMUSG00000025197:ENSRNOG00000013291	CYP2C23	gi|48374085|ref|NP_00	gi|48374085|ref|NP_001001446.2|	cytochrome P450, family 2, subfamily c, pol	494	56456	8.5	1	i3-25o	S	26	0.961	X	X	X	X	X	X	X	0	1	3	0	1	3	3	3.24	0.00113	1	0.001126	0.000802				1	3
180	ENSG00000115307:ENSMUSG00000068328:ENSRNOG00000007842	AUP1	gi|90403601|ref|NP_03	gi|90403601|ref|NP_031543.2|	ancient ubiquitous protein [Mus musculus]	439	49351	9.2	1	i52-74o	A	65	0	1	1	0	1	1	1	6.38	0.00101	X	X	X	X	X	X	X	0	1	0.000994	0.000712	CUE domain. CUE domains have been shown to bind ubiquitin.		acyltransferase activity	1	1
181	ENSG00000142655:ENSMUSG00000028975:ENSRNOG00000013498	PEX14	gi|9790153|ref|NP_062	gi|9790153|ref|NP_062755.1|	peroxisomal biogenesis factor 14 [Mus mus	376	41208	5.1	1	i109-127o	Q	0	0	X	X	X	X	X	X	X	0	2	2	0	2	2	2	5.85	0.00099	1	0.000986	0.000703	Peroxisomal membrane anchor protein (Pex14p) conserved	membrane; peroxisome		2	2
182	ENSG00000167536:ENSMUSG00000020834:ENSRNOG00000009673	DHRS13	gi|117647267|ref|NP_8	gi|117647267|ref|NP_899109.2|	dehydrogenase/reductase (SDR family) me	376	40745	7.9	0	o	S	26	0.62	X	X	X	X	X	X	X	0	1	2	0	1	2	2	2.66	0.00099	1	0.000986	0.000703	short chain dehydrogenase; PRK06197			1	2
183	ENSG00000167165:ENSMUSG00000054545:ENSRNOG00000018740	UGT1A9	gi|47059131|ref|NP_96	gi|47059131|ref|NP_964006.1|	UDP glucuronosyltransferase 1 family, polyp	528	59934	8.4	1	o486-508i	S	24	1	X	X	X	X	X	X	X	0	3	61	60	1	1	2.765	7.77	0.00098	1	0.000971	0.000692	Glycosyltransferase family 28 C-terminal domain. The		transferase activity; transferase activity, transferring	3	61
184	ENSG00000143870:ENSMUSG00000020571:NA	PDIA6	gi|149262992|ref|XP_0	gi|149262992|ref|XP_001476035.1|;gi|58037267|ref|NP_082235.1|	PREDICTED: similar to Protein disulfide iso	391	42858	6.7	1	i7-26o	S	28	0.966	X	X	X	X	X	X	X	0	1	2	0	0	2	2	3.58	0.00096	1	0.000948	0.000676	P5 family, C-terminal redox inactive TRX-like domain; P5 is a			1	2
185	ENSG00000211456:ENSMUSG00000025240:ENSRNOG00000005149	SACM1L	gi|13507622|ref|NP_10	gi|13507622|ref|NP_109617.1|	SAC1 (supressor of actin mutations 1, homo	587	66944	7.3	2	o521-543i5	Q	23	0	X	X	X	X	X	X	X	0	2	3	0	2	3	3	3.41	0.00095	1	0.000947	0.000675	SacI homology domain. This Pfam family represents a protein			2	3
186	ENSG00000148343:ENSMUSG00000026858:ENSRNOG00000017513	FAM73B	gi|30425102|ref|NP_78	gi|30425102|ref|NP_780601.1|	hypothetical protein LOC108958 [Mus musc	593	65548	5.4	0	o	A	62	0.276	X	X	X	X	X	X	X	0	2	3	0	2	3	3	6.75	0.00094	1	0.000938	0.000668				2	3
187	ENSG00000119688:ENSMUSG00000021240:ENSRNOG00000011964	ABCD4	gi|6680614|ref|NP_033	gi|6680614|ref|NP_033018.1|	ATP-binding cassette, sub-family D, membe	606	68549	6.4	2	o173-195i2	A	55	0.089	X	X	X	X	X	X	X	0	2	3	0	2	3	3	5.61	0.00092	1	0.000918	0.000654	ABC transporter transmembrane region 2. This domain covers	membrane; peroxisome	ATP binding; ATPase activity; ATPase activity, coupled	2	3
