

Supplementary Table S3. Cardiac gene expression. A GeneChip Mouse Genome 430 2.0 Array (Affymetrix, Santa Clara, CA, United States) was used to analyze the basal mRNA expression in hearts from PP2A-TG (n=3) and WT (n=3) mice. For analysis, the TM4 application MeV was used (Saeed et al., 2003). Here, analysis was performed with genes that were expressed in both PP2A-TG and WT. First, data were adjusted by a variance filter (percent mode; value 50) and, secondly, analyzed by a t-Test (Welch approximation; alpha (overall threshold p-value): 0.05; P-values based on t-distribution).

Gene descriptions	WT mean	WT SD	PP2A-TG mean	PP2A-TG SD	Absolute t value	Degrees of freedom	Adj p value	False discovery rate
gb.NM_007981.1/DB_XREF=gi:6679738/GEN=Fac2/FEA=FLmRNA/CNT=147/ITD=Mm.28962.1/ТИER=FL+Stack/STK=45 /UG=Mm.28962/LL=14081/DEF=Mus musculus fatty acid Coenzyme A ligase, long chain 2 (Fac2), mRNA./PROD=fatty acid Coenzyme A ligase, long chain 2/FL-gb.NM_007981.1 gb.U15977.1	3965.5664	415.30035	2066.2332	226.85002	6.9518514	3.0	0.006105606	2.7719452
gb.AK005586.1/DB_XREF=gi:12834343/FEA=mRNA/CNT=119/ITD=Mm.20488.1/ТИER=Stack/STK=50/UG=Mm.20488/LL=76301 /UG_PRODE=111000806Rik/UG_TITLE=RIKEN cDNA111000806, clone J0454.1 gb.NM.007533.1 gb.L47333.1 gb.BC004804.1/DB_XREF=gi:19335929/FEA=FLmRNA/CNT=1277/ITD=Mm.104540.1/ТИER=FL+Stack/STK=115/UG=Mm.104540/LL=108124/UG_GENE=Napa/DEF=Mus musculus, RIKEN cDNA 1500039N14 gene, clone MGC:6399 IMAGE:358469, mRNA, complete cds./PROD=RIKEN cDNA 1500039N14 gene/FL-gb.NM_025898.1 gb.BC004804.1	1412.2666	172.08234	591.0333	137.58932	6.455995	3.0	0.007538527	1.7112457
gb.BC006688.1/DB_XREF=gi:13879379/FEA=FLmRNA/CNT=135/ITD=Mm.20396.1/ТИER=FL+Stack/STK=60/UG=Mm.20396/LL=12908 /UG_GENE=Crat/DEF=Mus musculus, Similar to carnitine acetyltransferase, clone MGC:6046 IMAGE:3499169, mRNA, complete cds./PROD=Similar to carnitine acetyltransferase/FL-gb.BC006688.1 gb.NM_007760.1	4650.733	358.1267	2468.2334	466.95862	6.4237013	3.0	0.007646559	1.1571792
gb.NM_007533.1/DB_XREF=gi:6671623/GEN=Bckdha/FEA=FLmRNA/CNT=211/ITD=Mm.25848.1/ТИER=FL+Stack/STK=76 /UG=Mm.25848/LL=12039/DEF=Mus musculus branched chain ketoadid dehydrogenase E1, alpha polypeptide (Bckdha), mRNA. (Parar)-branched chain ketoadid dehydrogenase E1, alpha polypeptide/FL-gb.BC003787.1 gb.NM_007533.1 gb.L47333.1 /UG_PRODE=111000806Rik/UG_TITLE=RIKEN cDNA111000806, clone J0454.1 gb.NM.007533.1 gb.L47333.1 gb.BC004804.1/DB_XREF=gi:19335929/FEA=FLmRNA/CNT=1277/ITD=Mm.104540.1/ТИER=FL+Stack/STK=115/UG=Mm.104540/LL=108124/UG_GENE=Napa/DEF=Mus musculus, RIKEN cDNA 1500039N14 gene, clone MGC:6399 IMAGE:358469, mRNA, complete cds./PROD=RIKEN cDNA 1500039N14 gene/FL-gb.NM_025898.1 gb.BC004804.1	2700.0334	286.70358	1546.7666	192.90247	5.780555	3.0	0.010295443	1.1685328
gb.AB056479.1/DB_XREF=gi:15341205/FEA=FLmRNA/CNT=427/ITD=Mm.43822.1/ТИER=FL+Stack/STK=32/UG=Mm.43822/LL=12974 /UG_GENE=Cs/DEF=Mus musculus mRNA for citrate synthase, complete cds./PROD=citrate synthase/FL-gb.BC013554.1 gb.NM_026444.1 gb.AB056479.1	3668.7334	270.4928	2305.8333	327.08664	5.5616684	3.0	0.011467959	0.8677422
gb.NM_008916.1/DB_XREF=gi:6679448/GEN=Pps/FEA=FLmRNA/CNT=174/ITD=Mm.1458.1/ТИER=FL+Stack/STK=115/UG=Mm.1458/LL=19062/DEF=Mus musculus putative phosphatase (Pps), mRNA./PROD=putative phosphatase/FL-gb.BC013554.1 gb.AF483522.1 gb.NM_008916.1 gb.U96724.1	1440.2001	142.18462	787.8	161.60974	5.2495723	3.0	0.013461299	0.8730614
gb.NM_007968.1/DB_XREF=gi:66881272/GEN=Eef1a2/FEA=FLmRNA/CNT=64/ITD=Mm.2645.1/ТИER=FL+Stack/STK=31/UG=Mm.2645/LL=13628/DEF=Mus musculus eukaryotic translation elongation factor 1 alpha 2 (Eef1a2), mRNA./PROD=eukaryotic translation elongation factor 1 alpha2/FL-gb.L26479.1 gb.NM_007968.1 gb.BC018235.1	17134.666	2077.833	9926.967	1596.6765	4.7641034	3.0	0.017563034	0.9967022
gb.NM_029632.1/DB_XREF=gi:18390326/GEN=Ppp1r11/FEA=FLmRNA/CNT=146/ITD=Mm.46176.1/ТИER=FL+Stack/STK=58 /UG=Mm.46176/LL=76497/DEF=Mus musculus protein phosphatase 1, regulatory (inhibitor) subunit 11 (Ppp1r11), mRNA./PROD=protein phosphatase 1, regulatory (inhibitor) subunit 11/FL-gb.NM_029632.1	3319.6667	170.52585	1640.5333	382.8957	6.9386435	2.0	0.020145172	1.0162121
gb.BC018355.1/DB_XREF=gi:17390829/FEA=FLmRNA/CNT=80/ITD=Mm.23809.1/ТИER=FL+Stack/STK=2/UG=Mm.23809/LL=56748 /UG_GENE=Hirp5/DEF=Mus musculus, histone cell cycle regulation defective interacting protein 5, clone MGC:5675 IMAGE:3584656, mRNA, complete cds./PROD=histone cell cycle regulation defective interacting protein 5/FL-gb.NM_020045.1 gb.BC018355.1	3284.8333	224.78094	2328.8333	292.29797	4.490613	3.0	0.020605719	0.93549967
gb.AK002443.1/DB_XREF=gi:12832431/FEA=FLmRNA/CNT=204/ITD=Mm.180189.1/ТИER=Stack/STK=57/UG=Mm.180189/LL=67800 /UG_GENE=Dygl2/UG_TITLE=dacylglycerol O-acyltransferase 2/DEF=Mus musculus adult male kidney cDNA, RIKEN full-length enriched library, clone 0610010B06, homolog to WUGSC.H_DJ0747618.5 PROTEIN (FRAGMENT), full insert sequence./FL-gb.AF384160.1 gb.NM_026384.1	2753.4001	267.295	1639.7334	105.6523	6.7112303	2.0	0.021489117	0.88691443
gb.NM_007476.1/DB_XREF=gi:6680715/GEN=Arf1/FEA=FLmRNA/CNT=64/ITD=Mm.6836.1/ТИER=FL/STK=2/UG=Mm.6836/LL=11840 /DEF=Mus musculus ADP-ribosylation factor 1 (Arf1), mRNA./PROD=ADP-ribosylation factor 1/FL-gb.D87898.1 gb.NM_007476.1 gb.BC027445.1/DB_XREF=gi:20071862/FEA=FLmRNA/CNT=79/ITD=Mm.153891.1/ТИER=FL+Stack/STK=28/UG=Mm.153891/LL=19245/UG_GENE=Pp4a3/DEF=Mus musculus, protein tyrosine phosphatase 4a3, clone MGC:36146 IMAGE:4482106, mRNA, complete cds./PROD=protein tyrosine phosphatase 4a3/FL-gb.NM_007476.1 gb.BC027445.1 gb.BC027445.1	3634.5999	385.0914	2027.2666	170.24298	6.6120944	2.0	0.022116944	0.77239174
gb.BC017689.1/DB_XREF=gi:17389288/FEA=FLmRNA/CNT=148/ITD=Mm.19258.1/ТИER=FL+Stack/STK=47/UG=Mm.19258/LL=66951 /UG_GENE=2310028D0Rik/DEF=Mus musculus, Similar to tyrothroph embryonic factor, clone MGC:19233 IMAGE:4242534, mRNA, complete cds./PROD=Similar to tyrothroph embryonic factor/FL-gb.BC017689.1	2227.3333	188.9985	1486.5	238.61961	4.2153683	3.0	0.024394894	0.79109156
gb.AK005305.1/DB_XREF=gi:12833890/FEA=mRNA/CNT=51/ITD=Mm.46367.1/ТИER=Stack/STK=12/UG=Mm.46367/LL=68453 /UG_GENE=1110002J19Rik/UG_TITLE=RIKEN cDNA 1110002J19 gene/DEF=Mus musculus 18 days embryo whole body cDNA, RIKEN full-length enriched library, clone 1110002J19, unclassifiable, full insert sequence.	5818.1997	927.7161	3272.6667	519.24005	4.1471405	3.0	0.025470959	0.770921
gb.NM_011179.1/DB_XREF=gi:7242190/GEN=Psp/FEA=FLmRNA/CNT=332/ITD=Mm.3363.1/ТИER=FL/STK=1/UG=Mm.3363/LL=19159/DEF=Mus musculus Psp, clone MGC:5675 IMAGE:3584656, mRNA, complete cds./PROD=protein tyrosine phosphatase 4a3/FL-gb.NM_011179.1 gb.BC027445.1 gb.BC027445.1	5425.933	628.29877	2125.7332	1085.7566	4.06974	3.0	0.026767017	0.75951415
gb.BC024138.1/DB_XREF=gi:18892248/FEA=FLmRNA/CNT=267/ITD=Mm.22926.1/ТИER=FL+Stack/STK=1/UG=Mm.22926/LL=66698 /UG_GENE=231007L09Rik/DEF=Mus musculus, RIKEN cDNA 231007L09 gene, clone MGC:37973 IMAGE:5136320, mRNA, complete cds./PROD=RIKEN cDNA 231007L09 gene/FL-gb.BC024138.1	1782.4	251.44804	1036.3667	201.14285	4.012932	3.0	0.027772743	0.7416956
gb.AF422244.1/DB_XREF=gi:17026373/GEN=Mdp77/FEA=FLmRNA/CNT=35/ITD=Mm.33173.1/ТИER=FL/STK=4/UG=Mm.33173/LL=69508/DEF=Mus musculus muscle-derived protein MDP77 variant 1 (Mdp77) mRNA, complete cds./PROD=muscle-derived protein MDP77 variant 1/FL-gb.AF422244.1 gb.NM_138628.1 gb.AF422245.1	5097.6665	429.47256	3562.9666	519.5502	3.9434373	3.0	0.029070232	0.73321587
gb.BC018355.1/DB_XREF=gi:17390829/FEA=FLmRNA/CNT=80/ITD=Mm.23809.1/ТИER=FL+Stack/STK=2/UG=Mm.23809/LL=56748 /UG_GENE=Hirp5/DEF=Mus musculus, histone cell cycle regulation defective interacting protein 5, clone MGC:5675 IMAGE:3584656, mRNA, complete cds./PROD=histone cell cycle regulation defective interacting protein 5/FL-gb.NM_020045.1 gb.BC018355.1	2181.5	125.08818	1068.4	314.64484	5.693912	2.0	0.029487085	0.70458615
gb.AF206720.1/DB_XREF=gi:6636320/FEA=FLmRNA/CNT=130/ITD=Mm.38469.1/ТИER=FL+Stack/STK=83/UG=Mm.38469/LL=11785 /UG_GENE=Apb1/DEF=Mus musculus Fe65 mRNA, complete cds./PROD=Fe65/FL-gb.AF206720.1	1659.7334	267.31207	867.3	232.41673	3.8747864	3.0	0.030429503	0.69074976
gb.BI408679.1/DB_XREF=gi:15169602/DB_XREF=602964304F1/CLONE=IMAGE:5119896/FEA=mRNA/CNT=61/ITD=Mm.29389.1/ТИER=Stack/STK=30/UG=Mm.29389/LL=51939/DEF=Mus musculus, Similar to KIA1075 protein, clone IMAGE:5095927, mRNA, partial cds	1488.9	179.23257	810.2	246.92395	3.8527741	3.0	0.030882569	0.6676517
gb.NM_009883.1/DB_XREF=gi:6753555/FEA=FLmRNA/CNT=522/ITD=Mm.2747.1/ТИER=FL+Stack/STK=193/UG=Mm.2747/LL=13083/DEF=Mus musculus Cdh23, cathepsin D (Cdh23), mRNA./PROD=cathepsin D/FL-gb.NM_009883.1	5454.1333	777.9049	3241.0332	625.04315	3.8412483	3.0	0.031123256	0.6422708
gb.U82470.1/DB_XREF=gi:2690301/GEN=G32/FEA=FLmRNA/CNT=238/ITD=Mm.18916.1/ТИER=FL/STK=1/UG=Mm.18916/LL=14719/DEF=Mus musculus aspartate aminotransferase precursor (Got-2) mRNA, Got-2 a allele, complete cds; nuclear gene for mitochondrial product./PROD=aspartate aminotransferase precursor (Got-2) mRNA, Got-2 a allele, complete cds; nuclear gene for mitochondrial product./FL-gb.U82470.1 gb.UJ02622.1 gb.NM_010325.1	4684.267	741.73334	2668.0999	544.53687	3.795118	3.0	0.032111008	0.63384336
gb.AK003207.1/DB_XREF=gi:12833731/FEA=mRNA/CNT=179/ITD=Mm.29998.1/ТИER=Stack/STK=95/UG=Mm.29998/LL=66853 /UG_GENE=0610039C2Rik/UG_TITLE=RIKEN cDNA 0610039C2 gene/DEF=Mus musculus 18 days embryo whole body cDNA, RIKEN full-length enriched library, clone 1110001C14, similar to HYPOTHETICAL 19.8 KDA PROTEIN (FRAGMENT), full insert sequence.	4345.7	245.63489	2401.5999	592.12665	5.2527237	2.0	0.034385104	0.65045154
gb.BC003447.1/DB_XREF=gi:13097416/FEA=FLmRNA/CNT=395/ITD=Mm.12758.1/ТИER=FL+Stack/STK=94/UG=Mm.12758/LL=14228 /UG_GENE=Fkbp4/DEF=Mus musculus, FK506 binding protein 4 (59 kDa), clone MGC:6528 IMAGE:2651490, mRNA, complete cds./PROD=FK506 binding protein 4 (59 kDa)/FL-gb.NM_010219.1 gb.BC003447.1	1799.4	258.09253	969.4666	96.33808	5.217995	2.0	0.03482062	0.63234246
gb.AJ007905.1/DB_XREF=gi:3336885/GEN=edr/FEA=mRNA/CNT=7/ITD=Mm.35829.2/ТИER=ConsEnd/STK=5/UG=Mm.35829/LL=170942/DEF=Mus musculus mRNA for erythroid differentiation regulator, partial./PROD=erythroid differentiation regulator	3188.2668	328.84497	2022.2999	441.76965	3.6670012	3.0	0.03507333	0.61243427
gb.BC004613.1/DB_XREF=gi:13435485/FEA=FLmRNA/CNT=159/ITD=Mm.22597.1/ТИER=FL+Stack/STK=30/UG=Mm.22597/LL=69654 /UG_GENE=2310024E0Rik/DEF=Mus musculus, Similar to dynactin 2 (p50), clone MGC:6712 IMAGE:3585310, mRNA, complete cds./PROD=Similar to dynactin 2 (p50)/FL-gb.BC004613.1	3519.4336	404.615	2197.7	185.29951	5.144202	3.0	0.035773426	0.6015235
gb.NM_023464.1/DB_XREF=gi:12963686/GEN=1110003H09Rik/FEA=FLmRNA/CNT=95/ITD=Mm.21444.1/ТИER=FL+Stack/STK=50/UG=Mm.21444/LL=68475/DEF=Mus musculus RIKEN cDNA 1110003H09 gene (1110003H09Rik), mRNA./PROD=RIKEN cDNA 1110003H09/FL-gb.NM_023464.1	1704.7666	181.4112	1069.9333	244.86806	3.6081257	3.0	0.03655193	0.5926634
gb.NM_011390.1/DB_XREF=gi:555533/GEN=Slc12a7/FEA=FLmRNA/CNT=91/ITD=Mm.24510.1/ТИER=FL+Stack/STK=27/UG=Mm.24510/LL=20499/DEF=Mus musculus solute carrier family 12, member 7 (Slc12a7), mRNA./PROD=solute carrier family 12, member 7/FL-gb.NM_011390.1 gb.AF087436.1	2386.3	263.8338	1715.7999	187.08417	3.5906699	3.0	0.037005566	0.57932854
gb.NM_024225.1/DB_XREF=gi:18034768/GEN=Snx5/FEA=FLmRNA/CNT=386/ITD=Mm.20847.1/ТИER=FL+Stack/STK=39/UG=Mm.20847/LL=69178/DEF=Mus musculus sorting nexin 5 (Snx5), mRNA./PROD=sorting nexin 5/FL-gb.NM_024225.1 gb.BC002242.1	1845.6333	502.8171	3112.2	355.3908	3.562837	3.0	0.037743855	0.57119036
gb.BC011344.1/DB_XREF=gi:15030176/FEA=FLmRNA/CNT=135/ITD=Mm.22092.2/ТИER=FL+Stack/STK=83/UG=Mm.22092.1/LL=15467/UG_GENE=Erf2ak1/DEF=Mus musculus, clone MGC:5739 IMAGE:3481870, mRNA, complete cds./PROD=Unknown (protein for MGC:5739)/FL-gb.BC011344.1	1550.6333	267.75513	881.4333	195.2781	3.497545	3.0	0.039550956	0.5792301
gb.BC027346.1/DB_XREF=gi:20071091/FEA=FLmRNA/CNT=82/ITD=Mm.11545.1/ТИER=FL+Stack/STK=51/UG=Mm.11545/DEF=Mus musculus, clone MGC:28292 IMAGE:4011421, mRNA, complete cds./PROD=Unknown (protein for MGC:28292)/FL-gb.BC027346.1	1823.9	194.57033	1146.9333	274.02765	3.4888892	3.0	0.039798737	0.5646446
gb.AK010167.1/DB_XREF=gi:12845417/GEN=1cap/FEA=FLmRNA/CNT=567/ITD=Mm.10762.1/ТИER=FL+Stack/STK=40/UG=Mm.10762/LL=21393/UG_TITLE=1cap/DEF=Mus musculus adult male tongue cDNA, RIKEN full-length enriched library, clone 231007E03, 1cap, full insert sequence./FL-gb.NM_011540.1	18152.068	2419.692	11988.667	1911.9014	3.4616609	3.0	0.040591177	0.5584362
gb.BC003975.1/DB_XREF=gi:13278300/FEA=FLmRNA/CNT=232/ITD=Mm.29737.1/ТИER=FL+Stack/STK=79/UG=Mm.29737/DEF=Mus musculus, Similar to myeloid leukemia factor 2, clone MGC:7424 IMAGE:3488851, mRNA, complete cds./PROD=Similar to myeloid leukemia factor 2/FL-gb.BC003975.1	2250.6666	502.99188	1128.7333	275.59164	3.3869345	3.0	0.042871576	0.5724616
gb.NM_007383.1/DB_XREF=gi:6880619/GEN=Acads/FEA=FLmRNA/CNT=1137/ITD=Mm.18759.1/ТИER=FL+Stack/STK=35/UG=Mm.18759/DEF=Mus musculus acetyl-Coenzyme A dehydrogenase, short chain (Acads), mRNA./PROD=acetyl-Coenzyme A dehydrogenase, short chain/FL-gb.BC016259.1 gb.NM_007383.1 gb.L1163.1	2546.2332	583.8708	1251.8334	331.40588	3.3393998	3.0	0.044407293	0.576026
gb.AY028963.1/DB_XREF=gi:19847823/FEA=FLmRNA/CNT=18/ITD=Mm.38250.1/ТИER=FL/STK=1/UG=Mm.38250/LL=56490 /UG_GENE=Zfp288/DEF=Mus musculus BTBPOZ zinc finger protein DPZF mRNA, complete cds./PROD=BTBPOZ zinc finger protein DPZF/FL-gb.AF165576.1 gb.NM_019778.1 gb.AY028963.1	1758.9	300.57047	1063.5333	202.91864	3.3210924	3.0	0.04501735	0.5677188
gb.BC003744.1/DB_XREF=gi:13277677/FEA=FLmRNA/CNT=135/ITD=Mm.3284.1/ТИER=FL+Stack/STK=52/UG=Mm.3284/LL=19060 /UG_GENE=Pyp5c/DEF=Mus musculus, protein phosphatase 5, catalytic subunit, clone MGC:5847 IMAGE:3590322, mRNA, complete cds./PROD=protein phosphatase 5, catalytic subunit/FL-gb.BC003744.1 gb.AF018262.1	1179.0	253.04428	629.6667	141.64098	3.2810674	3.0	0.046388563	0.5692002
gb.NM_007876.1/DB_XREF=gi:6681216/GEN=Dpep1/FEA=FLmRNA/CNT=49/ITD=Mm.20388.1/ТИER=FL/STK=7/UG=Mm.20388/LL=13479/DEF=Mus musculus dipeptidase 1 (renal) (Dpep1), mRNA./PROD=dipeptidase 1 (renal)/FL-gb.NM_007876.1 gb.BC003492.1	2660.8667	501.4193	1360.6333	475.69363	3.25838	3.0	0.04718934	0.5637884
gb.BC015263.1/DB_XREF=gi:15929639/FEA=FLmRNA/CNT=72/ITD=Mm.6522.1/ТИER=FL+Stack/STK=40/UG=Mm.6522/LL=121778/UG_GENE=Chnkr1/DEF=Mus musculus, chemokine orphan receptor 1, clone MGC:18378 IMAGE:4242244, mRNA, complete cds./PROD=chemokine orphan receptor 1/FL-gb.BC015263.1 gb.NM_007722.1 gb.AF00026.1	3317.8333	177.26184	5048.1665	652.2934	4.433797	2.0	0.04728927	0.5504956
Mus musculus REF=M32599/DEF=Mus mouse glyceraldehyde 3-phosphate dehydrogenase mRNA, complete cds./LEN=1228 (5_3_M_3 represent transcript regions 5 prime, Middle, and 3 prime respectively)	34215.402	7139.477	16254.234	6410.5503	3.2422204	3.0	0.0477704	0.54219407
gb.BC025440.1/DB_XREF=gi:19343555/FEA=FLmRNA/CNT=93/ITD=Mm.22668.2/ТИER=FL+Stack/STK=21/UG=Mm.22668/LL=15356 /UG_GENE=Hmgcl/DEF=Mus musculus, 3-hydroxy-3-methylglutaryl-Coenzyme A lyase, clone MGC:29242 IMAGE:5049759, mRNA, complete cds./PROD=3-hydroxy-3-methylglutaryl-Coenzyme A lyase/FL-gb.BC025440.1	2477.4	257.76486	1629.1998	373.01678	3.2401416	3.0	0.047845803	0.52980477
gb.BC008273.1/DB_XREF=gi:14198433/FEA=FLmRNA/CNT=243/ITD=Mm.22514.1/ТИER=FL+Stack/STK=139/UG=Mm.22514/LL=183/UG_GENE=Chnkr1/DEF=Mus musculus, chemokine orphan receptor 1, clone MGC:6312 IMAGE:2811419, mRNA, complete cds./PROD=RIKEN cDNA 0610008F14 gene/FL-gb.BC008273.1	8549.866	1705.65	4106.4336	406.7802	4.3891153	2.0	0.048188154	0.520891
