

Table S1. The Expression of Genes Involved In HIP-55-knockdown A549 Cells

Entrez Gene	Representative Public ID	Gene Symbol	Gene Title	Fold change	Gene Ontology Biological Process	Gene Ontology Cellular Component	Gene Ontology Molecular Function
22858	NM_173041	ICK	intestinal cell (MAK-like) kinase	0.10	protein amino acid phosphorylation	nucleus, membrane-bounded organelle	nucleotide binding, magnesium ion binding
123036	NM_152332	TC2N	tandem C2 domains, nuclear	0.21		nucleus	
245972	NM_152565	ATP6V0D2	ATPase, H+ transporting, lysosomal 38kDa, V0 subunit d2	4.08	proton transport	proton-transporting domain	hydrogen ion transmembrane transporter activity
117157	BC022407	SH2D1B	SH2 domain containing 1B	8.03			protein binding
7798	NM_033631	LUZP1	leucine zipper protein 1	28.88		nucleus	
25914	NM_173630	RTTN	rotatin	4.51	multicellular organismal development, determination of left/right symmetry		binding
26223	NM_012159	FBXL21	F-box and leucine-rich repeat protein 21	4.28	protein ubiquitination	ubiquitin ligase complex	ubiquitin-protein ligase activity
130749	NM_173077	CPO	carboxypeptidase O	0.17	proteolysis	extracellular region	carboxypeptidase activity, metalloproteinase activity, hydrolase activity
148789	NM_152490	B3GALNT2	beta-1,3-N-acetylgalactosaminyltransferase 2	3.56	protein amino acid glycosylation	Golgi apparatus, membrane	galactosyltransferase activity
256356	NM_152776	GK5	glycerol kinase 5 (putative)	0.12	carbohydrate metabolic process, glycerol metabolic process		glycerol kinase activity, ATP binding, transferase activity,
146057	BC041876	TTBK2	tau tubulin kinase 2	33.39	cell death, peptidyl-serine phosphorylation	intermediate filament	protein serine/threonine kinase activity, ATP binding, transferase activity
51699	BC032462	VPS29	vacuolar protein sorting 29 homolog (S. cerevisiae)	0.29	protein transport	cytoplasm, membrane	phosphoserine phosphatase activity, zinc ion binding
717	BC029781	C2	complement component 2	0.10	proteolysis, immune response	extracellular region	serine-type endopeptidase activity, hydrolase activity
346157	BG722372	ZNF391	zinc finger protein 391	32.52	transcription	nucleus	DNA binding, zinc ion binding
1586	AK094106	CYP17A1		0.04	C-steroid hormone biosynthetic process	mitochondrion, endoplasmic reticulum	steroid -alpha-monooxygenase activity

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149461	BC030524	CLDN19	claudin 19	0.21	visual perception,calcium-independent cell-cell adhesion	tight junction	magnesium ion binding
8418	BC022302	CMAH	cytidine monophosphate-N-acetylneuraminic acid hydroxylase (CMP-N-acetylneuraminate monooxygenase) pseudogene	0.11	oxidation reduction	cytoplasm	electron carrier activity,oxidoreductase activity,CMP-N-acetylneuraminate monooxygenase activity
57565	BC021267	KLHL14	kelch-like 14 (Drosophila)	48.50			protein binding
5743	AY151286	PTGS2	prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase)	0.32	cell motion, regulation of blood pressure	nucleus,endoplasmic reticulum,microsome	peroxidase activity,heme binding
144406	BC036233	WDR66	WD repeat domain 66	12.28			
27133	BC043409	KCNH5	potassium voltage-gated channel	31.80	phosphorelay,rtranscription,,signal transduction	membrane	potassium channel activity
283933	BC036762	ZNF843	zinc finger protein 843	5.79		intracellular	nucleic acid binding,zinc ion binding
5737	BC035694	PTGFR	prostaglandin F receptor (FP)	3.59	parturition	plasma membrane	prostaglandin F receptor activity
23545	BC0223,	ATP6V0A2	lysosomal V0 subunit a2	3.88	immune response, proton transport	acrosomal vesicle,endosome,plasma membrane	protein binding,hydrogen ion transmembrane transporter activity
57728	BC032578	WDR19	WD repeat domain 19	0.29	vesicle-mediated transport		protein binding
8243	BC046147	SMC1A	structural maintenance of chromosomes 1A	14.38	cell cycle ,nuclear mRNA splicing,DNA repair	condensed chromosome kinetochore,cytoplasm,	chromatin binding,microtubule motor activity
64344	AK021881	HIF3A	hypoxia inducible factor 3	0.30	regulation of transcription	nucleus,cytoplasm	DNA binding,signal transducer activity

