

## Down-regulated genes with annotations

<b>Aebp1</b>	<b><a href="#">AE binding protein 1</a></b>	<b><a href="#">Related Genes</a></b>	<b><a href="#">Mus musculus</a></b>
GOTERM_BP_FAT	<a href="#">transcription</a> , <a href="#">regulation of transcription</a> , <a href="#">DNA-dependent</a> , <a href="#">proteolysis</a> , <a href="#">cell adhesion</a> , <a href="#">biological adhesion</a> , <a href="#">regulation of transcription</a> , <a href="#">regulation of RNA metabolic process</a> ,		
GOTERM_CC_FAT	<a href="#">extracellular region</a> ,		
GOTERM_MF_FAT	<a href="#">DNA binding</a> , <a href="#">transcription cofactor activity</a> , <a href="#">transcription corepressor activity</a> , <a href="#">carboxypeptidase activity</a> , <a href="#">metallocarboxypeptidase activity</a> , <a href="#">transcription factor binding</a> , <a href="#">peptidase activity</a> , <a href="#">metalloexopeptidase activity</a> , <a href="#">metallopeptidase activity</a> , <a href="#">exopeptidase activity</a> , <a href="#">zinc ion binding</a> , <a href="#">transcription repressor activity</a> , <a href="#">transcription regulator activity</a> , <a href="#">ion binding</a> , <a href="#">cation binding</a> , <a href="#">metal ion binding</a> , <a href="#">transition metal ion binding</a> , <a href="#">peptidase activity, acting on L-amino acid peptides</a> ,		
INTERPRO	<a href="#">Coagulation factor 5/8 type, C-terminal</a> , <a href="#">Peptidase M14</a> , <a href="#">carboxypeptidase A</a> , <a href="#">Carboxypeptidase, regulatory region</a> ,		
SMART	<a href="#">FA58C</a> , <a href="#">Zn_pept</a> ,		
SP_PIR_KEYWORDS	<a href="#">alternative splicing</a> , <a href="#">cytoplasm</a> , <a href="#">dna-binding</a> , <a href="#">glycoprotein</a> , <a href="#">nucleus</a> , <a href="#">repressor</a> , <a href="#">Secreted</a> , <a href="#">signal</a> , <a href="#">Transcription</a> , <a href="#">transcription regulation</a> ,		
UP_SEQ_FEATURE	chain:Adipocyte enhancer-binding protein 1, compositionally biased region:Glu-rich, compositionally biased region:Lys-rich, compositionally biased region:Poly-Leu, domain:F5/8 type C, glycosylation site:N-linked (GlcNAc...), mutagenesis site, region of interest:Interaction with MAPK1 and MAPK3, region of interest:Interaction with PTEN, region of interest:Required for DNA-binding and interaction with NFKBIA, region of interest:Required for transcriptional repression, sequence conflict, signal peptide, splice variant,		
<b>Dbp</b>	<b><a href="#">D site albumin promoter binding protein</a></b>	<b><a href="#">Related Genes</a></b>	<b><a href="#">Mus musculus</a></b>
GOTERM_BP_FAT	<a href="#">transcription</a> , <a href="#">regulation of transcription</a> , <a href="#">DNA-dependent</a> , <a href="#">circadian rhythm</a> , <a href="#">regulation of cell proliferation</a> , <a href="#">regulation of transcription</a> , <a href="#">rhythmic process</a> , <a href="#">regulation of RNA metabolic process</a> ,		
GOTERM_MF_FAT	<a href="#">DNA binding</a> , <a href="#">transcription factor activity</a> , <a href="#">transcription regulator activity</a> , <a href="#">sequence-specific DNA binding</a> , <a href="#">protein dimerization activity</a> ,		
INTERPRO	<a href="#">Basic-leucine zipper (bZIP) transcription factor</a> , <a href="#">Basic leucine zipper</a> ,		
SMART	<a href="#">BRLZ</a> ,		
SP_PIR_KEYWORDS	<a href="#">activator</a> , <a href="#">biological rhythms</a> , <a href="#">dna-binding</a> , <a href="#">nucleus</a> , <a href="#">Transcription</a> , <a href="#">transcription regulation</a> ,		
UP_SEQ_FEATURE	chain:D site-binding protein, compositionally biased region:Poly-Pro, compositionally biased region:Poly-Ser, compositionally biased region:Pro-rich (proline/acidic region (PAR)), DNA-binding region:Basic motif, domain:Leucine-zipper, sequence conflict,		
<b>Gpr116</b>	<b><a href="#">G protein-coupled receptor 116</a></b>	<b><a href="#">Related Genes</a></b>	<b><a href="#">Mus musculus</a></b>
GOTERM_BP_FAT	<a href="#">cell surface receptor linked signal transduction</a> , <a href="#">G-protein coupled receptor protein signaling pathway</a> , <a href="#">neuropeptide signaling pathway</a> ,		
GOTERM_CC_FAT	<a href="#">plasma membrane</a> , <a href="#">integral to membrane</a> , <a href="#">intrinsic to membrane</a> ,		
INTERPRO	<a href="#">GPS</a> , <a href="#">GPCR, family 2</a> , <a href="#">secretin-like</a> , <a href="#">Immunoglobulin subtype</a> , <a href="#">Immunoglobulin-like</a> , <a href="#">GPCR, family 2</a> , <a href="#">Ig-hepta receptor</a> , <a href="#">Immunoglobulin</a> , <a href="#">GPCR, family 2-like</a> , <a href="#">GPCR, family 2</a> , <a href="#">secretin-like</a> , <a href="#">conserved site</a> ,		
PIR_SUPERFAMILY	<a href="#">PIRSF038682:probable G protein-coupled receptor 116</a> , <a href="#">PIRSF800007:secretin receptor-like G protein-coupled receptors</a> ,		
SMART	<a href="#">GPS</a> , <a href="#">IG</a> ,		
SP_PIR_KEYWORDS	<a href="#">cell membrane</a> , <a href="#">membrane</a> , <a href="#">transmembrane</a> ,		
<b>Notch3</b>	<b><a href="#">Notch gene homolog 3 (Drosophila)</a></b>	<b><a href="#">Related Genes</a></b>	<b><a href="#">Mus musculus</a></b>
GOTERM_BP_FAT	<a href="#">transcription</a> , <a href="#">cell surface receptor linked signal transduction</a> , <a href="#">Notch signaling pathway</a> , <a href="#">neuron differentiation</a> , <a href="#">forebrain development</a> , <a href="#">cell</a>		

<b>Aebp1</b>	<b><u>AE binding protein 1</u></b>	<b><u>Related Genes</u></b>	<b><u>Mus musculus</u></b>
	<a href="#">fate commitment</a> , <a href="#">regulation of transcription</a> , <a href="#">negative regulation of cell differentiation</a> , <a href="#">regulation of neuron differentiation</a> , <a href="#">negative regulation of neuron differentiation</a> , <a href="#">neuron fate commitment</a> , <a href="#">regulation of neurogenesis</a> , <a href="#">regulation of nervous system development</a> , <a href="#">regulation of cell development</a> ,		
GOTERM_CC_FAT	<a href="#">plasma membrane</a> , <a href="#">integral to plasma membrane</a> , <a href="#">integral to membrane</a> , <a href="#">intrinsic to membrane</a> , <a href="#">intrinsic to plasma membrane</a> , <a href="#">plasma membrane part</a> ,		
GOTERM_MF_FAT	<a href="#">calcium ion binding</a> , <a href="#">ion binding</a> , <a href="#">cation binding</a> , <a href="#">metal ion binding</a> ,		
INTERPRO	<a href="#">EGF-type aspartate/asparagine hydroxylation conserved site</a> , <a href="#">EGF-like, type 3</a> , <a href="#">Notch region</a> , <a href="#">EGF-like, type 2</a> , <a href="#">EGF-like calcium-binding</a> , <a href="#">Ankyrin</a> , <a href="#">EGF</a> , <a href="#">EGF-like</a> , <a href="#">Notch</a> , <a href="#">Notch, NOD region</a> , <a href="#">Notch, NODP region</a> , <a href="#">EGF-like region</a> , <a href="#">conserved site</a> , <a href="#">EGF calcium-binding</a> , <a href="#">EGF</a> , <a href="#">extracellular</a> , <a href="#">EGF-like calcium-binding</a> , <a href="#">conserved site</a> ,		
KEGG_PATHWAY	<a href="#">Dorso-ventral axis formation</a> , <a href="#">Notch signaling pathway</a> ,		
PIR_SUPERFAMILY	PIRSF002279:Notch, PIRSF002279:notch protein,		
SMART	<a href="#">NL</a> , <a href="#">EGF_CA</a> , <a href="#">EGF</a> , <a href="#">ANK</a> ,		