gb.NM_008733.1/DB_XREF=gi:8679123/GEN=Nrap/FEA=FLmRNA/CNT=12/ITD=Mm.8384.1/ТИER=FL/STK=2/UG=Mm.8384/LL=18175/DEF=Mus musculus nebulin-related anchoring protein (Nrap), mRNA./PROD=nebulin-related anchoring protein/FL-gb.NM_008733.1 gb.U76618.1	4659.6	864.4257	2685.7666	622.2885	3.2097685	3.0	0.048964903	0.51697826

gb:AK012776.1 /DB_XREF=gi:12849742 /FEA=mRNA /CNT=22 /TID=Mm.154145.2 /TIER=ConsEnd /STK=6 /UG=Mm.154145 /LL=66376 /UG_GENE=2310011F05R1K /UG_TITLE=RIKEN cDNA 2310011F05 gene /DEF=Mus musculus, full 10, 11 days embryo whole body cDNA, RIKEN full-length enriched library, clone 2810011F05.2 Zinc finger, C2H2 type containing protein, full insert sequence.	550.86664	266.142	1449.6334	410.57803	3.1815608	3.0	0.05003401	0.51625997
gb:AF171315.1 /DB_XREF=gi:3389171 /GEN=U03670 /FEA=FlmRNA /CNT=115 /TID=Mm.38817 /TIER=FL*Stack /STK=9 /UG=Mm.3981 /LL=26893 /DEF=Mus musculus COP9 complex subunit 6 (COP9b) mRNA, complete cds. /PROD=COP9 complex subunit 6 /FL=gb:AF071315.1 gb:BC004466.1	4076.3333	382.2838	2798.6667	588.63916	3.1529322	3.0	0.05114939	0.5160405
gb:NM_013562.1 /DB_XREF=gi:305178 /GEN=Ifitd1 /FEA=FlmRNA /CNT=225 /TID=Mm.168.1 /TIER=FL*Stack /STK=134 /UG=Mm.168 /LL=15982 /DEF=Mus musculus interferon-related developmental regulator 1 (Ifitd1), mRNA. /PROD=interferon-related developmental regulator 1 /FL=gb:NM_013562.1	1775.8002	335.17688	2668.5	362.82657	3.1302788	3.0	0.052054286	0.5137532
gb:NM_019502.1 /DB_XREF=gi:9507186 /GEN=Foxc1 /FEA=FlmRNA /CNT=70 /TID=Mm.4050.1 /TIER=FL*Stack /STK=33 /UG=Mm.4050 /LL=1566 /DEF=Mus musculus gut-enriched transcript 1 (Foxc1), mRNA. /PROD=fractured calsia expressed transcript 1 /FL=gb:NM_019502.1 gb:AF150103.1 gb:BC009158.1	1996.7001	257.0728	1280.0667	302.79193	3.1249733	3.0	0.052269127	0.50489753
gb:NM_026252.1 /DB_XREF=gi:13385759 /GEN=493044 /D24Rik /FEA=FlmRNA /CNT=161 /TID=Mm.23178.1 /TIER=ConsEnd /STK=0 /UG=Mm.23178 /LL=67579 /DEF=Mus musculus RIKEN cDNA 493044/D24 gene (493044/D24Rik), mRNA. /PROD=RIKEN cDNA 493044/D24 /FL=gb:NM_026252.1	2246.3333	522.5565	3440.5332	407.56915	3.12117	3.0	0.052423827	0.495842
gb:U20344.1 /DB_XREF=gi:912487 /FEA=FlmRNA /CNT=140 /TID=Mm.4325.1 /TIER=FL*Stack /STK=46 /UG=Mm.4325 /LL=16600 /UG_GENE=Klf4 /DEF=Mus musculus gut-enriched Kruppel-like factor GKLf mRNA, complete cds. /PROD=gut-enriched Kruppel-like factor /FL=gb:BC010301.1 gb:U20344.1 gb:U20344.1 gb:U20344.1 gb:NM_016937.1	2218.3	658.10254	3810.5332	593.3005	3.1124587	3.0	0.05278034	0.48902604
gb:NM_01116.1 /DB_XREF=gi:1920789 /FEA=FlmRNA /CNT=246 /TID=Mm.104975.1 /TIER=FL*Stack /STK=90 /UG=Mm.104975 /LL=66001 /UG_GENE=1300012C15Rik /DEF=Mus musculus, RIKEN cDNA 1300012C15 gene, clone MGC:19018 IMAGE:4023354, mRNA, complete cds. /PROD=RIKEN cDNA 1300012C15 gene /FL=gb:NM_02836.1 gb:BC011116.1	1721.4332	308.0201	978.2334	88.368774	4.017092	2.0	0.056745864	0.5152525
gb:NM_016715.1 /DB_XREF=gi:7710051 /GEN=Islr /FEA=FlmRNA /CNT=43 /TID=Mm.35771.1 /TIER=FL*Stack /STK=30 /UG=Mm.35771 /LL=57914 /DEF=Mus musculus thymic stromal-derived lymphopoietin, receptor (Islr), mRNA. /PROD=thymic stromal-derived lymphopoietin, receptor /FL=gb:AF232936.1 gb:AB031333.1 gb:AB039945.1 gb:NM_016715.1	912.63336	302.9743	1570.6333	225.301	3.0185394	3.0	0.05682495	0.5058535
gb:BC016280.1 /DB_XREF=gi:16740779 /FEA=FlmRNA /CNT=210 /TID=Mm.19055.1 /TIER=FL*Stack /STK=103 /UG=Mm.19055 /LL=18673 /UG_GENE=1110006E1 /DEF=Mus musculus, RIKEN cDNA 111006E1 gene, clone MGC:28902 IMAGE:4914167, mRNA, complete cds. /PROD=RIKEN cDNA 111006E1 gene /FL=gb:NM_008831.1	2465.0332	287.6765	1808.0668	243.65489	3.018338	3.0	0.056834035	0.49620482
gb:NM_133734.1 /DB_XREF=gi:19528929 /GEN=0710008A13Rik /FEA=FlmRNA /CNT=134 /TID=Mm.11535.1 /TIER=FL*Stack /STK=76 /UG=Mm.11535 /LL=71700 /DEF=Mus musculus RIKEN cDNA 0710008A13 gene (0710008A13Rik), mRNA. /PROD=RIKEN cDNA 0710008A13 /FL=gb:NM_133734.1 gb:BC008545.1	2924.9336	463.44464	1932.334	332.68933	3.0135894	3.0	0.057048753	0.4886818
gb:BC019459.1 /DB_XREF=gi:1804385 /FEA=mRNA /CNT=128 /TID=Mm.31025.1 /TIER=Stack /STK=66 /UG=Mm.31025 /LL=76437 /UG_GENE=2310015K15Rik /UG_TITLE=RIKEN cDNA 2310015K15 gene /DEF=Mus musculus, Similar to RIKEN cDNA 2310015K15 gene, clone IMAGE:4035590, mRNA.	682.73334	297.8792	1340.9333	235.16748	3.003885	3.0	0.057490736	0.48334804
gb:BC010586.1 /DB_XREF=gi:14714881 /FEA=FlmRNA /CNT=95 /TID=Mm.198238.1 /TIER=FL*Stack /STK=141 /UG=Mm.198239 /LL=66734 /UG_GENE=4922501H04Rik /DEF=Mus musculus, MAP1 light chain 3-like protein 1, clone MGC:6325 IMAGE:3256801, mRNA, complete cds. /PROD=MAP1 light chain 3-like protein 1 /FL=gb:BC010586.1	8346.8	1826.1411	4220.5	181.96098	3.8944106	2.0	0.060056616	0.49574006
gb:AB005361.1 /DB_XREF=gi:2317285 /FEA=FlmRNA /CNT=130 /TID=Mm.1008.1 /TIER=FL*Stack /STK=89 /UG=Mm.1008 /LL=19215 /UG_GENE=Pldgs /DEF=Mus musculus mRNA for prostaglandin D synthetase, complete cds. /PROD=prostaglandin D synthetase /FL=gb:AB005361.1	5255.2	1303.1003	2508.8	978.30804	2.9193041	3.0	0.06153079	0.4988389
gb:NM_008831.1 /DB_XREF=gi:6672918 /GEN=Phb /FEA=FlmRNA /CNT=260 /TID=Mm.2355.1 /TIER=FL*Stack /STK=58 /UG=Mm.2355 /LL=18673 /UG_GENE=Prohibitin (Phb), mRNA. /PROD=prohibitin /FL=gb:NM_008831.1	6689.0664	1162.0282	4307.933	824.85596	2.894155	3.0	0.06280016	0.50019777
gb:NM_013892.1 /DB_XREF=gi:7305570 /GEN=Itgag /FEA=FlmRNA /CNT=194 /TID=Mm.4292.1 /TIER=FL*Stack /STK=141 /UG=Mm.4292 /LL=21847 /DEF=Mus musculus TGFb inducible early growth response (Tieg), mRNA. /PROD=TGFb inducible early growth response /FL=gb:AF04088.1 gb:BC003316.1 gb:NM_013692.1 gb:AF049879.1	528.2	266.4009	1155.1333	107.51492	3.7798882	3.0	0.06340678	0.49632204
gb:BC010817.1 /DB_XREF=gi:14789892 /FEA=FlmRNA /CNT=138 /TID=Mm.3979.1 /TIER=FL*Stack /STK=25 /UG=Mm.3979 /DEF=Mus musculus, Similar to ubiquitin-like 4, clone MGC:19132 IMAGE:4215699, mRNA, complete cds. /PROD=Similar to ubiquitin-like 4 /FL=gb:BC010817.1	1884.5333	340.92563	1204.4667	226.77893	2.8767273	3.0	0.063699044	0.49015874
gb:NM_00592.1 /DB_XREF=gi:14714874 /FEA=FlmRNA /CNT=119 /TID=Mm.29553.1 /TIER=FL*Stack /STK=53 /UG=Mm.29553 /LL=60071 /UG_GENE=0610025L15Rik /DEF=Mus musculus, RIKEN cDNA 0610025L15 gene, clone MGC:7048 IMAGE:3156338, mRNA, complete cds. /PROD=RIKEN cDNA 0610025L15 gene /FL=gb:BC010592.1 gb:AB049623.1 gb:NM_023154.1	1405.4667	213.8315	834.73334	270.21564	2.8687627	3.0	0.06411519	0.48513827
gb:NM_007408.1 /DB_XREF=gi:6680849 /GEN=Adfp /FEA=FlmRNA /CNT=309 /TID=Mm.381.1 /TIER=FL*Stack /STK=92 /UG=Mm.381 /LL=1520 /DEF=Mus musculus adipose differentiation related protein (Adfp), mRNA. /PROD=adipose differentiation related protein /FL=gb:M93275.1 gb:NM_007408.1	2498.2666	257.47202	1771.2334	357.4763	2.8584013	3.0	0.06466167	0.4812524
gb:BI076714 /DB_XREF=gi:14515371 /DB_XREF=U0223810-3 /CLONE=U0223810 /FEA=mRNA /CNT=167 /TID=Mm.216195.1 /TIER=Stack /STK=18 /UG=Mm.216195 /UG_TITLE=Mus musculus mV330.1 retroelement mRNA sequence	12693.434	2625.5188	6953.3003	530.13385	3.7118473	2.0	0.065527044	0.47982705
gb:AK005326.1 /DB_XREF=gi:12834026 /FEA=mRNA /CNT=52 /TID=Mm.41330.1 /TIER=Stack /STK=17 /UG=Mm.41330 /LL=76291 /UG_GENE=1110003008Rik /UG_TITLE=RIKEN cDNA 1110003008 gene /DEF=Mus musculus 18 days embryo whole body cDNA, RIKEN full-length enriched library, clone:1110003008 hypothetical protein, full insert sequence.	1215.3334	282.99225	629.76666	51.017086	3.5270977	2.0	0.07182983	0.48672754
gb:NM_016738.1 /DB_XREF=gi:7949126 /GEN=Rpl13 /FEA=FlmRNA /CNT=11 /TID=Mm.42578.1 /TIER=FL*STK=2 /UG=Mm.42578 /LL=19898 /DEF=Mus musculus ribosomal protein L13 (Rpl13), mRNA. /PROD=ribosomal protein L13 /FL=gb:U28917.1 gb:NM_016738.1	19578.768	4562.7007	10923.566	3138.9824	2.7068903	3.0	0.07335706	0.48976624
gb:NM_025570.1 /DB_XREF=gi:20270193 /GEN=Mrp20 /FEA=FlmRNA /CNT=181 /TID=Mm.23825.1 /TIER=FL*Stack /STK=128 /UG=Mm.23825 /LL=66448 /DEF=Mus musculus mitochondrial ribosomal protein L20 (Mrp20), mRNA. /PROD=mitochondrial ribosomal protein L20 /FL=gb:AB049645.1 gb:BC016591.1 gb:NM_025570.1	3240.5664	473.0782	2285.8	388.91672	2.700274	3.0	0.07376892	0.48537812
gb:NM_133721.1 /DB_XREF=gi:19526903 /GEN=Iga9 /FEA=FlmRNA /CNT=110 /TID=Mm.23386.1 /TIER=FL*STK=2 /UG=Mm.23386 /LL=70107 /DEF=Mus musculus integrin alpha 9 (Iga9), mRNA. /PROD=integrin alpha 9 /FL=gb:NM_133721.1	1774.6666	433.60614	2705.9	413.57755	2.691753	3.0	0.074303575	0.48191175
gb:AF168781.1 /DB_XREF=gi:12833287 /GEN=Dnpep /FEA=FlmRNA /CNT=197 /TID=Mm.24680.1 /TIER=FL*Stack /STK=123 /UG=Mm.24680 /LL=13437 /DEF=Mus musculus aspartyl aminopeptidase (Dnpep), mRNA. /PROD=aspartyl aminopeptidase /FL=gb:AF005051.1 gb:NM_016878.1	1693.6334	243.04478	1160.1666	242.70084	2.6901348	3.0	0.07440565	0.47577694
gb:NM_053162.1 /DB_XREF=gi:16716448 /GEN=Mrp34 /FEA=FlmRNA /CNT=111 /TID=Mm.29489.1 /TIER=FL*Stack /STK=96 /UG=Mm.29489 /LL=94065 /DEF=Mus musculus mitochondrial ribosomal protein L34 (Mrp34), mRNA. /PROD=mitochondrial ribosomal protein L34 /FL=gb:NM_053162.1 gb:AB049653.1	2390.8	640.9675	1195.1666	431.3994	2.6803503	3.0	0.07502657	0.47308424
gb:BC003744.1 /DB_XREF=gi:13277677 /FEA=FlmRNA /CNT=135 /TID=Mm.3294.1 /TIER=FL*Stack /STK=52 /UG=Mm.3294 /LL=19080 /UG_GENE=Pp5c /DEF=Mus musculus, protein phosphatase 5, catalytic subunit, clone MGC:5847 IMAGE:3593022, mRNA, complete cds. /PROD=protein phosphatase 5, catalytic subunit /FL=gb:BC003744.1 gb:AF181862.1	974.39996	279.2426	455.9	185.42218	2.6792161	3.0	0.075098954	0.46705377
gb:AF078667.1 /DB_XREF=gi:4322307 /FEA=FlmRNA /CNT=54 /TID=Mm.29030.2 /TIER=FL*STK=1 /UG=Mm.29030 /LL=20411 /UG_GENE=Sorts1 /DEF=Mus musculus ponsin-1 mRNA, complete cds. /PROD=ponsin-1 /FL=gb:AF078667.1	4500.3335	454.3644	2470.4	926.83795	3.4062045	2.0	0.07643881	0.46896243
gb:NM_019990.1 /DB_XREF=gi:9910481 /GEN=Sdcca28 /FEA=FlmRNA /CNT=125 /TID=Mm.28896.1 /TIER=FL*Stack /STK=29 /UG=Mm.28896 /LL=56018 /DEF=Mus musculus serologically defined colon cancer antigen 28 (Sdcca28), mRNA. /PROD=serologically defined colon cancer antigen 28 /FL=gb:AB031550.1 gb:NM_019990.1	2981.7666	774.46027	1355.2666	307.86032	3.380319	3.0	0.0774809	0.4690177
gb:NM_011875.1 /DB_XREF=gi:6755209 /GEN=Psm13 /FEA=FlmRNA /CNT=192 /TID=Mm.29760.1 /TIER=FL*Stack /STK=95 /UG=Mm.29760 /LL=29907 /DEF=Mus musculus proleukine (prosome, macrophage) 26S subunit, non-ATPase, 13 (Psm13), mRNA. /PROD=proleukine (prosome, macrophage) 26S subunit, non-ATPase, 13 (Psm13) /FL=gb:AF107838.1	1570.9667	226.58565	1053.6	253.27943	2.6368415	3.0	0.07786655	0.46515015
gb:BC024394.1 /DB_XREF=gi:19354424 /FEA=FlmRNA /CNT=2007 /TID=Mm.34570.2 /TIER=FL*Stack /STK=108 /UG=Mm.34570 /LL=20018 /UG_GENE=Rpo1-3 /DEF=Mus musculus, RNA polymerase 1-3 (16 kDa subunit), clone MGC:36184 IMAGE:4987975, mRNA, complete cds. /PROD=RNA polymerase 1-3 (16 kDa subunit) /FL=gb:BC024394.1	1394.3667	266.72238	763.7	316.98865	2.6367848	3.0	0.07787033	0.45913157
gb:NM_007638.1 /DB_XREF=gi:8671703 /GEN=Ce7 /FEA=FlmRNA /CNT=513 /TID=Mm.914.1 /TIER=FL*Stack /STK=236 /UG=Mm.914 /LL=12468 /DEF=Mus musculus chaperonin subunit 7 (eta) (Cet7), mRNA. /PROD=chaperonin subunit 7 (eta) /FL=gb:BC008255.1 gb:U07638.1	2315.9333	46.717625	1610.0668	360.1172	3.3667843	2.0	0.07803395	0.4541976
gb:BC013486.1 /DB_XREF=gi:15489676 /FEA=FlmRNA /CNT=189 /TID=Mm.41389.1 /TIER=FL*Stack /STK=141 /UG=Mm.41389 /LL=66277 /UG_GENE=Klf15 /DEF=Mus musculus, Kruppel-like factor 15, clone MGC:19125 IMAGE:421067, mRNA, complete cds. /PROD=Kruppel-like factor 15 /FL=gb:NM_023184.1 gb:AF317225.1 gb:BC013486.1	1641.1333	293.1515	993.8667	309.8631	2.6290479	3.0	0.07838921	0.45048988
gb:NM_009777.1 /DB_XREF=gi:6753219 /GEN=C1qb /FEA=FlmRNA /CNT=149 /TID=Mm.2570.1 /TIER=FL*Stack /STK=58 /UG=Mm.2570 /LL=12260 /DEF=Mus musculus complement component 1, q subcomponent, beta polypeptide (C1qb), mRNA. /PROD=complement component 1, q subcomponent, betapolypeptide /FL=gb:M22531.1 gb:M36293.1 gb:NM_009777.1	2006.4667	304.08218	1285.4332	365.01932	2.6287265	3.0	0.078410864	0.44498166
gb:NM_023371.1 /DB_XREF=gi:12663652 /GEN=Pn1 /FEA=FlmRNA /CNT=173 /TID=Mm.7906.1 /TIER=FL*Stack /STK=110 /UG=Mm.7906 /LL=23988 /DEF=Mus musculus protein (peptidyl-prolyl cis-trans isomerase) NIMA-interacting 1 (Pn1), mRNA. /PROD=protein (peptidyl-prolyl cis-trans isomerase) NIMA-interacting 1 /FL=gb:NM_023371.1	3336.7666	475.0641	1999.5333	480.16516	2.613035	3.0	0.07947676	0.44546235
gb:NM_008155.1 /DB_XREF=gi:6680066 /GEN=Gp1 /FEA=FlmRNA /CNT=26 /TID=Mm.589.1 /TIER=FL*Stack /STK=2 /UG=Mm.589 /LL=14751 /DEF=Mus musculus glucose phosphate isomerase 1 complex (Gp1), mRNA. /PROD=glucose phosphate isomerase 1 complex /FL=gb:M14220.1 gb:NM_008155.1	6017.467	1636.3217	3145.5999	981.9437	2.6065686	3.0	0.07992121	0.4424906
gb:U48800.1 /DB_XREF=gi:1234824 /GEN=VEGf-B /FEA=FlmRNA /CNT=7 /TID=Mm.15807.2 /TIER=FL*STK=1 /UG=Mm.15807 /LL=22340 /DEF=Mus musculus vascular endothelial growth factor B precursor (VEGF-B) mRNA, complete cds. /PROD=vascular endothelial growth factor B precursor /FL=gb:U48800.1 gb:U48800.1	3644.2334	921.23413	1713.7333	417.65958	3.3057415	2.0	0.08060011	0.4408729
gb:AK010811.1 /DB_XREF=gi:12848197 /GEN=Phb /FEA=FlmRNA /CNT=260 /TID=Mm.2355.1 /TIER=Stack /STK=55 /UG=Mm.2355 /LL=18673 /UG_TITLE=RIKEN cDNA 2310015K15 gene /DEF=Mus musculus, Similar to RIKEN cDNA 2310015K15 gene, clone:241003008 hypothetical protein, full insert sequence. /FL=gb:NM_008831.1	3106.8665	494.61856	2189.1	362.6443	2.5918353	3.0	0.080945365	0.43749043
gb:NM_130881.1 /DB_XREF=gi:18700019 /GEN=MGC6885 /FEA=FlmRNA /CNT=43 /TID=Mm.12267.1 /TIER=FL*STK=2 /UG=Mm.12267 /LL=170715 /DEF=Mus musculus similar to poly(A)-binding protein, cytoplasmic 4 (inducible form) (MGC6885), mRNA. /PROD=similar to poly(A)-binding protein, cytoplasmic4 (inducible form) /FL=gb:NM_130881.1 gb:BC003283.1	2363.5667	555.67523	1319.0	424.0053	2.5884504	3.0	0.081182934	0.43361238
gb:NM_033882.1 /DB_XREF=gi:16716364 /GEN=Itm67 /FEA=FlmRNA /CNT=174 /TID=Mm.195498.1 /TIER=FL*Stack /STK=105 /UG=Mm.195498 /LL=20524 /DEF=Mus musculus transmembrane 4 superfamily member 7 (Tms4f7), mRNA. /PROD=transmembrane 4 superfamily member 7 /FL=gb:NM_053082.1 gb:BC003482.1	1432.9668	371.01614	723.1333	83.90889	3.2321563	2.0	0.083857775	0.44269103
gb:NM_015816.1 /DB_XREF=gi:7657316 /GEN=Lsm4-pending /FEA=FlmRNA /CNT=133 /TID=Mm.14585.1 /TIER=FL*Stack /STK=52 /UG=Mm.14585 /LL=50783 /DEF=Mus musculus U6 snRNA-associated SM-like protein 4 (Lsm4-pending), mRNA. /PROD=U6 snRNA-associated SM-like protein 4 /FL=gb:NM_015816.1 gb:BC026747.1	2082.0667	419.71677	1322.8334	300.10544	2.5486553	3.0	0.08404149	0.43856132
gb:NM_007940.1 /DB_XREF=gi:6679664 /FEA=FlmRNA /CNT=154 /TID=Mm.15295.1 /TIER=FL*Stack /STK=66 /UG=Mm.15295 /LL=13850 /DEF=Mus musculus epoxide hydrolase 2, cytoplasmic (Ephx2), mRNA. /PROD=epoxide hydrolase 2, cytoplasmic /FL=gb:NM_007940.1 gb:BC001587.1	6488.4336	906.62756	4647.6	401.75757	3.2152436	2.0	0.08463317	0.43663022
gb:NM_009045.1 /DB_XREF=gi:6877708 /GEN=Hga /FEA=FlmRNA /CNT=107 /TID=Mm.28170.1 /TIER=FL*Stack /STK=9 /UG=Mm.28170 /LL=19697 /DEF=Mus musculus v-rel reticuloendotheliosis viral oncogene homolog A (vian) (RelA), mRNA. /PROD=avian reticuloendotheliosis viral (v-ret) oncogene homolog A /FL=gb:NM_009045.1 gb:M1909.1	1960.0332	383.5544	1213.4333	334.97433	2.5393877	3.0	0.08472489	0.43219215
gb:NM_019503.1 /DB_XREF=gi:9506704 /GEN=Foxp1 /FEA=FlmRNA /CNT=7 /TID=Mm.1491.1 /TIER=FL*Stack /STK=2 /UG=Mm.1491 /LL=56188 /DEF=Mus musculus FXYD domain-containing ion transport regulator 1 (Fxyd1), mRNA. /PROD=FXYD domain-containing ion transport regulator 1 /FL=gb:AF089734.1 gb:NM_019503.1	14909.3	2605.9375	10422.3	1641.9779	2.5232031	3.0	0.0859348	0.43349335
gb:NM_011125.1 /DB_XREF=gi:1455117 /FEA=FlmRNA /CNT=67 /TID=Mm.6105.1 /TIER=FL*Stack /STK=32 /UG=Mm.6105 /LL=18830 /DEF=Mus musculus phospholipid transfer protein (Pltp), mRNA. /PROD=phospholipid transfer protein /FL=gb:BC003782.1	2012.7001	384.84665	1234.1333	370.92523	2.5229409	3.0	0.085954584	0.42882836