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1974	BC039344	EIF4A2	eukaryotic translation initiation factor 4A, isoform 2	0.27	translation,interspecies interaction between organisms	eukaryotic translation initiation factor 4F complex	translation initiation factor activity,helicase activity
5081	AI250939	PAX7	paired box 7	0.30	transcription, anti-apoptosis,multicellular organismal development	nucleus	transcription factor activity
1915	BE622780	EEF1A1	Eukaryotic translation elongation factor 1 alpha 1	4.67	translational elongation	eukaryotic translation elongation factor 1 complex	translation elongation factor activity,GTPase activity
5337	AK091897	PLD1	phospholipase D1, phosphatidylcholine-specific	0.03	Ras protein signal transduction,lipid catabolic process	Golgi membrane,cytoplasm	phospholipase D activity
57498	AA992480	KIDINS220	kinase D-interacting substrate, 220kDa	0.16	intracellular signaling cascade	cytosol ,membrane	kinase activity
2335	W73431	FN1	fibronectin 1	3.50	acute-phase response,cell adhesion	extracellular region,fibrinogen complex,apical plasma membrane	collagen binding,peptidase activator activity
8091	AI990940	HMGA2	high mobility group AT-hook 2	0.21	regulation of transcription, cell cycle,	chromosome	DNA binding,protein binding
1729	AL832054	DIAPH1	diaphanous homolog 1 (Drosophila)	3.37	sensory perception of sound,actin cytoskeleton organization	cytoskeleton	actin binding,receptor binding,Rho GTPase binding
29880	BG94,96	ALG5	Asparagine-linked glycosylation 5, dolichyl-phosphate beta-glucosyltransferase homolog (S. cerevisiae)	0.30	protein glycosylation, determination of left/right symmetry	endoplasmic reticulum membrane	oligosaccharyl transferase activity
6546	Y12885	SLC8A1	solute carrier family 8 (sodium/calcium exchanger), member 1	3.21	Heart contraction, regulation of ion transport	plasma membraneT-tubule,sarcolemma	calcium:sodium antiporter activity
8874	AL831814	ARHGEF7	Rho guanine nucleotide exchange factor (GEF) 7	4.18	regulation of Rho protein signal transduction	nucleolus,cytosol	Rho guanyl-nucleotide exchange factor activity
1262	BC040277	CNGA4	cyclic nucleotide gated channel alpha 4	0.14	ion transport,sensory perception of smell	membrane	nucleotide binding,ion channel activity,cAMP binding
163051	BI830259	ZNF709	zinc finger protein 709	4.92	transcription	nucleus	DNA binding,zinc ion binding