SP_PIR_KEYWORDS	<a href="#">activator</a> , <a href="#">ank repeat</a> , <a href="#">cell membrane</a> , <a href="#">developmental protein</a> , <a href="#">differentiation</a> , <a href="#">disulfide bond</a> , <a href="#">egf-like domain</a> , <a href="#">glycoprotein</a> , <a href="#">membrane</a> , <a href="#">notch signaling pathway</a> , <a href="#">nucleus</a> , <a href="#">phosphoprotein</a> , <a href="#">receptor</a> , <a href="#">repeat</a> , <a href="#">signal</a> , <a href="#">Transcription</a> , <a href="#">transcription regulation</a> , <a href="#">transmembrane</a> ,		
UP_SEQ_FEATURE	chain:Neurogenic locus notch homolog protein 3, chain:Notch 3 extracellular truncation, chain:Notch 3 intracellular domain, disulfide bond, domain:EGF-like 1, domain:EGF-like 10; calcium-binding, domain:EGF-like 11; calcium-binding, domain:EGF-like 12; calcium-binding, domain:EGF-like 13; calcium-binding, domain:EGF-like 14; calcium-binding, domain:EGF-like 15; calcium-binding, domain:EGF-like 16; calcium-binding, domain:EGF-like 17; calcium-binding, domain:EGF-like 18, domain:EGF-like 19, domain:EGF-like 2, domain:EGF-like 20, domain:EGF-like 21; calcium-binding, domain:EGF-like 22; calcium-binding, domain:EGF-like 23; calcium-binding, domain:EGF-like 24, domain:EGF-like 25, domain:EGF-like 26, domain:EGF-like 27, domain:EGF-like 28, domain:EGF-like 29; calcium-binding, domain:EGF-like 3, domain:EGF-like 30; calcium-binding, domain:EGF-like 31, domain:EGF-like 32, domain:EGF-like 33, domain:EGF-like 34, domain:EGF-like 4; calcium-binding, domain:EGF-like 5, domain:EGF-like 6; calcium-binding, domain:EGF-like 7, domain:EGF-like 8; calcium-binding, domain:EGF-like 9, glycosylation site:N-linked (GlcNAc...), mutagenesis site, region of interest:PEST-like, repeat:ANK 1, repeat:ANK 2, repeat:ANK 3, repeat:ANK 4, repeat:ANK 5, repeat:LNR 1, repeat:LNR 2, repeat:LNR 3, signal peptide, site:Cleavage; by furin-like protease, topological domain:Cytoplasmic, topological domain:Extracellular, transmembrane region,		
<b>2010007H12Rik</b>	<b><u>RIKEN cDNA 2010007H12 gene</u></b>	<b><u>Related Genes</u></b>	<b><u>Mus musculus</u></b>
SP_PIR_KEYWORDS	<a href="#">phosphoprotein</a> ,		
UP_SEQ_FEATURE	chain:UPF0683 protein C7orf47 homolog, compositionally biased region:Pro-rich, modified residue,		
<b>Agri</b>	<b><u>agrin</u></b>	<b><u>Related Genes</u></b>	<b><u>Mus musculus</u></b>
BIOCARTA	<a href="#">Agrin in Postsynaptic Differentiation</a> ,		
GOTERM_BP_FAT	<a href="#">regulation of transcription</a> , <a href="#">DNA-dependent</a> , <a href="#">regulation of transcription from RNA polymerase II promoter</a> , <a href="#">protein complex assembly</a> , <a href="#">plasma membrane organization</a> , <a href="#">cell surface receptor linked signal transduction</a> , <a href="#">enzyme linked receptor protein signaling pathway</a> , <a href="#">transmembrane receptor protein tyrosine kinase signaling pathway</a> , <a href="#">signal complex assembly</a> , <a href="#">G-protein coupled receptor protein signaling pathway</a> , <a href="#">muscarinic acetylcholine receptor signaling pathway</a> , <a href="#">cell-cell signaling</a> , <a href="#">synaptic transmission</a> , <a href="#">muscle organ development</a> , <a href="#">skeletal muscle tissue development</a> , <a href="#">neuromuscular junction development</a> , <a href="#">regulation of synaptic growth at neuromuscular junction</a> , <a href="#">positive regulation of biosynthetic process</a> , <a href="#">positive regulation of macromolecule biosynthetic process</a> , <a href="#">positive regulation of macromolecule metabolic process</a> , <a href="#">positive regulation of gene expression</a> , <a href="#">striated muscle tissue development</a> , <a href="#">membrane organization</a> , <a href="#">regulation of striated muscle tissue development</a> , <a href="#">transmission of nerve impulse</a> , <a href="#">positive regulation of cellular biosynthetic process</a> , <a href="#">cellular macromolecular complex subunit organization</a> , <a href="#">cellular macromolecular complex assembly</a> , <a href="#">regulation of growth</a> , <a href="#">muscle cell differentiation</a> , <a href="#">extracellular structure organization</a> , <a href="#">receptor metabolic process</a> , <a href="#">receptor clustering</a> , <a href="#">cellular protein complex assembly</a> , <a href="#">macromolecular</a>		

<b>Aebp1</b>	<b><a href="#">AE binding protein 1</a></b>	<b><a href="#">Related Genes</a></b>	<b><a href="#">Mus musculus</a></b>
	<a href="#">complex subunit organization</a> , <a href="#">regulation of cellular component biogenesis</a> , <a href="#">neurotransmitter receptor metabolic process</a> , <a href="#">regulation of transcription</a> , <a href="#">positive regulation of transcription, DNA-dependent</a> , <a href="#">positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process</a> , <a href="#">positive regulation of transcription</a> , <a href="#">positive regulation of transcription from RNA polymerase II promoter</a> , <a href="#">regulation of muscle development</a> , <a href="#">regulation of developmental growth</a> , <a href="#">regulation of skeletal muscle tissue development</a> , <a href="#">skeletal muscle fiber development</a> , <a href="#">regulation of skeletal muscle fiber development</a> , <a href="#">muscle fiber development</a> , <a href="#">regulation of synapse structure and activity</a> , <a href="#">regulation of synapse organization</a> , <a href="#">synapse organization</a> , <a href="#">neurological system process</a> , <a href="#">striated muscle cell differentiation</a> , <a href="#">regulation of muscle cell differentiation</a> , <a href="#">regulation of striated muscle cell differentiation</a> , <a href="#">positive regulation of nitrogen compound metabolic process</a> , <a href="#">regulation of RNA metabolic process</a> , <a href="#">positive regulation of RNA metabolic process</a> , <a href="#">regulation of nervous system development</a> , <a href="#">regulation of synaptogenesis</a> , <a href="#">muscle cell development</a> , <a href="#">striated muscle cell development</a> , <a href="#">regulation of cell development</a> , <a href="#">muscle tissue development</a> , <a href="#">skeletal muscle organ development</a> , <a href="#">macromolecular complex assembly</a> , <a href="#">protein complex biogenesis</a> ,		
GOTERM_CC_FAT	<a href="#">extracellular region</a> , <a href="#">proteinaceous extracellular matrix</a> , <a href="#">basement membrane</a> , <a href="#">basal lamina</a> , <a href="#">extracellular space</a> , <a href="#">cell surface</a> , <a href="#">extracellular matrix</a> , <a href="#">extracellular matrix part</a> , <a href="#">extracellular region part</a> , <a href="#">synapse</a> ,		
GOTERM_MF_FAT	<a href="#">receptor regulator activity</a> , <a href="#">acetylcholine receptor regulator activity</a> , <a href="#">laminin binding</a> , <a href="#">extracellular matrix binding</a> ,		
INTERPRO	<a href="#">SEA</a> , <a href="#">EGF-like, type 3</a> , <a href="#">Laminin G</a> , <a href="#">EGF-like</a> , <a href="#">laminin</a> , <a href="#">Proteinase inhibitor I1</a> , <a href="#">Kazal</a> , <a href="#">Follistatin-like</a> , <a href="#">N-terminal</a> , <a href="#">Agrin NtA</a> , <a href="#">EGF</a> , <a href="#">EGF-like</a> , <a href="#">Laminin G, subdomain 1</a> , <a href="#">EGF-like region, conserved site</a> , <a href="#">Concanavalin A-like lectin/glucanase, subgroup</a> ,		