gb U081551.1 DB_XREF=gi 8580066 GEN=Gap1 FEA=FLmRNA CNT=26 TID=Mm.589.1 TIER=FL STK=2 UG=Mm.589 ILL=14751 DEF=Mus musculus glucose phosphate isomerase 1 complex (Gp1), mRNA, /PROD=glucose phosphate isomerase 1 complex /FL=gb M14220.1 gb.NM_008155.1	8020.0	2118.5437	4423.6665	1272.875	2.5203187	3.0	0.08615266	0.42514464
gb NM_024223.1 DB_XREF=gi 13195845 GEN=U61002 U63R FEA=FLmRNA CNT=180 TID=Mm.133825.1 TIER=FL STK=gb U63R ILL=14751 UG=Mm.133825 ILL=6833 DEF=Mus musculus RIKEN cDNA 061001023 (U63R), mRNA, /PROD=RIKEN cDNA 061001023 /FL=gb.NM_024223.1 gb.BC002096.1 gb.BC002093.1	24228.334	3708.0068	16887.434	3422.41	2.519776	3.0	0.08619372	0.42077363
gb NM_025529.1 DB_XREF=gi 13398997 GEN=U61002 U63R FEA=FLmRNA CNT=180 TID=Mm.133825.1 TIER=FL STK=gb U63R ILL=14751 UG=Mm.133825 ILL=6833 DEF=Mus musculus RIKEN cDNA 2310039H17 (U63R), mRNA, /PROD=RIKEN cDNA 2310039H17 /FL=gb.NM_025529.1	3700.1335	1125.2148	1606.6998	191.09187	3.1769488	2.0	0.08642728	0.41742536
gb AB054000.1 DB_XREF=gi 14017172 GEN=Cg10671-like FEA=FLmRNA CNT=35 TID=Mm.38758.1 TIER=FL STK=gb U63R ILL=14751 UG=Mm.38758 ILL=6880 DEF=Mus musculus Cg10671-like (mRNA), complete cds. /PROD=Cg10671-like /FL=gb AB054000.1	1886.9332	390.19482	1093.9	189.40694	3.1668425	2.0	0.086909845	0.41533756
gb BC024621.1 DB_XREF=gi 19354257 FEA=FLmRNA CNT=209 TID=Mm.30064.1 TIER=FL+Stk STK=62 UG=Mm.30064 ILL=56486 UG=CE-Gabru ILL=56486 DEF=Mus musculus Gabru (GABRA4) protein, complete cds. /PROD=GABRA4 protein, complete cds. /FL=gb BC024621.1 gb.BC002126.1 gb.BC024621.1 gb.AF161587.1	10245.833	2222.5093	5753.9663	1048.8822	3.165773	2.0	0.086961135	0.4112537
gb AF250139.1 DB_XREF=gi 7644381 FEA=FLmRNA CNT=159 TID=Mm.21549.1 TIER=FL STK=gb U63R ILL=14751 UG=Mm.21549 ILL=80888 UG=GENE=Cryac DEF=Mus musculus small stress protein-like protein HSP22 mRNA, complete cds. /PROD=small stress protein-like protein HSP22 /FL=gb BC011219.1 gb.NM_030704.1 gb.AF250139.1 gb.AF273453.1	2011.4	564.6096	1067.7667	328.73923	2.501638	3.0	0.08758011	0.40991104
gb NM_019414.1 DB_XREF=gi 9507076 GEN=Selensbp2 FEA=FLmRNA CNT=105 TID=Mm.196558.1 TIER=FL STK=gb U63R ILL=14751 UG=Mm.196558 ILL=20342 DEF=Mus musculus selenin binding protein 2 (Selensbp2), mRNA, /PROD=selenin binding protein 2 /FL=gb NM_019414.1 gb.BC024106.1 gb.BC024106.1	4026.9336	494.99008	2721.0667	759.7327	2.4944136	3.0	0.088139914	0.40832165
gb NM_024741.1 DB_XREF=gi 19320214 GEN=Mpr23 FEA=FLmRNA CNT=543 TID=Mm.41910.1 TIER=FL STK=gb U63R ILL=14751 UG=Mm.41910 ILL=64656 DEF=Mus musculus mitochondrial ribosomal protein S23 (Mpr23), mRNA, /PROD=mitochondrial ribosomal protein S23 /FL=gb NM_024741.1	2356.1335	299.46243	1698.9668	349.67368	2.4724076	3.0	0.08987236	0.41214195
gb AK013135.1 DB_XREF=gi 12850309 FEA=mRNA CNT=121 TID=Mm.141864.1 TIER=Stk STK=79 UG=Mm.141864 ILL=75620 UG=GENE=2810422J05R UG_TITLE=RIKEN cDNA 2810422J05 (U63R), mRNA, complete cds. /PROD=RIKEN cDNA 2810422J05 (U63R), mRNA, complete cds. /FL=gb AK013135.1 gb.BC024106.1 gb.BC024106.1	1843.7001	200.65141	1282.5333	344.3946	2.4385602	3.0	0.09261915	0.42049095
Mus musculus REF332599 DEF=Mouse glyceroldehyde 3-phosphate dehydrogenase mRNA, complete cds /LEN=1228 [2..5..M..3 represent transcripts 5 prime, Middle, and 3 prime respectively	38164.9	9613.984	22698.932	5409.2744	2.4283547	3.0	0.093467414	0.42014065
gb NM_025554.1 DB_XREF=gi 13398997 GEN=U61002 U63R FEA=FLmRNA CNT=180 TID=Mm.133825.1 TIER=FL STK=gb U63R ILL=14751 UG=Mm.133825 ILL=6833 DEF=Mus musculus RIKEN cDNA 2310039H17 (U63R), mRNA, complete cds. /PROD=RIKEN cDNA 2310039H17 /FL=gb NM_025554.1 gb.BC002096.1 gb.BC002093.1	3954.4001	400.78058	2848.5667	680.5213	2.4252167	3.0	0.09373015	0.41719106
gb NM_017393.1 DB_XREF=gi 8393155 GEN=Cp FEA=FLmRNA CNT=134 TID=Mm.15243.1 TIER=FL STK=gb U63R ILL=14751 UG=Mm.15243 ILL=53895 DEF=Mus musculus caseinolytic protease, ATP-dependent, proteolytic subunit homolog (E. coli) (Cp), mRNA, /PROD=caseinolytic protease, ATP-dependent, proteolytic subunit homolog (E. coli) (Cp) /FL=gb NM_017393.1 gb.BC001998.1	1832.3666	349.50354	1118.9667	371.0742	2.4240038	3.0	0.09383194	0.41358933
gb BC019408.1 DB_XREF=gi 13398997 GEN=U61002 U63R FEA=FLmRNA CNT=180 TID=Mm.133825.1 TIER=FL STK=gb U63R ILL=14751 UG=Mm.133825 ILL=6833 DEF=Mus musculus RIKEN cDNA 2310039H17 (U63R), mRNA, complete cds. /PROD=RIKEN cDNA 2310039H17 /FL=gb BC019408.1 gb.BC002096.1 gb.BC002093.1	1815.1333	453.52466	927.93335	445.7683	2.416461	3.0	0.09446801	0.4123892
gb NM_015493.1 DB_XREF=gi 8393155 GEN=Cp FEA=FLmRNA CNT=134 TID=Mm.15243.1 TIER=FL STK=gb U63R ILL=14751 UG=Mm.15243 ILL=53895 DEF=Mus musculus caseinolytic protease, ATP-dependent, proteolytic subunit homolog (E. coli) (Cp), mRNA, /PROD=caseinolytic protease, ATP-dependent, proteolytic subunit homolog (E. coli) (Cp) /FL=gb NM_015493.1 gb.BC001998.1	1815.1333	453.52466	927.93335	445.7683	2.416461	3.0	0.09446801	0.4123892
gb NM_018681.1 DB_XREF=gi 13994194 GEN=Ppp1a FEA=FLmRNA CNT=386 TID=Mm.1970.1 TIER=FL+Stk STK=206 UG=Mm.1970 ILL=19045 DEF=Mus musculus protein phosphatase 1, catalytic subunit, alpha isoform (Ppp1a), mRNA, /PROD=protein phosphatase 1,	5705.3667	1490.353	3345.9333	800.3353	2.4157786	3.0	0.09452581	0.40871158
gb AK009753.1 DB_XREF=gi 12844759 FEA=mRNA CNT=8 TID=Mm.34838.1 TIER=ConsE STK=3 UG=Mm.34838 ILL=76463 UG=GENE=231022J05R UG_TITLE=RIKEN cDNA 231022J05 (U63R), mRNA, complete cds. /PROD=RIKEN cDNA 231022J05 (U63R), mRNA, complete cds. /FL=gb AK009753.1 gb.BC024106.1 gb.BC024106.1	2922.1003	540.96954	1978.4667	35.65691	3.0147402	2.0	0.09466275	0.40544236
Mus musculus REF332599 DEF=Mouse glyceroldehyde 3-phosphate dehydrogenase mRNA, complete cds /LEN=1228 [2..5..M..3 represent transcripts 5 prime, Middle, and 3 prime respectively	38164.9	9613.984	22698.932	5409.2744	2.4283547	3.0	0.093467414	0.42014065
gb NM_025554.1 DB_XREF=gi 13398997 GEN=U61002 U63R FEA=FLmRNA CNT=180 TID=Mm.133825.1 TIER=FL STK=gb U63R ILL=14751 UG=Mm.133825 ILL=6833 DEF=Mus musculus RIKEN cDNA 2310039H17 (U63R), mRNA, complete cds. /PROD=RIKEN cDNA 2310039H17 /FL=gb NM_025554.1 gb.BC002096.1 gb.BC002093.1	3954.4001	400.78058	2848.5667	680.5213	2.4252167	3.0	0.09373015	0.41719106
gb NM_017393.1 DB_XREF=gi 8393155 GEN=Cp FEA=FLmRNA CNT=134 TID=Mm.15243.1 TIER=FL STK=gb U63R ILL=14751 UG=Mm.15243 ILL=53895 DEF=Mus musculus caseinolytic protease, ATP-dependent, proteolytic subunit homolog (E. coli) (Cp), mRNA, /PROD=caseinolytic protease, ATP-dependent, proteolytic subunit homolog (E. coli) (Cp) /FL=gb NM_017393.1 gb.BC001998.1	1832.3666	349.50354	1118.9667	371.0742	2.4240038	3.0	0.09383194	0.41358933
gb BC019408.1 DB_XREF=gi 13398997 GEN=U61002 U63R FEA=FLmRNA CNT=180 TID=Mm.133825.1 TIER=FL STK=gb U63R ILL=14751 UG=Mm.133825 ILL=6833 DEF=Mus musculus RIKEN cDNA 2310039H17 (U63R), mRNA, complete cds. /PROD=RIKEN cDNA 2310039H17 /FL=gb BC019408.1 gb.BC002096.1 gb.BC002093.1	1815.1333	453.52466	927.93335	445.7683	2.416461	3.0	0.09446801	0.4123892
gb NM_015493.1 DB_XREF=gi 8393155 GEN=Cp FEA=FLmRNA CNT=134 TID=Mm.15243.1 TIER=FL STK=gb U63R ILL=14751 UG=Mm.15243 ILL=53895 DEF=Mus musculus caseinolytic protease, ATP-dependent, proteolytic subunit homolog (E. coli) (Cp), mRNA, /PROD=caseinolytic protease, ATP-dependent, proteolytic subunit homolog (E. coli) (Cp) /FL=gb NM_015493.1 gb.BC001998.1	1815.1333	453.52466	927.93335	445.7683	2.416461	3.0	0.09446801	0.4123892
gb NM_018681.1 DB_XREF=gi 13994194 GEN=Ppp1a FEA=FLmRNA CNT=386 TID=Mm.1970.1 TIER=FL+Stk STK=206 UG=Mm.1970 ILL=19045 DEF=Mus musculus protein phosphatase 1, catalytic subunit, alpha isoform (Ppp1a), mRNA, /PROD=protein phosphatase 1,	5705.3667	1490.353	3345.9333	800.3353	2.4157786	3.0	0.09452581	0.40871158
gb AK009753.1 DB_XREF=gi 12844759 FEA=mRNA CNT=8 TID=Mm.34838.1 TIER=ConsE STK=3 UG=Mm.34838 ILL=76463 UG=GENE=231022J05R UG_TITLE=RIKEN cDNA 231022J05 (U63R), mRNA, complete cds. /PROD=RIKEN cDNA 231022J05 (U63R), mRNA, complete cds. /FL=gb AK009753.1 gb.BC024106.1 gb.BC024106.1	2922.1003	540.96954	1978.4667	35.65691	3.0147402	2.0	0.09466275	0.40544236
Mus musculus REF332599 DEF=Mouse glyceroldehyde 3-phosphate dehydrogenase mRNA, complete cds /LEN=1228 [2..5..M..3 represent transcripts 5 prime, Middle, and 3 prime respectively	38164.9	9613.984	22698.932	5409.2744	2.4283547	3.0	0.093467414	0.42014065
gb NM_025554.1 DB_XREF=gi 13398997 GEN=U61002 U63R FEA=FLmRNA CNT=180 TID=Mm.133825.1 TIER=FL STK=gb U63R ILL=14751 UG=Mm.133825 ILL=6833 DEF=Mus musculus RIKEN cDNA 2310039H17 (U63R), mRNA, complete cds. /PROD=RIKEN cDNA 2310039H17 /FL=gb NM_025554.1 gb.BC002096.1 gb.BC002093.1	3954.4001	400.78058	2848.5667	680.5213	2.4252167	3.0	0.09373015	0.41719106
gb NM_017393.1 DB_XREF=gi 8393155 GEN=Cp FEA=FLmRNA CNT=134 TID=Mm.15243.1 TIER=FL STK=gb U63R ILL=14751 UG=Mm.15243 ILL=53895 DEF=Mus musculus caseinolytic protease, ATP-dependent, proteolytic subunit homolog (E. coli) (Cp), mRNA, /PROD=caseinolytic protease, ATP-dependent, proteolytic subunit homolog (E. coli) (Cp) /FL=gb NM_017393.1 gb.BC001998.1	1832.3666	349.50354	1118.9667	371.0742	2.4240038	3.0	0.09383194	0.41358933
gb BC019408.1 DB_XREF=gi 13398997 GEN=U61002 U63R FEA=FLmRNA CNT=180 TID=Mm.133825.1 TIER=FL STK=gb U63R ILL=14751 UG=Mm.133825 ILL=6833 DEF=Mus musculus RIKEN cDNA 2310039H17 (U63R), mRNA, complete cds. /PROD=RIKEN cDNA 2310039H17 /FL=gb BC019408.1 gb.BC002096.1 gb.BC002093.1	1815.1333	453.52466	927.93335	445.7683	2.416461	3.0	0.09446801	0.4123892
gb NM_015493.1 DB_XREF=gi 8393155 GEN=Cp FEA=FLmRNA CNT=134 TID=Mm.15243.1 TIER=FL STK=gb U63R ILL=14751 UG=Mm.15243 ILL=53895 DEF=Mus musculus caseinolytic protease, ATP-dependent, proteolytic subunit homolog (E. coli) (Cp), mRNA, /PROD=caseinolytic protease, ATP-dependent, proteolytic subunit homolog (E. coli) (Cp) /FL=gb NM_015493.1 gb.BC001998.1	1815.1333	453.52466	927.93335	445.7683	2.416461	3.0	0.09446801	0.4123892
gb NM_018681.1 DB_XREF=gi 13994194 GEN=Ppp1a FEA=FLmRNA CNT=386 TID=Mm.1970.1 TIER=FL+Stk STK=206 UG=Mm.1970 ILL=19045 DEF=Mus musculus protein phosphatase 1, catalytic subunit, alpha isoform (Ppp1a), mRNA, /PROD=protein phosphatase 1,	5705.3667	1490.353	3345.9333	800.3353	2.4157786	3.0	0.09452581	0.40871158
gb AK009753.1 DB_XREF=gi 12844759 FEA=mRNA CNT=8 TID=Mm.34838.1 TIER=ConsE STK=3 UG=Mm.34838 ILL=76463 UG=GENE=231022J05R UG_TITLE=RIKEN cDNA 231022J05 (U63R), mRNA, complete cds. /PROD=RIKEN cDNA 231022J05 (U63R), mRNA, complete cds. /FL=gb AK009753.1 gb.BC024106.1 gb.BC024106.1	2922.1003	540.96954	1978.4667	35.65691	3.0147402	2.0	0.09466275	0.40544236
Mus musculus REF332599 DEF=Mouse glyceroldehyde 3-phosphate dehydrogenase mRNA, complete cds /LEN=1228 [2..5..M..3 represent transcripts 5 prime, Middle, and 3 prime respectively	38164.9	9613.984	22698.932	5409.2744	2.4283547	3.0	0.093467414	0.42014065
gb NM_025554.1 DB_XREF=gi 13398997 GEN=U61002 U63R FEA=FLmRNA CNT=180 TID=Mm.133825.1 TIER=FL STK=gb U63R ILL=14751 UG=Mm.133825 ILL=6833 DEF=Mus musculus RIKEN cDNA 2310039H17 (U63R), mRNA, complete cds. /PROD=RIKEN cDNA 2310039H17 /FL=gb NM_025554.1 gb.BC002096.1 gb.BC002093.1	3954.4001	400.78058	2848.5667	680.5213	2.4252167	3.0	0.09373015	0.41719106
gb NM_017393.1 DB_XREF=gi 8393155 GEN=Cp FEA=FLmRNA CNT=134 TID=Mm.15243.1 TIER=FL STK=gb U63R ILL=14751 UG=Mm.15243 ILL=53895 DEF=Mus musculus caseinolytic protease, ATP-dependent, proteolytic subunit homolog (E. coli) (Cp), mRNA, /PROD=caseinolytic protease, ATP-dependent, proteolytic subunit homolog (E. coli) (Cp) /FL=gb NM_017393.1 gb.BC001998.1	1832.3666	349.50354	1118.9667	371.0742	2.4240038	3.0	0.09383194	0.41358933
gb BC019408.1 DB_XREF=gi 13398997 GEN=U61002 U63R FEA=FLmRNA CNT=180 TID=Mm.133825.1 TIER=FL STK=gb U63R ILL=14751 UG=Mm.133825 ILL=6833 DEF=Mus musculus RIKEN cDNA 2310039H17 (U63R), mRNA, complete cds. /PROD=RIKEN cDNA 2310039H17 /FL=gb BC019408.1 gb.BC002096.1 gb.BC002093.1	1815.1333	453.52466	927.93335	445.7683	2.416461	3.0	0.09446801	0.4123892
gb NM_015493.1 DB_XREF=gi 8393155 GEN=Cp FEA=FLmRNA CNT=134 TID=Mm.15243.1 TIER=FL STK=gb U63R ILL=14751 UG=Mm.15243 ILL=53895 DEF=Mus musculus caseinolytic protease, ATP-dependent, proteolytic subunit homolog (E. coli) (Cp), mRNA, /PROD=caseinolytic protease, ATP-dependent, proteolytic subunit homolog (E. coli) (Cp) /FL=gb NM_015493.1 gb.BC001998.1	1815.1333	453.52466	927.93335	445.7683	2.416461	3.0	0.09446801	0.4123892
gb NM_018681.1 DB_XREF=gi 13994194 GEN=Ppp1a FEA=FLmRNA CNT=386 TID=Mm.1970.1 TIER=FL+Stk STK=206 UG=Mm.1970 ILL=19045 DEF=Mus musculus protein phosphatase 1, catalytic subunit, alpha isoform (Ppp1a), mRNA, /PROD=protein phosphatase 1,	5705.3667	1490.353	3345.9333	800.3353	2.4157786	3.0	0.09452581	0.40871158
gb AK009753.1 DB_XREF=gi 12844759 FEA=mRNA CNT=8 TID=Mm.34838.1 TIER=ConsE STK=3 UG=Mm.34838 ILL=76463 UG=GENE=231022J05R UG_TITLE=RIKEN cDNA 231022J05 (U63R), mRNA, complete cds. /PROD=RIKEN cDNA 231022J05 (U63R), mRNA, complete cds. /FL=gb AK009753.1 gb.BC024106.1 gb.BC024106.1	2922.1003	540.96954	1978.4667	35.65691	3.0147402	2.0	0.09466275	0.40544236
Mus musculus REF332599 DEF=Mouse glyceroldehyde 3-phosphate dehydrogenase mRNA, complete cds /LEN=1228 [2..5..M..3 represent transcripts 5 prime, Middle, and 3 prime respectively	38164.9	9613.984	22698.932	5409.2744	2.4283547	3.0	0.093467414	0.42014065
gb NM_025554.1 DB_XREF=gi 13398997 GEN=U61002 U63R FEA=FLmRNA CNT=180 TID=Mm.133825.1 TIER=FL STK=gb U63R ILL=14751 UG=Mm.133825 ILL=6833 DEF=Mus musculus RIKEN cDNA 2310039H17 (U63R), mRNA, complete cds. /PROD=RIKEN cDNA 2310039H17 /FL=gb NM_025554.1 gb.BC002096.1 gb.BC002093.1	3954.4001	400.78058	2848.5667	680.5213	2.4252167	3.0	0.09373015	0.41719106
gb NM_017393.1 DB_XREF=gi 8393155 GEN=Cp FEA=FLmRNA CNT=134 TID=Mm.15243.1 TIER=FL STK=gb U63R ILL=14751 UG=Mm.15243 ILL=53895 DEF=Mus musculus caseinolytic protease, ATP-dependent, proteolytic subunit homolog (E. coli) (Cp), mRNA, /PROD=caseinolytic protease, ATP-dependent, proteolytic subunit homolog (E. coli) (Cp) /FL=gb NM_017393.1 gb.BC001998.1	1832.3666	349.50354	1118.9667	371.0742	2.4240038	3.0	0.09383194	0.41358933
gb BC019408.1 DB_XREF=gi 13398997 GEN=U61002 U63R FEA=FLmRNA CNT=180 TID=Mm.133825.1 TIER=FL STK=gb U63R ILL=14751 UG=Mm.133825 ILL=6833 DEF=Mus musculus RIKEN cDNA 2310039H17 (U63R), mRNA, complete cds. /PROD=RIKEN cDNA 2310039H17 /FL=gb BC019408.1 gb.BC002096.1 gb.BC002093.1	1815.1333	453.52466	927.93335	445.7683	2.416461	3.0	0.09446801	0.4123892
gb NM_015493.1 DB_XREF=gi 8393155 GEN=Cp FEA=FLmRNA CNT=134 TID=Mm.15243.1 TIER=FL STK=gb U63R ILL=14751 UG=Mm.15243 ILL=53895 DEF=Mus musculus caseinolytic protease, ATP-dependent, proteolytic subunit homolog (E. coli) (Cp), mRNA, /PROD=caseinolytic protease, ATP-dependent, proteolytic subunit homolog (E. coli) (Cp) /FL=gb NM_015493.1 gb.BC001998.1	1815.1333	453.52466	927.93335	445.7683	2.416461	3.0	0.09446801	0.4123892
gb NM_018681.1 DB_XREF=gi 13994194 GEN=Ppp1a FEA=FLmRNA CNT=386 TID=Mm.1970.1 TIER=FL+Stk STK=206 UG=Mm.1970 ILL=19045 DEF=Mus musculus protein phosphatase 1, catalytic subunit, alpha isoform (Ppp1a), mRNA, /PROD=protein phosphatase 1,	5705.3667	1490.353	3345.9333	800.3353	2.4157786	3.0	0.09452581	0.40871158
gb AK009753.1 DB_XREF=gi 12844759 FEA=mRNA CNT=8 TID=Mm.34838.1 TIER=ConsE STK=3 UG=Mm.34838 ILL=76463 UG=GENE=231022J05R UG_TITLE=RIKEN cDNA 231022J05 (U63R), mRNA, complete cds. /PROD=RIKEN cDNA 231022J05 (U63R), mRNA, complete cds. /FL=gb AK009753.1 gb.BC024106.1 gb.BC024106.1	2922.1003	540.96954	1978.4667	35.65691	3.0147402	2.0	0.09466275	0.40544236
Mus musculus REF332599 DEF=Mouse glyceroldehyde 3-phosphate dehydrogenase mRNA, complete cds /LEN=1228 [2..5..M..3 represent transcripts 5 prime, Middle, and 3 prime respectively	38164.9	9613.984	22698.					