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162998	AK095468	OR7D2	olfactory receptor, family 7, subfamily D, member 2	5.79	sensory perception of smell	plasma membrane	olfactory receptor activity
5166	AL832708	PDK4	pyruvate dehydrogenase kinase, isozyme 4	0.15	glucose metabolic process,signal transduction,peptidyl-histidine phosphorylation	mitochondrial	two-component sensor activity,protein histidine kinase activity,pyruvate dehydrogenase (acetyl-transferring) kinase activity
25862	AL049937	USP49	ubiquitin specific peptidase 49	21.64	ubiquitin-dependent protein catabolic process		ubiquitin thiolesterase activity,zinc ion binding
55191	BF,1535	NADSYN1	NAD synthetase 1	0.09	nitrogen compound metabolic process	cytosol	NAD+ synthase (glutamine-hydrolyzing) activity
5054	BC020765	SERPINE1	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1	4.46	chronological cell aging,blood coagulation,angiogenesis	extracellular region,plasma membrane	serine-type endopeptidase inhibitor activity
11320	BC031487	MGAT4A	Mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase, isozyme A	3.07	carbohydrate metabolic process,9N-glycan processing	extracellular region,Golgi apparatus,membrane	transferring glycosyl groups
81931	BC020837	ZNF93	zinc finger protein 93	0.08	transcription	nucleus	transcription factor activity,zinc ion binding
9970	BC030972	NR113	nuclear receptor subfamily 1, group I, member 3	9.67	transcription	nucleus	transcription factor activity,steroid hormone receptor activity
3987	BC015843	LIMS1	LIM and senescent cell antigen-like domains 1	15.36	cell aging	plasma membrane,focal adhesion	protein binding,zinc ion binding
472	BG623786	ATM	ataxia telangiectasia mutated	0.04	DNA repair,female gamete generation,brain development	nucleus,nucleoplasm ,spindle,cytoplasmic vesicle	DNA binding,protein serine/threonine kinase activity
473	AI920976	RERE	arginine-glutamic acid dipeptide (RE) repeats	14.14	transcription,multicellular organismal development	nucleus	transcription factor activity,protein binding,zinc ion binding
3728	NM_021991	JUP	junction plakoglobin	0.29	cell adhesion	cytoplasm,cytoplasm	cytoskeletal protein binding
999	NM_04360	CDH1	cadherin 1, type 1, E-cadherin (epithelial)	0.27	cell adhesion,regulation of caspase activity	Golgi apparatus,plasma membrane	calcium ion binding

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3490	NM_,1553	IGFBP7	insulin-like growth factor binding protein 7	3.65	cell adhesion,negative regulation of cell proliferation	extracellular region	insulin-like growth factor binding
6414	NM_,5410	SEPP1	selenoprotein P, plasma, 1	0.09	selenium metabolic process,response to oxidative stress,brain development	extracellular region	selenium binding
6426	M69040	SFRS1	splicing factor, arginine/serine-rich 1	7.78	RNA splicing	nucleus,spliceosome	RNA binding
4811	BF94,43	NID1	nidogen 1	4.12	cell adhesion	extracellular region,basement membrane	calcium ion binding
7102	NM_,4615	TSPAN7	tetraspanin 7	4.12	protein amino acid N-linked glycosylation	extracellular region,plasma membrane	calcium ion binding
1277	NM_,088	COL1A1	collagen, type I, alpha 1	0.31	skeletal system development, ossification,blood vessel development	extracellular regionn,collagen type I	extracellular matrix structural constituent,platelet-derived growth factor binding
6695	AF231124	SPOCK1	sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 1	3.68	cell motion,cell adhesion,signal transduction	extracellular matrix	calcium ion binding
28951	NM_021643	TRIB2	tribbles homolog 2 (Drosophila)	0.24	protein amino acid phosphorylation,regulation of MAP kinase activity	nucleus,cytoplasm,cytoskeleton	nucleotide binding,protein kinase inhibitor activity
3709	AI963873	ITPR2	inositol 1,4,5-triphosphate receptor, type 2	0.32	response to hypoxia,ion transport,calcium ion transport	endoplasmic reticulum	receptor activity,ion channel activity,
8743	U57059	TNFSF10	tumor necrosis factor (ligand) superfamily, member 10	0.16	apoptosis	extracellular region	receptor binding,cytokine activitytumor necrosis factor receptor binding
6507	NM_,4172	SLC1A3	solute carrier family 1 (glial high affinity glutamate transporter), member 3	0.05	neurotransmitter uptake	plasma membrane	high-affinity glutamate transmembrane transporter activity
290	NM_,1150	ANPEP	alanyl (membrane) aminopeptidase	11.58	angiogenesis,proteolysis	cytoplasm,ER-Golgi intermediate compartment	aminopeptidase activity,receptor activity
4646	AA877789	MYO6	myosin VI	0.29	protein transport,endocytosis	ruffle,nucleus,cytoplasm	nucleotide binding,motor activity