KEGG_PATHWAY	<a href="#">ECM-receptor interaction</a> ,		
PIR_SUPERFAMILY	PIRSF002277:agrin,		
SMART	<a href="#">EGF Lam</a> , <a href="#">EGF</a> , <a href="#">SEA</a> , <a href="#">FOLN</a> , <a href="#">KAZAL</a> , <a href="#">LamG</a> ,		
SP_PIR_KEYWORDS	<a href="#">alternative splicing</a> , <a href="#">disulfide bond</a> , <a href="#">egf-like domain</a> , <a href="#">extracellular matrix</a> , <a href="#">glycoprotein</a> , <a href="#">heparan sulfate</a> , <a href="#">laminin egf-like domain</a> , <a href="#">proteoglycan</a> , <a href="#">repeat</a> , <a href="#">Secreted</a> , <a href="#">signal</a> ,		
UP_SEQ_FEATURE	chain:Agirin, compositionally biased region:Ser/Thr-rich, disulfide bond, domain:EGF-like 1, domain:EGF-like 2, domain:EGF-like 3, domain:EGF-like 4, domain:Kazal-like 1, domain:Kazal-like 2, domain:Kazal-like 3, domain:Kazal-like 4, domain:Kazal-like 5, domain:Kazal-like 6, domain:Kazal-like 7, domain:Kazal-like 8, domain:Kazal-like 9, domain:Laminin EGF-like 1, domain:Laminin EGF-like 2, domain:Laminin G-like 1, domain:Laminin G-like 2, domain:Laminin G-like 3, domain:SEA, glycosylation site:N-linked (GlcNAc...), sequence conflict, signal peptide, splice variant,		
<b>Naglu</b>	<b><a href="#">alpha-N-acetylglucosaminidase (Sanfilippo disease IIIB)</a></b>	<b><a href="#">Related Genes</a></b>	<b><a href="#">Mus musculus</a></b>
GOTERM_MF_FAT	<a href="#">alpha-N-acetylglucosaminidase activity</a> , <a href="#">hexosaminidase activity</a> ,		
INTERPRO	<a href="#">Alpha-N-acetylglucosaminidase</a> ,		
KEGG_PATHWAY	<a href="#">Glycosaminoglycan degradation</a> , <a href="#">Lysosome</a> ,		
PIR_SUPERFAMILY	PIRSF001091:alpha-N-acetylglucosaminidase,		
SP_PIR_KEYWORDS	<a href="#">glycosidase</a> , <a href="#">hydrolase</a> ,		
<b>Capn5</b>	<b><a href="#">calpain 5</a></b>	<b><a href="#">Related Genes</a></b>	<b><a href="#">Mus musculus</a></b>
GOTERM_BP_FAT	<a href="#">proteolysis</a> ,		
GOTERM_MF_FAT	<a href="#">endopeptidase activity</a> , <a href="#">cysteine-type endopeptidase activity</a> , <a href="#">calcium-dependent cysteine-type endopeptidase activity</a> , <a href="#">peptidase activity</a> , <a href="#">cysteine-type peptidase activity</a> , <a href="#">peptidase activity, acting on L-amino acid peptides</a> ,		
INTERPRO	<a href="#">C2 calcium-dependent membrane targeting</a> , <a href="#">Peptidase</a> , <a href="#">cysteine peptidase active site</a> , <a href="#">Peptidase C2</a> , <a href="#">calpain</a> ,		
PIR_SUPERFAMILY	PIRSF006670:human tissue-specific calpain htra-3,		
SMART	<a href="#">CysPc</a> , <a href="#">C2</a> , <a href="#">calpain_III</a> ,		
SP_PIR_KEYWORDS	<a href="#">hydrolase</a> , <a href="#">polymorphism</a> , <a href="#">Protease</a> , <a href="#">thiol protease</a> ,		

<b>Aebp1</b>	<b><a href="#">AE binding protein 1</a></b>	<b><a href="#">Related Genes</a></b>	<b><a href="#">Mus musculus</a></b>
UP_SEQ_FEATURE	chain:Calpain-5, domain:C2, domain:Calpain catalytic, region of interest:Domain III, sequence variant,		
<b>Col4a6</b>	<b><a href="#">collagen, type IV, alpha 6</a></b>	<b><a href="#">Related Genes</a></b>	<b><a href="#">Mus musculus</a></b>
GOTERM_BP_FAT	<a href="#">extracellular matrix organization</a> , <a href="#">extracellular structure organization</a> ,		
GOTERM_CC_FAT	<a href="#">extracellular region</a> , <a href="#">proteinaceous extracellular matrix</a> , <a href="#">collagen</a> , <a href="#">collagen type IV</a> , <a href="#">basement membrane</a> , <a href="#">sheet-forming collagen</a> , <a href="#">extracellular matrix</a> , <a href="#">extracellular matrix part</a> , <a href="#">extracellular region part</a> ,		
GOTERM_MF_FAT	<a href="#">structural molecule activity</a> , <a href="#">extracellular matrix structural constituent</a> ,		
INTERPRO	<a href="#">Type 4 procollagen, C-terminal repeat</a> , <a href="#">Collagen triple helix repeat</a> ,		
KEGG_PATHWAY	<a href="#">Focal adhesion</a> , <a href="#">ECM-receptor interaction</a> , <a href="#">Pathways in cancer</a> , <a href="#">Small cell lung cancer</a> ,		
PIR_SUPERFAMILY	PIRSF002258:collagen alpha 1(IV) chain,		
SMART	<a href="#">C4</a> ,		
SP_PIR_KEYWORDS	<a href="#">collagen</a> ,		
<b>H2-Q7, H2-Q2</b>	<b><a href="#">histocompatibility 2, Q region locus 1; histocompatibility 2, Q region locus 9; similar to H-2 class I histocompatibility antigen, L-D alpha chain precursor; histocompatibility 2, Q region locus 8; histocompatibility 2, Q region locus 2; similar to MHC class Ib antigen; histocompatibility 2, Q region locus 7; histocompatibility 2, Q region locus 6; hypothetical protein LOC100044307; similar to H-2 class I histocompatibility antigen, Q7 alpha chain precursor (QA-2 antigen); RIKEN cDNA 0610037M15 gene</a></b>	<b><a href="#">Related Genes</a></b>	<b><a href="#">Mus musculus</a></b>
GOTERM_BP_FAT	<a href="#">regulation of cytokine production</a> , <a href="#">positive regulation of cytokine production</a> , <a href="#">regulation of leukocyte mediated cytotoxicity</a> , <a href="#">positive regulation of leukocyte mediated cytotoxicity</a> , <a href="#">regulation of T cell mediated cytotoxicity</a> , <a href="#">positive regulation of T cell mediated cytotoxicity</a> , <a href="#">immune effector process</a> , <a href="#">antigen processing and presentation of peptide antigen via MHC class Ib</a> , <a href="#">antigen processing and presentation of peptide antigen via MHC class I</a> , <a href="#">antigen processing and presentation via MHC class Ib</a> , <a href="#">antigen processing and presentation of endogenous peptide antigen via MHC class Ib</a> , <a href="#">antigen processing and presentation of endogenous peptide antigen</a> , <a href="#">positive regulation of immune system process</a> , <a href="#">regulation of immune effector process</a> , <a href="#">positive regulation of immune effector process</a> , <a href="#">regulation of leukocyte mediated immunity</a> , <a href="#">positive regulation of leukocyte mediated immunity</a> , <a href="#">regulation of lymphocyte mediated immunity</a> , <a href="#">positive regulation of lymphocyte mediated immunity</a> , <a href="#">regulation of T cell mediated immunity</a> , <a href="#">positive regulation of T cell mediated immunity</a> , <a href="#">regulation of adaptive immune response</a> , <a href="#">positive regulation of adaptive immune response</a> , <a href="#">regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains</a> , <a href="#">positive regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains</a> , <a href="#">defense response</a> , <a href="#">immune response</a> , <a href="#">response to virus</a> , <a href="#">antigen processing and presentation</a> , <a href="#">antigen processing and presentation of endogenous antigen</a> , <a href="#">regulation of cell killing</a> , <a href="#">positive regulation of cell killing</a> , <a href="#">regulation of interferon-gamma production</a> , <a href="#">positive regulation of interferon-gamma production</a> , <a href="#">antigen processing and presentation of peptide antigen</a> , <a href="#">positive regulation of response to stimulus</a> , <a href="#">positive regulation of immune response</a> , <a href="#">positive regulation of multicellular organismal process</a> , <a href="#">defense response to virus</a> ,		