gbNM_007964.1/DB_XREF=gi6679706/GEN=Ew5/FEA=FLmRNA/CNT=132/TID=Mm.35796.1/TIER=FL+Stack/STK=43 /UG=Mm.35796.1/DB_XREF=gi6679706/GEN=Ew5/FEA=FLmRNA/CNT=132/TID=Mm.35796.1/TIER=FL+Stack/STK=43 /FL-gb.U53586.1 gb-NM_007964.1	792.3667	377.52588	1390.3002	92.49189	2.6644602	2.0	0.11670841	0.38395375
gbNM_010438.1/DB_XREF=gi8754205/GEN=HK1/FEA=FLmRNA/CNT=117/TID=Mm.196605.1/TIER=FL+Stack/STK=2/UG=Mm.196605 /FL-gb.U53586.1 gb-NM_010438.1	1239.2334	485.96017	504.16666	328.2567	2.1710267	3.0	0.118341856	0.38652664
gbBC001527.1/DB_XREF=gi13938071/FEA=FLmRNA/CNT=413/TID=Mm.27818.1/TIER=FL+Stack/STK=17/UG=Mm.27818.1/LL=13629 /UG_GENE=Eef2/DEF=Mus musculus, eukaryotic translation elongation factor 2, clone MGC:6761 IMAGE:3600352, mRNA, complete cds. /PROD=eukaryotic translation elongation factor 2 /FL-gb.BC007152.1	14758.233	2760.599	10545.767	1951.1	2.1583295	3.0	0.11976393	0.3883773
gbNM_001572.1/DB_XREF=gi6671649/GEN=Ct1ga/FEA=FLmRNA/CNT=119/TID=Mm.370.1/TIER=FL+Stack/STK=46/UG=Mm.370 /LL=12259/DEF=Mus musculus complement component 1, q subcomponent, alpha polypeptide (C1qa), mRNA, /PROD=complement component 1, q subcomponent, alpha polypeptide /FL-gb.BC002686.1 gb-NM_001572.1	1808.0332	915.5151	389.43335	199.11038	2.6225247	2.0	0.11982115	0.38580713
gbBC0027166.1/DB_XREF=gi20073307/FEA=FLmRNA/CNT=223/TID=Mm.219670.1/TIER=Stack/STK=22/UG=Mm.219670/DEF=Mus musculus, Similar to eukaryotic translation initiation factor 4 gamma, 1, clone IMAGE:4950789, mRNA, partial cds. /PROD=Similar to eukaryotic translation initiation factor 4 gamma, 1	1914.3334	535.31134	1075.0	149.95964	2.6150708	2.0	0.120386615	0.38489804
gbNM_033617.1/DB_XREF=gi15991794/GEN=AtP6v0b/FEA=FLmRNA/CNT=145/TID=Mm.3479.1/TIER=FL+Stack/STK=70 /UG=Mm.3479.1/LL=114143/DEF=Mus musculus ATPase, H+ transporting, lysosomal 21kDa, V0 subunit B (AtP6v0b), mRNA, /PROD=ATPase, H+ transporting, lysosomal 21kDa, V0subunit B /FL-gb.NM_033617.1 gb-AB060654.1 gb-AF356006.1	2499.8333	531.6897	1691.5333	374.72598	2.1523097	2.0	0.12044529	0.38239273
gbU25533.1/DB_XREF=gi1028496/GEN=TMP/FEA=FLmRNA/CNT=216/TID=Mm.30024.1/TIER=FL+Stack/STK=83/UG=Mm.30024 /LL=13730/DEF=Mus musculus tumor-associated membrane protein (TMP) mRNA, complete cds. /PROD=tumor-associated membrane protein /FL-gb.U25533.1 gb-NM_010128.1	3414.7334	885.31415	5353.6997	1285.9819	2.1510766	3.0	0.120585434	0.3801791
gbAK019319.1/DB_XREF=gi12859466/GEN=ApoE/FEA=mRNA/CNT=1/TID=Mm.138866.2/TIER=ConsEnd/STK=0/UG=Mm.138866 /LL=11816/UG_TITLE=apolipoprotein E /DEF=Mus musculus adult mice hippocampus cDNA, RIKEN full-length enriched library, clone:2900019G12/apolipoprotein E, full insert sequence	15604.3	4270.9517	9267.634	2806.9692	2.147504	3.0	0.12099254	0.3788318
gbNM_008512.1/DB_XREF=gi6678719/GEN=LtP1/FEA=FLmRNA/CNT=182/TID=Mm.7221.1/TIER=FL+Stack/STK=49/UG=Mm.7221 /LL=16971/DEF=Mus musculus low density lipoprotein receptor-related protein 1 (Lrp1), mRNA, /PROD=low density lipoprotein receptor-related protein1 /FL-gb-AF36720.1 gb-NM_008512.1	2616.4001	712.1777	1542.8334	493.1368	2.1465883	3.0	0.12109717	0.37656245
gb-NM_011918.1/DB_XREF=gi6756042/GEN=Ldb3/FEA=FLmRNA/CNT=97/TID=Mm.29733.1/TIER=FL+Stack/STK=71/UG=Mm.29733 /LL=24131/DEF=Mus musculus LIM domain binding 3 (Ldb3), mRNA, /PROD=LIM domain binding 3 /FL-gb.AF114379.2 gb-NM_011918.1	14779.5	2508.98	10855.767	719.2049	2.6038458	2.0	0.12124525	0.3744581
gbNM_009208.1/DB_XREF=gi6678022/GEN=SC4a3/FEA=FLmRNA/CNT=45/TID=Mm.5053.1/TIER=FL+Stack/STK=23/UG=Mm.5053 /LL=20536/DEF=Mus musculus solute carrier family 4 (anion exchanger), member 3 (SC4a3), mRNA, /PROD=solute carrier family 4 (anion exchanger) member 3 /FL-gb.M28383.1 gb-NM_009208.1	2166.0	661.7367	1131.3334	191.27336	2.601667	2.0	0.12141292	0.37244233
gbAF225808.1/DB_XREF=gi6717123/DB_XREF=gi15991794/GEN=AtP6v0b/FEA=FLmRNA/CNT=145/TID=Mm.3479.1/TIER=FL+Stack/STK=70 /UG=Mm.3479.1/LL=114143/DEF=Mus musculus ATPase, H+ transporting, lysosomal 21kDa, V0 subunit B (AtP6v0b), mRNA, /PROD=ATPase, H+ transporting, lysosomal 21kDa, V0subunit B /FL-gb.NM_033617.1 gb-AB060654.1 gb-AF356006.1	2209.2	1237.3901	4263.6665	585.0482	2.599816	2.0	0.1215556	0.37037745
gbNM_010240.1/DB_XREF=gi6753913/GEN=Fb1/FEA=FLmRNA/CNT=109/TID=Mm.7500.1/TIER=FL+Stack/STK=24/UG=Mm.7500 /LL=14325/DEF=Mus musculus ferritin light chain 1 (Fb1), mRNA, /PROD=ferritin light chain 1 /FL-gb.U04716.1 gb-NM_010240.1	5862.8335	943.54614	4308.5664	432.8185	2.5933146	2.0	0.122058645	0.36943084
gbNM_019840.1/DB_XREF=gi14971094/FEA=FLmRNA/CNT=5/TID=Mm.2400.2/TIER=FL+Stack/STK=2/UG=Mm.2400.2/LL=14779 /UG_GENE=Gp4/DEF=Mus musculus phospholipid hydroperoxide glutathione peroxidase, mRNA, complete cds, alternatively spliced. /PROD=phospholipid hydroperoxide glutathione peroxidase /FL-gb-AF24027.1	23738.666	5152.416	15873.466	1223.0314	2.5725076	2.0	0.12368836	0.3718842
gbBC006753.1/DB_XREF=gi13879545/FEA=FLmRNA/CNT=190/TID=Mm.3634.1/TIER=FL+Stack/STK=71/UG=Mm.3634/DEF=Mus musculus, clone MGC:11670 IMAGE:3709076, mRNA, complete cds. /PROD=Unknown (protein for MGC:11670) /FL-gb.U028317.1 gb-BC006753.1	1298.4333	74.20587	789.0334	335.8784	2.5650096	2.0	0.12428313	0.37121406
gbNM_021538.1/DB_XREF=gi10946971/GEN=Cope/FEA=FLmRNA/CNT=222/TID=Mm.28668.1/TIER=FL+Stack/STK=93 /UG=Mm.28668.1/LL=59042/DEF=Mus musculus coatomer protein complex, subunit epsilon (Cope), mRNA, /PROD=coatomer protein complex, subunit epsilon /FL-gb-AB033837.1 gb-BC009170.1 gb-NM_021538.1	2886.7668	464.41937	2023.2333	537.0535	2.1065724	3.0	0.12577623	0.3732184
gbNM_009349.1/DB_XREF=gi10946971/GEN=Cope/FEA=FLmRNA/CNT=222/TID=Mm.28668.1/TIER=FL+Stack/STK=93/UG=Mm.299 /LL=1743/DEF=Mus musculus thioester S-methyltransferase (Tent), mRNA, /PROD=thioester S-methyltransferase /FL-gb.M88694.1 gb-NM_009349.1 gb-BC013518.1	3501.0999	800.25867	2259.0667	277.9903	2.539362	2.0	0.12634811	0.37248078
gbAK003715.1/DB_XREF=gi12634551/GEN=D11Wsu686/FEA=mRNA/CNT=48/TID=Mm.24855.1/TIER=Stack/STK=29 /UG=Mm.24855.1/LL=28084/UG_TITLE=DNA segment, Chr 11, Wayne State University 68, expressed /DEF=Mus musculus 18 days embryo whole body cDNA, RIKEN full-length enriched library, clone:1110014N10.DNA segment, Chr 11, Wayne State University 68, expressed, full insert sequence	2237.9	257.32095	1627.3334	434.5673	2.0939682	3.0	0.12729448	0.37284964
gb-NM_009077.1/DB_XREF=gi6677770/GEN=Rpl18/FEA=FLmRNA/CNT=2/TID=Mm.41923.1/TIER=FL+Stack/STK=2/UG=Mm.41923 /LL=19899/DEF=Mus musculus ribosomal protein L18 (Rpl18), mRNA, /PROD=ribosomal protein L18 /FL-gb.NM_009077.1 gb-U04128.1	12883.8	2866.7754	8467.8	986.7063	2.5228121	2.0	0.12770614	0.3716576
gbAK017523.1/DB_XREF=gi12658802/FEA=mRNA/CNT=39/TID=Mm.29092.2/TIER=ConsEnd/STK=1/UG=Mm.29092.2/LL=70510 /UG_GENE=5730408C10R1K/UG_TITLE=RIKEN cDNA 5730408C10 gene /DEF=Mus musculus 8 days embryo whole body cDNA, RIKEN full- length enriched library, clone:5730408C10.C3HC4 type (RING finger) Zinc finger containing protein, full insert sequence	1612.5	484.06375	910.66675	328.9321	2.0770903	3.0	0.12936181	0.3740781
gbNM_020255.1/DB_XREF=gi9937979/GEN=SGand1/FEA=FLmRNA/CNT=74/TID=Mm.29477.1/TIER=FL+Stack/STK=34 /UG=Mm.29477.1/LL=19018/DEF=Mus musculus SCAN domain-containing 1 (Scand1), mRNA, /PROD=paroxysmal proliferative activated receptor, gamma, coactivator 1 /FL-gb-BC010724.1 gb-NM_020255.1 gb-AF106473.1 gb-AF220501.1	1806.9667	392.72913	1233.5	58.524418	2.5015333	2.0	0.1294824	0.37205702
gb-NM_017379.1/DB_XREF=gi8394492/GEN=Tuba8/FEA=FLmRNA/CNT=31/TID=Mm.32884.1/TIER=FL+Stack/STK=9/UG=Mm.32884 /LL=53857/DEF=Mus musculus tubulin, alpha 8 (Tuba8), mRNA, /PROD=tubulin, alpha 8 /FL-gb-BC017631.1 gb-NM_017379.1	3518.2668	731.5148	2430.4001	541.90027	2.069757	2.0	0.13027246	0.37197295
gbNM_008906.1/DB_XREF=gi6679436/GEN=Ppgb/FEA=FLmRNA/CNT=327/TID=Mm.7046.1/TIER=FL+Stack/STK=187/UG=Mm.7046 /LL=19025/DEF=Mus musculus protective protein for beta-galactosidase (Ppgb), mRNA, /PROD=protective protein for beta-galactosidase /FL-gb-BC016534.1 gb-U056261.1 gb-NM_008906.1	3347.4336	684.5403	2355.2668	469.90833	2.069697	3.0	0.13027996	0.3696694
gbBC025650.1/DB_XREF=gi10946971/GEN=Cope/FEA=FLmRNA/CNT=222/TID=Mm.28668.1/TIER=FL+Stack/STK=93/UG=Mm.299 /LL=1743/DEF=Mus musculus thioester S-methyltransferase (Tent), mRNA, /PROD=thioester S-methyltransferase /FL-gb.M88694.1 gb-NM_009349.1 gb-BC013518.1	6629.7007	1163.0481	4860.3335	919.62646	2.0669303	3.0	0.13062552	0.36834773
gbNM_009149.1/DB_XREF=gi6677904/GEN=Sele/FEA=FLmRNA/CNT=216/TID=Mm.488.1/TIER=FL+Stack/STK=57/UG=Mm.488 /LL=20340/DEF=Mus musculus selectin, endothelial cell, ligand (Sele), mRNA, /PROD=selectin, endothelial cell, ligand /FL-gb-NM_009149.1 gb-BC021306.1	4186.1665	1061.3314	2741.0332	597.75024	2.054902	3.0	0.13214059	0.37031993
gbAK003436.1/DB_XREF=gi12634106/GEN=Pn0b8/FEA=FLmRNA/CNT=285/TID=Mm.35812.1/TIER=FL+Stack/STK=17/UG=Mm.35812 /LL=57296/UG_TITLE=proteasome (prosome, macropain) 26S subunit, non-ATPase, 8 /DEF=Mus musculus 18 days embryo whole body cDNA, RIKEN full-length enriched library, clone:1110004L21.proteasome (prosome, macropain) 26S subunit, non-ATPase, 8, full insert sequence, /FL-gb-BC005717.1 gb-BC004075.1 gb-NM_026451.1	3733.7	823.347	2583.7334	512.53284	2.0537407	3.0	0.13228798	0.36845854
gbBC028256.1/DB_XREF=gi2389524/FEA=mRNA/CNT=19/TID=Mm.45357.2/TIER=ConsEnd/STK=0/UG=Mm.45357.2/LL=59079 /UG_GENE=ErbB2ip/DEF=Mus musculus, Similar to erbB2 interacting protein, clone IMAGE:4988135, mRNA, partial cds. /PROD=Similar to erbB2 interacting protein	1193.3667	589.4717	2155.9001	562.5233	2.0460775	3.0	0.1332654	0.36891764
gbNM_008968.1/DB_XREF=gi6679534/GEN=Ppgis/FEA=FLmRNA/CNT=85/TID=Mm.2339.1/TIER=FL+Stack/STK=38/UG=Mm.2339 /LL=19223/DEF=Mus musculus prostaglandin I2 (prostaglandin) synthase (Pgis), mRNA, /PROD=prostaglandin I2 (prostaglandin) synthase /FL-gb-AB001607.1 gb-NM_008968.1	3961.1667	958.07043	2481.9668	417.30057	2.4517064	2.0	0.13377887	0.3680946
gb-NM_008896.1/DB_XREF=gi6679416/GEN=Pon2/FEA=FLmRNA/CNT=70/TID=Mm.22681.1/TIER=FL+Stack/STK=27/UG=Mm.22681 /LL=18990/DEF=Mus musculus paraoxonase 2 (Pon2), mRNA, /PROD=paraoxonase 2 /FL-gb-L48514.1 gb-NM_008896.1	1238.8	514.217	1998.3667	390.5902	2.0373657	3.0	0.13438699	0.36754033
gbNM_025933.1/DB_XREF=gi13385425/GEN=2010110M21R1K/FEA=FLmRNA/CNT=99/TID=Mm.29353.1/TIER=FL+Stack/STK=31 /UG=Mm.29353.1/LL=67044/DEF=Mus musculus RIKEN cDNA 2010110M21 (2010110M21R1k), mRNA, /PROD=RIKEN cDNA 2010110M21 /FL-gb-NM_025933.1 gb-BC021471.1	9029.7	1679.2811	6378.6333	848.9092	2.440287	2.0	0.13479145	0.366439
gb-BC013670.1/DB_XREF=gi15489119/FEA=FLmRNA/CNT=368/TID=Mm.30074.1/TIER=FL+Stack/STK=142/UG=Mm.30074/DEF=Mus musculus, clone MGC:19042 IMAGE:4188988, mRNA, complete cds. /PROD=Unknown (protein for MGC:19042) /FL-gb-BC013670.1	9587.733	1456.2542	6396.4336	2294.6082	2.0338852	3.0	0.1348382	0.36438417
gbNM_011892.1/DB_XREF=gi6755487/GEN=SGcg/FEA=FLmRNA/CNT=12/TID=Mm.7217.3/TIER=FL+Stack/STK=2/UG=Mm.7217/3 /LL=24053/DEF=Mus musculus sarcoglycan, gamma (35kD dystrophin-associated glycoprotein) (Sgog), mRNA, /PROD=sarcoglycan, gamma (35kD dystrophin-associated glycoprotein) /FL-gb-NM_011892.1 gb-AB024922.1	3929.0	206.34653	2650.0	888.793	2.4278996	2.0	0.13590199	0.36508584
gbNM_008749.1/DB_XREF=gi6679157/GEN=Nucb/FEA=FLmRNA/CNT=332/TID=Mm.2283.1/TIER=FL+Stack/STK=64/UG=Mm.2283 /LL=8220/DEF=Mus musculus nucleobindin (Nucb), mRNA, /PROD=nucleobindin /FL-gb-NM_008749.1 gb-M58623.1	2056.5332	457.68692	1335.7333	414.98807	2.020778	3.0	0.13655357	0.36467835
gbBC024681.1/DB_XREF=gi10071462/FEA=FLmRNA/CNT=174/TID=Mm.2381.1/TIER=FL+Stack/STK=138/UG=Mm.2381 /DEF=Mus musculus, Similar to LGN protein, clone MGC:31563 IMAGE:4504055, mRNA, complete cds. /PROD=Similar to LGN protein /FL-gb-BC024681.1	1239.2333	239.45042	746.6333	348.11758	2.0193365	3.0	0.1367438	0.3630508
gbBC021463.1/DB_XREF=gi18204796/FEA=FLmRNA/CNT=46/TID=Mm.29372.1/TIER=FL+Stack/STK=27/UG=Mm.29372/LL=67675 /UG_GENE=0610039D01R1K/DEF=Mus musculus, Similar to RIKEN cDNA 0610039D01 gene, clone MGC:29169 IMAGE:5053934, mRNA, complete cds. /PROD=Similar to RIKEN cDNA 0610039D01 gene /FL-gb-BC021463.1	2120.3	536.66815	1357.9	103.11544	2.4163818	2.0	0.13694601	0.36147377
gbBC027021.1/DB_XREF=gi20071695/FEA=FLmRNA/CNT=11/TID=Mm.2857.1/TIER=FL+Stack/STK=38/UG=Mm.2857.1/LL=88463 /UG_GENE=111000611R1K/DEF=Mus musculus, RIKEN cDNA 111000611 gene, clone MGC:36524 IMAGE:5374870, mRNA, complete cds. /PROD=RIKEN cDNA 111000611 gene /FL-gb-BC027021.1	2301.3	584.0858	1471.8667	408.19916	2.0160584	3.0	0.13717754	0.35999194
gb-NM_023133.1/DB_XREF=gi12963510/GEN=Rps19/FEA=FLmRNA/CNT=72/TID=Mm.103634.1/TIER=FL+Stack/STK=17 /UG=Mm.103634.1/LL=20085/DEF=Mus musculus ribosomal protein S19 (Rps19), mRNA, /PROD=ribosomal protein S19 /FL-gb-NM_023133.1	12766.899	2580.3882	8981.033	886.1002	2.4034498	2.0	0.13813154	0.36041218
gbNM_023341.1/DB_XREF=gi12963648/GEN=4632432J1R1K/FEA=FLmRNA/CNT=129/TID=Mm.28337.1/TIER=FL+Stack/STK=58 /UG=Mm.28337.1/LL=67428/DEF=Mus musculus RIKEN cDNA 4632432J16 gene (4632432J16R1k), mRNA, /PROD=RIKEN cDNA 4632432J16 /FL-gb-NM_023341.1	7496.6665	1431.8107	5438.7334	389.1163	2.402333	2.0	0.13823459	0.35862002
gbBC006701.1/DB_XREF=gi13879559/FEA=FLmRNA/CNT=160/TID=Mm.24353.1/TIER=FL+Stack/STK=69/UG=Mm.24353.1/LL=56418 /UG_GENE=Yk6-pending /DEF=Mus musculus, prnylated SNARE protein, clone MGC:5770 IMAGE:3257673, mRNA, complete cds. /PROD=prnylated SNARE protein /FL-gb-AF076956.1 gb-NM_019661.1 gb-BC006701.1	1423.2999	314.74496	936.23334	278.5027	2.0073311	3.0	0.13834026	0.35685498
gbBM24557.2/DB_XREF=gi17880842/DB_XREF=K0726D05.3/CLONE=K0726D05/FEA=mRNA/CNT=10/TID=Mm.204648.1 /TIER=ConsEnd/STK=7/UG=Mm.204648/UG_TITLE=Mus musculus adult male kidney cDNA, RIKEN full-length enriched library, clone:0610010005 lymphocyte antigen 6 complex, locus E, full insert sequence	7878.033	2055.934	5033.4663	1347.9259	2.0044116	3.0	0.13877152	0.35594502
gbBC025450.1/DB_XREF=gi1934374/FEA=mRNA/CNT=171/TID=Mm.24463.1/TIER=Stack/STK=124/UG=Mm.24463.1/LL=70049 /UG_GENE=261004482R1K/UG_TITLE=RIKEN cDNA 2610044822 gene /DEF=Mus musculus, clone IMAGE:5345597, mRNA, complete cds. /PROD=Unknown (protein for MGC:19042) /FL-gb-BC013670.1	2023.8334	822.1557	3157.9336	534.31946	2.0033257	3.0	0.1388778	0.3542164
gbBC00562.1/DB_XREF=gi13542843/FEA=FLmRNA/CNT=178/TID=Mm.29097.1/TIER=FL+Stack/STK=27/UG=Mm.29097 /LL=110829/UG_GENE=Lims1/DEF=Mus musculus, RIKEN cDNA 4921524A02 gene, clone MGC:11585 IMAGE:3711611, mRNA, complete cds. /PROD=RIKEN cDNA 4921524A02 gene /FL-gb-NM_026148.1 gb-BC00562.1	3386.3333	739.64	2136.9666	790.78	1.9985387	3.0	0.13952343	0.35387507
gbNM_007752.1/DB_XREF=gi6680996/GEN=Cp/FEA=FLmRNA/CNT=332/TID=Mm.13787.1/TIER=FL+Stack/STK=43/UG=Mm.13787 /LL=12870/DEF=Mus musculus ceruloplasmin (Cp), mRNA, /PROD=ceruloplasmin /FL-gb-U49430.1 gb-NM_007752.1	4454.0	455.7452	2840.6335	1083.2803	2.3777456	2.0	0.14053063	0.35444948
gb-NM_019966.1/DB_XREF=gi9910433/GEN=Mlycd/FEA=FLmRNA/CNT=83/TID=Mm.20260.1/TIER=FL+Stack/STK=3/UG=Mm.20260 /LL=56690/DEF=Mus musculus malonyl-CoA decarboxylase (Mlycd), mRNA, /PROD=malonyl-CoA decarboxylase /FL-gb-NM_019966.1	1357.1666	386.15103	839.89996	232.48802	1.9877075	2.0	0.14099741	0.353662
gbBC027285.1/DB_XREF=gi20071022/FEA=FLmRNA/CNT=65/TID=Mm.175681.1/TIER=FL+Stack/STK=42/UG=Mm.175681 /LL=68713/UG_GENE=1110036C17R1K/DEF=Mus musculus, Similar to RIKEN cDNA 1110036C17 gene, clone MGC:27862 IMAGE:332212, mRNA, complete cds. /PROD=Similar to RIKEN cDNA 1110036C17 gene /FL-gb-BC027285.1	1052.9667	369.74796	534.93335	259.89047	1.9853188	3.0	0.14132495	0.35253587
gbAK019396.1/DB_XREF=gi12859581/FEA=mRNA/CNT=68/TID=Mm.44226.2/TIER=Stack/STK=38/UG=Mm.44226.2/LL=68066 /UG_GENE=3010027G13R1K/UG_TITLE=RIKEN cDNA 3010027G13 gene /DEF=Mus musculus 12 days embryo head cDNA, R								

gbNM_016763.1/DB_XREF=gi:7949046/GEN=Hsd17b10/FEA=FLmRNA/CNT=195/7/ID=Mm.6994.1/7/IER=FL+Stack/STK=101/UG=Mm.6994/LL=15108/DEF=Mus musculus hydroxysteroid (17-beta) dehydrogenase 10 (Hsd17b10), mRNA, /PROD=hydroxysteroid (17-beta) dehydrogenase 10 /FL=gb:AF233585.1 gb:NM_016763.1 gb:UgNM_013620.1	7606.8335	1108.047	5424.6333	1571.2577	1.9658613	3.0	0.14402652	0.35344887
gbNM_009739.1/DB_XREF=gi:7331587/GEN=Hsd17b10/FEA=FLmRNA/CNT=129/7/ID=Mm.8903.1/7/IER=FL+Stack/STK=88/UG=Mm.8903/LL=12041/DEF=Mus musculus branched chain ketoacid dehydrogenase kinase (Bckdk), mRNA, /PROD=branched chain keto acid dehydrogenase kinase /FL=gb:AF043070.1 gb:NM_009739.1	1531.5	364.39032	1027.8334	89.51983	2.3249393	2.0	0.14564368	0.35549587
gbNM_030561.1/DB_XREF=gi:13385411/GEN=BC004004/FEA=FLmRNA/CNT=146/7/ID=Mm.25308.1/7/IER=FL+Stack/STK=78/UG=Mm.25308/LL=80748/DEF=Mus musculus hypothetical protein, MGC:7550 (BC004004), mRNA, /PROD=hypothetical protein MGC7550 /FL=gb:BC004004.1 gb:NM_030561.1	7795.6333	1556.6836	5527.3667	672.38983	2.3169024	2.0	0.14644434	0.35553867
gbNM_013602.7/DB_XREF=gi:7305284/GEN=MIT/FEA=FLmRNA/CNT=145/7/ID=Mm.219629.1/7/IER=FL+Stack/STK=36/UG=Mm.219629/LL=17748/DEF=Mus musculus mitogen-activated protein kinase 1 (Mit1), mRNA, /PROD=mitogen-activated protein kinase 1 /FL=gb:U03620.1	11612.833	3314.8948	7316.1665	1936.7217	1.9384388	3.0	0.14793773	0.35725388
gbU13884.1/DB_XREF=gi:124782/GEN=Hsd17b10/FEA=FLmRNA/CNT=37/ID=Mm.444.2/7/IER=FL+Stack/STK=1/UG=Mm.444/LL=15901/DEF=Mus musculus transcription factor IIdB (IIdB), mRNA, complete cds, /PROD=IIdB /FL=gb:U43884.1	1394.6	364.95178	889.7	273.0372	1.9186989	3.0	0.15083033	0.36231202
gbBC026751.1/DB_XREF=gi:20071192/FEA=FLmRNA/CNT=36/7/ID=Mm.41486.1/7/IER=FL+Stack/STK=1/UG=Mm.41486/LL=70103/UG_GENE=2700001K05Rf/DEF=Mus musculus, Similar to putative cyclin G1 interacting protein, clone MGC:3153902, mRNA, complete cds, /PROD=Similar to putative cyclin G1 interacting protein /FL=gb:BC026751.1	1355.3667	312.11258	905.0999	262.02222	1.9137493	3.0	0.15156595	0.36216286
gbBC025071.1/DB_XREF=gi:19264072/FEA=FLmRNA/CNT=132/7/ID=Mm.2875.2/7/IER=FL+Stack/STK=58/UG=Mm.2875/LL=66855/UG_GENE=1100001J13Rf/DEF=Mus musculus, Similar to RIKEN cDNA 1100001J13 gene, clone MGC:36794 IMAGE:3498003, mRNA, complete cds, /PROD=Similar to RIKEN cDNA 1100001J13 gene /FL=gb:BC025071.1	2475.1667	329.6616	1750.5	568.4756	1.9100156	3.0	0.15212366	0.36159238