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6337	NM_,1038	SCNN1A	sodium channel, nonvoltage-gated 1 alpha	0.27	ion transport,excretion	plasma membrane	actin binding,ion channel activity,sodium channel activity
2487	U91903	FRZB	frizzled-related protein	4.93	multicellular organismal development,negative regulation of Wnt receptor signaling pathway	extracellular region	Wnt-protein binding
3109	NM_,2118	HLA-DMB	major histocompatibility complex, class II, DM beta	0.22	antigen processing and presentation	lysosome,plasma membrane	nucleotide binding
9923	AI557467	ZBTB40	zinc finger and BTB domain containing 40	3.96	transcription	nucleus	DNA binding,zinc ion binding
607	NM_,4326	BCL9	B-cell CLL/lymphoma 9	5.36	Wnt receptor signaling pathway	nucleus	protein binding
4316	NM_,2423	MMP7	matrix metalloproteinase 7 (matrilysin, uterine)	0.25	proteolysis	extracellular region	metalloendopeptidase activity
4015	NM_,2317	LOX	lysyl oxidase	3.44	blood vessel development,lung development	extracellular region	protein-lysine 6-oxidase activity
9730	NM_014703	VPRBP	Vpr (HIV-1) binding protein	3.26	modification-dependent protein catabolic process	cytoplasm	binding
4128	NM_,240	MAOA	monoamine oxidase A	0.30	catecholamine metabolic process,behavior	mitochondrion	amine oxidase activity,electron carrier activity
240	NM_,698	ALOX5	arachidonate 5-lipoxygenase	0.29	leukotriene metabolic process	nucleus,cytoplasm,membrane	arachidonate 5-lipoxygenase activity,calcium ion binding
6622	NM_,345	SNCA	synuclein, alpha (non A4 component of amyloid precursor)	0.18	anti-apoptosis	nucleus,cytoplasm	protein binding
4312	NM_,2421	MMP1	matrix metalloproteinase 1 (interstitial collagenase)	0.25	proteolysis	extracellular region	metalloendopeptidase activity,zinc ion binding
7020	NM_,3220	TFAP2A	transcription factor AP-2 alpha (activating enhancer binding protein 2 alpha)	0.10	regulation of transcription	nucleus	transcription factor activity

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3384	NM_,873	ICAM2	intercellular adhesion molecule 2	0.27	cell adhesion	plasma membrane	integrin binding
2244	NM_,5141	FGB	fibrinogen beta chain	0.19	signal transduction,platelet activation	extracellular region,platelet alpha granule	eukaryotic cell surface binding
11216	NM_,7202	AKAP10	A kinase (PRKA) anchor protein 10	0.21	signal transduction	cytoplasm,mitochondrion	signal transducer activity
316	NM_,1159	AOX1	aldehyde oxidase 1	3.04	oxygen and reactive oxygen species metabolic process	cytoplasm	aldehyde oxidase activity,electron carrier activity
3569	NM_,6,	IL6	interleukin 6 (interferon, beta 2)	3.14	neutrophil apoptosis,positive regulation of MAPKKK cascade	extracellular region	interleukin-6 receptor binding
350	NM_,042	APOH	apolipoprotein H (beta-2-glycoprotein I)	0.32	negative regulation of endothelial cell proliferation,positive regulation of lipoprotein lipase activity	extracellular region,intracellular membrane-bounded organelle	lipoprotein lipase activator activity
4306	NM_,901	NR3C2	nuclear receptor subfamily 3, group C, member 2	0.21	transcription,excretion	nucleus,cytoplasm,endoplasmic reticulum	transcription factor activity,steroid hormone receptor activity
5450	NM_,6235	POU2AF1	POU class 2 associating factor 1	13.26	transcription,humoral immune response	nucleus	transcription cofactor activity
3764	BF514158	KCNJ8	potassium inwardly-rectifying channel, subfamily J, member 8	7.86	kidney developmenttransport,ion transport,defense response to virus	mitochondrion,membrane	inward rectifier potassium channel activity
5324	NM_,2655	PLAG1	pleiomorphic adenoma gene 1	9.31	regulation of transcription	nucleus	transcription factor activity,zinc ion binding
286	M28880	ANK1	ankyrin 1, erythrocytic	0.05	exocytosis,cytoskeleton organization	cytoskeleton,plasma membrane	structural molecule activity,cytoskeletal adaptor activity
6876	NM_,3186	TAGLN	transgelin	3.31	muscle organ development	cytoplasm	actin binding
4488	D31771	MSX2	msh homeobox 2	0.24	skeletal system development,regulation of transcription	nucleus	transcription factor activity
27074	NM_014398	LAMP3	lysosomal-associated membrane protein 3	0.19	cell proliferation	lysosome	
7425	NM_,3378	VGF	VGF nerve growth factor inducible	3.40	ovarian follicle development	extracellular space	neuropeptide hormone activity