188	ENSG00000185187:ENSMUSG00000025494:ENSRNOG00000015593	SIGIRR	gi|110625701|ref|NP_0	gi|110625701|ref|NP_075546.2|	single Ig IL-1 receptor related protein [Mus	409	46159	5.7	1	i117-139o	Q	39	0.002	X	X	X	X	X	X	X	0	1	2	0	1	2	2	3.67	0.00091	1	0.000907	0.000646	TIR domain. The Toll/interleukin-1 receptor (TIR) homology	integral to membrane; membrane	protein binding; receptor activity	1	2
189	ENSG00000172482:ENSMUSG00000026272:ENSRNOG00000023856	AGXT	gi|111038130|ref|NP_0	gi|111038130|ref|NP_057911.2|	alanine-glyoxylate aminotransferase [Mus m	414	45912	8.2	0	o	S	38	0.614	X	X	X	X	X	X	X	0	1	2	0	1	2	2	3.14	0.0009	1	0.000896	0.000638	Aminotransferase class-V. This domain is found in amino	mitochondrion; peroxisome	alanine-glyoxylate transaminase activity; serine-pyruvate	1	2
190	ENSG00000127463:ENSMUSG00000078517:ENSRNOG00000018097	KIAA0090	gi|31542273|ref|NP_66	gi|31542273|ref|NP_666269.2|;gi|85861260|ref|NP_001034289.1|	hypothetical protein LOC230866 isoform 1 [	997	111605	7.4	1	i2-24o	S	23	0.999	2	2	0	0	2	2	3.61	0.00089	X	X	X	X	X	X	X	0	1	0.000876	0.000627	Protein of unknown function (DUF1620). These sequences are	integral to membrane; membrane		2	2
191	ENSG00000167114:ENSMUSG00000059316:ENSRNOG00000014369	SLC27A4	gi|45597453|ref|NP_03	gi|45597453|ref|NP_036119.1|	solute carrier family 27 (fatty acid transporte	643	72319	8.6	2	o20-42i139	S	38	0.885	X	X	X	X	X	X	X	0	1	3	0	1	3	3	1.4	0.00087	1	0.000865	0.000616	acyl-CoA synthase; PRK08279	integral to membrane; membrane; plasma membrane	catalytic activity; ligase activity; long-chain-fatty-acid-	1	3
192	ENSG00000188338:ENSMUSG00000010064:ENSRNOG00000016827	SLC38A3	gi|34328322|ref|NP_07	gi|34328322|ref|NP_076294.2|	N system amino acids transporter NAT-1 [M	505	55592	7.1	11	i69-91o95-1	Q	33	0	1	1	0	1	1	1	3.37	0.00088	X	X	X	X	X	X	X	0	1	0.000864	0.000619	Transmembrane amino acid transporter protein. This	integral to plasma membrane	amino acid transporter activity; antiporter activity; L-	1	1
193	ENSG00000164040:ENSMUSG00000049940:ENSRNOG00000014051	PGRMC2	gi|82889417|ref|XP_13	gi|82889417|ref|XP_130859.7|	PREDICTED: progesterone receptor memb	217	23334	5.1	1	o40-62i	Q	63	0.005	X	X	X	X	X	X	X	0	1	1	0	1	1	1	6.45	0.00086	1	0.000854	0.000609	Ribosomal protein L31e; pfam01198			1	1
194	ENSG00000142973:ENSMUSG00000028713:ENSRNOG00000009741	CYP4B1	gi|6681123|ref|NP_031	gi|6681123|ref|NP_031849.1|	cytochrome P450, family 4, subfamily b, pol	511	58900	8.4	1	i13-35o	S	32	0.547	1	1	0	1	1	1	2.35	0.00087	X	X	X	X	X	X	X	0	1	0.000854	0.000612	Cytochrome P450. Cytochrome P450s are haem-thiolate	endoplasmic reticulum; membrane; microsome	heme binding; iron ion binding; metal ion binding;	1	1
195	ENSG00000139641:ENSMUSG00000025366:ENSRNOG00000003909	FAM62A	gi|33859650|ref|NP_03	gi|33859650|ref|NP_035973.1|	extended synaptotagmin-like protein 1 [Mus	1104	122856	5.8	2	o68-90i241	Q	0	0	X	X	X	X	X	X	X	0	2	5	0	0	5	5	2.63	0.00085	1	0.00084	0.000598	Protein kinase C conserved region 2 (CalB); Ca2+-binding motif	integral to membrane; membrane		2	5