gbNM_024227.1/DB_XREF=gi:13195649/GEN=1110015G04Rf/FEA=FLmRNA/CNT=160/7/ID=Mm.27332.1/7/IER=FL+Stack/STK=102/UG=Mm.27332/LL=68611/DEF=Mus musculus RIKEN cDNA 1110015G04 gene (1110015G04Rf), mRNA, /PROD=RIKEN cDNA 1110015G04 /FL=gb:NM_024227.1 gb:BC002293.1 gb:BC005797.1	4231.767	809.5277	3110.2998	290.3462	2.2585943	2.0	0.15243916	0.3604551
gbBC024610.1/DB_XREF=gi:19354311/FEA=FLmRNA/CNT=39/7/ID=Mm.46628.2/7/IER=FL+Stack/STK=21/UG=Mm.46628/LL=22344/UG_GENE=Vedf1/DEF=Mus musculus, vascular endothelial zinc finger 1, clone MGC:28455 IMAGE:4159675, mRNA, complete cds, /PROD=vascular endothelial zinc finger 1 /FL=gb:BC024610.1	1260.9	340.7898	789.93335	122.7772	2.251978	2.0	0.15314065	0.3602376
gbAK011360.1/DB_XREF=gi:12847432/FEA=mRNA/CNT=64/7/ID=Mm.142187.1/7/IER=Stack/STK=24/UG=Mm.142187/LL=69202/UG_GENE=2610009E16Rf/UG_TITLE=RIKEN cDNA 2610009E16 gene/DEF=Mus musculus 10 days embryo whole body cDNA, RIKEN full-length enriched library, clone:2610009E16.homolog to PARATHYMOXIN (ZINC-BINDING 11.5 KDA PROTEIN), full insert sequence.	3908.8	1215.2148	2384.5	673.47577	1.9002765	3.0	0.15358968	0.35943154
gbAK007208.1/DB_XREF=gi:12840620/GEN=Cappb1/FEA=mRNA/CNT=27/7/ID=Mm.2945.3/7/IER=ConsEnd/STK=1/UG=Mm.2945/LL=12345/UG_TITLE=capping protein beta 1 /DEF=Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:1700120C01.capping protein beta 1, full insert sequence.	3347.5	1118.8156	1890.4668	725.1011	1.892879	3.0	0.15471424	0.36020648
gbBC026137.1/DB_XREF=gi:20071192/FEA=FLmRNA/CNT=36/7/ID=Mm.2875.2/7/IER=FL+Stack/STK=58/UG=Mm.2875/LL=66855/UG_GENE=2700001K05Rf/DEF=Mus musculus, Similar to putative cyclin G1 interacting protein, clone MGC:3153902, mRNA, complete cds, /PROD=Unknown (protein for MGC:41260)	2423.5	500.8672	1659.0332	496.18042	1.8780776	3.0	0.15699328	0.36364773
gbBC007140.1/DB_XREF=gi:1938048/FEA=FLmRNA/CNT=129/7/ID=Mm.219663.2/7/IER=FL+Stack/STK=107/UG=Mm.219663/LL=14114/UG_GENE=Fbln1/DEF=Mus musculus, Similar to fibulin 1, clone MGC:6128 IMAGE:3495754, mRNA, complete cds, /PROD=Similar to fibulin 1 /FL=gb:BC007140.1	2261.4333	914.7857	1040.7667	275.78848	2.2128296	2.0	0.15738344	0.3627009
gbNM_019932.1/DB_XREF=gi:9910485/GEN=PH4/FEA=FLmRNA/CNT=47/7/ID=Mm.23905.1/7/IER=FL+Stack/STK=28/UG=Mm.23905/LL=56744/DEF=Mus musculus platelet factor 4 (PF4), mRNA, /PROD=platelet factor 4 /FL=gb:AB01491.2 gb:NM_019932.1	3736.8665	923.7606	2606.4666	488.46692	1.8736765	3.0	0.15767846	0.36154556
gbNM_010312.1/DB_XREF=gi:13337390/GEN=Gnb2/FEA=FLmRNA/CNT=387/7/ID=Mm.30141.1/7/IER=FL+Stack/STK=141/UG=Mm.30141/LL=14693/DEF=Mus musculus guanine nucleotide binding protein, beta 2 (Gnb2), mRNA, /PROD=guanine nucleotide-binding protein, beta-2subunit /FL=gb:U34960.1 gb:NM_010312.1	1156.7001	482.16302	477.7333	227.77388	2.2053285	2.0	0.15821478	0.3609523
gbNM_011797.1/DB_XREF=gi:8753263/GEN=Car14/FEA=FLmRNA/CNT=541/7/ID=Mm.34556.1/7/IER=FL+Stack/STK=16/UG=Mm.34556/LL=123831/DEF=Mus musculus carbonic anhydrase 14 (Car14), mRNA, /PROD=carbonic anhydrase 14 /FL=gb:NM_011797.1 gb:AB005450.1	1273.2001	392.50107	750.2666	284.58118	1.8682411	3.0	0.15852948	0.3598619
gbNM_008081.1/DB_XREF=gi:12835132/FEA=mRNA/CNT=542/7/ID=Mm.29458.1/7/IER=Stack/STK=17/UG=Mm.29458/LL=68748/UG_GENE=1110034G11Rf/UG_TITLE=RIKEN cDNA 1110034G11 gene/DEF=Mus musculus 18 days embryo whole body cDNA, RIKEN full-length enriched library, clone:1110034G11.related to CG12379 PROTEIN, full insert sequence.	2279.8	659.10315	1438.1333	63.327145	2.2016687	2.0	0.15862256	0.3582818
gbU16321.1/DB_XREF=gi:1185384/FEA=FLmRNA/CNT=80/7/ID=Mm.4269.2/7/IER=FL+Stack/STK=55/UG=Mm.4269/LL=21413/UG_GENE=Tcf4/DEF=Mus musculus basic transcription factor MITF-2A mRNA, complete cds, /PROD=MITF-2A protein /FL=gb:U16321.1 gb:BC014293.1	1709.9332	440.62988	1114.2999	333.23102	1.8675402	3.0	0.15865374	0.3565782
gbAF332085.1/DB_XREF=gi:14193736/GEN=Rad21/FEA=FLmRNA/CNT=282/7/ID=Mm.182628.1/7/IER=FL+Stack/STK=2/UG=Mm.182628/LL=18597/DEF=Mus musculus strain ISS Rad21 (Rad21), mRNA, complete cds, /PROD=Rad21 /FL=gb:AF332086.1 gb:AF332085.1	823.76666	335.08176	380.09998	241.96138	1.8592664	3.0	0.15994632	0.35771248
gbNM_133739.1/DB_XREF=gi:19526937/GEN=2310075C12Rf/FEA=FLmRNA/CNT=150/7/ID=Mm.148516.1/7/IER=FL+Stack/STK=52/UG=Mm.148516/LL=71929/DEF=Mus musculus RIKEN cDNA 2310075C12 gene (2310075C12Rf), mRNA, /PROD=RIKEN cDNA 2310075C12 /FL=gb:NM_133739.1	797.3333	489.41528	1390.7999	263.78073	1.8488518	3.0	0.16160896	0.35965917
gbBC004829.1/DB_XREF=gi:13435995/FEA=FLmRNA/CNT=206/7/ID=Mm.2079.1/7/IER=FL+Stack/STK=57/UG=Mm.2079/LL=20973/UG_GENE=Syngr2/DEF=Mus musculus, synaptogyrin 2, clone MGC:6483 IMAGE:2646657, mRNA, complete cds, /PROD=synaptogyrin 2 /FL=gb:AF364049.1 gb:BC004829.1 gb:AF11985.1 gb:NM_009304.1	1566.0868	384.5148	1058.5	310.58392	1.8486891	3.0	0.1616351	0.3579626
gbNM_026468.1/DB_XREF=gi:13385699/GEN=Atf7/FEA=FLmRNA/CNT=334/7/ID=Mm.10314.1/7/IER=FL+Stack/STK=154/UG=Mm.10314/LL=67942/DEF=Mus musculus ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 2 (Atf5g2), mRNA, /PROD=ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 2 /FL=gb:NM_026468.1 gb:BC006813.1	13885.966	3905.741	8379.966	1993.4896	2.1748064	2.0	0.16166022	0.3562803
gbNM_019719.1/DB_XREF=gi:9789906/GEN=Stub1/FEA=FLmRNA/CNT=166/7/ID=Mm.29000.1/7/IER=FL+Stack/STK=80/UG=Mm.29000/LL=56424/DEF=Mus musculus STP1 homology and U-Box containing protein 1 (Stub1), mRNA, /PROD=STP1 homology and U-Box containing protein 1 /FL=gb:NM_019719.1 gb:AF129086.1	4352.6333	730.2896	3130.9333	883.24316	1.8463746	3.0	0.16200738	0.35532054
gbBC026760.1/DB_XREF=gi:20071192/FEA=FLmRNA/CNT=36/7/ID=Mm.2875.2/7/IER=FL+Stack/STK=58/UG=Mm.2875/LL=66855/UG_GENE=Myfn1/DEF=Mus musculus, clone MGC:25573 IMAGE:3990090, mRNA, complete cds, /PROD=Unknown (protein for MGC:25573) /FL=gb:BC026760.1	10349.899	2328.1802	7504.567	1345.0183	1.8329034	3.0	0.16419399	0.35838494
gbNM_010347.1/DB_XREF=gi:8679089/GEN=Nos3/FEA=FLmRNA/CNT=49/7/ID=Mm.12837.1/7/IER=FL+Stack/STK=25/UG=Mm.12837/LL=18127/DEF=Mus musculus nitric oxide synthase 3, endothelial cell (Nos3), mRNA, /PROD=nitric oxide synthase 3, endothelial cell /FL=gb:U53142.1 gb:NM_008713.1	1535.2333	382.03305	1020.6995	303.48578	1.8265747	3.0	0.16523309	0.3589274
gbNM_010347.1/DB_XREF=gi:8679089/GEN=Nos3/FEA=FLmRNA/CNT=49/7/ID=Mm.12837.1/7/IER=FL+Stack/STK=25/UG=Mm.12837/LL=18127/DEF=Mus musculus nitric oxide synthase 3, endothelial cell (Nos3), mRNA, /PROD=nitric oxide synthase 3, endothelial cell /FL=gb:U53142.1 gb:NM_008713.1	1535.2333	382.03305	1020.6995	303.48578	1.8265747	3.0	0.16523309	0.3589274
gbNM_010347.1/DB_XREF=gi:8679089/GEN=Nos3/FEA=FLmRNA/CNT=49/7/ID=Mm.12837.1/7/IER=FL+Stack/STK=25/UG=Mm.12837/LL=18127/DEF=Mus musculus nitric oxide synthase 3, endothelial cell (Nos3), mRNA, /PROD=nitric oxide synthase 3, endothelial cell /FL=gb:U53142.1 gb:NM_008713.1	1535.2333	382.03305	1020.6995	303.48578	1.8265747	3.0	0.16523309	0.3589274
gbNM_010347.1/DB_XREF=gi:8679089/GEN=Nos3/FEA=FLmRNA/CNT=49/7/ID=Mm.12837.1/7/IER=FL+Stack/STK=25/UG=Mm.12837/LL=18127/DEF=Mus musculus nitric oxide synthase 3, endothelial cell (Nos3), mRNA, /PROD=nitric oxide synthase 3, endothelial cell /FL=gb:U53142.1 gb:NM_008713.1	1535.2333	382.03305	1020.6995	303.48578	1.8265747	3.0	0.16523309	0.3589274
gbNM_010347.1/DB_XREF=gi:8679089/GEN=Nos3/FEA=FLmRNA/CNT=49/7/ID=Mm.12837.1/7/IER=FL+Stack/STK=25/UG=Mm.12837/LL=18127/DEF=Mus musculus nitric oxide synthase 3, endothelial cell (Nos3), mRNA, /PROD=nitric oxide synthase 3, endothelial cell /FL=gb:U53142.1 gb:NM_008713.1	1535.2333	382.03305	1020.6995	303.48578	1.8265747	3.0	0.16523309	0.3589274
gbNM_010347.1/DB_XREF=gi:8679089/GEN=Nos3/FEA=FLmRNA/CNT=49/7/ID=Mm.12837.1/7/IER=FL+Stack/STK=25/UG=Mm.12837/LL=18127/DEF=Mus musculus nitric oxide synthase 3, endothelial cell (Nos3), mRNA, /PROD=nitric oxide synthase 3, endothelial cell /FL=gb:U53142.1 gb:NM_008713.1	1535.2333	382.03305	1020.6995	303.48578	1.8265747	3.0	0.16523309	0.3589274
gbNM_010347.1/DB_XREF=gi:8679089/GEN=Nos3/FEA=FLmRNA/CNT=49/7/ID=Mm.12837.1/7/IER=FL+Stack/STK=25/UG=Mm.12837/LL=18127/DEF=Mus musculus nitric oxide synthase 3, endothelial cell (Nos3), mRNA, /PROD=nitric oxide synthase 3, endothelial cell /FL=gb:U53142.1 gb:NM_008713.1	1535.2333	382.03305	1020.6995	303.48578	1.8265747	3.0	0.16523309	0.3589274
gbNM_010347.1/DB_XREF=gi:8679089/GEN=Nos3/FEA=FLmRNA/CNT=49/7/ID=Mm.12837.1/7/IER=FL+Stack/STK=25/UG=Mm.12837/LL=18127/DEF=Mus musculus nitric oxide synthase 3, endothelial cell (Nos3), mRNA, /PROD=nitric oxide synthase 3, endothelial cell /FL=gb:U53142.1 gb:NM_008713.1	1535.2333	382.03305	1020.6995	303.48578	1.8265747	3.0	0.16523309	0.3589274
gbNM_010347.1/DB_XREF=gi:8679089/GEN=Nos3/FEA=FLmRNA/CNT=49/7/ID=Mm.12837.1/7/IER=FL+Stack/STK=25/UG=Mm.12837/LL=18127/DEF=Mus musculus nitric oxide synthase 3, endothelial cell (Nos3), mRNA, /PROD=nitric oxide synthase 3, endothelial cell /FL=gb:U53142.1 gb:NM_008713.1	1535.2333	382.03305	1020.6995	303.48578	1.8265747	3.0	0.16523309	0.3589274
gbNM_010347.1/DB_XREF=gi:8679089/GEN=Nos3/FEA=FLmRNA/CNT=49/7/ID=Mm.12837.1/7/IER=FL+Stack/STK=25/UG=Mm.12837/LL=18127/DEF=Mus musculus nitric oxide synthase 3, endothelial cell (Nos3), mRNA, /PROD=nitric oxide synthase 3, endothelial cell /FL=gb:U53142.1 gb:NM_008713.1	1535.2333	382.03305	1020.6995	303.48578	1.8265747	3.0	0.16523309	0.3589274
gbNM_010347.1/DB_XREF=gi:8679089/GEN=Nos3/FEA=FLmRNA/CNT=49/7/ID=Mm.12837.1/7/IER=FL+Stack/STK=25/UG=Mm.12837/LL=18127/DEF=Mus musculus nitric oxide synthase 3, endothelial cell (Nos3), mRNA, /PROD=nitric oxide synthase 3, endothelial cell /FL=gb:U53142.1 gb:NM_008713.1	1535.2333	382.03305	1020.6995	303.48578	1.8265747	3.0	0.16523309	0.3589274
gbNM_010347.1/DB_XREF=gi:8679089/GEN=Nos3/FEA=FLmRNA/CNT=49/7/ID=Mm.12837.1/7/IER=FL+Stack/STK=25/UG=Mm.12837/LL=18127/DEF=Mus musculus nitric oxide synthase 3, endothelial cell (Nos3), mRNA, /PROD=nitric oxide synthase 3, endothelial cell /FL=gb:U53142.1 gb:NM_008713.1	1535.2333	382.03305	1020.6995	303.48578	1.8265747	3.0	0.16523309	0.3589274
gbNM_010347.1/DB_XREF=gi:8679089/GEN=Nos3/FEA=FLmRNA/CNT=49/7/ID=Mm.12837.1/7/IER=FL+Stack/STK=25/UG=Mm.12837/LL=18127/DEF=Mus musculus nitric oxide synthase 3, endothelial cell (Nos3), mRNA, /PROD=nitric oxide synthase 3, endothelial cell /FL=gb:U53142.1 gb:NM_008713.1	1535.2333	382.03305	1020.6995	303.48578	1.8265747	3.0	0.16523309	0.3589274
gbNM_010347.1/DB_XREF=gi:8679089/GEN=Nos3/FEA=FLmRNA/CNT=49/7/ID=Mm.12837.1/7/IER=FL+Stack/STK=25/UG=Mm.12837/LL=18127/DEF=Mus musculus nitric oxide synthase 3, endothelial cell (Nos3), mRNA, /PROD=nitric oxide synthase 3, endothelial cell /FL=gb:U53142.1 gb:NM_008713.1	1535.2333	382.03305	1020.6995	303.48578	1.8265747	3.0	0.16523309	0.3589274
gbNM_010347.1/DB_XREF=gi:8679089/GEN=Nos3/FEA=FLmRNA/CNT=49/7/ID=Mm.12837.1/7/IER=FL+Stack/STK=25/UG=Mm.12837/LL=18127/DEF=Mus musculus nitric oxide synthase 3, endothelial cell (Nos3), mRNA, /PROD=nitric oxide synthase 3, endothelial cell /FL=gb:U53142.1 gb:NM_008713.1	1535.2333	382.03305	1020.6995	303.48578	1.8265747	3.0	0.16523309	0.3589274
gbNM_010347.1/DB_XREF=gi:8679089/GEN=Nos3/FEA=FLmRNA/CNT=49/7/ID=Mm.12837.1/7/IER=FL+Stack/STK=25/UG=Mm.12837/LL=18127/DEF=Mus musculus nitric oxide synthase 3, endothelial cell (Nos3), mRNA, /PROD=nitric oxide synthase 3, endothelial cell /FL=gb:U53142.1 gb:NM_008713.1	1535.2333	382.03305	1020.6995	303.48578	1.8265747	3.0	0.16523309	0.3589274
gbNM_010347.1/DB_XREF=gi:8679089/GEN=Nos3/FEA=FLmRNA/CNT=49/7/ID=Mm.12837.1/7/IER=FL+Stack/STK=25/UG=Mm.12837/LL=18127/DEF=Mus musculus nitric oxide synthase 3, endothelial cell (Nos3), mRNA, /PROD=nitric oxide synthase 3, endothelial cell /FL=gb:U53142.1 gb:NM_008713.1	1535.2333	382.03305	1020.6995	303.48578	1.8265747	3.0	0.16523309	0.3589274
gbNM_010347.1/DB_XREF=gi:8679089/GEN=Nos3/FEA=FLmRNA/CNT=49/7/ID=Mm.12837.1/7/IER=FL+Stack/STK=25/UG=Mm.12837/LL=18127/DEF=Mus musculus nitric oxide synthase 3, endothelial cell (Nos3), mRNA, /PROD=nitric oxide synthase 3, endothelial cell /FL=gb:U53142.1 gb:NM_008713.1	1535.2333	382.03305	1020.6995	303.48578	1.8265747	3.0	0.16523309	0.3589274
gbNM_010347.1/DB_XREF=gi:8679089/GEN=Nos3/FEA=FLmRNA/CNT=49/7/ID=Mm.12837.1/7/IER=FL+Stack/STK=25/UG=Mm.12837/LL=18127/DEF=Mus musculus nitric oxide synthase 3, endothelial cell (Nos3), mRNA, /PROD=nitric oxide synthase 3, endothelial cell /FL=gb:U53142.1 gb:NM_008713.1	1535.2333	382.03305	1020.6995	303.48578	1.8265747	3.0	0.16523309	0.3589274
gbNM_010347.1/DB_XREF=gi:8679089/GEN=Nos3/FEA=FLmRNA/CNT=49/7/ID=Mm.12837.1/7/IER=FL+Stack/STK=25/UG=Mm.12837/LL=18127/DEF=Mus musculus nitric oxide synthase 3, endothelial cell (Nos3), mRNA, /PROD=nitric oxide synthase 3, endothelial cell /FL=gb:U53142.1 gb:NM_008713.1	1535.2333	382.03305	1020.6995	303.48578	1.8265747	3.0	0.16523309	0.3589274
gbNM_010347.1/DB_XREF=gi:8679089/GEN=Nos3/FEA=FLmRNA/CNT=49/7/ID=Mm.12837.1/7/IER=FL+Stack/STK=25/UG=Mm.12837/LL=18127/DEF=Mus musculus nitric oxide synthase 3, endothelial cell (Nos3), mRNA, /PROD=nitric oxide synthase 3, endothelial cell /FL=gb:U53142.1 gb:NM_008713.1	1535.2333	382.03305	1020.6995	303.48578	1.8265747	3.0	0.16523309	0.3589274
gbNM_010347.1/DB_XREF=gi:8679089/GEN=Nos3/FEA=FLmRNA/CNT=49/7/ID=Mm.12837.1/7/IER=FL+Stack/STK=25/UG=Mm.12837/LL=18127/DEF=Mus musculus nitric oxide synthase 3, endothelial cell (Nos3), mRNA, /PROD=nit								

[illegible]

gbNM_011072.1/DB_XREF=gi 8755039/ GEN=Prl1/FEA=FLmRNA/CNT=168/7/ID=Mm.2647.1/7/IER=FL+Stack/STK=26/UG=Mm.2647/LL=18643/DEF=Mus musculus profilin 1 (Prl1), mRNA, /PROD=profilin 1 /FL=gb:BC002080.1 gbNM_011072.1	1880.2666	486.36215	1148.6666	624.1759	1.6013907	3.0	0.20760737	0.33782706
gbBC019131.1/DB_XREF=gi 7512319/FEA=FLmRNA/CNT=897/ID=Mm.7694.1/7/IER=FL+Stack/STK=38/UG=Mm.7694/LL=68864/LL=13894/DEF=Mus musculus, clone MGC-29165 IMAGE 5036749, mRNA, complete cds. /PROD=Unknown (protein for MGC-29165) /FL=gb:BC019131.1	1780.6666	942.588	2963.0667	868.2394	1.5980754	3.0	0.20831712	0.33777133
gbNM_025650.1/DB_XREF=gi 13385111/GEN=07/1008090R/FEA=FLmRNA/CNT=200/7/ID=Mm.43162.1/7/IER=FL+Stack/STK=100/UG=Mm.43162/LL=66594/DEF=Mus musculus RIKEN cDNA 071008090R (071008090R), mRNA, /PROD=RIKEN cDNA 071008090R /FL=gbNM_025650.1	17802.533	6000.5195	10966.7	2426.666	1.8292425	2.0	0.20886318	0.33745155
gbNM_023119.1/DB_XREF=gi 12963490/GEN=Eno1/FEA=FLmRNA/CNT=270/7/ID=Mm.90587.1/7/IER=FL+Stack/STK=14/UG=Mm.90587/LL=13806/DEF=Mus musculus enolase 1, alpha non-neuron (Eno1), mRNA, /PROD=enolase 1, alpha non-neuron (FL=gb:BC024844.1 gbNM_023119.1) /FL=gb:BC024844.1 gbNM_023119.1	6644.033	2078.6033	4233.8335	1600.5298	1.5912825	3.0	0.20977983	0.33773065
gbBC016534.1/DB_XREF=gi 16741429/FEA=FLmRNA/CNT=237/ID=Mm.144899.2/7/IER=FL+Stack/STK=8/UG=Mm.144899.2/LL=56409/UG_GENE=Nud3/DEF=Mus musculus, nudix (nucleotide diphosphate linked moiety X)-type motif 3, clone MGC-28998 IMAGE 2615904, mRNA, complete cds. /PROD=nudix (nucleotide diphosphate linked moiety X)-type motif 3 /FL=gb:BC016534.1	4924.8003	1210.6158	3560.6335	466.26718	1.8213212	3.0	0.21015003	0.33713117
gbNM_007751.1/DB_XREF=gi 6880994/GEN=Cox8b/FEA=FLmRNA/CNT=27/7/ID=Mm.3841.1/7/IER=FL+Stack/STK=18/UG=Mm.3841/LL=12869/DEF=Mus musculus cytochrome c oxidase, subunit VIIIb (Cox8b), mRNA, /PROD=cytochrome c oxidase, subunit VIIIb /FL=gb:U15541.1 gbNM_007751.1	30768.635	9435.1045	20126.934	3702.992	1.8185111	2.0	0.21060908	0.33667788
gbAJ002587.1/DB_XREF=gi 2598561/FEA=mRNA/CNT=14/7/ID=Mm.918.2/7/IER=ConsEnd/STK=0/UG=Mm.918/LL=14828/UG_GENE=Hspas/DEF=Mus musculus mRNA for Hsp, /PROD=Hsp	3538.3337	1849.5023	5593.8667	464.41464	1.8179885	2.0	0.2106946	0.3356328
gbNM_017608.1/DB_XREF=gi 7949157/FEA=FLmRNA/CNT=113/7/ID=Mm.12914.1/7/IER=FL+Stack/STK=54/UG=Mm.12914/LL=53376/DEF=Mus musculus ubiquitin specific protease 2 (Usp2), mRNA, /PROD=ubiquitin-specific protease 2 /FL=gbNM_016808.1 gbNM_017608.1	3728.6335	542.1459	2686.4001	1003.7924	1.5823406	3.0	0.21172279	0.33609143
gbNM_007899.1/DB_XREF=gi 6681256/GEN=Ecm1/FEA=FLmRNA/CNT=126/7/ID=Mm.3433.1/7/IER=FL+Stack/STK=53/UG=Mm.3433/LL=13601/DEF=Mus musculus extracellular matrix protein 1 (Ecm1), mRNA, /PROD=extracellular matrix protein 1 /FL=gbNM_007899.1 gb133416.1	2801.5664	1210.8658	1481.3999	358.34644	1.8107661	2.0	0.21188116	0.3351709
gbAK002681.1/DB_XREF=gi 12832810/FEA=mRNA/CNT=777/ID=Mm.27395.1/7/IER=Stack/STK=34/UG=Mm.27395/LL=76263/UG_GENE=061002519R/UG_TITLE=RIKEN cDNA 061002519 gene /DEF=Mus musculus adult male kidney cDNA, RIKEN full-length enriched library, clone 061002519 homolog to GLUTATHIONE S-TRANSFERASE, MITOCHONDRIAL (EC 2.5.1.18) (GST 13-13) (GLUTATHIONE S-TRANSFERASE SUBUNIT 13) (GST CLASS-KAPPA) (HDCMD47P), full insert...	3342.1003	954.06024	2284.0	660.2486	1.5795715	3.0	0.21232854	0.33471236
gbNM_053122.1/DB_XREF=gi 1674620/GEN=Imp2/DEF=Mus musculus inner mitochondrial membrane peptidase 2-like (S. cerevisiae) (Imp2), mRNA, /PROD=inner mitochondrial membrane peptidase 2-like (S. cerevisiae) /FL=gb:AF359564.1 gbNM_053122.1	1377.0668	475.85724	873.3333	85.10619	1.8048774	3.0	0.21285515	0.33438143
gbBM235840/DB_XREF=gi 7871110/DB_XREF=gi K04260C63/CLONE=K04260C6/FEA=mRNA/CNT=147/7/ID=Mm.159813.1/7/IER=Stack/STK=11/UG=Mm.159813.1/UG_GENE=Usp2/DEF=Mus musculus, clone IMAGE 5102112, mRNA, partial cds.	1349.6	955.2317	2434.4333	712.7231	1.5765651	3.0	0.21298838	0.33343697
gbAK018713.1/DB_XREF=gi 12858581/GEN=Cyba/FEA=mRNA/CNT=17/ID=Mm.448.2/7/IER=ConsEnd/STK=0/UG=Mm.448/UG_GENE=Nud3/DEF=Mus musculus, nudix (nucleotide diphosphate linked moiety X)-type motif 3, clone MGC-28998 IMAGE 2615904, mRNA, complete cds. /PROD=nudix (nucleotide diphosphate linked moiety X)-type motif 3 /FL=gb:BC016534.1	1930.9332	586.1127	1270.2334	430.65775	1.5734007	3.0	0.21368538	0.33337855