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5152	NM_,2606	PDE9A	phosphodiesterase 9A	0.16	signal transduction	cytosol	5'-cyclic-nucleotide phosphodiesterase activity
8997	NM_,3947	KALRN	kalirin, RhoGEF kinase	4.07	protein amino acid phosphorylation,regulation of Rho protein signal transduction	cytoplasm,cytoskeleton	protein serine/threonine kinase activity,Rho guanyl-nucleotide exchange factor activity
2243	NM_,508	FGA	fibrinogen alpha chain	0.23	platelet activation,tissue regeneration	,extracellular region ,platelet alpha granule lumen	eukaryotic cell surface binding
7306	NM_,550	TYRP1	tyrosinase-related protein 1	3.90	melanin biosynthetic process from tyrosine,pigmentation	nucleus,cytoplasm,plasma membrane	monooxygenase activity,copper ion binding
1040	NM_,1263	CDS1	CDP-diacylglycerol synthase (phosphatidate cytidyltransferase) 1	0.14	lipid metabolic process	endoplasmic reticulum	diacylglycerol cholinephosphotransferase activity
8631	NM_,3726	SKAP1	src kinase associated phosphoprotein 1	0.26	immune response	nucleus,cytoplasm,membrane	SH3/SH2 adaptor activity
1551	NM_,765	CYP3A7	cytochrome P450, family 3, subfamily A, polypeptide 7	0.11	oxidation reduction	endoplasmic reticulum,membrane	monooxygenase activity
7474	NM_,3392	WNT5A	wingless-type MMTV integration site family, member 5A	0.31	Wnt receptor signaling pathway, calcium modulating pathway,JNK cascade	extracellular region	signal transducer activity
7644	NM_,3430	ZNF91	zinc finger protein 91	44.98	regulation of transcription	intracellular,nucleus	transcription factor activity,zinc ion binding
1491	NM_,1902	CTH	cystathionase (cystathionine gamma-lyase)	0.27	cysteine metabolic process,negative regulation of cell growth	cytoplasm	catalytic activity
54575	NM_,1072	UGT1A1	UDP glucuronosyl transferase 1 family, polypeptide A1 / glucuronosyltransferase 1 family, polypeptide A9	7.49	xenobiotic metabolic process	endoplasmic reticulum,integral to membrane	,UDP-glycosyltransferase activity
6036	NM_,2934	RNASE2	ribonuclease, RNase A family, 2 (liver, eosinophil-derived neurotoxin)	0.03	RNA catabolic process,chemotaxis	extracellular region,lysosome	ribonuclease activity, hydrolase activity

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6,5	AF178841	RHAG	Rh-associated glycoprotein	3.31	cellular ion homeostasis,blood circulation	plasma membrane	ammonium transmembrane transporter activity,ankyrin binding
140	NM_,677	ADORA3	adenosine A3 receptor	22.89	inflammatory response, regulation of heart contraction	plasma membrane	adenosine receptor activity
762	NM_,717	CA4	carbonic anhydrase IV	0.12	one-carbon compound metabolic process,visual perception	membrane fraction,plasma membrane	carbonate dehydratase activity
552	NM_,706	AVPR1A	arginine vasopressin receptor 1A	0.15	regulation of systemic arterial blood pressure by vasopressin	plasma membrane	protein kinase C binding, V1A vasopressin receptor binding
4922	NM_,6183	NTS	neurotensin	0.10	regulation of blood vessel size	extracellular region,cytoplasmic vesicle	neuropeptide hormone activity
5319	NM_,928	PLA2G1B	phospholipase A2, group IB (pancreas)	0.04	activation of MAPK activity,neutrophil mediated immunity	extracellular region	phospholipase A2 activity,
866	NM_,1756	SERPINA6	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 6	0.26	glucocorticoid metabolic process	extracellular region	serine-type endopeptidase inhibitor activity,steroid binding
1013	NM_,4933	CDH15	cadherin 15, type 1, M-cadherin (myotubule)	7.64	cell adhesion	plasma membrane,membrane	calcium ion binding
9971	NM_,5123	NR1H4	nuclear receptor subfamily 1, group H, member 4	0.21	negative regulation of transcription from RNA polymerase II promoter	nucleus	transcription factor activity,transcription factor activity,steroid hormone receptor activity
9021	NM_,3955	SOCS3	suppressor of cytokine signaling 3	0.13	regulation of protein amino acid phosphorylation,anti-apoptosis,JAK-STAT cascade		protein kinase inhibitor activity
288	NM_020987	ANK3	ankyrin 3, node of Ranvier (ankyrin G)	0.19	cytoskeletal anchoring at plasma membrane	endoplasmic reticulum,Golgi apparatus	protein C-terminus binding
7092	AI769310	TLL1	tolloid-like 1	0.26	cell differentiation	extracellular region	metalloendopeptidase activity
1259	NM_,087	CNGA1	cyclic nucleotide gated channel alpha 1	0.18	ion transport,immune response	photoreceptor outer segmen	cGMP binding