GOTERM_CC_FAT	<a href="#">plasma membrane</a> , <a href="#">external side of plasma membrane</a> , <a href="#">cell surface</a> , <a href="#">integral to membrane</a> , <a href="#">intrinsic to membrane</a> , <a href="#">MHC class Ib protein complex</a> , <a href="#">MHC protein complex</a> , <a href="#">MHC class I protein complex</a> , <a href="#">plasma membrane part</a> ,		
GOTERM_MF_FAT	<a href="#">antigen binding</a> , <a href="#">peptide binding</a> , <a href="#">peptide antigen binding</a> ,		
INTERPRO	<a href="#">MHC class I, alpha chain, alpha1 and alpha2</a> , <a href="#">Immunoglobulin/major histocompatibility complex, conserved site</a> , <a href="#">Immunoglobulin C1-set, Immunoglobulin-like</a> , <a href="#">MHC class I, alpha chain, C-terminal</a> , <a href="#">MHC class I-like antigen recognition</a> , <a href="#">Immunoglobulin-like fold</a> , <a href="#">LPXTG-motif cell wall anchor</a> ,		
KEGG_PATHWAY	<a href="#">Endocytosis</a> , <a href="#">Cell adhesion molecules (CAMs)</a> , <a href="#">Antigen processing and presentation</a> , <a href="#">Type I diabetes mellitus</a> , <a href="#">Autoimmune thyroid</a>		

<b>Aebp1</b>	<b><a href="#">AE binding protein 1</a></b>	<b><a href="#">Related Genes</a></b>	<b><a href="#">Mus musculus</a></b>
	<a href="#">disease</a> , <a href="#">Allograft rejection</a> , <a href="#">Graft-versus-host disease</a> , <a href="#">Viral myocarditis</a> ,		
PIR_SUPERFAMILY	PIRSF001990:class I histocompatibility antigen,		
SMART	<a href="#">IGc1</a> ,		
SP_PIR_KEYWORDS	<a href="#">3d-structure</a> , <a href="#">disulfide bond</a> , <a href="#">glycoprotein</a> , <a href="#">immune response</a> , <a href="#">membrane</a> , <a href="#">mhc i</a> , <a href="#">signal</a> , <a href="#">transmembrane</a> , <a href="#">transmembrane protein</a> , <a href="#">transplantation antigen</a> ,		
UP_SEQ_FEATURE	chain:class Ib MHC antigen Qa-2, chain:H-2 class I histocompatibility antigen, Q7 alpha chain, chain:H-2 class I histocompatibility antigen, Q8 alpha chain, chain:H-2 class I histocompatibility antigen, Q9 alpha chain, disulfide bond, domain:Ig-like C1-type, glycosylation site:N-linked (GlcNAc...), helix, region of interest:Alpha-1, region of interest:Alpha-2, region of interest:Alpha-3, region of interest:Connecting peptide, sequence conflict, signal peptide, strand, topological domain:Extracellular, transmembrane region, turn,		
<b>H2-T23</b>	<b><a href="#">histocompatibility 2, T region locus 23; similar to RT1 class Ib, locus H2-Q-like, grc region</a></b>	<b><a href="#">Related Genes</a></b>	<b><a href="#">Mus musculus</a></b>
GOTERM_BP_FAT	<a href="#">antigen processing and presentation of peptide antigen via MHC class I</a> , <a href="#">immune response</a> , <a href="#">antigen processing and presentation</a> , <a href="#">antigen processing and presentation of peptide antigen</a> ,		
GOTERM_CC_FAT	<a href="#">plasma membrane</a> , <a href="#">integral to membrane</a> , <a href="#">intrinsic to membrane</a> , <a href="#">MHC protein complex</a> , <a href="#">MHC class I protein complex</a> , <a href="#">plasma membrane part</a> ,		
INTERPRO	<a href="#">MHC class I, alpha chain, alpha1 and alpha2</a> , <a href="#">Immunoglobulin/major histocompatibility complex</a> , <a href="#">conserved site</a> , <a href="#">Immunoglobulin C1-set, Immunoglobulin-like</a> , <a href="#">MHC class I-like antigen recognition</a> , <a href="#">Immunoglobulin-like fold</a> ,		
KEGG_PATHWAY	<a href="#">Endocytosis</a> , <a href="#">Cell adhesion molecules (CAMs)</a> , <a href="#">Antigen processing and presentation</a> , <a href="#">Natural killer cell mediated cytotoxicity</a> , <a href="#">Type I diabetes mellitus</a> , <a href="#">Autoimmune thyroid disease</a> , <a href="#">Allograft rejection</a> , <a href="#">Graft-versus-host disease</a> , <a href="#">Viral myocarditis</a> ,		
PIR_SUPERFAMILY	PIRSF001990:class I histocompatibility antigen,		
SMART	<a href="#">IGc1</a> ,		
SP_PIR_KEYWORDS	<a href="#">disulfide bond</a> , <a href="#">glycoprotein</a> , <a href="#">heterodimer</a> , <a href="#">immune response</a> , <a href="#">membrane</a> , <a href="#">mhc i</a> , <a href="#">phosphoprotein</a> , <a href="#">signal</a> , <a href="#">transmembrane</a> , <a href="#">transmembrane protein</a> ,		
UP_SEQ_FEATURE	chain:H-2 class I histocompatibility antigen, D-37 alpha chain, disulfide bond, domain:Ig-like C1-type, glycosylation site:N-linked (GlcNAc...), modified residue, region of interest:Alpha-1, region of interest:Alpha-2, region of interest:Alpha-3, region of interest:Connecting peptide, signal peptide, topological domain:Cytoplasmic, topological domain:Extracellular, transmembrane region,		
<b>C630004H02Rik</b>	<b><a href="#">hypothetical protein LOC100043986; RIKEN cDNA C630004H02 gene</a></b>	<b><a href="#">Related Genes</a></b>	<b><a href="#">Mus musculus</a></b>
GOTERM_BP_FAT	<a href="#">sensory organ development</a> , <a href="#">sensory perception</a> , <a href="#">sensory perception of sound</a> , <a href="#">neuron differentiation</a> , <a href="#">ear morphogenesis</a> , <a href="#">inner ear morphogenesis</a> , <a href="#">mechanoreceptor differentiation</a> , <a href="#">ear development</a> , <a href="#">embryonic organ morphogenesis</a> , <a href="#">embryonic organ development</a> , <a href="#">embryonic morphogenesis</a> , <a href="#">inner ear development</a> , <a href="#">neurological system process</a> , <a href="#">cognition</a> , <a href="#">sensory perception of mechanical stimulus</a> , <a href="#">inner ear receptor cell differentiation</a> ,		
GOTERM_CC_FAT	<a href="#">integral to membrane</a> , <a href="#">intrinsic to membrane</a> ,		
GOTERM_MF_FAT	<a href="#">identical protein binding</a> , <a href="#">protein homodimerization activity</a> , <a href="#">protein dimerization activity</a> ,		
INTERPRO	<a href="#">High-temperature-induced dauer-formation protein-like</a> ,		
SP_PIR_KEYWORDS	<a href="#">alternative splicing</a> , <a href="#">membrane</a> , <a href="#">phosphoprotein</a> , <a href="#">transmembrane</a> ,		
UP_SEQ_FEATURE	chain:UPF0663 transmembrane protein C17orf28 homolog, modified residue, sequence conflict, splice variant, transmembrane region,		
<b>Nlgn2</b>	<b><a href="#">neuroligin 2</a></b>	<b><a href="#">Related Genes</a></b>	<b><a href="#">Mus musculus</a></b>
COG_ONTOLOGY	<a href="#">Lipid metabolism</a> ,		

<b>Aebp1</b>	<b><a href="#">AE binding protein 1</a></b>	<b><a href="#">Related Genes</a></b>	<b><a href="#">Mus musculus</a></b>
GOTERM_BP_FAT	<a href="#">regulation of respiratory gaseous exchange by neurological system process</a> , <a href="#">cell adhesion</a> , <a href="#">biological adhesion</a> , <a href="#">regulation of neurological system process</a> , <a href="#">extracellular structure organization</a> , <a href="#">regulation of respiratory gaseous exchange</a> , <a href="#">regulation of system process</a> , <a href="#">regulation of respiratory system process</a> , <a href="#">regulation of synaptic transmission</a> , <a href="#">synapse organization</a> , <a href="#">neurological system process</a> , <a href="#">regulation of transmission of nerve impulse</a> ,		
GOTERM_CC_FAT	<a href="#">integral to membrane</a> , <a href="#">intrinsic to membrane</a> , <a href="#">synapse</a> ,		
INTERPRO	<a href="#">Neurologin</a> , <a href="#">Carboxylesterase, type B</a> , <a href="#">Carboxylesterase type B</a> , <a href="#">conserved site</a> ,		