gbNM_011722.1/DB_XREF=gi 8756008/GEN=Dnab6/FEA=FLmRNA/CNT=129/7/ID=Mm.90496.1/7/IER=FL+Stack/STK=85/UG=Mm.90496/LL=22428/DEF=Mus musculus dynactin 6 (Dnab6), mRNA, /PROD=dynactin 6 /FL=gb:AF124788.1 gbNM_011722.1	1629.3002	83.222305	1194.2333	410.49402	1.7991323	2.0	0.21381108	0.3324323
gbAF10796.1/DB_XREF=gi 12857270/GEN=Dnab6/FEA=FLmRNA/CNT=129/7/ID=Mm.90496.1/7/IER=FL+Stack/STK=85/UG=Mm.90496/LL=22428/DEF=Mus musculus dynactin 6 (Dnab6), mRNA, /PROD=dynactin 6 /FL=gb:AF124788.1 gbNM_011722.1	1629.3002	83.222305	1194.2333	410.49402	1.7991323	2.0	0.21381108	0.3324323
gbNM_017622.1/DB_XREF=gi 12857270/GEN=Dnab6/FEA=FLmRNA/CNT=129/7/ID=Mm.90496.1/7/IER=FL+Stack/STK=85/UG=Mm.90496/LL=22428/DEF=Mus musculus dynactin 6 (Dnab6), mRNA, /PROD=dynactin 6 /FL=gb:AF124788.1 gbNM_011722.1	1629.3002	83.222305	1194.2333	410.49402	1.7991323	2.0	0.21381108	0.3324323
gbNM_025650.1/DB_XREF=gi 13384929/GEN=2310008M10R/FEA=FLmRNA/CNT=192/7/ID=Mm.3811.1/7/IER=FL+Stack/STK=21/UG=Mm.3811/LL=66357/DEF=Mus musculus RIKEN cDNA 2310008M10 (2310008M10R), mRNA, /PROD=RIKEN cDNA 2310008M10 /FL=gb:BC021935.1 gbNM_025650.1	1907.1666	421.60797	1362.2667	432.72708	1.5621666	3.0	0.21618043	0.33382964
gbNM_007931.1/DB_XREF=gi 6679546/GEN=Eno3/FEA=FLmRNA/CNT=217/ID=Mm.4449.1/7/IER=FL+Stack/STK=2/UG=Mm.4449/LL=13806/DEF=Mus musculus enolase 3, alpha non-neuron (Eno3), mRNA, /PROD=enolase 3, alpha non-neuron (FL=gb:BC024844.1 gbNM_007931.1) /FL=gb:BC024844.1 gbNM_007931.1	2059.8667	481.12747	1506.5333	383.07217	1.5583705	3.0	0.21703082	0.33400676
gbBC025821.1/DB_XREF=gi 20070721/FEA=FLmRNA/CNT=85/ID=Mm.87433.1/7/IER=FL+Stack/STK=33/UG=Mm.87433/LL=16649/UG_GENE=Kpnal/DEF=Mus musculus, karyopherin (importin) alpha 4, clone MGC-19244 IMAGE 3672708, mRNA, complete cds. /PROD=karyopherin (importin) alpha 4 /FL=gb:AF020771.1 gbNM_008467.1 gbBC025821.1	4096.9004	875.8401	6336.9	2006.1893	1.7723727	2.0	0.21833913	0.33488503
gbNM_011722.1/DB_XREF=gi 12857270/GEN=Dnab6/FEA=FLmRNA/CNT=129/7/ID=Mm.90496.1/7/IER=FL+Stack/STK=85/UG=Mm.90496/LL=22428/DEF=Mus musculus dynactin 6 (Dnab6), mRNA, /PROD=dynactin 6 /FL=gb:AF124788.1 gbNM_011722.1	1629.3002	83.222305	1194.2333	410.49402	1.7991323	2.0	0.21381108	0.3324323
gbNM_017622.1/DB_XREF=gi 12857270/GEN=Dnab6/FEA=FLmRNA/CNT=129/7/ID=Mm.90496.1/7/IER=FL+Stack/STK=85/UG=Mm.90496/LL=22428/DEF=Mus musculus dynactin 6 (Dnab6), mRNA, /PROD=dynactin 6 /FL=gb:AF124788.1 gbNM_011722.1	1629.3002	83.222305	1194.2333	410.49402	1.7991323	2.0	0.21381108	0.3324323
gbNM_025650.1/DB_XREF=gi 13384929/GEN=2310008M10R/FEA=FLmRNA/CNT=192/7/ID=Mm.3811.1/7/IER=FL+Stack/STK=21/UG=Mm.3811/LL=66357/DEF=Mus musculus RIKEN cDNA 2310008M10 (2310008M10R), mRNA, /PROD=RIKEN cDNA 2310008M10 /FL=gb:BC021935.1 gbNM_025650.1	1907.1666	421.60797	1362.2667	432.72708	1.5621666	3.0	0.21618043	0.33382964
gbNM_007931.1/DB_XREF=gi 6679546/GEN=Eno3/FEA=FLmRNA/CNT=217/ID=Mm.4449.1/7/IER=FL+Stack/STK=2/UG=Mm.4449/LL=13806/DEF=Mus musculus enolase 3, alpha non-neuron (Eno3), mRNA, /PROD=enolase 3, alpha non-neuron (FL=gb:BC024844.1 gbNM_007931.1) /FL=gb:BC024844.1 gbNM_007931.1	2059.8667	481.12747	1506.5333	383.07217	1.5583705	3.0	0.21703082	0.33400676
gbBC025821.1/DB_XREF=gi 20070721/FEA=FLmRNA/CNT=85/ID=Mm.87433.1/7/IER=FL+Stack/STK=33/UG=Mm.87433/LL=16649/UG_GENE=Kpnal/DEF=Mus musculus, karyopherin (importin) alpha 4, clone MGC-19244 IMAGE 3672708, mRNA, complete cds. /PROD=karyopherin (importin) alpha 4 /FL=gb:AF020771.1 gbNM_008467.1 gbBC025821.1	4096.9004	875.8401	6336.9	2006.1893	1.7723727	2.0	0.21833913	0.33488503
gbNM_011722.1/DB_XREF=gi 12857270/GEN=Dnab6/FEA=FLmRNA/CNT=129/7/ID=Mm.90496.1/7/IER=FL+Stack/STK=85/UG=Mm.90496/LL=22428/DEF=Mus musculus dynactin 6 (Dnab6), mRNA, /PROD=dynactin 6 /FL=gb:AF124788.1 gbNM_011722.1	1629.3002	83.222305	1194.2333	410.49402	1.7991323	2.0	0.21381108	0.3324323
gbNM_017622.1/DB_XREF=gi 12857270/GEN=Dnab6/FEA=FLmRNA/CNT=129/7/ID=Mm.90496.1/7/IER=FL+Stack/STK=85/UG=Mm.90496/LL=22428/DEF=Mus musculus dynactin 6 (Dnab6), mRNA, /PROD=dynactin 6 /FL=gb:AF124788.1 gbNM_011722.1	1629.3002	83.222305	1194.2333	410.49402	1.7991323	2.0	0.21381108	0.3324323
gbNM_025650.1/DB_XREF=gi 13384929/GEN=2310008M10R/FEA=FLmRNA/CNT=192/7/ID=Mm.3811.1/7/IER=FL+Stack/STK=21/UG=Mm.3811/LL=66357/DEF=Mus musculus RIKEN cDNA 2310008M10 (2310008M10R), mRNA, /PROD=RIKEN cDNA 2310008M10 /FL=gb:BC021935.1 gbNM_025650.1	1907.1666	421.60797	1362.2667	432.72708	1.5621666	3.0	0.21618043	0.33382964
gbNM_007931.1/DB_XREF=gi 6679546/GEN=Eno3/FEA=FLmRNA/CNT=217/ID=Mm.4449.1/7/IER=FL+Stack/STK=2/UG=Mm.4449/LL=13806/DEF=Mus musculus enolase 3, alpha non-neuron (Eno3), mRNA, /PROD=enolase 3, alpha non-neuron (FL=gb:BC024844.1 gbNM_007931.1) /FL=gb:BC024844.1 gbNM_007931.1	2059.8667	481.12747	1506.5333	383.07217	1.5583705	3.0	0.21703082	0.33400676
gbBC025821.1/DB_XREF=gi 20070721/FEA=FLmRNA/CNT=85/ID=Mm.87433.1/7/IER=FL+Stack/STK=33/UG=Mm.87433/LL=16649/UG_GENE=Kpnal/DEF=Mus musculus, karyopherin (importin) alpha 4, clone MGC-19244 IMAGE 3672708, mRNA, complete cds. /PROD=karyopherin (importin) alpha 4 /FL=gb:AF020771.1 gbNM_008467.1 gbBC025821.1	4096.9004	875.8401	6336.9	2006.1893	1.7723727	2.0	0.21833913	0.33488503
gbNM_011722.1/DB_XREF=gi 12857270/GEN=Dnab6/FEA=FLmRNA/CNT=129/7/ID=Mm.90496.1/7/IER=FL+Stack/STK=85/UG=Mm.90496/LL=22428/DEF=Mus musculus dynactin 6 (Dnab6), mRNA, /PROD=dynactin 6 /FL=gb:AF124788.1 gbNM_011722.1	1629.3002	83.222305	1194.2333	410.49402	1.7991323	2.0	0.21381108	0.3324323
gbNM_017622.1/DB_XREF=gi 12857270/GEN=Dnab6/FEA=FLmRNA/CNT=129/7/ID=Mm.90496.1/7/IER=FL+Stack/STK=85/UG=Mm.90496/LL=22428/DEF=Mus musculus dynactin 6 (Dnab6), mRNA, /PROD=dynactin 6 /FL=gb:AF124788.1 gbNM_011722.1	1629.3002	83.222305	1194.2333	410.49402	1.7991323	2.0	0.21381108	0.3324323
gbNM_025650.1/DB_XREF=gi 13384929/GEN=2310008M10R/FEA=FLmRNA/CNT=192/7/ID=Mm.3811.1/7/IER=FL+Stack/STK=21/UG=Mm.3811/LL=66357/DEF=Mus musculus RIKEN cDNA 2310008M10 (2310008M10R), mRNA, /PROD=RIKEN cDNA 2310008M10 /FL=gb:BC021935.1 gbNM_025650.1	1907.1666	421.60797	1362.2667	432.72708	1.5621666	3.0	0.21618043	0.33382964
gbNM_007931.1/DB_XREF=gi 6679546/GEN=Eno3/FEA=FLmRNA/CNT=217/ID=Mm.4449.1/7/IER=FL+Stack/STK=2/UG=Mm.4449/LL=13806/DEF=Mus musculus enolase 3, alpha non-neuron (Eno3), mRNA, /PROD=enolase 3, alpha non-neuron (FL=gb:BC024844.1 gbNM_007931.1) /FL=gb:BC024844.1 gbNM_007931.1	2059.8667	481.12747	1506.5333	383.07217	1.5583705	3.0	0.21703082	0.33400676
gbBC025821.1/DB_XREF=gi 20070721/FEA=FLmRNA/CNT=85/ID=Mm.87433.1/7/IER=FL+Stack/STK=33/UG=Mm.87433/LL=16649/UG_GENE=Kpnal/DEF=Mus musculus, karyopherin (importin) alpha 4, clone MGC-19244 IMAGE 3672708, mRNA, complete cds. /PROD=karyopherin (importin) alpha 4 /FL=gb:AF020771.1 gbNM_008467.1 gbBC025821.1	4096.9004	875.8401	6336.9	2006.1893	1.7723727	2.0	0.21833913	0.33488503
gbNM_011722.1/DB_XREF=gi 12857270/GEN=Dnab6/FEA=FLmRNA/CNT=129/7/ID=Mm.90496.1/7/IER=FL+Stack/STK=85/UG=Mm.90496/LL=22428/DEF=Mus musculus dynactin 6 (Dnab6), mRNA, /PROD=dynactin 6 /FL=gb:AF124788.1 gbNM_011722.1	1629.3002	83.222305	1194.2333	410.49402	1.7991323	2.0	0.21381108	0.3324323
gbNM_017622.1/DB_XREF=gi 12857270/GEN=Dnab6/FEA=FLmRNA/CNT=129/7/ID=Mm.90496.1/7/IER=FL+Stack/STK=85/UG=Mm.90496/LL=22428/DEF=Mus musculus dynactin 6 (Dnab6), mRNA, /PROD=dynactin 6 /FL=gb:AF124788.1 gbNM_011722.1	1629.3002	83.222305	1194.2333	410.49402	1.7991323	2.0	0.21381108	0.3324323
gbNM_025650.1/DB_XREF=gi 13384929/GEN=2310008M10R/FEA=FLmRNA/CNT=192/7/ID=Mm.3811.1/7/IER=FL+Stack/STK=21/UG=Mm.3811/LL=66357/DEF=Mus musculus RIKEN cDNA 2310008M10 (2310008M10R), mRNA, /PROD=RIKEN cDNA 2310008M10 /FL=gb:BC021935.1 gbNM_025650.1	1907.1666	421.60797	1362.2667	432.72708	1.5621666	3.0	0.21618043	0.33382964
gbNM_007931.1/DB_XREF=gi 6679546/GEN=Eno3/FEA=FLmRNA/CNT=217/ID=Mm.4449.1/7/IER=FL+Stack/STK=2/UG=Mm.4449/LL=13806/DEF=Mus musculus enolase 3, alpha non-neuron (Eno3), mRNA, /PROD=enolase 3, alpha non-neuron (FL=gb:BC024844.1 gbNM_007931.1) /FL=gb:BC024844.1 gbNM_007931.1	2059.8667	481.12747	1506.5333	383.07217	1.5583705	3.0	0.21703082	0.33400676
gbBC025821.1/DB_XREF=gi 20070721/FEA=FLmRNA/CNT=85/ID=Mm.87433.1/7/IER=FL+Stack/STK=33/UG=Mm.87433/LL=16649/UG_GENE=Kpnal/DEF=Mus musculus, karyopherin (importin) alpha 4, clone MGC-19244 IMAGE 3672708, mRNA, complete cds. /PROD=karyopherin (importin) alpha 4 /FL=gb:AF020771.1 gbNM_008467.1 gbBC025821.1	4096.9004	875.8401	6336.9	2006.1893	1.7723727	2.0	0.21833913	0.33488503
gbNM_011722.1/DB_XREF=gi 12857270/GEN=Dnab6/FEA=FLmRNA/CNT=129/7/ID=Mm.90496.1/7/IER=FL+Stack/STK=85/UG=Mm.90496/LL=22428/DEF=Mus musculus dynactin 6 (Dnab6), mRNA, /PROD=dynactin 6 /FL=gb:AF124788.1 gbNM_011722.1	1629.3002	83.222305	1194.2333	410.49402	1.7991323	2.0	0.21381108	0.3324323
gbNM_017622.1/DB_XREF=gi 12857270/GEN=Dnab6/FEA=FLmRNA/CNT=129/7/ID=Mm.90496.1/7/IER=FL+Stack/STK=85/UG=Mm.90496/LL=22428/DEF=Mus musculus dynactin 6 (Dnab6), mRNA, /PROD=dynactin 6 /FL=gb:AF124788.1 gbNM_011722.1	1629.3002	83.222305	1194.2333	410.49402	1.7991323	2.0	0.21381108	0.3324323
gbNM_025650.1/DB_XREF=gi 13384929/GEN=2310008M10R/FEA=FLmRNA/CNT=192/7/ID=Mm.3811.1/7/IER=FL+Stack/STK=21/UG=Mm.3811/LL=66357/DEF=Mus musculus RIKEN cDNA 2310008M10 (2310008M10R), mRNA, /PROD=RIKEN cDNA 2310008M10 /FL=gb:BC021935.1 gbNM_025650.1	1907.1666	421.60797	1362.2667	432.72708	1.5621666	3.0	0.21618043	0.33382964
gbNM_007931.1/DB_XREF=gi 6679546/GEN=Eno3/FEA=FLmRNA/CNT=217/ID=Mm.4449.1/7/IER=FL+Stack/STK=2/UG=Mm.4449/LL=13806/DEF=Mus musculus enolase 3, alpha non-neuron (Eno3), mRNA, /PROD=enolase 3, alpha non-neuron (FL=gb:BC024844.1 gbNM_007931.1) /FL=gb:BC024844.1 gbNM_007931.1	2059.8667	481.12747	1506.5333	383.07217	1.5583705	3.0	0.21703082	0.33400676
gbBC025821.1/DB_XREF=gi 20070721/FEA=FLmRNA/CNT=85/ID=Mm.87433.1/7/IER=FL+Stack/STK=33/UG=Mm.87433/LL=16649/UG_GENE=Kpnal/DEF=Mus musculus, karyopherin (importin) alpha 4, clone MGC-19244 IMAGE 3672708, mRNA, complete cds. /PROD=karyopherin (importin) alpha 4 /FL=gb:AF020771.1 gbNM_008467.1 gbBC025821.1	4096.9004	875.8401	6336.9	2006.1893	1.7723727	2.0	0.21833913	0.33488503
gbNM_011722.1/DB_XREF=gi 12857270/GEN=Dnab6/FEA=FLmRNA/CNT=129/7/ID=Mm.90496.1/7/IER=FL+Stack/STK=85/UG=Mm.90496/LL=22428/DEF=Mus musculus dynactin 6 (Dnab6), mRNA, /PROD=dynactin 6 /FL=gb:AF124788.1 gbNM_011722.1	1629.3002	83.222305	1194.2333	410.49402	1.799132			

gb:NM_024243.1/DB_XREF=gi:1885906/GEN=0610006A03Rik/FEA=FLmRNA/CNT=204/7/ID=Mm.21580.1/7/IER=FL+Stack/STK=126/UG=Mm.21580/LL=17665/DEF=Mus musculus RIKEN cDNA 0610006A03 gene (0610006A03Rik), mRNA, /PROD=RIKEN cDNA 0610006A03/FL=gb:NM_024243.1 gb:BC003235.1	2050.0999	373.57025	1488.3667	560.70416	1.4440475	3.0	0.24444532	0.34042385
gb:NM_012248.1/DB_XREF=gi:12481/DEF=Mouse cytoplasmic beta-actin mRNA/IENT=1109(_5_,_M_,_3 represent transcript regions 5 prime, Middle, and 3 prime respectively)	7098.533	3205.232	3795.8333	1436.3824	1.6286589	2.0	0.24493289	0.34005973
gb:AK006418.1/DB_XREF=gi:12839509/FEA=mRNA/CNT=9/7/ID=Mm.139700.2/7/IER=ConsEnd/STK=7/UG=Mm.139700/LL=76171/UG_GENE=6330544805Rik/UG_TITLE=RIKEN cDNA 6330544805 gene /DEF=Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:170027H16:homolog to ARF-LIKE 2 BINDING PROTEIN BART1 (BINDER OF ARL TWO), full insert sequence.	1334.9333	456.44818	879.5999	167.46419	1.6220952	2.0	0.24624552	0.34083983
gb:CT6322.1/DB_XREF=gi:2516652/DB_XREF=ct6322/CLONE=J000811/FEA=FLmRNA/CNT=215/7/ID=Mm.22632.1/7/IER=Stack/STK=91/UG=Mm.14601/LL=14863/DEF=Mus musculus, Similar to transgelin 2, clone MGC:6300 IMAGE:2654361, mRNA, complete cds /FL=gb:BC009076.1 gb:AF149291.1	1422.2999	547.77124	888.6667	163.41887	1.6169243	2.0	0.247286	0.34123966
gb:AK012780.1/DB_XREF=gi:12849748/FEA=mRNA/CNT=10/7/ID=Mm.1980.2/7/IER=ConsEnd/STK=6/UG=Mm.1980/LL=69253/UG_GENE=Hspb2/UG_TITLE=heat shock 27kD protein 2/DEF=Mus musculus 10, 11 days embryo whole body cDNA, RIKEN full-length enriched library, clone:2810021G24:homolog to HEAT-SHOCK PROTEIN, BETA-2 (DMPK-BINDING PROTEIN) (MKBP), full insert sequence.	1949.6333	717.2411	1206.8	345.3317	1.6162702	2.0	0.24741803	0.34038723
gb:NM_008163.1/DB_XREF=gi:6680120/GEN=Gsm2z/FEA=FLmRNA/CNT=135/7/ID=Mm.14601.1/7/IER=FL+Stack/STK=91/UG=Mm.14601/LL=14863/DEF=Mus musculus glutathione S-transferase, mu 2 (Gsm2), mRNA, /PROD=glutathione S-transferase, mu 2 /FL=gb:J04696.1 gb:NM_008163.1	2698.0	388.65005	1897.5333	767.24585	1.6120245	2.0	0.24827717	0.34053728
gb:NM_010798.1/DB_XREF=gi:54895/GEN=MF/FEA=FLmRNA/CNT=216/7/ID=Mm.2326.1/7/IER=FL+Stack/STK=96/UG=Mm.2326/LL=17319/DEF=Mus musculus macrophage migration inhibitory factor (Mif), mRNA, /PROD=macrophage migration inhibitory factor /FL=gb:NM_010798.1 gb:1.0613.1 gb:BC024895.1	5992.4336	1752.3951	4222.6333	1240.7228	1.4276481	3.0	0.24868712	0.34007215
gb:NM_019391.1/DB_XREF=gi:1225263/GEN=Lsp1/FEA=FLmRNA/CNT=562/7/ID=Mm.2183.1/7/IER=FL+Stack/STK=37/UG=Mm.2183/LL=16985/DEF=Mus musculus lymphocyte specific 1 (Lsp1), mRNA, /PROD=lymphocyte specific 1 /FL=gb:NM_019391.1 gb:M90316.1 gb:BC003796.1	1213.8667	345.4198	850.1667	274.75565	1.4272609	3.0	0.24878806	0.33918855
gb:NM_00744.1/DB_XREF=gi:8680981/GEN=Camt/FEA=FLmRNA/CNT=84/7/ID=Mm.35853.1/7/IER=FL+Stack/STK=19/UG=Mm.35853/LL=12846/DEF=Mus musculus catechol-O-methyltransferase (Comt), mRNA, /PROD=catechol-O-methyltransferase /FL=gb:AF076156.1 gb:NM_00744.1 gb:BC010402.1	6855.0996	1962.6735	4987.967	434.9332	1.60871	2.0	0.24895056	0.33839387
gb:NM_138749.1/DB_XREF=gi:20270280/GEN=P16nb2/FEA=FLmRNA/CNT=197/7/ID=Mm.28780.1/7/IER=FL+Stack/STK=74/UG=Mm.28780/LL=140570/DEF=Mus musculus plxin B2 (P16nb2), mRNA, /PROD=plxin B2 /FL=gb:NM_138749.1 gb:BC007481.1 gb:BC003293.1	1338.4667	664.8858	697.9333	183.63422	1.6083946	2.0	0.24901477	0.33747074
gb:NM_003694.1/DB_XREF=gi:13507625/GEN=Ifitm3i/FEA=FLmRNA/CNT=102/7/ID=Mm.14747.1/7/IER=FL+Stack/STK=44/UG=Mm.14747/LL=140878/DEF=Mus musculus interferon induced transmembrane protein 3-like (Ifitm3), mRNA, /PROD=interferon induced transmembrane protein, like /FL=gb:BC002160.1 gb:BC002102.1 gb:AY082486.1 gb:NM_003694.1	7020.6	2221.2522	4749.467	1641.2349	1.4243245	3.0	0.249555	0.33719635
gb:BC025117.1/DB_XREF=gi:19264026/FEA=FLmRNA/CNT=85/7/ID=Mm.21793.1/7/IER=FL+Stack/STK=13/UG=Mm.21793/LL=66363/UG_GENE=2310005G07Rik/DEF=Mus musculus, RIKEN cDNA 2310005G07 gene, clone MGC:35747 IMAGE:3984181, mRNA, complete cds, /PROD=RIKEN cDNA 2310005G07 gene /FL=gb:NM_025514.1 gb:BC025117.1	2440.0667	653.6071	1782.5668	282.57137	1.5993049	2.0	0.25087416	0.3379729
gb:BC027196.1/DB_XREF=gi:20071133/FEA=FLmRNA/CNT=203/7/ID=Mm.34411.1/7/IER=FL+Stack/STK=128/UG=Mm.34411/DEF=Mus musculus, Similar to pyruvate dehydrogenase kinase, isoenzyme 1, clone MGC:28719 IMAGE:4458562, mRNA, complete cds, /PROD=Similar to pyruvate dehydrogenase kinase, isoenzyme 1 /FL=gb:BC027196.1	1481.2001	424.4901	269.0334	1182.8103	1.5958194	2.0	0.25159192	0.3379371
gb:BC013496.1/DB_XREF=gi:15488700/FEA=mRNA/CNT=2/7/ID=Mm.10477.19/7/IER=ConsEnd/STK=0/UG=Mm.10477/LL=16114/UG_GENE=Ilgk-V28/DEF=Mus musculus, clone IMAGE:4219618, mRNA, partial cds, /PROD=Unknown (protein for IMAGE:4219618)	2536.7	1346.0999	5748.767	3229.9329	1.5899211	2.0	0.2528125	0.33857486
gb:NM_013670.1/DB_XREF=gi:3055508/GEN=Snripn/FEA=FLmRNA/CNT=253/7/ID=Mm.43721.1/7/IER=FL+Stack/STK=178/UG=Mm.43721/LL=20646/DEF=Mus musculus small nuclear ribonucleoprotein N (Snripn), mRNA, /PROD=small nuclear ribonucleoprotein N /FL=gb:BC024880.1 gb:NM_013670.1 gb:BC019589.1	4073.7668	1357.4027	2778.2334	400.39764	1.5855645	2.0	0.25371894	0.3387894
gb:NM_013771.1/DB_XREF=gi:349863/FEA=FLmRNA/CNT=98/7/ID=Mm.821.1/7/IER=FL+Stack/STK=47/UG=Mm.821/LL=57086/UG_GENE=5210005G07Rik/DEF=Mus musculus, RIKEN cDNA 5210005G07 gene, clone MGC:6298 IMAGE:2651704, mRNA, complete cds, /PROD=Unknown (protein for MGC:6298) /FL=gb:AF230356.1 gb:BC013771.1 gb:NM_021336.1	1188.9333	656.97046	1902.2999	693.9675	1.4081479	3.0	0.2538262	0.3379387
gb:NM_008816.1/DB_XREF=gi:8679272/GEN=Pecam/FEA=FLmRNA/CNT=15/7/ID=Mm.2822.1/7/IER=FL/STK=2/UG=Mm.2822/LL=18613/DEF=Mus musculus plateletendothelial cell adhesion molecule (Pecam), mRNA, /PROD=plateletendothelial cell adhesion molecule /FL=gb:NM_008816.1 gb:U06039.1	1024.2666	261.8756	663.30005	358.61865	1.407957	3.0	0.2538771	0.33701816
gb:BC004096.1/DB_XREF=gi:13278617/FEA=FLmRNA/CNT=7/7/ID=Mm.167102.2/7/IER=FL/STK=1/UG=Mm.16710/LL=16211/UG_GENE=Impnb/DEF=Mus musculus, clone MGC:8315 IMAGE:3594201, mRNA, complete cds, /PROD=Unknown (protein for MGC:8315) /FL=gb:BC004096.1	2197.7332	580.041	3536.7668	1344.1012	1.5842928	2.0	0.2539843	0.33617747
gb:AF205078.1/DB_XREF=gi:9828172/FEA=mRNA/CNT=116/7/ID=Mm.29933.1/7/IER=Stack/STK=76/UG=Mm.29933/LL=72333/UG_GENE=2410003B18Rik/DEF=Mus musculus strain Swiss WebsterNIH actin-associated protein palladin mRNA, partial cds, /PROD=actin-associated protein palladin	2120.3	569.42145	1508.4332	496.02515	1.4033719	3.0	0.25510228	0.33667567
gb:NM_026612.1/DB_XREF=gi:13386095/GEN=1810011001Rik/FEA=FLmRNA/CNT=92/7/ID=Mm.29415.1/7/IER=FL+Stack/STK=67/UG=Mm.29415/LL=68198/DEF=Mus musculus RIKEN cDNA 1810011001 gene (1810011001Rik), mRNA, /PROD=RIKEN cDNA 1810011001/FL=gb:BC013510.1 gb:NM_026612.1	15384.167	4013.6558	11335.101	1932.8859	1.5742899	2.0	0.25608414	0.33699188
gb:NM_011141.1/DB_XREF=gi:1285991/FEA=FLmRNA/CNT=211/7/ID=Mm.41928.1/7/IER=Stack/STK=55/UG=Mm.41928/LL=17992/UG_GENE=Ndufa4/DEF=Mus musculus, NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4, clone MGC:7218 IMAGE:3483026, mRNA, complete cds, /PROD=NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4 /FL=gb:BC011141.1	20005.533	6725.475	13639.532	1986.9003	1.5722948	2.0	0.2565056	0.33657095
gb:NM_011793.1/DB_XREF=gi:8753177/GEN=Bcrp1-pending/FEA=FLmRNA/CNT=167/7/ID=Mm.7508.1/7/IER=FL/STK=2/UG=Mm.7508/LL=23825/DEF=Mus musculus breakpoint cluster region protein 1 (Bcrp1-pending), mRNA, /PROD=breakpoint cluster region protein 1 /FL=gb:NM_011793.1 gb:AB025349.1	1859.2999	494.08163	1304.1666	480.25177	1.3954734	3.0	0.25722775	0.33654583