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10202	NM_,5794	DHRS2	dehydrogenase/reductase (SDR family) member 2	0.08	C-steroid hormone metabolic process,negative regulation of cell proliferation	nucleus,cytoplasm	carbonyl reductase (NADPH) activity
6595	NM_,3070	SMARCA2	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2	0.07	regulation of transcription	nucleus	DNA binding
3641	NM_,2195	INSL4	insulin-like 4 (placenta)	0.29	signal transduction	extracellular region	insulin-like growth factor receptor binding
786	NM_,727	CACNG1	calcium channel, voltage-dependent, gamma subunit 1	26.69	calcium ion transport	calcium channel complex	ion channel activity
9534	NM_,4876	ZNF254	zinc finger protein 254	0.12	negative regulation of transcription	nucleus	DNA binding
8739	NM_,3806	HRK	harakiri, BCL2 interacting protein (contains only BH3 domain)	3.12	apoptosis		protein binding
5465	NM_,5036	PPARA	peroxisome proliferator-activated receptor alpha	0.12	hypoxia transcription	nucleus	DNA binding
6299	NM_,2968	SALL1	sal-like 1 (Drosophila)	0.16	transcription	nucleus	DNA binding
8744	NM_,3811	TNFSF9	tumor necrosis factor (ligand) superfamily, member 9	0.26	apoptosis,immune response	extracellular space,membrane	cytokine activitytumor necrosis factor receptor binding
8366	NM_,3545	HIST1H4B	Histone cluster 1, H4b	3.56	nucleosome assembly	nucleosome	DNA binding
1235	NM_,4367	CCR6	chemokine (C-C motif) receptor 6	0.05	immune response, signal transduction	membrane	receptor activity
6538	NM_014229	SLC6A11	solute carrier family 6 (neurotransmitter transporter, GABA), member 11	9.02	neurotransmitter transport	membrane	neurotransmitter
3760	NM_,2239	KCNJ3	potassium inwardly-rectifying channel, subfamily J, member 3	22.87	potassium ion transport	potassium channel complex	inward rectifier potassium channel activity