196	ENSG00000149485:ENSMUSG00000010663:ENSRNOG00000020480	FADS1	gi|22164784|ref|NP_66	gi|22164784|ref|NP_666206.1|	delta-5 desaturase [Mus musculus]	447	52323	9.3	4	i134-156o1	Q	20	0	X	X	X	X	X	X	X	0	2	2	0	2	2	2	5.82	0.00084	1	0.000829	0.000591	Heme oxygenase catalyzes the rate limiting step in the	endoplasmic reticulum; microsome	electron carrier activity [pmid 1575508]; heme	2	2
197	ENSG00000119777:ENSMUSG00000038828:ENSRNOG00000008812	TMEM214	gi|31559970|ref|NP_65	gi|31559970|ref|NP_653108.2|	hypothetical protein LOC68796 [Mus muscu	687	76430	9.3	0	o	Q	18	0	X	X	X	X	X	X	X	0	1	3	0	1	3	3	1.75	0.00082	1	0.00081	0.000577	Domain of unknown function. This family of proteins has no			1	3
198	ENSG00000125912:ENSMUSG00000020238:ENSRNOG00000004793	NCLN	gi|33469043|ref|NP_59	gi|33469043|ref|NP_598770.1|;gi|51873031|ref|NP_064555.2|	nicalin homolog [Mus musculus]	563	62908	6.5	2	i12-34o521	A	43	0.281	1	1	0	0	1	1	2.49	0.00079	X	X	X	X	X	X	X	0	1	0.000775	0.000555	Peptidase family M28; pfam04389	endoplasmic reticulum; membrane		1	1
199	ENSG00000138115:ENSMUSG00000025003:ENSRNOG00000013241	CYP2C8	gi|6857777|ref|NP_034	gi|6857777|ref|NP_034133.1|	cytochrome P450, family 2, subfamily c, pol	490	55903	7.9	0	o	S	26	0.994	2	3	3	0	0	0	2.86	0	2	4	4	0	0	2	7.14	0.00076	1	0.000757	0.000539	Globins are heme proteins, which bind and transport oxygen;	hemoglobin complex	heme binding; iron ion binding; metal ion binding; oxygen	4	7
200	ENSG00000086848:ENSMUSG00000032059:ENSRNOG00000010877	ALG9	gi|19527202|ref|NP_59	gi|19527202|ref|NP_598742.1|	alpha-1,2-mannosyltransferase ALG9 [Mus	613	69428	8.8	9	i136-158o1	Q	24	0.001	1	1	0	0	1	1	3.43	0.00072	X	X	X	X	X	X	X	0	1	0.000712	0.00051				1	1
201	ENSG00000204221:ENSMUSG00000024312:ENSRNOG00000029500	WDR46	gi|10181122|ref|NP_06	gi|10181122|ref|NP_065628.1|	WD repeat domain 46 [Mus musculus]	622	69048	9.8	0	o	Q	0	0	1	1	0	1	1	1	4.02	0.00071	X	X	X	X	X	X	X	0	1	0.000702	0.000503	WD40 domain, found in a number of eukaryotic proteins that	cellular_component		1	1
202	ENSG00000196620:ENSMUSG00000070704:ENSRNOG00000001980	UGT2B15	gi|71274184|ref|NP_00	gi|71274184|ref|NP_001025038.1|	UDP glucuronosyltransferase 2 family, polyp	530	61041	8.3	1	o495-517i	S	24	0.999	X	X	X	X	X	X	X	0	2	8	7	1	1	2	7.17	0.0007	1	0.0007	0.000498	Helicase superfamily c-terminal domain; associated with			2	8
203	ENSG00000109971:ENSMUSG00000015656:ENSRNOG00000030228	HSPA8	gi|31981690|ref|NP_11	gi|31981690|ref|NP_112442.2|	heat shock protein 8 [Mus musculus]	646	70871	5.5	0	o	Q	17	0.004	1	1	0	1	1	1	2.01	0.00068	X	X	X	X	X	X	X	0	1	0.000676	0.000484	Hsp70 protein. Hsp70 chaperones help to fold many proteins.	nucleus	ATP binding; ATPase activity, coupled; nucleotide	1	1