gb:NM_025706.1/DB_XREF=gi:13385163/GEN=4432405K22Rik/FEA=FLmRNA/CNT=232/7/ID=Mm.2252.1/7/IER=FL+Stack/STK=137/UG=Mm.2252/LL=166887/DEF=Mus musculus RIKEN cDNA 4432405K22 gene (4432405K22Rik), mRNA, /PROD=RIKEN cDNA 4432405K22/FL=gb:BC020760.1 gb:NM_025706.1	2074.0334	925.5119	3127.4668	926.4323	1.3933324	3.0	0.25780717	0.33633462
gb:AK004661.1/DB_XREF=gi:1285991/FEA=FLmRNA/CNT=211/7/ID=Mm.22179.1/7/IER=Stack/STK=28/UG=Mm.22179/LL=67456/UG_GENE=1200009B18Rik/UG_TITLE=RIKEN cDNA 1200009B18 gene /DEF=Mus musculus adult male lung cDNA, RIKEN full-length enriched library, clone:1200009B18:homolog to CDA14, full insert sequence. /FL=gb:BC006895.1 gb:BC018188.1 gb:BC026558.1	963.0	467.03268	1549.3334	564.1123	1.3867055	3.0	0.25960946	0.33771545
gb:BC023060.1/DB_XREF=gi:18606201/FEA=mRNA/CNT=19/7/ID=Mm.44176.1/7/IER=Stack/STK=17/UG=Mm.44176/DEF=Mus musculus, Similar to EGF-containing fibulin-like extracellular matrix protein 1 /FL=gb:BC023060.1	1247.9333	767.05914	1964.3334	217.40591	1.5563558	2.0	0.25990483	0.3371337
gb:NM_026533.1/DB_XREF=gi:13386033/GEN=Rps13/FEA=FLmRNA/CNT=343/7/ID=Mm.14798.1/7/IER=FL+Stack/STK=170/UG=Mm.14798/LL=168052/DEF=Mus musculus ribosomal protein S13 (Rps13), mRNA, /PROD=ribosomal protein S13 /FL=gb:NM_026533.1 gb:BC011192.1	17834.967	5539.1167	12845.399	941.7359	1.538138	2.0	0.26386073	0.34128997
gb:NM_013670.1/DB_XREF=gi:3055508/GEN=Snripn/FEA=FLmRNA/CNT=253/7/ID=Mm.43721.1/7/IER=FL+Stack/STK=178/UG=Mm.43721/LL=20646/DEF=Mus musculus small nuclear ribonucleoprotein N (Snripn), mRNA, /PROD=small nuclear ribonucleoprotein N /FL=gb:BC024880.1 gb:NM_013670.1 gb:BC019589.1	3676.5	1964.3711	1895.9	476.49503	1.5257676	2.0	0.26659068	0.34384137
gb:AK005096.1/DB_XREF=gi:12836790/FEA=mRNA/CNT=38/7/ID=Mm.44075.1/7/IER=Stack/STK=22/UG=Mm.44075/LL=70364/UG_GENE=150000103Rik/UG_TITLE=RIKEN cDNA 150000103 gene /DEF=Mus musculus adult male cerebellum cDNA, RIKEN full-length enriched library, clone:15000103:homolog to CDNA1/FL22362 FIS, CLONE HRC0854, full insert sequence.	1331.4	363.54633	911.39996	398.89136	1.34789	2.0	0.2704402	0.34781826
gb:NM_011793.1/DB_XREF=gi:8753177/GEN=Bcrp1-pending/FEA=FLmRNA/CNT=167/7/ID=Mm.7508.1/7/IER=FL/STK=2/UG=Mm.7508/LL=23825/DEF=Mus musculus breakpoint cluster region protein 1 (Bcrp1-pending), mRNA, /PROD=breakpoint cluster region protein 1 /FL=gb:NM_011793.1 gb:AB025349.1	1313.1333	341.6223	867.7	460.86154	1.348688	2.0	0.27130315	0.34794244
gb:NM_022318.1/DB_XREF=gi:11612496/GEN=Pop2-pending/FEA=FLmRNA/CNT=49/7/ID=Mm.23890.1/7/IER=FL+Stack/STK=36/UG=Mm.23890/LL=64082/DEF=Mus musculus popeye 2 (Pop2-pending), mRNA, /PROD=popeye 2 /FL=gb:AF204175.1 gb:NM_022318.1	7395.8667	2724.9272	4811.0	1195.4429	1.504601	2.0	0.2713454	0.3470164
gb:BC025501.1/DB_XREF=gi:1285991/FEA=FLmRNA/CNT=211/7/ID=Mm.10091.2/7/IER=FL+Stack/STK=74/UG=Mm.10091/LL=18769/UG_GENE=Pkg/DEF=Mus musculus, protein kinase inhibitor, gamma, clone MGC:36052 IMAGE:5006826, mRNA, complete cds, /PROD=protein kinase inhibitor, gamma /FL=gb:BC026550.1	4608.9336	575.2312	3331.2	1355.7172	1.5027447	2.0	0.2717675	0.3465799
gb:NM_031176.1/DB_XREF=gi:13928671/GEN=Tnxb/FEA=FLmRNA/CNT=413/7/ID=Mm.183266.1/7/IER=FL/STK=2/UG=Mm.183266/LL=81877/DEF=Mus musculus tenascin XB (Tnxb), mRNA, /PROD=tenascin XB /FL=gb:NM_031176.1	1731.1666	907.9988	932.7	486.432	1.342591	3.0	0.27195567	0.34584838
gb:NM_007750.1/DB_XREF=gi:6680992/GEN=Cox8a/FEA=FLmRNA/CNT=189/7/ID=Mm.14022.1/7/IER=FL+Stack/STK=125/UG=Mm.14022/LL=12688/DEF=Mus musculus cytochrome c oxidase, subunit VIIIa (Cox8a), mRNA, /PROD=cytochrome c oxidase, subunit VIIIa /FL=gb:U37721.1 gb:NM_007750.1	2268.0	424.9446	1662.5	663.0841	1.3316449	3.0	0.2751148	0.3488886
gb:NM_009982.1/DB_XREF=gi:6753553/GEN=Ctsc/FEA=FLmRNA/CNT=280/7/ID=Mm.684.1/7/IER=FL+Stack/STK=93/UG=Mm.684/LL=13032/DEF=Mus musculus cathepsin C (Ctsc), mRNA, /PROD=cathepsin C /FL=gb:U74683.3 gb:NM_009982.1 gb:U89269.1	4534.1333	1361.0074	3302.5999	532.1105	1.4596839	2.0	0.28179538	0.3563652
gb:BC002090.1/DB_XREF=gi:12805254/FEA=FLmRNA/CNT=31/7/ID=Mm.27128.1/7/IER=FL/STK=2/UG=Mm.27128/LL=86556/UG_GENE=2310074H19Rik/DEF=Mus musculus, Similar to DR1-associated protein 1 (negative cofactor 2 alpha), clone MGC:6341 IMAGE:3481839, mRNA, complete cds, /PROD=Similar to DR1-associated protein 1 (negative cofactor 2 alpha) /FL=gb:BC002090.1	3833.4668	1725.8673	2366.5999	262.58167	1.40553742	2.0	0.28282443	0.35667303
gb:BC027290.1/DB_XREF=gi:20070999/FEA=FLmRNA/CNT=23/7/ID=Mm.48232.1/7/IER=FL+Stack/STK=14/UG=Mm.48232/LL=8888/UG_GENE=B430311C09Rik/DEF=Mus musculus, RIKEN cDNA B430311C09 gene, clone MGC:27734 IMAGE:2647023, mRNA, complete cds, /PROD=RIKEN cDNA B430311C09 gene /FL=gb:BC027290.1	1301.5	433.59323	899.60004	206.88048	1.448966	2.0	0.28436327	0.35762027
gb:BC024398.1/DB_XREF=gi:19353453/FEA=FLmRNA/CNT=102/7/ID=Mm.10586.1/7/IER=FL+Stack/STK=33/UG=Mm.10586/LL=71966/UG_GENE=2410003M04Rik/DEF=Mus musculus, RIKEN cDNA 2410003M04 gene, clone MGC:36234 IMAGE:5003001, mRNA, complete cds, /PROD=RIKEN cDNA 2410003M04 gene /FL=gb:BC013469.1 gb:BC024398.1	1527.3666	475.4801	1109.0333	157.3033	1.4467617	2.0	0.28498503	0.3572993
gb:BC020068.1/DB_XREF=gi:18043363/FEA=FLmRNA/CNT=31/7/ID=Mm.172352.1/7/IER=FL/STK=6/UG=Mm.172352/DEF=Mus musculus, Similar to RIKEN cDNA 953053H05 gene, clone MGC:28371 IMAGE:4020866, mRNA, complete cds, /PROD=Similar to RIKEN cDNA 953053H05 gene /FL=gb:BC020068.1	610.4333	222.68494	1039.9	463.5047	1.4465678	2.0	0.28494188	0.35637358
gb:NM_022976.1/DB_XREF=gi:1818334/GEN=Lrg-pending/FEA=FLmRNA/CNT=132/7/ID=Mm.176946.1/7/IER=FL+Stack/STK=49/UG=Mm.176946/LL=76905/DEF=Mus musculus leucine-rich alpha-2-glycoprotein (Lrg-pending), mRNA, /PROD=leucine-rich alpha-2-glycoprotein /FL=gb:AF403429.1 gb:AB055885.1 gb:NM_022976.1	990.1667	377.34503	612.86664	335.041	1.2950386	3.0	0.2859639	0.35666925
gb:BC010331.1/DB_XREF=gi:16307568/FEA=FLmRNA/CNT=140/7/ID=Mm.6586.1/7/IER=FL+Stack/STK=86/UG=Mm.6586/DEF=Mus musculus, clone MGC:6299 IMAGE:2654341, mRNA, complete cds, /PROD=Unknown (protein for MGC:6299) /FL=gb:BC010331.1 gb:AF071546.1	1688.6666	570.3714	1201.7999	318.48758	1.2908622	3.0	0.28722993	0.3572668
gb:NM_007750.1/DB_XREF=gi:6680992/GEN=Cox8a/FEA=FLmRNA/CNT=189/7/ID=Mm.14022.1/7/IER=FL+Stack/STK=125/UG=Mm.14022/LL=12688/DEF=Mus musculus cytochrome c oxidase, subunit VIIIa (Cox8a), mRNA, /PROD=cytochrome c oxidase, subunit VIIIa /FL=gb:U37721.1 gb:NM_007750.1	2348.0667	582.6127	1683.4332	680.7008	1.2848178	2.0	0.28907257	0.35857636
gb:AK007959.1/DB_XREF=gi:12841843/GEN=Kif3/FEA=mRNA/CNT=9/7/ID=Mm.28787.2/7/IER=Stack/STK=31/UG=Mm.28787/LL=16599/UG_TITLE=Kruppel-like factor 3 (basic) /DEF=Mus musculus 10 day old male pancreas cDNA, RIKEN full-length enriched library, clone:1810073A04:Kruppel-like factor 3 (basic), full insert sequence.	1284.3334	330.9694	894.1333	409.0531	1.2844399	3.0	0.2891882	0.35774237
gb:AK01872.1/DB_XREF=gi:12858675/FEA=mRNA/CNT=90/7/ID=Mm.45683.1/7/IER=Stack/STK=34/UG=Mm.45683/LL=78304/UG_GENE=1500034E06Rik/UG_TITLE=RIKEN cDNA 1500034E06 gene /DEF=Mus musculus adult male cerebellum cDNA, RIKEN full-length enriched library, clone:1500034E06:Sm protein containing protein, full insert sequence.	6024.7993	1744.9688	4426.1	861.1195	1.4230223	2.0	0.2907013	0.35863695
gb:AK017291.1/DB_XREF=gi:1285421/FEA=FLmRNA/CNT=52/7/ID=Mm.23242.1/7/IER=Stack/STK=27/UG=Mm.23242/LL=17408/UG_GENE=5430405D02Rik/UG_TITLE=RIKEN cDNA 5430405D02 gene /DEF=Mus musculus 6 days neonate head cDNA, RIKEN full-length enriched library, clone:5430405D02:unclassified transcript, full insert sequence.	851.36664	128.27292	1371.7666	598.14606	1.4156123	2.0	0.29254377	0.35993192
gb:BC005547.1/DB_XREF=gi:13542679/FEA=FLmRNA/CNT=515/7/ID=Mm.21840.1/7/IER=FL+Stack/STK=279/UG=Mm.21840/LL=68222/UG_GENE=4930542G03Rik/DEF=Mus musculus, clone MGC:6713 IMAGE:3585500, mRNA, complete cds, /PROD=Unknown (protein for MGC:6713) /FL=gb:BC022919.1 gb:BC005547.1	7940.133	2849.038	5353.1	1400.036	1.4115437	2.0		

gb NM_003033.1 DB_XREF=gi 6880308 GEN=Hspc1 FEA=FLmRNA CNT=27 TID=Mm.197601.1 TIER=FL+Stack STK=32 /UG=Mm.197601.1 DB_XREF=gi 15528 DEF=Mus musculus heat shock 10 kDa protein 1 (chaperonin 10) (Hspc1), mRNA, /PROD=heat shock 10 kDa protein 1 (chaperonin 10) /FL=gb NM_003033.1 gb U06599.1 gb BC024385.1	2460.5999	742.7351	1814.6666	298.21667	1.3978438	2.0	0.2970214	0.36249384
gb NM_010050.1 DB_XREF=gi 5753637 GEN=U062 FEA=FLmRNA CNT=27 TID=Mm.21389.1 TIER=FL+Stack STK=16 UG=Mm.21389 /LL=13371 DEF=Mus musculus deiodinase, iodothyronine, type 1 (Dio2), mRNA, /PROD=deiodinase, iodothyronine, type 1 /FL=gb AF177196.1 gb NM_010050.1 gb AF093137.1 gb AF096875.1	400.40002	116.28194	767.9666	442.2855	1.3921314	2.0	0.2984789	0.36329603
gb NM_010907.1 DB_XREF=gi 5754339 GEN=NR1Kb3 FEA=FLmRNA CNT=183 TID=Mm.8884.1 TIER=FL+Stack STK=97 UG=Mm.8884 /LL=168 DEF=Mus musculus nuclear factor of kappa light chain gene enhancer in B-cells inhibitor, alpha (Nfkbia), mRNA, /PROD=nuclear factor of kappa light chain gene enhancer in B-cells inhibitor, alpha (Nfkbia) /FL=gb NM_010907.1 gb U36277.1	2398.0999	1137.4896	1406.9668	523.849	1.3708122	2.0	0.30399716	0.3690233
gb BC008166.1 DB_XREF=gi 14198212 FEA=FLmRNA CNT=157 TID=Mm.186.1 TIER=FL+Stack STK=47 UG=Mm.186 LL=76281 /UG_GENE=130001 C24Rik DEF=Mus musculus, RIKEN cDNA 130001 C24 gene MGC:7169 IMAGE:3257323, mRNA, complete cds, /PROD=RIKEN cDNA 130001 C24 gene /FL=gb BC008166.1	2138.5667	693.2226	1549.7666	272.3373	1.3692713	2.0	0.30440086	0.36852798
gb BC021383.1 DB_XREF=gi 16204067 FEA=FLmRNA CNT=181 TID=Mm.22682.1 TIER=FL+Stack STK=93 UG=Mm.22682 /LL=117150 UG_GENE=Pp5k2c DEF=Mus musculus, phosphatidylinositol-4-phosphate 5-kinase, type I, gamma, clone MGC:29371 /UG_GENE=130001 C24Rik DEF=Mus musculus, complete cds, /PROD=phosphatidylinositol-4-phosphate 5-kinase, type I, gamma /FL=gb AB054591.1 gb BC021383.1 gb NM_054097.1	1285.8334	300.57645	910.33344	432.14334	1.2355403	3.0	0.30456167	0.36774203
gb NM_009161.1 DB_XREF=gi 6671922 GEN=Scga FEA=FLmRNA CNT=357 TID=Mm.18709.1 TIER=FL+Stack STK=21 UG=Mm.18709 /LL=20391 DEF=Mus musculus, serine hydroxymethyl transferase 1 (soluble), clone MGC:14007 IMAGE:4160579, mRNA, complete cds, /PROD=serine hydroxymethyl transferase 1 (soluble) /FL=gb AB024920.1 gb AF019564.1 gb NM_009161.1	2397.4001	819.89575	1718.4	267.866	1.3634822	2.0	0.30592343	0.36840647
gb AF28255.1 DB_XREF=gi 9652249 GEN=Dsg1 FEA=FLmRNA CNT=119 TID=Mm.56.1 TIER=FL+Stack STK=1 UG=Mm.56 LL=54720 /DEF=Mus musculus Down syndrome candidate region 1 protein (Dscr1) mRNA, complete cds, /PROD=Down syndrome candidate region 1 protein /FL=gb AF28255.1 gb AF32789.1 gb U04956.1	870.0999	438.59137	487.6	314.48032	1.2275844	3.0	0.30714175	0.3688951
gb NM_080555.1 DB_XREF=gi 18017589 GEN=Pap2b FEA=FLmRNA CNT=81 TID=Mm.29124.1 TIER=FL+Stack STK=32 /UG=Mm.29124 LL=67916 DEF=Mus musculus phosphatidic acid phosphatase type 2B (Pap2b), mRNA, /PROD=phosphatidic acid phosphatase type 2B /FL=gb NM_080555.1 gb BC005558.1	2908.0999	967.49896	2102.5999	605.9832	1.2221063	3.0	0.3089313	0.37006545
gb BC026055.1 DB_XREF=gi 19913455 FEA=FLmRNA CNT=113 TID=Mm.3379.2 TIER=FL+Stack STK=4 UG=Mm.3379 LL=20425 /UG_GENE=Shnrt1 DEF=Mus musculus, serine hydroxymethyl transferase 1 (soluble), clone MGC:14007 IMAGE:4160579, mRNA, complete cds, /PROD=serine hydroxymethyl transferase 1 (soluble) /FL=gb AF237702.1 gb BC026055.1	459.9	176.8502	1045.8334	731.91003	1.3478124	2.0	0.31009194	0.37047827
gb NM_010907.1 DB_XREF=gi 5754339 GEN=NR1Kb3 FEA=FLmRNA CNT=183 TID=Mm.8884.1 TIER=FL+Stack STK=97 UG=Mm.8884 /LL=168 DEF=Mus musculus nuclear factor of kappa light chain gene enhancer in B-cells inhibitor, alpha (Nfkbia), mRNA, /PROD=nuclear factor of kappa light chain gene enhancer in B-cells inhibitor, alpha (Nfkbia) /FL=gb NM_010907.1 gb U36277.1	2398.0999	1137.4896	1406.9668	523.849	1.3708122	2.0	0.30399716	0.3690233
gb NM_080555.1 DB_XREF=gi 18017589 GEN=Pap2b FEA=FLmRNA CNT=81 TID=Mm.29124.1 TIER=FL+Stack STK=32 /UG=Mm.29124 LL=67916 DEF=Mus musculus phosphatidic acid phosphatase type 2B (Pap2b), mRNA, /PROD=phosphatidic acid phosphatase type 2B /FL=gb NM_080555.1 gb BC005558.1	2908.0999	967.49896	2102.5999	605.9832	1.2221063	3.0	0.3089313	0.37006545
gb BC026055.1 DB_XREF=gi 19913455 FEA=FLmRNA CNT=113 TID=Mm.3379.2 TIER=FL+Stack STK=4 UG=Mm.3379 LL=20425 /UG_GENE=Shnrt1 DEF=Mus musculus, serine hydroxymethyl transferase 1 (soluble), clone MGC:14007 IMAGE:4160579, mRNA, complete cds, /PROD=serine hydroxymethyl transferase 1 (soluble) /FL=gb AF237702.1 gb BC026055.1	459.9	176.8502	1045.8334	731.91003	1.3478124	2.0	0.31009194	0.37047827
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gb NM_080555.1 DB_XREF=gi 18017589 GEN=Pap2b FEA=FLmRNA CNT=81 TID=Mm.29124.1 TIER=FL+Stack STK=32 /UG=Mm.29124 LL=67916 DEF=Mus musculus phosphatidic acid phosphatase type 2B (Pap2b), mRNA, /PROD=phosphatidic acid phosphatase type 2B /FL=gb NM_080555.1 gb BC005558.1	2908.0999	967.49896	2102.5999	605.9832	1.2221063	3.0	0.3089313	0.37006545
gb BC026055.1 DB_XREF=gi 19913455 FEA=FLmRNA CNT=113 TID=Mm.3379.2 TIER=FL+Stack STK=4 UG=Mm.3379 LL=20425 /UG_GENE=Shnrt1 DEF=Mus musculus, serine hydroxymethyl transferase 1 (soluble), clone MGC:14007 IMAGE:4160579, mRNA, complete cds, /PROD=serine hydroxymethyl transferase 1 (soluble) /FL=gb AF237702.1 gb BC026055.1	459.9	176.8502	1045.8334	731.91003	1.3478124	2.0	0.31009194	0.37047827
gb NM_010907.1 DB_XREF=gi 5754339 GEN=NR1Kb3 FEA=FLmRNA CNT=183 TID=Mm.8884.1 TIER=FL+Stack STK=97 UG=Mm.8884 /LL=168 DEF=Mus musculus nuclear factor of kappa light chain gene enhancer in B-cells inhibitor, alpha (Nfkbia), mRNA, /PROD=nuclear factor of kappa light chain gene enhancer in B-cells inhibitor, alpha (Nfkbia) /FL=gb NM_010907.1 gb U36277.1	2398.0999	1137.4896	1406.9668	523.849	1.3708122	2.0	0.30399716	0.3690233
gb NM_080555.1 DB_XREF=gi 18017589 GEN=Pap2b FEA=FLmRNA CNT=81 TID=Mm.29124.1 TIER=FL+Stack STK=32 /UG=Mm.29124 LL=67916 DEF=Mus musculus phosphatidic acid phosphatase type 2B (Pap2b), mRNA, /PROD=phosphatidic acid phosphatase type 2B /FL=gb NM_080555.1 gb BC005558.1	2908.0999	967.49896	2102.5999	605.9832	1.2221063	3.0	0.3089313	0.37006545
gb BC026055.1 DB_XREF=gi 19913455 FEA=FLmRNA CNT=113 TID=Mm.3379.2 TIER=FL+Stack STK=4 UG=Mm.3379 LL=20425 /UG_GENE=Shnrt1 DEF=Mus musculus, serine hydroxymethyl transferase 1 (soluble), clone MGC:14007 IMAGE:4160579, mRNA, complete cds, /PROD=serine hydroxymethyl transferase 1 (soluble) /FL=gb AF237702.1 gb BC026055.1	459.9	176.8502	1045.8334	731.91003	1.3478124	2.0	0.31009194	0.37047827
gb NM_010907.1 DB_XREF=gi 5754339 GEN=NR1Kb3 FEA=FLmRNA CNT=183 TID=Mm.8884.1 TIER=FL+Stack STK=97 UG=Mm.8884 /LL=168 DEF=Mus musculus nuclear factor of kappa light chain gene enhancer in B-cells inhibitor, alpha (Nfkbia), mRNA, /PROD=nuclear factor of kappa light chain gene enhancer in B-cells inhibitor, alpha (Nfkbia) /FL=gb NM_010907.1 gb U36277.1	2398.0999	1137.4896	1406.9668	523.849	1.3708122	2.0	0.30399716	0.3690233
gb NM_080555.1 DB_XREF=gi 18017589 GEN=Pap2b FEA=FLmRNA CNT=81 TID=Mm.29124.1 TIER=FL+Stack STK=32 /UG=Mm.29124 LL=67916 DEF=Mus musculus phosphatidic acid phosphatase type 2B (Pap2b), mRNA, /PROD=phosphatidic acid phosphatase type 2B /FL=gb NM_080555.1 gb BC005558.1	2908.0999	967.49896	2102.5999	605.9832	1.2221063	3.0	0.3089313	0.37006545
gb BC026055.1 DB_XREF=gi 19913455 FEA=FLmRNA CNT=113 TID=Mm.3379.2 TIER=FL+Stack STK=4 UG=Mm.3379 LL=20425 /UG_GENE=Shnrt1 DEF=Mus musculus, serine hydroxymethyl transferase 1 (soluble), clone MGC:14007 IMAGE:4160579, mRNA, complete cds, /PROD=serine hydroxymethyl transferase 1 (soluble) /FL=gb AF237702.1 gb BC026055.1	459.9	176.8502	1045.8334	731.91003	1.3478124	2.0	0.31009194	0.37047827
gb NM_010907.1 DB_XREF=gi 5754339 GEN=NR1Kb3 FEA=FLmRNA CNT=183 TID=Mm.8884.1 TIER=FL+Stack STK=97 UG=Mm.8884 /LL=168 DEF=Mus musculus nuclear factor of kappa light chain gene enhancer in B-cells inhibitor, alpha (Nfkbia), mRNA, /PROD=nuclear factor of kappa light chain gene enhancer in B-cells inhibitor, alpha (Nfkbia) /FL=gb NM_010907.1 gb U36277.1	2398.0999	1137.4896	1406.9668	523.849	1.3708122	2.0	0.30399716	0.3690233
gb NM_080555.1 DB_XREF=gi 18017589 GEN=Pap2b FEA=FLmRNA CNT=81 TID=Mm.29124.1 TIER=FL+Stack STK=32 /UG=Mm.29124 LL=67916 DEF=Mus musculus phosphatidic acid phosphatase type 2B (Pap2b), mRNA, /PROD=phosphatidic acid phosphatase type 2B /FL=gb NM_080555.1 gb BC005558.1	2908.0999	967.49896	2102.5999	605.9832	1.2221063	3.0	0.3089313	0.37006545
gb BC026055.1 DB_XREF=gi 19913455 FEA=FLmRNA CNT=113 TID=Mm.3379.2 TIER=FL+Stack STK=4 UG=Mm.3379 LL=20425 /UG_GENE=Shnrt1 DEF=Mus musculus, serine hydroxymethyl transferase 1 (soluble), clone MGC:14007 IMAGE:4160579, mRNA, complete cds, /PROD=serine hydroxymethyl transferase 1 (soluble) /FL=gb AF237702.1 gb BC026055.1	459.9	176.8502	1045.8334	731.91003	1.3478124	2.0	0.31009194	0.37047827
gb NM_010907.1 DB_XREF=gi 5754339 GEN=NR1Kb3 FEA=FLmRNA CNT=183 TID=Mm.8884.1 TIER=FL+Stack STK=97 UG=Mm.8884 /LL=168 DEF=Mus musculus nuclear factor of kappa light chain gene enhancer in B-cells inhibitor, alpha (Nfkbia), mRNA, /PROD=nuclear factor of kappa light chain gene enhancer in B-cells inhibitor, alpha (Nfkbia) /FL=gb NM_010907.1 gb U36277.1	2398.0999	1137.4896	1406.9668	523.849	1.3708122	2.0	0.30399716	0.3690233
gb NM_080555.1 DB_XREF=gi 18017589 GEN=Pap2b FEA=FLmRNA CNT=81 TID=Mm.29124.1 TIER=FL+Stack STK=32 /UG=Mm.29124 LL=67916 DEF=Mus musculus phosphatidic acid phosphatase type 2B (Pap2b), mRNA, /PROD=phosphatidic acid phosphatase type 2B /FL=gb NM_080555.1 gb BC005558.1	2908.0999	967.49896	2102.5999	605.9832	1.2221063	3.0	0.3089313	0.37006545
gb BC026055.1 DB_XREF=gi 19913455 FEA=FLmRNA CNT=113 TID=Mm.3379.2 TIER=FL+Stack STK=4 UG=Mm.3379 LL=20425 /UG_GENE=Shnrt1 DEF=Mus musculus, serine hydroxymethyl transferase 1 (soluble), clone MGC:14007 IMAGE:4160579, mRNA, complete cds, /PROD=serine hydroxymethyl transferase 1 (soluble) /FL=gb AF237702.1 gb BC026055.1	459.9	176.8502	1045.8334	731.91003	1.3478124	2.0	0.31009194	0.37047827