KEGG_PATHWAY	<a href="#">Cell adhesion molecules (CAMs)</a> ,		
SP_PIR_KEYWORDS	<a href="#">3d-structure</a> , <a href="#">cell adhesion</a> , <a href="#">disulfide bond</a> , <a href="#">glycoprotein</a> , <a href="#">membrane</a> , <a href="#">phosphoprotein</a> , <a href="#">signal</a> , <a href="#">transmembrane</a> ,		
UP_SEQ_FEATURE	chain:Neurologin-2, disulfide bond, glycosylation site:N-linked (GlcNAc...), helix, modified residue, sequence conflict, signal peptide, strand, topological domain:Cytoplasmic, topological domain:Extracellular, transmembrane region, turn,		
<b>Pltp</b>	<b><a href="#">phospholipid transfer protein</a></b>	<b><a href="#">Related Genes</a></b>	<b><a href="#">Mus musculus</a></b>
GOTERM_BP_FAT	<a href="#">lipid transport</a> , <a href="#">lipid localization</a> ,		
GOTERM_CC_FAT	<a href="#">extracellular region</a> ,		
GOTERM_MF_FAT	<a href="#">lipid binding</a> ,		
INTERPRO	<a href="#">Lipid-binding serum glycoprotein, C-terminal</a> , <a href="#">Lipid-binding serum glycoprotein, N-terminal</a> , <a href="#">Lipid-binding serum glycoprotein, conserved site</a> ,		
KEGG_PATHWAY	<a href="#">PPAR signaling pathway</a> ,		
PIR_SUPERFAMILY	PIRSF002417:lipopolysaccharide-binding protein,		
SMART	<a href="#">BPI1</a> , <a href="#">BPI2</a> ,		
SP_PIR_KEYWORDS	<a href="#">disulfide bond</a> , <a href="#">glycoprotein</a> , <a href="#">lipid transport</a> , <a href="#">phosphoprotein</a> , <a href="#">Secreted</a> , <a href="#">signal</a> , <a href="#">transport</a> ,		
UP_SEQ_FEATURE	chain:Phospholipid transfer protein, disulfide bond, glycosylation site:N-linked (GlcNAc...), modified residue, sequence conflict, signal peptide,		
<b>Pcsk9</b>	<b><a href="#">proprotein convertase subtilisin/kexin type 9</a></b>	<b><a href="#">Related Genes</a></b>	<b><a href="#">Mus musculus</a></b>
GOTERM_BP_FAT	<a href="#">urogenital system development</a> , <a href="#">kidney development</a> , <a href="#">liver development</a> , <a href="#">proteolysis</a> , <a href="#">neutral lipid metabolic process</a> , <a href="#">acylglycerol metabolic process</a> , <a href="#">triglyceride metabolic process</a> , <a href="#">phospholipid metabolic process</a> , <a href="#">glycerol ether metabolic process</a> , <a href="#">induction of apoptosis</a> , <a href="#">steroid metabolic process</a> , <a href="#">cholesterol metabolic process</a> , <a href="#">macromolecule catabolic process</a> , <a href="#">cellular response to starvation</a> , <a href="#">response to endogenous stimulus</a> , <a href="#">response to hormone stimulus</a> , <a href="#">regulation of catabolic process</a> , <a href="#">response to extracellular stimulus</a> , <a href="#">response to organic substance</a> , <a href="#">regulation of cell death</a> , <a href="#">positive regulation of cell death</a> , <a href="#">induction of programmed cell death</a> , <a href="#">sterol metabolic process</a> , <a href="#">protein processing</a> , <a href="#">protein autoprocessing</a> , <a href="#">organic ether metabolic process</a> , <a href="#">organophosphate metabolic process</a> , <a href="#">protein catabolic process</a> , <a href="#">neuron differentiation</a> , <a href="#">regulation of cellular catabolic process</a> , <a href="#">response to nutrient levels</a> , <a href="#">cellular response to extracellular stimulus</a> , <a href="#">cellular response to nutrient levels</a> , <a href="#">regulation of cellular protein metabolic process</a> , <a href="#">low-density lipoprotein receptor metabolic process</a> , <a href="#">receptor catabolic process</a> , <a href="#">low-density lipoprotein receptor catabolic process</a> , <a href="#">regulation of low-density lipoprotein receptor catabolic process</a> , <a href="#">response to insulin stimulus</a> , <a href="#">cellular response to insulin stimulus</a> , <a href="#">cellular response to hormone stimulus</a> , <a href="#">cellular response to stress</a> , <a href="#">lipoprotein metabolic process</a> , <a href="#">regulation of protein catabolic process</a> , <a href="#">homeostatic process</a> , <a href="#">response to starvation</a> , <a href="#">cholesterol homeostasis</a> , <a href="#">regulation of apoptosis</a> , <a href="#">positive regulation of apoptosis</a> , <a href="#">regulation of programmed cell death</a> , <a href="#">positive regulation of programmed cell death</a> , <a href="#">negative regulation of catalytic activity</a> , <a href="#">receptor metabolic process</a> , <a href="#">response to peptide hormone stimulus</a> , <a href="#">regulation of neuron apoptosis</a> , <a href="#">positive regulation of neuron apoptosis</a> , <a href="#">negative regulation of molecular function</a> , <a href="#">cellular protein catabolic process</a> , <a href="#">cellular macromolecule catabolic process</a> , <a href="#">glycerolipid metabolic process</a> , <a href="#">chemical homeostasis</a> , <a href="#">protein maturation</a> , <a href="#">protein maturation by peptide bond cleavage</a> , <a href="#">lipid homeostasis</a> , <a href="#">sterol homeostasis</a> ,		
GOTERM_CC_FAT	<a href="#">extracellular region</a> , <a href="#">extracellular space</a> , <a href="#">endoplasmic reticulum</a> , <a href="#">rough endoplasmic reticulum</a> , <a href="#">extracellular region part</a> ,		



<b>Aebp1</b>	<b><u>AE binding protein 1</u></b>	<b><u>Related Genes</u></b>	<b><u>Mus musculus</u></b>
GOTERM_MF_FAT	<a href="#">endopeptidase activity</a> , <a href="#">serine-type endopeptidase activity</a> , <a href="#">calcium ion binding</a> , <a href="#">peptidase activity</a> , <a href="#">serine-type peptidase activity</a> , <a href="#">serine hydrolase activity</a> , <a href="#">identical protein binding</a> , <a href="#">ion binding</a> , <a href="#">cation binding</a> , <a href="#">metal ion binding</a> , <a href="#">low-density lipoprotein receptor binding</a> , <a href="#">peptidase activity, acting on L-amino acid peptides</a> , <a href="#">lipoprotein receptor binding</a> ,		
INTERPRO	<a href="#">Peptidase S8 and S53</a> , <a href="#">subtilisin</a> , <a href="#">kexin</a> , <a href="#">sedolisin</a> , <a href="#">Proteinase inhibitor I9</a> , <a href="#">subtilisin propeptide</a> , <a href="#">Peptidase S8</a> , <a href="#">subtilisin-related</a> ,		
SP_PIR_KEYWORDS	<a href="#">autocatalytic cleavage</a> , <a href="#">calcium</a> , <a href="#">cholesterol metabolism</a> , <a href="#">disulfide bond</a> , <a href="#">glycoprotein</a> , <a href="#">hydrolase</a> , <a href="#">lipid metabolism</a> , <a href="#">phosphoprotein</a> , <a href="#">Protease</a> , <a href="#">Secreted</a> , <a href="#">Serine protease</a> , <a href="#">signal</a> , <a href="#">steroid metabolism</a> , <a href="#">zymogen</a> ,		
UP_SEQ_FEATURE	active site: <a href="#">Charge relay system</a> , chain: <a href="#">Proprotein convertase subtilisin/kexin type 9</a> , <a href="#">disulfide bond</a> , domain: <a href="#">Peptidase S8</a> , <a href="#">glycosylation site:N-linked (GlcNAc...)</a> , <a href="#">modified residue</a> , <a href="#">sequence conflict</a> , <a href="#">short sequence motif:Cell attachment site</a> , <a href="#">signal peptide</a> , site: <a href="#">Cleavage; by autolysis</a> ,		
<b>Psmb8</b>	<b><u>proteasome (prosome, macropain) subunit, beta type 8 (large multifunctional peptidase 7)</u></b>	<b><u>Related Genes</u></b>	<b><u>Mus musculus</u></b>