204	NA:NA:ENSRNOG00000000790	LOC676837	gi|149269298|ref|XP_0	[illegible]	PREDICTED: similar to MHC class I antiger	552	61771	8.1	1	o476-498i	Q	23	0.003	X	X	X	X	X	X	X	0	1	2	0	0	2	2	2.17	0.00068	1	0.000672	0.000479	Immunoglobulin domain constant region subfamily; members of			1	2
205	ENSG00000103227:ENSMUSG00000002279:ENSRNOG00000000230	TMEM112	gi|31981342|ref|NP_08	gi|31981342|ref|NP_083900.2|	hypothetical protein LOC76483 [Mus muscu	567	65094	9.3	5	o43-65i90-1	A	65	0	X	X	X	X	X	X	X	0	1	2	0	1	2	2	1.59	0.00066	1	0.000654	0.000466	Protein of unknown function (DUF1222). This family, which			1	2
206	ENSG00000065361:ENSMUSG00000018166:ENSRNOG00000004964	ERBB3	gi|61098019|ref|NP_03	gi|61098019|ref|NP_034283.1|	v-erb-b2 erythroblastic leukemia viral oncog	1339	147613	6.6	1	o642-664i	S	20	0.998	1	2	0	1	2	2	2.02	0.00066	X	X	X	X	X	X	X	0	1	0.000652	0.000467	Receptor L domain. The L domains from these receptors make	apical plasma membrane; integral to membrane; intracellular;	ATP binding; epidermal growth factor receptor activity;	1	2
207	ENSG00000108829:ENSMUSG00000020869:ENSRNOG00000003524	LRRC59	gi|19527026|ref|NP_59	gi|19527026|ref|NP_598568.1|;gi|56605670|ref|NP_001008281.1|	leucine rich repeat containing 59 [Mus musc	307	34877	9.5	1	o244-266i	Q	0	0	X	X	X	X	X	X	X	0	1	1	0	0	1	1	3.91	0.00061	1	0.000604	0.00043	Leucine-rich repeat (LRR) protein [Function unknown];	membrane	transferase activity	1	1
208	ENSG00000153707:ENSMUSG00000028399:ENSRNOG00000005711	PTPRD	gi|62177150|ref|NP_00	gi|62177150|ref|NP_001014310.1|;gi|90403603|ref|NP_035341.2|	protein tyrosine phosphatase, receptor type	1254	141640	6.5	1	o610-632i	Q	17	0.029	X	X	X	X	X	X	X	0	2	4	0	0	4	4	2.79	0.0006	1	0.000591	0.000421	Fibronectin type 3 domain; One of three types of internal	integral to membrane; integral to plasma membrane; membrane;	hydrolase activity; phosphoprotein phosphatase activity;	2	4
209	ENSG00000130714:ENSMUSG00000039254:ENSRNOG00000010477	POMT1	gi|21553107|ref|NP_66	gi|21553107|ref|NP_660127.1|	protein-O-mannosyltransferase 1 [Mus mus	746	85234	8.3	10	i31-53o88-1	Q	56	0.016	1	1	0	1	1	1	1.74	0.00059	X	X	X	X	X	X	X	0	1	0.000585	0.000419	Dolichyl-phosphate-mannose-protein mannosyltransferase. This	endoplasmic reticulum; endoplasmic reticulum membrane	dolichyl-phosphate-mannose-protein	1	1
210	ENSG00000197635:ENSMUSG00000035000:ENSRNOG00000030763	DPP4	gi|6753674|ref|NP_034	gi|6753674|ref|NP_034204.1|	dipeptidylpeptidase 4 [Mus musculus]	760	87437	6.4	1	i7-29o	A	23	0.404	1	1	0	1	1	1	2.76	0.00058	X	X	X	X	X	X	X	0	1	0.000574	0.000411	Dipeptidyl peptidase IV (DPP IV) N-terminal region. This family	intercellular canaliculus; membrane	aminopeptidase activity; dipeptidyl-peptidase IV activity;	1	1
211	ENSG00000168036:ENSMUSG00000006932:ENSRNOG00000019139	CTNNB1	gi|6671684|ref|NP_031	gi|6671684|ref|NP_031640.1|	catenin (cadherin associated protein), beta	781	85471	5.9	0	o	Q	22	0	1	1	0	1	1	1	2.69	0.00057	X	X	X	X	X	X	X	0	1	0.000559	0.0004	Armadillo/beta-catenin-like repeats; Approx. 40 amino acid	adherens junction; apical part of cell; basolateral plasma	alpha-catenin binding; binding; cadherin binding;	1	1