gb NM_010907.1 DB_XREF=gi 5754339 GEN=NR1Kb3 FEA=FLmRNA CNT=183 TID=Mm.8884.1 TIER=FL+Stack STK=97 UG=Mm.8884 /LL=168 DEF=Mus musculus nuclear factor of kappa light chain gene enhancer in B-cells inhibitor, alpha (Nfkbia), mRNA, /PROD=nuclear factor of kappa light chain gene enhancer in B-cells inhibitor, alpha (Nfkbia) /FL=gb NM_010907.1 gb U36277.1	2398.0999	1137.4896	1406.9668	523.849	1.3708122	2.0	0.30399716	0.3690233
gb NM_080555.1 DB_XREF=gi 18017589 GEN=Pap2b FEA=FLmRNA CNT=81 TID=Mm.29124.1 TIER=FL+Stack STK=32 /UG=Mm.29124 LL=67916 DEF=Mus musculus phosphatidic acid phosphatase type 2B (Pap2b), mRNA, /PROD=phosphatidic acid phosphatase type 2B /FL=gb NM_080555.1 gb BC005558.1	2908.0999	967.49896	2102.5999	605.9832	1.2221063	3.0	0.3089313	0.37006545
gb BC026055.1 DB_XREF=gi 19913455 FEA=FLmRNA CNT=113 TID=Mm.3379.2 TIER=FL+Stack STK=4 UG=Mm.3379 LL=20425 /UG_GENE=Shnrt1 DEF=Mus musculus, serine hydroxymethyl transferase 1 (soluble), clone MGC:14007 IMAGE:4160579, mRNA, complete cds, /PROD=serine hydroxymethyl transferase 1 (soluble) /FL=gb AF237702.1 gb BC026055.1	459.9	176.8502	1045.8334	731.91003	1.3478124	2.0	0.31009194	0.37047827
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gb NM_080555.1 DB_XREF=gi 18017589 GEN=Pap2b FEA=FLmRNA CNT=81 TID=Mm.29124.1 TIER=FL+Stack STK=32 /UG=Mm.29124 LL=67916 DEF=Mus musculus phosphatidic acid phosphatase type 2B (Pap2b), mRNA, /PROD=phosphatidic acid phosphatase type 2B /FL=gb NM_080555.1 gb BC005558.1	2908.0999	967.49896	2102.5999	605.9832	1.2221063	3.0	0.3089313	0.37006545
gb BC026055.1 DB_XREF=gi 19913455 FEA=FLmRNA CNT=113 TID=Mm.3379.2 TIER=FL+Stack STK=4 UG=Mm.3379 LL=20425 /UG_GENE=Shnrt1 DEF=Mus musculus, serine hydroxymethyl transferase 1 (soluble), clone MGC:14007 IMAGE:4160579, mRNA, complete cds, /PROD=serine hydroxymethyl transferase 1 (soluble) /FL=gb AF237702.1 gb BC026055.1	459.9	176.8502	1045.8334	731.91003	1.3478124	2.0	0.31009194	0.37047827
gb NM_010907.1 DB_XREF=gi 5754339 GEN=NR1Kb3 FEA=FLmRNA CNT=183 TID=Mm.8884.1 TIER=FL+Stack STK=97 UG=Mm.8884 /LL=168 DEF=Mus musculus nuclear factor of kappa light chain gene enhancer in B-cells inhibitor, alpha (Nfkbia), mRNA, /PROD=nuclear factor of kappa light chain gene enhancer in B-cells inhibitor, alpha (Nfkbia) /FL=gb NM_010907.1 gb U36277.1	2398.0999	1137.4896	1406.9668	523.849	1.3708122	2.0	0.30399716	0.3690233
gb NM_080555.1 DB_XREF=gi 18017589 GEN=Pap2b FEA=FLmRNA CNT=81 TID=Mm.29124.1 TIER=FL+Stack STK=32 /UG=Mm.29124 LL=67916 DEF=Mus musculus phosphatidic acid phosphatase type 2B (Pap2b), mRNA, /PROD=phosphatidic acid phosphatase type 2B /FL=gb NM_080555.1 gb BC005558.1	2908.0999	967.49896	2102.5999	605.9832	1.2221063	3.0	0.3089313	0.37006545
gb BC026055.1 DB_XREF=gi 19913455 FEA=FLmRNA CNT=113 TID=Mm.3379.2 TIER=FL+Stack STK=4 UG=Mm.3379 LL=20425 /UG_GENE=Shnrt1 DEF=Mus musculus, serine hydroxymethyl transferase 1 (soluble), clone MGC:14007 IMAGE:4160579, mRNA, complete cds, /PROD=serine hydroxymethyl transferase 1 (soluble) /FL=gb AF237702.1 gb BC026055.1	459.9	176.8502	1045.8334	731.91003	1.3478124	2.0	0.31009194	0.37047827
gb NM_010907.1 DB_XREF=gi 5754339 GEN=NR1Kb3 FEA=FLmRNA CNT=183 TID=Mm.8884.1 TIER=FL+Stack STK=97 UG=Mm.8884 /LL=168 DEF=Mus musculus nuclear factor of kappa light chain gene enhancer in B-cells inhibitor, alpha (Nfkbia), mRNA, /PROD=nuclear factor of kappa light chain gene enhancer in B-cells inhibitor, alpha (Nfkbia) /FL=gb NM_010907.1 gb U36277.1	2398.0999	1137.4896	1406.9668	523.849	1.3708122	2.0	0.30399716	0.3690233
gb NM_080555.1 DB_XREF=gi 18017589 GEN=Pap2b FEA=FLmRNA CNT=81 TID=Mm.29124.1 TIER=FL+Stack STK=32 /UG=Mm.29124 LL=67916 DEF=Mus musculus phosphatidic acid phosphatase type 2B (Pap2b), mRNA, /PROD=phosphatidic acid phosphatase type 2B /FL=gb NM_080555.1 gb BC005558.1	2908.0999	967.49896	2102.5999	605.9832	1.2221063	3.0	0.3089313	0.37006545
gb BC026055.1 DB_XREF=gi 19913455 FEA=FLmRNA CNT=113 TID=Mm.3379.2 TIER=FL+Stack STK=4 UG=Mm.3379 LL=20425 /UG_GENE=Shnrt1 DEF=Mus musculus, serine hydroxymethyl transferase 1 (soluble), clone MGC:14007 IMAGE:4160579, mRNA, complete cds, /PROD=serine hydroxymethyl transferase 1 (soluble) /FL=gb AF237702.1 gb BC026055.1	459.9	176.8502	1045.8334	731.91003	1.3478124	2.0	0.31009194	0.37047827
gb NM_010907.1 DB_XREF=gi 5754339 GEN=NR1Kb3 FEA=FLmRNA CNT=183 TID=Mm.8884.1 TIER=FL+Stack STK=97 UG=Mm.8884 /LL=168 DEF=Mus musculus nuclear factor of kappa light chain gene enhancer in B-cells inhibitor, alpha (Nfkbia), mRNA, /PROD=nuclear factor of kappa light chain gene enhancer in B-cells inhibitor, alpha (Nfkbia) /FL=gb NM_010907.1 gb U36277.1	2398.0999	1137.4896	1406.9668	523.849	1.3708122	2.0	0.30399716	0.3690233
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gb BC026055.1 DB_XREF=gi 19913455 FEA=FLmRNA CNT=113 TID=Mm.3379.2 TIER=FL+Stack STK=4 UG=Mm.3379 LL=20425 /UG_GENE=Shnrt1 DEF=Mus musculus, serine hydroxymethyl transferase 1 (soluble), clone MGC:14007 IMAGE:4160579, mRNA, complete cds, /PROD=serine hydroxymethyl transferase 1 (soluble) /FL=gb AF237702.1 gb BC026055.1	459.9	176.8502	1045.8334	731.91003	1.3478124	2.0	0.31009194	0.37047827
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gb:NM_007657.1/DB_XREF=gi:6680893/GEN=Cd9/FEA=FLmRNA/CNT=324/TID=Mm.2956.1/TIER=FL+Stack/STK=135/UG=Mm.2956/LL=12527/DEF=Mus musculus CD9 antigen (Cd9), mRNA, /PROD=CD9 antigen /FL=gb:L08115.1 gb:NM_007657.1	2590.3333	1327.7048	1686.2667	684.79297	1.0481877	2.0	0.40454426	0.43938538
gb:NM_009870.7/DB_XREF=gi:6753379/GEN=CDk4/FEA=FLmRNA/CNT=239/TID=Mm.6839.1/TIER=FL+Stack/STK=122/UG=Mm.6839/LL=1267/DEF=Mus musculus cyclin-dependent kinase 4 (Cd4), mRNA, /PROD=cyclin-dependent kinase 4 /FL=gb:L01640.1 gb:NM_009870.1	993.26666	444.49567	694.5334	217.49274	1.0456059	2.0	0.40549216	0.43936384
gb:AK004342.1/DB_XREF=gi:12635491/FEA=mRNA/CNT=37/TID=Mm.178550.2/TIER=Stack/STK=19/UG=Mm.178550/LL=66478/UG_GENE=2410026K10Rik/UG_TITLE=RIKEN cDNA 2410026K10 gene /DEF=Mus musculus 18 days embryo whole body cDNA, RIKEN full-length enriched library, clone:1110061M03.homolog to T-CELL SURFACE GLYCOPROTEIN E2 PRECURSOR (E2 ANTIGEN) (CD99) (MIC2 PROTEIN) (I2E7), full insert sequence.	849.5334	656.2247	453.93335	76.852875	1.0370659	2.0	0.40864527	0.44172606
gb:BC025654.1/DB_XREF=gi:19343912/FEA=FLmRNA/CNT=105/TID=Mm.25602.1/TIER=FL+Stack/STK=80/UG=Mm.25602/DEF=Mus musculus, Similar to DKFZP586L151 protein, clone MGC:35286 IMAGE:5342879, mRNA, complete cds, /PROD=Similar to DKFZP586L151 protein /FL=gb:BC025654.1	1097.0668	515.759	756.93335	245.942	1.0310311	2.0	0.41088986	0.44309738
gb:NM_019521.1/DB_XREF=gi:9506714/GEN=Gas6/FEA=FLmRNA/CNT=147/TID=Mm.3982.1/TIER=FL+Stack/STK=46/UG=Mm.3982/LL=14456/DEF=Mus musculus growth arrest specific 6 (Gas6), mRNA, /PROD=growth arrest specific 6 /FL=gb:BC005444.1 gb:NM_019521.1 gb:BC010584.1/DB_XREF=gi:14714826/FEA=FLmRNA/CNT=83/TID=Mm.219659.1/TIER=FL+Stack/STK=24/UG=Mm.219659/LL=15267/UG_GENE=Hst2/DEF=Mus musculus, H2A histone family, member O, clone MGC:5956 IMAGE:3582122, mRNA, complete cds.	1537.0668	912.65375	992.8333	134.19629	1.0218685	2.0	0.41432413	0.44468832
gb:BC015439.1/DB_XREF=gi:15830030/FEA=FLmRNA/CNT=83/TID=Mm.18814.1/TIER=FL+Stack/STK=10/UG=Mm.18814/LL=66898/UG_GENE=1300006M19Rik/DEF=Mus musculus, RIKEN cDNA 1300006M19 gene, clone MGC:8269 IMAGE:3592632, mRNA, complete cds, /PROD=RIKEN cDNA 1300006M19 gene /FL=gb:BC015439.1	992.26666	1056.4161	371.96667	48.13329	1.015961	2.0	0.41655517	0.4460284
gb:NM_008788.1/DB_XREF=gi:6679220/GEN=Poolce/FEA=FLmRNA/CNT=152/TID=Mm.18808.1/TIER=FL+Stack/STK=74/UG=Mm.18808/LL=18542/DEF=Mus musculus procollagen C-proteinase enhancer protein (Poolce), mRNA, /PROD=procollagen C-proteinase enhancer protein /FL=gb:NM_008788.1	3300.6667	1719.5554	2233.6333	697.6866	0.99593264	2.0	0.42421845	0.4531651
gb:NM_007826.1/DB_XREF=gi:12841627/FEA=mRNA/CNT=37/TID=Mm.157783.14/TIER=Stack/STK=27/UG=Mm.157783/LL=104911/UG_GENE=AIB93585/UG_TITLE=expressed sequence AIB93585 /DEF=Mus musculus, 10 day old male pancreas cDNA, RIKEN full-length enriched library, clone:1810048H17.immunoglobulin heavy chain, (J558 family), full insert sequence.	536.60004	343.23163	1281.9667	1260.6519	0.98811466	2.0	0.42725167	0.45533392
gb:NM_010890.1/DB_XREF=gi:13994148/GEN=Nedd3a4/FEA=FLmRNA/CNT=23/TID=Mm.16553.1/TIER=FL/STK=17/UG=Mm.16553/LL=17999/DEF=Mus musculus neural precursor cell expressed, developmentally down-regulated gene 4a (Nedd4), mRNA, /PROD=neural precursor cell expressed, developmentally down-regulated gene 4a /FL=gb:NM_010890.1	1768.7333	992.5988	1140.6	479.7904	0.98683304	2.0	0.42775115	0.45479864
gb:BC025131.1/DB_XREF=gi:19264044/FEA=FLmRNA/CNT=81/TID=Mm.41931.1/TIER=FL+Stack/STK=23/UG=Mm.41931/LL=50530/UG_GENE=Mtaps-pending /DEF=Mus musculus, Similar to microfibrillar associated protein 5, clone MGC:35969 IMAGE:3982519, mRNA, complete cds, /PROD=Similar to microfibrillar associated protein 5 /FL=gb:AF180805.1 gb:NM_015776.1 gb:BC025131.1	4995.033	2107.182	3669.4668	1422.718	0.9030253	3.0	0.43307415	0.45938239
gb:NM_013472.1/DB_XREF=gi:7304890/GEN=Anxa6/FEA=FLmRNA/CNT=413/TID=Mm.22619.1/TIER=FL+Stack/STK=233/UG=Mm.22619/LL=11749/DEF=Mus musculus annexin A6 (Anxa6), mRNA, /PROD=annexin A6 /FL=gb:NM_013472.1 gb:BC005595.1 gb:BC019775.1/DB_XREF=gi:18043602/FEA=FLmRNA/CNT=156/TID=Mm.214514.1/TIER=FL+Stack/STK=98/UG=Mm.214514/LL=116847/UG_GENE=Prep /DEF=Mus musculus, proline arginine-rich end leucine-rich repeat, clone MGC:52825 IMAGE:4165772, mRNA, complete cds, /PROD=proline arginine-rich end leucine-rich repeat /FL=gb:BC019775.1 gb:NM_054077.1	2057.4666	881.61163	1507.8334	424.67703	0.97284544	2.0	0.43324443	0.45849165
gb:NM_032541.1/DB_XREF=gi:14221154/GEN=Hamp/FEA=FLmRNA/CNT=18/TID=Mm.23995.1/TIER=FL+Stack/STK=12/UG=Mm.23995/LL=84506/DEF=Mus musculus, hepcidin antimicrobial peptide (Hamp), mRNA, /PROD=hepcidin antimicrobial peptide /FL=gb:NM_032541.1 gb:AF297664.1 gb:BC021587.1	4090.6667	2158.8376	2871.2	441.99368	0.95850414	2.0	0.43895587	0.46238044
gb:AK008203.1/DB_XREF=gi:12842246/FEA=FLmRNA/CNT=83/TID=Mm.18814.1/TIER=Stack/STK=25/UG=Mm.18814/LL=66898/UG_GENE=1300006M19Rik/UG_TITLE=RIKEN cDNA 130006M19 gene /DEF=Mus musculus adult male intestine cDNA, RIKEN full-length enriched library, clone:2010012D17.homolog to INSULIN RECEPTOR TYROSINE KINASE SUBSTRATE, full insert sequence.	2052.7	2641.6304	592.10004	181.3516	0.95542985	2.0	0.4401908	0.46260792
gb:BC015459.1/DB_XREF=gi:13933834/FEA=FLmRNA/CNT=521/TID=Mm.140785.1/TIER=FL+Stack/STK=158/UG=Mm.140785/LL=140785/UG_GENE=20249/UG_GENE=Scd1/DEF=Mus musculus, steroyl-Coenzyme A desaturase 1, clone MGC:6427 IMAGE:3599932, mRNA, complete cds, /PROD=steroyl-Coenzyme A desaturase 1 /FL=gb:BC007474.1 gb:NM_009127.1	6781.533	901.3425	11328.734	8234.607	0.95077056	2.0	0.44206956	0.46350944
gb:BC025161.1/DB_XREF=gi:19263792/FEA=FLmRNA/CNT=98/TID=Mm.29503.1/TIER=FL+Stack/STK=47/UG=Mm.29503/LL=68479/UG_GENE=111000780Rik/DEF=Mus musculus, hypothetical protein MGC1346, clone MGC:36856 IMAGE:4235469, mRNA, complete cds, /PROD=hypothetical protein MGC1346 /FL=gb:BC025161.1	990.4001	521.377	693.3333	156.94771	0.94498926	2.0	0.4444127	0.46489254
gb:NM_013550.1/DB_XREF=gi:7305140/GEN=Hist4/FEA=FLmRNA/CNT=9/TID=Mm.193557.1/TIER=FL/STK=1/UG=Mm.193557/LL=15269/DEF=Mus musculus histone 4 protein (Hist4), mRNA, /PROD=histone 4 protein /FL=gb:NM_013550.1	2056.1667	1616.3438	1194.2001	14.616449	0.9236334	2.0	0.45318398	0.4729782
gb:NM_019427.1/DB_XREF=gi:14221154/GEN=Hamp/FEA=FLmRNA/CNT=18/TID=Mm.23995.1/TIER=FL+Stack/STK=12/UG=Mm.23995/LL=84506/DEF=Mus musculus, hepcidin antimicrobial peptide (Hamp), mRNA, /PROD=hepcidin antimicrobial peptide /FL=gb:NM_019427.1 gb:AF297664.1 gb:BC021587.1	1015.76666	444.64703	1562.2001	960.1859	0.8944442	2.0	0.46547025	0.48468689
gb:AK011936.1/DB_XREF=gi:12849366/FEA=mRNA/CNT=86/TID=Mm.203875.1/TIER=Stack/STK=50/UG=Mm.203875/LL=72478/UG_GENE=2610209L21Rik/UG_TITLE=RIKEN cDNA 2610209L21 gene /DEF=Mus musculus 10 days embryo whole body cDNA, RIKEN full-length enriched library, clone:2610209L21.unclassifiable transcript, full insert sequence.	1655.0	803.78375	1204.4667	482.45084	0.8324072	3.0	0.4662473	0.48438507
gb:NM_010664.1/DB_XREF=gi:6754481/GEN=Krt18/FEA=FLmRNA/CNT=380/TID=Mm.22479.1/TIER=FL+Stack/STK=149/UG=Mm.22479/LL=16689/DEF=Mus musculus keratin complex 1, acidic, gene 18 (Krt1-18), mRNA, /PROD=keratin complex 1, acidic, gene 18 /FL=gb:M36376.1 gb:NM_010664.1 gb:M11686.1	497.56665	1510.219	883.39996	751.11115	0.8897052	2.0	0.46749777	0.48457533
gb:BB204720/DB_XREF=gi:16351882/DB_XREF=BB204720/CLONE=AA30059G22/FEA=FLmRNA/CNT=74/TID=Mm.182434.2/TIER=Stack/STK=16/UG=Mm.182434/UG_TITLE=Mus musculus, Similar to RIKEN cDNA 1700066C05 gene, clone MGC:28125 IMAGE:3980327, mRNA, complete cds /FL=gb:BC020078.1	416.06668	181.6803	901.2	929.3317	0.88737375	2.0	0.4684986	0.48450652
gb:NM_009156.1/DB_XREF=gi:6677916/GEN=Sepw1/FEA=FLmRNA/CNT=217/TID=Mm.42829.1/TIER=FL+Stack/STK=83/UG=Mm.42829/LL=20364/DEF=Mus musculus selenoprotein W, muscle 1 (Sepw1), mRNA, /PROD=selenoprotein W, muscle 1 /FL=gb:U67890.1 gb:A241527.2 gb:AF015284.1 gb:NM_009156.1	2498.2	1507.5862	1717.6	341.65616	0.8746445	2.0	0.4740024	0.48908427
gb:NM_134051.1/DB_XREF=gi:19267267/FEA=FLmRNA/CNT=3/TID=Mm.157783.1/TIER=FL/STK=2/UG=Mm.157783/LL=104911/DEF=Mus musculus expressed sequence AIB93585 (AIB93585), mRNA, /PROD=expressed sequence AIB93585 /FL=gb:NM_134051.1 gb:BC013488.1	1823.8334	1609.4973	5154.1665	6440.4775	0.8689117	2.0	0.47650295	0.49054953
gb:BC019425.1/DB_XREF=gi:18043870/FEA=FLmRNA/CNT=5/TID=Mm.157783.67/TIER=FL/STK=1/UG=Mm.157783/LL=104911/UG_GENE=AIB93585/DEF=Mus musculus, clone MGC:30346 IMAGE:4459683, mRNA, complete cds, /PROD=Unknown (protein for MGC:30346) /FL=gb:BC019425.1	893.8333	797.18445	2621.0002	3428.4812	0.8498838	2.0	0.48490024	0.49806497
gb:NM_032541.1/DB_XREF=gi:14221154/GEN=Hamp/FEA=FLmRNA/CNT=18/TID=Mm.23995.1/TIER=FL+Stack/STK=12/UG=Mm.23995/LL=84506/DEF=Mus musculus hepcidin antimicrobial peptide (Hamp), mRNA, /PROD=hepcidin antimicrobial peptide /FL=gb:NM_032541.1 gb:AF297664.1 gb:BC021587.1	3380.7666	2024.4442	2395.367	236.9967	0.8373586	2.0	0.4905101	0.5026898
gb:AK017926.1/DB_XREF=gi:12857423/FEA=mRNA/CNT=124/TID=Mm.21697.1/TIER=Stack/STK=56/UG=Mm.21697/LL=74747/UG_GENE=5830413E08Rik/UG_TITLE=RIKEN cDNA 5830413E08 gene /DEF=Mus musculus adult male thymus cDNA, RIKEN full-length enriched library, clone:5830413E08.homolog to HYPOTHETICAL 25.4 KDA PROTEIN, full insert sequence.	2388.0667	451.77954	1741.9	1306.4413	0.8096306	2.0	0.50316334	0.51449585
gb:NM_017370.1/DB_XREF=gi:8850218/GEN=Hpf/FEA=FLmRNA/CNT=154/TID=Mm.26730.1/TIER=FL+Stack/STK=33/UG=Mm.26730/LL=15439/DEF=Mus musculus haptoglobin (Hp), mRNA, /PROD=haptoglobin /FL=gb:NM_017370.1 gb:M96827.1	705.19995	506.99698	440.69998	253.31256	0.8083316	2.0	0.5037641	0.51395255
gb:AF127033.1/DB_XREF=gi:9937096/FEA=FLmRNA/CNT=402/TID=Mm.3760.1/TIER=FL+Stack/STK=97/UG=Mm.3760/LL=14104/UG_GENE=Fasn/DEF=Mus musculus fatty acid synthase mRNA, complete cds, /PROD=fatty acid synthase /FL=gb:AF127033.1	1379.7334	459.9069	2322.4333	1995.7894	0.797231	2.0	0.5089267	0.51805544
gb:NM_010180.1/DB_XREF=gi:6753821/GEN=Fbn1/FEA=FLmRNA/CNT=91/TID=Mm.219663.1/TIER=FL+Stack/STK=41/UG=Mm.219663/LL=14114/DEF=Mus musculus fibulin 1 (Fbn1), mRNA, /PROD=fibulin 1 /FL=gb:NM_010180.1	835.6333	728.61206	505.8666	168.10336	0.76385224	2.0	0.52476585	0.53298366
gb:NM_009052.1/DB_XREF=gi:6677720/GEN=Rea3/FEA=FLmRNA/CNT=77/TID=Mm.14768.1/TIER=FL+Stack/STK=56/UG=Mm.14768/LL=19716/DEF=Mus musculus reduced expression 3 (Rea3), mRNA, /PROD=reduced expression 3 /FL=gb:AF051347.1 gb:NM_009052.1 gb:AF097438.1	1297.2999	1452.1323	657.06665	84.7658	0.76234937	2.0	0.5254902	0.53252804
gb:AK010307.1/DB_XREF=gi:12845853/FEA=mRNA/CNT=161/TID=Mm.3014.1/TIER=ConsEnd/STK=0/UG=Mm.3014/LL=66386/UG_GENE=2310039H15Rik/UG_TITLE=RIKEN cDNA 2310039H15 gene /DEF=Mus musculus ES cells cDNA, RIKEN full-length enriched library, clone:2810470K21Rik.homolog to ACYL CARRIER PROTEIN, MITOCHONDRIAL PRECURSOR (ACP) (NADH-UBIQUINONE OXIDOREDUCTASE 9.6 KDA SUBUNIT) (EC 1.6.5.3) (EC 1.6.99.3) (CI-SADP), full insert sequ...	1906.5	288.7541	2880.9336	2196.1677	0.7619484	2.0	0.5256836	0.53153753
gb:NM_021400.1/DB_XREF=gi:10946747/GEN=Prg4/FEA=FLmRNA/CNT=10/TID=Mm.212696.1/TIER=FL/STK=6/UG=Mm.212696/LL=65022/DEF=Mus musculus proteoglycan 4 (megakaryocyte stimulating factor, articular superficial zone protein) (Prg4), mRNA, /PROD=proteoglycan 4 (megakaryocyte stimulating factor, articular superficial zone protein) /FL=gb:AB034730.1 gb:NM_021400.1	2187.3333	1512.217	1530.1998	243.50616	0.74308985	2.0	0.5348581	0.5396124
gb:BC021831.1/DB_XREF=gi:16256103/FEA=mRNA/CNT=7/TID=Mm.218360.1/TIER=ConsEnd/STK=0/UG=Mm.218360/DEF=Mus musculus, clone IMAGE:3983821, mRNA, partial cds, /PROD=Unknown (protein for IMAGE:3983821)	828.2	179.45923	1305.7333	1128.0948	0.72408855	2.0	0.54425615	0.5478765
gb:NM_008979.2/DB_XREF=gi:15638941/GEN=Cdv1/FEA=FLmRNA/CNT=48/TID=Mm.10125.1/TIER=FL+Stack/STK=11/UG=Mm.10125/LL=12589/DEF=Mus musculus carnitine deficiency-associated gene expressed in ventricle 1 (Cdv1), mRNA, /PROD=carnitine deficiency-associated gene expressed in ventricle 1 /FL=gb:AF354757.1 gb:NM_008979.2	2408.5	1793.4084	1702.0	263.94318	0.6750568	2.0	0.569223	0.57174164
gb:BC025093.1/DB_XREF=gi:19263816/FEA=FLmRNA/CNT=37/TID=Mm.11480.2/TIER=FL/STK=1/UG=Mm.11480/LL=67239/UG_GENE=2810470K21Rik/DEF=Mus musculus, RIKEN cDNA 2810470K21 gene, clone MGC:35797 IMAGE:4009314, mRNA, complete cds, /PROD=RIKEN cDNA 2810470K21 gene /FL=gb:BC025093.1	1150.7666	101.20684	2018.6	2279.5244	0.6587568	2.0	0.5777513	0.57902664
gb:NM_054037.1/DB_XREF=gi:16905068/GEN=Scg3a1/FEA=FLmRNA/CNT=13/TID=Mm.22802.1/TIER=FL/STK=7/UG=Mm.22802/LL=68662/DEF=Mus musculus secretoglobulin, family 3A, member 1 (Scg3a1), mRNA, /PROD=UGRP2 type A /FL=gb:NM_054037.1 gb:AF313456.1	6362.733	6998.1064	3526.5332	5637.334	0.5466609	3.0	0.62264764	0.62264764