COG_ONTOLOGY	<a href="#">Posttranslational modification</a> , <a href="#">protein turnover</a> , <a href="#">chaperones</a> ,		
GOTERM_BP_FAT	<a href="#">proteolysis</a> , <a href="#">immune response</a> , <a href="#">macromolecule catabolic process</a> , <a href="#">antigen processing and presentation</a> , <a href="#">protein catabolic process</a> , <a href="#">cellular protein catabolic process</a> , <a href="#">cellular macromolecule catabolic process</a> , <a href="#">proteolysis involved in cellular protein catabolic process</a> ,		
GOTERM_CC_FAT	<a href="#">proteasome complex</a> , <a href="#">endoplasmic reticulum</a> , <a href="#">proteasome core complex</a> , <a href="#">MHC class I peptide loading complex</a> , <a href="#">TAP complex</a> , <a href="#">endoplasmic reticulum part</a> ,		
GOTERM_MF_FAT	<a href="#">nucleotide binding</a> , <a href="#">nucleoside binding</a> , <a href="#">purine nucleoside binding</a> , <a href="#">endopeptidase activity</a> , <a href="#">threonine-type endopeptidase activity</a> , <a href="#">ATP binding</a> , <a href="#">peptidase activity</a> , <a href="#">purine nucleotide binding</a> , <a href="#">adenyl nucleotide binding</a> , <a href="#">ribonucleotide binding</a> , <a href="#">purine ribonucleotide binding</a> , <a href="#">adenyl ribonucleotide binding</a> , <a href="#">peptide binding</a> , <a href="#">MHC protein binding</a> , <a href="#">MHC class I protein binding</a> , <a href="#">threonine-type peptidase activity</a> , <a href="#">peptidase activity, acting on L-amino acid peptides</a> ,		
INTERPRO	<a href="#">Peptidase T1A</a> , <a href="#">proteasome beta-subunit</a> , <a href="#">Proteasome, alpha and beta subunits</a> , <a href="#">Proteasome, subunit alpha/beta</a> , <a href="#">Proteasome, beta-type subunit</a> , <a href="#">conserved site</a> ,		
KEGG_PATHWAY	<a href="#">Proteasome</a> ,		
PIR_SUPERFAMILY	<a href="#">PIRSF001212:multicatalytic endopeptidase complex chain C9</a> ,		
SP_PIR_KEYWORDS	<a href="#">cytoplasm</a> , <a href="#">hydrolase</a> , <a href="#">immune response</a> , <a href="#">nucleus</a> , <a href="#">polymorphism</a> , <a href="#">Protease</a> , <a href="#">proteasome</a> , <a href="#">threonine protease</a> , <a href="#">zymogen</a> ,		
UP_SEQ_FEATURE	active site: <a href="#">Nucleophile</a> , chain: <a href="#">Proteasome subunit beta type-8</a> , <a href="#">propeptide:Removed in mature form</a> , <a href="#">sequence conflict</a> , <a href="#">sequence variant</a> , site: <a href="#">Cleavage; by autocatalysis</a> ,		
<b>Rpl22</b>	<b><u>similar to 60S ribosomal protein L22 (Heparin binding protein HBp15); ribosomal protein L22 pseudogene; predicted gene 6784; ribosomal protein L22</u></b>	<b><u>Related Genes</u></b>	<b><u>Mus musculus</u></b>
GOTERM_BP_FAT	<a href="#">cell activation</a> , <a href="#">immune system development</a> , <a href="#">leukocyte differentiation</a> , <a href="#">translation</a> , <a href="#">hemopoiesis</a> , <a href="#">lymphocyte differentiation</a> , <a href="#">T cell differentiation</a> , <a href="#">T cell activation</a> , <a href="#">leukocyte activation</a> , <a href="#">alpha-beta T cell activation</a> , <a href="#">alpha-beta T cell differentiation</a> , <a href="#">lymphocyte activation</a> , <a href="#">hemopoietic or lymphoid organ development</a> ,		
GOTERM_CC_FAT	<a href="#">ribosome</a> , <a href="#">ribonucleoprotein complex</a> , <a href="#">non-membrane-bounded organelle</a> , <a href="#">intracellular non-membrane-bounded organelle</a> ,		
GOTERM_MF_FAT	<a href="#">pattern binding</a> , <a href="#">RNA binding</a> , <a href="#">structural constituent of ribosome</a> , <a href="#">structural molecule activity</a> , <a href="#">glycosaminoglycan binding</a> , <a href="#">heparin binding</a> , <a href="#">carbohydrate binding</a> , <a href="#">polysaccharide binding</a> ,		
INTERPRO	<a href="#">Ribosomal protein L22e</a> ,		
KEGG_PATHWAY	<a href="#">Ribosome</a> ,		
PIR_SUPERFAMILY	<a href="#">PIRSF002223:ribosomal protein L22</a> ,		
SP_PIR_KEYWORDS	<a href="#">heparin binding</a> , <a href="#">heparin-binding</a> , <a href="#">protein biosynthesis</a> , <a href="#">ribonucleoprotein</a> , <a href="#">ribosomal protein</a> , <a href="#">ribosome</a> , <a href="#">rna-binding</a> ,		

<b>Aebp1</b>	<b><a href="#">AE binding protein 1</a></b>	<b><a href="#">Related Genes</a></b>	<b><a href="#">Mus musculus</a></b>
UP_SEQ_FEATURE	chain:60S ribosomal protein L22, compositionally biased region:Asp/Glu-rich (highly acidic),		
<b>Slc25a1</b>	<b><a href="#">solute carrier family 25 (mitochondrial carrier, citrate transporter), member 1</a></b>	<b><a href="#">Related Genes</a></b>	<b><a href="#">Mus musculus</a></b>
BIOCARTA	<a href="#">Shuttle for transfer of acetyl groups from mitochondria to the cytosol,</a>		
GOTERM_CC_FAT	<a href="#">mitochondrion, mitochondrial envelope, mitochondrial inner membrane, integral to membrane, organelle inner membrane, organelle membrane, intrinsic to membrane, mitochondrial membrane, organelle envelope, envelope, mitochondrial part,</a>		
INTERPRO	<a href="#">Mitochondrial substrate carrier, Mitochondrial carrier protein, Adenine nucleotide translocator 1, Mitochondrial substrate/solute carrier,</a>		
PIR_SUPERFAMILY	PIRSF002458:ADP,ATP carrier protein,		
SP_PIR_KEYWORDS	<a href="#">membrane, repeat, transmembrane, transport,</a>		
<b>Thra</b>	<b><a href="#">thyroid hormone receptor alpha; similar to thyroid hormone receptor</a></b>	<b><a href="#">Related Genes</a></b>	<b><a href="#">Mus musculus</a></b>
GOTERM_BP_FAT	<a href="#">skeletal system development, cartilage condensation, ossification, transcription, regulation of transcription, DNA-dependent, regulation of transcription from RNA polymerase II promoter, cell adhesion, regulation of heart contraction, negative regulation of biosynthetic process, positive regulation of biosynthetic process, positive regulation of macromolecule biosynthetic process, negative regulation of macromolecule biosynthetic process, positive regulation of macromolecule metabolic process, negative regulation of macromolecule metabolic process, positive regulation of gene expression, negative regulation of gene expression, cell-cell adhesion, negative regulation of transcription, biological adhesion, negative regulation of cellular biosynthetic process, positive regulation of cellular biosynthetic process, negative regulation of DNA binding, negative regulation of transcription factor activity, regulation of system process, negative regulation of molecular function, regulation of transcription, positive regulation of transcription, DNA-dependent, negative regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process, positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process, positive regulation of transcription, positive regulation of transcription from RNA polymerase II promoter, skeletal system morphogenesis, regulation of transcription factor activity, regulation of binding, negative regulation of binding, regulation of DNA binding, negative regulation of nitrogen compound metabolic process, positive regulation of nitrogen compound metabolic process, cartilage development, regulation of RNA metabolic process, positive regulation of RNA metabolic process, bone development,</a>		
GOTERM_CC_FAT	<a href="#">cytosol,</a>		