212	ENSG00000072274:ENSMUSG00000022797:ENSRNOG00000001766	TFRC	gi|11596855|ref|NP_03	gi|11596855|ref|NP_035768.1|	transferrin receptor [Mus musculus]	763	85731	6.6	1	i66-88o	Q	27	0.002	X	X	X	X	X	X	X	0	1	2	0	1	2	2	2.1	0.00049	1	0.000486	0.000346	PA_TfR: Protease-associated domain containing proteins like	cytoplasmic membrane-bound vesicle; endosome; integral to	iron ion transporter activity; peptidase activity; receptor	1	2
213	ENSG00000004939:ENSMUSG00000006574:ENSRNOG00000020951	SLC4A1	gi|6755560|ref|NP_035	gi|6755560|ref|NP_035533.1|	solute carrier family 4 (anion exchanger), m	929	103135	5.4	12	o425-447i4	Q	0	0	1	1	0	1	1	1	1.18	0.00048	X	X	X	X	X	X	X	0	1	0.00047	0.000336	HCO3- transporter family. This family contains Band 3 anion	integral to plasma membrane; membrane	anion exchanger activity; carrier activity; inorganic anion	1	1
214	ENSG00000205702:ENSMUSG00000068085:ENSRNOG00000029128	CYP2D7P1	gi|82958348|ref|XP_91	gi|149266772|ref|XP_001479975.1|;gi|82958348|ref|XP_910862.1|	PREDICTED: similar to Cytochrome P450 2	504	57002	6.5	2	o4-23i301-3	A	26	0.084	4	14	14	0	0	0.5	16.87	0.00044	3	52	52	0	0	0	6.35	0	1	0.000433	0.00031	Cytochrome P450. Cytochrome P450s are haem-thiolate			7	66
215	ENSG00000205702:ENSMUSG00000068085:ENSRNOG00000029128	CYP2D7P1	gi|149266772|ref|XP_0	gi|149266772|ref|XP_001479975.1|;gi|82958348|ref|XP_910862.1|	PREDICTED: similar to P45016a-ms2 [Mus	504	56988	6.3	1	i7-26o	A	26	0.084	5	18	18	0	0	0.5	20.04	0.00044	3	52	52	0	0	0	6.35	0	1	0.000433	0.00031	Cytochrome P450. Cytochrome P450s are haem-thiolate			8	70
216	ENSG00000101290:ENSMUSG00000058793:ENSRNOG00000021265	CDS2	gi|20149726|ref|NP_61	gi|20149726|ref|NP_619592.1|	phosphatidate cytidylyltransferase 2 [Mus m	444	51314	7	8	i67-89o94-1	Q	0	0	X	X	X	X	X	X	X	0	1	1	0	1	1	1	3.83	0.00042	1	0.000418	0.000297	Cytidylyltransferase family. The members of this family are	endoplasmic reticulum; integral to membrane	nucleotidyltransferase activity; transferase activity	1	1
217	ENSG00000198561:ENSMUSG00000034101:ENSRNOG00000030790	CTNND1	gi|83745122|ref|NP_03	gi|83745122|ref|NP_031641.2|	catenin, delta 1 isoform 1 [Mus musculus]	938	104925	6.9	0	o	Q	22	0	X	X	X	X	X	X	X	0	2	2	0	2	2	2	2.35	0.0004	1	0.000395	0.000282	Armadillo/beta-catenin-like repeats; cd00020	cytoskeleton; lamellipodium; membrane fraction; nucleus	binding; protein binding; structural molecule activity	2	2
218	ENSG00000046604:ENSMUSG00000044393:ENSRNOG00000016526	DSG2	gi|22779879|ref|NP_03	gi|22779879|ref|NP_031909.1|	desmoglein 2 [Mus musculus]	1122	122397	5.3	1	o618-640i	S	29	0.921	1	1	0	1	1	1	1.07	0.00039	X	X	X	X	X	X	X	0	1	0.000389	0.000279	Cadherin repeat domain; Cadherins are glycoproteins involved	cytoskeleton; desmosome; integral to membrane; membrane	calcium ion binding; protein binding	1	1
219	ENSG00000087111:ENSMUSG00000041958:ENSRNOG00000011366	PIGS	gi|41351529|ref|NP_95	gi|41351529|ref|NP_958808.1|	phosphatidylinositol glycan anchor biosynth	555	61711	6.9	2	i19-36o519	S	42	0.864	X	X	X	X	X	X	X	0	1	1	0	1	1	1	3.06	0.00034	1	0.000334	0.000238		endoplasmic reticulum; GPI-anchor transamidase complex;	GPI-anchor transamidase activity; protein binding	1	1
220	ENSG00000167930:ENSMUSG00000024187:ENSRNOG00000028241	ITFG3	gi|46402185|ref|NP_99	gi|46402185|ref|NP_997100.1|	integrin alpha FG-GAP repeat containing 3	555	60576	5.7	1	i50-72o	A	0	0	X	X	X	X	X	X	X	0	1	1	0	1	1	1	2.88	0.00034	1	0.000334	0.000238		integral to membrane; membrane		1	1
221	ENSG00000033867:ENSMUSG00000021733:ENSRNOG00000005957	SLC4A7	gi|117320529|ref|NP_0	gi|117320529|ref|NP_001028442.2|	solute carrier family 4, sodium bicarbonate	1131	127221	6.4	11	o490-512i5	Q	0	0	X	X	X	X	X	X	X	0	1	2	0	1	2	2	1.59	0.00033	1	0.000328	0.000234	HCO3- transporter family. This family contains Band 3 anion	integral to membrane	anion exchanger activity; sodium ion binding; symporter	1	2
222	ENSG00000179087:ENSMUSG00000068587:ENSRNOG00000026177	MGAM	gi|149255014|ref|XP_0	gi|149255014|ref|XP_001481364.1|;gi|149255059|ref|XP_001481327.1|	PREDICTED: similar to maltase-glucoamyla	3629	414322	5.7	1	i12-34o	A	36	0.005	X	X	X	X	X	X	X	0	1	6	0	0	6	6	0.28	0.00031	1	0.000307	0.000218	Glycosyl hydrolases family 31. Glycosyl hydrolases are key			1	6
223	ENSG00000118705:ENSMUSG00000027642:ENSRNOG00000007492	RPN2	gi|34996495|ref|NP_06	gi|34996495|ref|NP_062616.2|	ribophorin II [Mus musculus]	631	69063	5.8	3	o539-561i5	S	23	1	X	X	X	X	X	X	X	0	1	1	0	1	1	1	3.49	0.0003	1	0.000294	0.000209	Ribophorin II (RPN2). This family consists of several eukaryotic	cellular_component; endoplasmic reticulum; endoplasmic	dolichyl-diphosphooligosaccharide-protein	1	1
224	ENSG00000091039:ENSMUSG00000020189:ENSRNOG00000026962	OSBPL8	gi|51243036|ref|NP_00	gi|51243036|ref|NP_001003717.1|	oxysterol-binding protein-like protein 8 isofo	846	96928	7.4	1	o828-845i	Q	31	0	X	X	X	X	X	X	X	0	1	1	0	0	1	1	1.3	0.00022	1	0.000219	0.000156				1	1
225	ENSG00000130402:ENSMUSG00000054808:ENSRNOG00000020433	ACTN4	gi|11230802|ref|NP_06	gi|11230802|ref|NP_068695.1|;gi|61097906|ref|NP_598917.1|	actinin alpha 4 [Mus musculus]	912	104977	5.4	0	o	Q	0	0	X	X	X	X	X	X	X	0	1	1	0	0	1	1	1.32	0.0002	1	0.000203	0.000145	Spectrin repeats, found in several proteins involved in	cortical cytoskeleton; cytoplasm; pseudopodium; stress fiber	actin binding; actin filament binding; calcium ion binding;	1	1
226	ENSG00000032444:ENSMUSG00000004565:ENSRNOG00000000977	PNPLA6	gi|7657401|ref|NP_056	gi|7657401|ref|NP_056616.1|	patatin-like phospholipase domain containin	1327	146562	8	1	i9-31o	A	26	0.002	X	X	X	X	X	X	X	0	1	1	0	1	1	1	1.13	0.00014	1	0.00014	9.95E-05	effector domain of the CAP family of transcription factors;	membrane fraction	molecular_function; serine esterase activity	1	1