GOTERM_MF_FAT	<a href="#">DNA binding, transcription factor activity, steroid hormone receptor activity, RNA binding, single-stranded RNA binding, ligand-dependent nuclear receptor activity, thyroid hormone receptor activity, zinc ion binding, transcription activator activity, transcription repressor activity, transcription regulator activity, identical protein binding, protein homodimerization activity, ion binding, cation binding, sequence-specific DNA binding, metal ion binding, transition metal ion binding, protein heterodimerization activity, protein dimerization activity,</a>		
INTERPRO	<a href="#">Nuclear hormone receptor, ligand-binding, core, Zinc finger, nuclear hormone receptor-type, Steroid hormone receptor, Thyroid hormone receptor, Nuclear hormone receptor, ligand-binding, Zinc finger, NHR/GATA-type,</a>		
KEGG_PATHWAY	<a href="#">Neuroactive ligand-receptor interaction,</a>		
PIR_SUPERFAMILY	PIRSF002533:thyroid hormone receptor,		
SMART	<a href="#">ZnF_C4, HOLI,</a>		
SP_PIR_KEYWORDS	<a href="#">alternative splicing, cytoplasm, DNA binding, dna-binding, isopeptide bond, metal-binding, nucleus, Proto-oncogene, receptor, rna editing, thyroid hormone receptor, Transcription, transcription regulation, ubl conjugation, zinc, zinc finger, zinc-finger,</a>		
UP_SEQ_FEATURE	chain:Thyroid hormone receptor alpha, cross-link:Glycyl lysine isopeptide (Lys-Gly) (interchain with G-Cter in ubiquitin), DNA-binding region:Nuclear receptor, region of interest:Ligand-binding, region of interest:Modulating, sequence conflict, splice variant, zinc finger region:NR C4-type,		
<b>Tgfb1</b>	<b><a href="#">transforming growth factor, beta induced</a></b>	<b><a href="#">Related Genes</a></b>	<b><a href="#">Mus musculus</a></b>
GOTERM_BP_FAT	<a href="#">cell adhesion, biological adhesion, extracellular matrix organization, extracellular structure organization,</a>		



<b>Aebp1</b>	<b><a href="#">AE binding protein 1</a></b>	<b><a href="#">Related Genes</a></b>	<b><a href="#">Mus musculus</a></b>
GOTERM_CC_FAT	<a href="#">extracellular region</a> , <a href="#">proteinaceous extracellular matrix</a> , <a href="#">extracellular space</a> , <a href="#">extracellular matrix</a> , <a href="#">extracellular region part</a> ,		
<b>Notch3</b>	<b><a href="#">Notch gene homolog 3 (Drosophila)</a></b>	<b><a href="#">Related Genes</a></b>	<b><a href="#">Mus musculus</a></b>

GOTERM_MF_FAT	<a href="#">extracellular matrix binding</a> ,		
INTERPRO	<a href="#">FAS1 domain</a> , <a href="#">EMI domain</a> , <a href="#">TGF beta-induced protein bIGH3/osteoblast-specific factor 2</a> ,		
PIR_SUPERFAMILY	PIRSF016553:BIGH3_OSF2, PIRSF016553:TGF beta-induced protein bIGH3/osteoblast-specific factor 2,		
SMART	<a href="#">FAS1</a> ,		
SP_PIR_KEYWORDS	<a href="#">cell adhesion</a> , <a href="#">disulfide bond</a> , <a href="#">extracellular matrix</a> , <a href="#">gamma-carboxyglutamic acid</a> , <a href="#">repeat</a> , <a href="#">Secreted</a> , <a href="#">signal</a> ,		
UP_SEQ_FEATURE	chain:Transforming growth factor-beta-induced protein ig-h3, disulfide bond, domain:EMI, domain:FAS1 1, domain:FAS1 2, domain:FAS1 3, domain:FAS1 4, modified residue, short sequence motif:Cell attachment site, signal peptide,		
<b>Trim65</b>	<b><a href="#">tripartite motif-containing 65</a></b>	<b><a href="#">Related Genes</a></b>	<b><a href="#">Mus musculus</a></b>
GOTERM_BP_FAT	<a href="#">proteolysis</a> , <a href="#">macromolecule catabolic process</a> , <a href="#">modification-dependent protein catabolic process</a> , <a href="#">protein catabolic process</a> , <a href="#">modification-dependent macromolecule catabolic process</a> , <a href="#">cellular protein catabolic process</a> , <a href="#">cellular macromolecule catabolic process</a> , <a href="#">proteolysis involved in cellular protein catabolic process</a> ,		
GOTERM_MF_FAT	<a href="#">protein C-terminus binding</a> , <a href="#">zinc ion binding</a> , <a href="#">protein domain specific binding</a> , <a href="#">ion binding</a> , <a href="#">cation binding</a> , <a href="#">metal ion binding</a> , <a href="#">transition metal ion binding</a> ,		
INTERPRO	<a href="#">Zinc finger, B-box</a> , <a href="#">Zinc finger, RING-type</a> , <a href="#">B302 (SPRY)-like</a> , <a href="#">SPla/Ryanodine receptor SPRY</a> , <a href="#">Butyrophilin-like</a> , <a href="#">SPRY-associated</a> , <a href="#">Zinc finger, RING-type</a> , <a href="#">conserved site</a> , <a href="#">SPla/Ryanodine receptor subgroup</a> , <a href="#">Zinc finger, C3HC4 RING-type</a> ,		
SMART	<a href="#">RING</a> , <a href="#">BBOX</a> , <a href="#">SPRY</a> , <a href="#">PRY</a> ,		
SP_PIR_KEYWORDS	<a href="#">acetylation</a> , <a href="#">alternative splicing</a> , <a href="#">coiled coil</a> , <a href="#">cytoplasm</a> , <a href="#">ligase</a> , <a href="#">metal-binding</a> , <a href="#">nucleus</a> , <a href="#">ubl conjugation pathway</a> , <a href="#">zinc</a> , <a href="#">zinc-finger</a> ,		
UP_SEQ_FEATURE	chain:Tripartite motif-containing protein 11, chain:Tripartite motif-containing protein 65, domain:B30.2/SPRY, modified residue, splice variant, zinc finger region:B box-type, zinc finger region:RING-type,		
<b>Vegfb</b>	<b><a href="#">vascular endothelial growth factor B</a></b>	<b><a href="#">Related Genes</a></b>	<b><a href="#">Mus musculus</a></b>
GOTERM_BP_FAT	<a href="#">angiogenesis</a> , <a href="#">blood vessel development</a> , <a href="#">vasculature development</a> , <a href="#">blood vessel morphogenesis</a> , <a href="#">regulation of cell division</a> , <a href="#">positive regulation of cell division</a> ,		
GOTERM_CC_FAT	<a href="#">extracellular region</a> ,		
GOTERM_MF_FAT	<a href="#">pattern binding</a> , <a href="#">glycosaminoglycan binding</a> , <a href="#">growth factor activity</a> , <a href="#">heparin binding</a> , <a href="#">carbohydrate binding</a> , <a href="#">polysaccharide binding</a> ,		
INTERPRO	<a href="#">Platelet-derived growth factor (PDGF)</a> ,		
KEGG_PATHWAY	<a href="#">Cytokine-cytokine receptor interaction</a> , <a href="#">mTOR signaling pathway</a> , <a href="#">Focal adhesion</a> , <a href="#">Pathways in cancer</a> , <a href="#">Renal cell carcinoma</a> , <a href="#">Pancreatic cancer</a> , <a href="#">Bladder cancer</a> ,		
SMART	<a href="#">PDGF</a> ,		
SP_PIR_KEYWORDS	<a href="#">alternative splicing</a> , <a href="#">angiogenesis</a> , <a href="#">developmental protein</a> , <a href="#">differentiation</a> , <a href="#">disulfide bond</a> , <a href="#">glycoprotein</a> , <a href="#">growth factor</a> , <a href="#">heparin-binding</a> , <a href="#">mitogen</a> , <a href="#">Secreted</a> , <a href="#">signal</a> ,		
UP_SEQ_FEATURE	chain:Vascular endothelial growth factor B, disulfide bond, sequence conflict, signal peptide, splice variant,		

KEGG_PATHWAY	<a href="#">Dorso-ventral axis formation</a> , <a href="#">Notch signaling pathway</a> ,		
<b>Agrn</b>	<a href="#">agrin</a>	<a href="#">Related Genes</a>	<a href="#">Mus musculus</a>
KEGG_PATHWAY	<a href="#">ECM-receptor interaction</a> ,		
<b>Nagln3</b>	<a href="#">alpha-N-acetylglucosaminidase (Sanfilippo disease IIIB)</a>	<a href="#">Related Genes</a>	<a href="#">MUS MUSCULUS</a>
KEGG_PATHWAY	<a href="#">Dorso-ventral axis formation</a> , <a href="#">Notch signaling pathway</a> ,		
<b>Col4a6</b>	<a href="#">collagen, type IV, alpha 6</a>	<a href="#">Related Genes</a>	<a href="#">MUS MUSCULUS</a>
KEGG_PATHWAY	<a href="#">Focal adhesion</a> , <a href="#">ECM-receptor interaction</a> , <a href="#">Pathways in cancer</a> , <a href="#">Small cell lung cancer</a> ,		
<b>H2-Q7, H2-Q2</b>	<a href="#">histocompatibility 2, Q region locus 1</a> ; <a href="#">histocompatibility 2, Q region locus 9</a> ; <a href="#">similar to H-2 class I histocompatibility antigen, L-D alpha chain precursor</a> ; <a href="#">histocompatibility 2, Q region locus 8</a> ; <a href="#">histocompatibility 2, Q region locus 2</a> ; <a href="#">similar to MHC class Ib antigen</a> ; <a href="#">histocompatibility 2, Q region locus 7</a> ; <a href="#">histocompatibility 2, Q region locus 6</a> ; <a href="#">hypothetical protein LOC100044307</a> ; <a href="#">similar to H-2 class I histocompatibility antigen, Q7 alpha chain precursor (QA-2 antigen)</a> ; <a href="#">RIKEN cDNA 0610037M15 gene</a>	<a href="#">Related Genes</a>	<a href="#">Mus musculus</a>
KEGG_PATHWAY	<a href="#">Endocytosis</a> , <a href="#">Cell adhesion molecules (CAMs)</a> , <a href="#">Antigen processing and presentation</a> , <a href="#">Type I diabetes mellitus</a> , <a href="#">Autoimmune thyroid disease</a> , <a href="#">Allograft rejection</a> , <a href="#">Graft-versus-host disease</a> , <a href="#">Viral myocarditis</a> ,		
<b>H2-T23</b>	<a href="#">histocompatibility 2, T region locus 23</a> ; <a href="#">similar to RT1 class Ib, locus H2-Q-like, grc region</a>	<a href="#">Related Genes</a>	<a href="#">Mus musculus</a>
KEGG_PATHWAY	<a href="#">Endocytosis</a> , <a href="#">Cell adhesion molecules (CAMs)</a> , <a href="#">Antigen processing and presentation</a> , <a href="#">Natural killer cell mediated cytotoxicity</a> , <a href="#">Type I diabetes mellitus</a> , <a href="#">Autoimmune thyroid disease</a> , <a href="#">Allograft rejection</a> , <a href="#">Graft-versus-host disease</a> , <a href="#">Viral myocarditis</a> ,		
<b>Nlgn2</b>	<a href="#">neuroligin 2</a>	<a href="#">Related Genes</a>	<a href="#">Mus musculus</a>
KEGG_PATHWAY	<a href="#">Cell adhesion molecules (CAMs)</a> ,		
<b>Pltp</b>	<a href="#">phospholipid transfer protein</a>	<a href="#">Related Genes</a>	<a href="#">Mus musculus</a>
KEGG_PATHWAY	<a href="#">PPAR signaling pathway</a> ,		
<b>Psmb8</b>	<a href="#">proteasome (prosome, macropain) subunit, beta type 8 (large multifunctional peptidase 7)</a>	<a href="#">Related Genes</a>	<a href="#">Mus musculus</a>
KEGG_PATHWAY	<a href="#">Proteasome</a> ,		
<b>Rpl22</b>	<a href="#">similar to 60S ribosomal protein L22 (Heparin binding protein HBp15)</a> ; <a href="#">ribosomal protein L22 pseudogene</a> ; <a href="#">predicted gene 6784</a> ; <a href="#">ribosomal protein L22</a>	<a href="#">Related Genes</a>	<a href="#">Mus musculus</a>
KEGG_PATHWAY	<a href="#">Ribosome</a> ,		
<b>Thra</b>	<a href="#">thyroid hormone receptor alpha</a> ; <a href="#">similar to thyroid hormone receptor</a>	<a href="#">Related Genes</a>	<a href="#">Mus musculus</a>
KEGG_PATHWAY	<a href="#">Neuroactive ligand-receptor interaction</a> ,		
<b>Vegfb</b>	<a href="#">vascular endothelial growth factor B</a>	<a href="#">Related Genes</a>	<a href="#">Mus musculus</a>
KEGG_PATHWAY	<a href="#">Cytokine-cytokine receptor interaction</a> , <a href="#">mTOR signaling pathway</a> , <a href="#">Focal adhesion</a> , <a href="#">Pathways in cancer</a> , <a href="#">Renal cell carcinoma</a> , <a href="#">Pancreatic cancer</a> , <a href="#">Bladder cancer</a> ,		

KEGG_PATHWAY	<a href="#">ECM-receptor interaction</a> ,		
<b>Naglu</b>	<a href="#">alpha-N-acetylglucosaminidase (Sanfilippo disease IIIB)</a>	<a href="#">Related Genes</a>	<a href="#">Mus musculus</a>
KEGG_PATHWAY	<a href="#">Glycosaminoglycan degradation</a> , <a href="#">Lysosome</a> ,		
<b>Col4a6</b>	<a href="#">collagen, type IV, alpha 6</a>	<a href="#">Related Genes</a>	<a href="#">Mus musculus</a>
KEGG_PATHWAY	<a href="#">Focal adhesion</a> , <a href="#">ECM-receptor interaction</a> , <a href="#">Pathways in cancer</a> , <a href="#">Small cell lung cancer</a> ,		
<b>H2-Q7, H2-Q2</b>	<a href="#">histocompatibility 2, Q region locus 1</a> ; <a href="#">histocompatibility 2, Q region locus 9</a> ; <a href="#">similar to H-2 class I histocompatibility antigen, L-D alpha chain precursor</a> ; <a href="#">histocompatibility 2, Q region locus 8</a> ; <a href="#">histocompatibility 2, Q region locus 2</a> ; <a href="#">similar to MHC class Ib antigen</a> ; <a href="#">histocompatibility 2, Q region locus 7</a> ; <a href="#">histocompatibility 2, Q region locus 6</a> ; <a href="#">hypothetical protein LOC100044307</a> ; <a href="#">similar to H-2 class I histocompatibility antigen, Q7 alpha chain precursor (QA-2 antigen)</a> ; <a href="#">RIKEN cDNA 0610037M15 gene</a>	<a href="#">Related Genes</a>	<a href="#">Mus musculus</a>
KEGG_PATHWAY	<a href="#">Endocytosis</a> , <a href="#">Cell adhesion molecules (CAMs)</a> , <a href="#">Antigen processing and presentation</a> , <a href="#">Type I diabetes mellitus</a> , <a href="#">Autoimmune thyroid disease</a> , <a href="#">Allograft rejection</a> , <a href="#">Graft-versus-host disease</a> , <a href="#">Viral myocarditis</a> ,		
<b>H2-T23</b>	<a href="#">histocompatibility 2, T region locus 23</a> ; <a href="#">similar to RT1 class Ib, locus H2-Q-like, grc region</a>	<a href="#">Related Genes</a>	<a href="#">Mus musculus</a>
KEGG_PATHWAY	<a href="#">Endocytosis</a> , <a href="#">Cell adhesion molecules (CAMs)</a> , <a href="#">Antigen processing and presentation</a> , <a href="#">Natural killer cell mediated cytotoxicity</a> , <a href="#">Type I diabetes mellitus</a> , <a href="#">Autoimmune thyroid disease</a> , <a href="#">Allograft rejection</a> , <a href="#">Graft-versus-host disease</a> , <a href="#">Viral myocarditis</a> ,		
<b>Nlgn2</b>	<a href="#">neuroligin 2</a>	<a href="#">Related Genes</a>	<a href="#">Mus musculus</a>
KEGG_PATHWAY	<a href="#">Cell adhesion molecules (CAMs)</a> ,		
<b>Pltp</b>	<a href="#">phospholipid transfer protein</a>	<a href="#">Related Genes</a>	<a href="#">Mus musculus</a>
KEGG_PATHWAY	<a href="#">PPAR signaling pathway</a> ,		
<b>Psmb8</b>	<a href="#">proteasome (prosome, macropain) subunit, beta type 8 (large multifunctional peptidase 7)</a>	<a href="#">Related Genes</a>	<a href="#">Mus musculus</a>
KEGG_PATHWAY	<a href="#">Proteasome</a> ,		
<b>Rpl22</b>	<a href="#">similar to 60S ribosomal protein L22 (Heparin binding protein HBp15)</a> ; <a href="#">ribosomal protein L22 pseudogene</a> ; <a href="#">predicted gene 6784</a> ; <a href="#">ribosomal protein L22</a>	<a href="#">Related Genes</a>	<a href="#">Mus musculus</a>
KEGG_PATHWAY	<a href="#">Ribosome</a> ,		
<b>Thra</b>	<a href="#">thyroid hormone receptor alpha</a> ; <a href="#">similar to thyroid hormone receptor</a>	<a href="#">Related Genes</a>	<a href="#">Mus musculus</a>
KEGG_PATHWAY	<a href="#">Neuroactive ligand-receptor interaction</a> ,		
<b>Vegfb</b>	<a href="#">vascular endothelial growth factor B</a>	<a href="#">Related Genes</a>	<a href="#">Mus musculus</a>
KEGG_PATHWAY	<a href="#">Cytokine-cytokine receptor interaction</a> , <a href="#">mTOR signaling pathway</a> , <a href="#">Focal adhesion</a> , <a href="#">Pathways in cancer</a> , <a href="#">Renal cell carcinoma</a> , <a href="#">Pancreatic cancer</a> , <a href="#">Bladder cancer</a> ,		

## Down-regulated Gene Pathway Analysis