227	ENSG00000112851:ENSMUSG00000021709:NA	ERBB2IP	gi|54607112|ref|NP_06	gi|54607112|ref|NP_067538.2|;gi|54607114|ref|NP_001005868.1|	Erbb2 interacting protein isoform 2 [Mus mu	1376	154327	5.6	0	o	Q	20	0.366	X	X	X	X	X	X	X	0	1	1	0	1	1	1	0.87	0.00014	1	0.000135	9.6E-05	Leucine-rich repeats (LRRs), ribonuclease inhibitor (RI)-like	basolateral plasma membrane	protein binding; transferase activity	1	1
228	ENSG00000075568:ENSMUSG00000026116:ENSRNOG00000017265	TMEM131	gi|119372306|ref|NP_0	gi|119372306|ref|NP_061360.2|;gi|149233754|ref|XP_001477925.1|	transmembrane protein 131 [Mus musculus]	1877	204650	8.5	2	o1081-1103	S	58	0.996	X	X	X	X	X	X	X	0	1	1	0	0	1	1	0.75	1E-04	1	0.000099	7.04E-05		membrane		1	1
													Protein Counts							153								180									
229			Contaminant_GR78_H	[illegible]	owl|P11021| 78 KD GLUCOSE REGULATE	653	72116	5.1						1	1	0	0	1	1	2.14	0.00068	1	1	0	0	1	1	2.14	0.00029	2	0.000476	0.000276				2	2
230			Contaminant_gi|74630	Contaminant_gi|7463016|pir||S77957	lysyl endopeptidase (EC 3.4.21.50) - Lysoba	269	27961	6.7						1	2	0	1	2	2	7.06	0.00329	2	4	0	2	4	4	11.9	0.00278	2	0.003001	0.00036				3	6
231			Contaminant_TRYPSIN	Contaminant_TRYPSIN	no description	229	23993	7.9						2	5	0	2	5	5	18.34	0.00965	1	2	0	1	2	2	8.73	0.00163	2	0.005574	0.005672				3	7
232			Contaminant_KERATI	Contaminant_KERATIN03	no description	593	59519	5.2						X	X	X	X	X	X	X	0	1	1	0	0	1	1	1.52	0.00031	1	0.000313	0.000223				1	1
233			Contaminant_KERATI	Contaminant_KERATIN13	no description	643	65494	6.6						X	X	X	X	X	X	X	0	1	1	0	1	1	1	1.87	0.00029	1	0.000288	0.000205				1	1
234			gi|114145561|ref|NP_1	gi|114145561|ref|NP_112447.2|	keratin complex 2, basic, gene 8 [Mus musc	490	54565	5.8						X	X	X	X	X	X	X	0	1	2	0	1	2	2	2.45	0.00076	1	0.000757	0.000539				1	2
													Contaminant Protein Count							17								20									
													Total Distributed Spectral Counts						779								2421										
						AVG	SDV						Total Protein Count							170								200									
					Spectral FDR (%)	0.164948	0.233272						Spectral FDR (%)						0								0.33										
					Protein FDR (%)	0.5	0.707107						Protein FDR (%)							0								1									
													SHUFFLED Protein Counts							0								2									
													SHUFFLED Spectral Counts						0								4										
			SHUFFLED_gi|30425204|ref|NP_780675.1|		FALSE POSITIVE	705	81252	9.2						X	X	X	X	X	X	X	X	1	2	0	1	2	2	1.7	X							1	2
			SHUFFLED_gi|124486933|ref|NP_001074828.1		FALSE POSITIVE	2799	309095	5.8						X	X	X	X	X	X	X	X	1	2	0	1	2	2	0.29	X							1	2

	Total	% Total	ΣdNSAFavg	% Total normalized spectral counts
Detected Proteins	228			
Proteins with PredHel>=1	158	69.30	0.98	77.81
Proteins with Signal Peptide/Anchor only	27	11.84	0.14	11.21
Soluble Proteins (no TM, no signal peptide)	43	18.86	0.14	10.98