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23373	NM_025021	CRTC1	CREB regulated transcription coactivator 1	9.41	transcription	nucleus,cytoplasm	transcription coactivator
941	NM_,5191	CD80	CD80 molecule	3.94	intracellular signaling cascade	membrane	transcription activator activity
242	NM_,1139	ALOX12B	arachidonate 12-lipoxygenase, 12R type	0.19	leukotriene metabolic proces		arachidonate -lipoxygenase activity
9420	NM_,4820	CYP7B1	cytochrome P450, family 7, subfamily B, polypeptide 1 UDP	4.49	bile acid biosynthetic process	endoplasmic reticulum	oxysterol 7-alpha-hydroxylase activity
7366	NM_,1076	UGT2B15	glucuronosyltransferase 2 family, polypeptide B15	0.16	steroid metabolic process	endoplasmic reticulum	glucuronosyltransferase activity
3354	NM_,865	HTR1E	5-hydroxytryptamine (serotonin) receptor 1E	3.22	signal transduction	membrane	serotonin receptor activity
7355	NM_,5660	SLC35A2	solute carrier family 35 (UDP-galactose transporter), member A2	0.26	UDP-galactose transport	Golgi membrane	UDP-galactose transmembrane transporter activity
130	NM_,672	ADH6	alcohol dehydrogenase 6 (class V)	0.29	ethanol oxidation	cytosol	alcohol dehydrogenase activity
4868	NM_,4646	NPHS1	nephrosis 1, congenital, Finnish type (nephrin)	0.23	MAPKKK cascade,JNK cascade,excretion	membrane	protein binding
1142	NM_,749	CHRNA3	cholinergic receptor, nicotinic, beta 3	0.26	transport	membrane	nicotinic acetylcholine-activated cation-selective channel activity
6332	NM_,2976	SCN7A	sodium channel, voltage-gated, type VII, alpha	25.87	sodium ion transport,muscle contraction	sodium channel complex,nucleus	sodium channel activity
5078	NM_,6193	PAX4	paired box 4	17.70	multicellular organismal development	nucleus,cytoplasm	transcription regulator activity
5579	NM_,2738	PRKCB	protein kinase C, beta	0.18	phosphorylation,calcium ion transport,cellular calcium ion homeostasis	nucleus,cytoplasm	nucleotide binding,protein kinase C activity
6354	NM_,6273	CCL7	chemokine (C-C motif) ligand 7	7.97	inflammatory response,immune response	extracellular region	cytokine activity

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3578	NM_,590	IL9	interleukin 9	14.69	inflammatory response,immune response	extracellular region	cytokine activity
4481	NM_,2445	MSR1	macrophage scavenger receptor 1	3.30	endocytosis	membrane	scavenger receptor activity
4762	NM_,6161	NEUROG1	neurogenin 1	0.11	transcription,neuron differentiation	nucleus	DNA binding
26333	NM_030901	OR7A17	olfactory receptor, family 7, subfamily A, member 17	7.08	sensory perception of smell	plasma membrane	olfactory receptor activity
8342	NM_,3521	HIST1H2BM	histone cluster 1, H2bm	3.00	nucleosome assembly	nucleus	DNA binding
690	NM_,1208	BTF3L1	basic transcription factor 3, like 1 pseudogene	0.09		nucleus	,transcription factor activity
59347	NM_021631	FKSG2	apoptosis inhibitor	4.94	apoptosis	cytoplasm	
2824	AW148844	GPM6B	glycoprotein M6B	0.28	nervous system development	nucleolus,membrane	
55361	BC,3167	PI4K2A	phosphatidylinositol 4-kinase type 2 alpha	0.12	phosphatidylinositol biosynthetic process	cytoplasm,membrane	1-phosphatidylinositol 4-kinase activity
2053	AF233336	EPHX2	epoxide hydrolase 2, cytoplasmic	0.33	prostaglandin production	peroxisome,cytosol	,4-nitrophenylphosphatase activity
634	X16354	CEACAM1	carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein)	0.07	angiogenesis	extracellular region,plasma membrane	
125	M21692	ADH1B	alcohol dehydrogenase 1B (class I), beta polypeptide	0.08	ethanol oxidation	cytoplasm	alcohol dehydrogenase activity
2861	U87460	GPR37	G protein-coupled receptor 37 (endothelin receptor type B-like)	0.22	signal transduction	endoplasmic reticulum	receptor activity
23127	AF288389	GLT25D2	glycosyltransferase 25 domain containing 2	3.18	lipopolysaccharide biosynthetic process	endoplasmic reticulum	transferring glycosyl groups
7104	BC,1386	TM4SF4	transmembrane 4 L six family member 4	0.18	glycosylation	membrane	

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7108	AF096304	TM7SF2	transmembrane 7 superfamily member 2	0.31	cholesterol biosynthetic process	endoplasmic reticulum	delta-sterol reductase activity
4336	D28114	MOBP	myelin-associated oligodendrocyte basic protein WW domain containing E3 ubiquitin protein ligase 2	14.85	nervous system development	mitochondrion	structural constituent of myelin sheath
11060	BC,108	WWP2	WW domain containing E3 ubiquitin protein ligase 2	3.10	protein modification	ubiquitin ligase complex	ubiquitin-protein ligase activity
6672	U36501	SP1,	SP1, nuclear antigen	4.47	negative regulation of transcription	chromosome	,DNA binding
4635	AF116676	MYL4	myosin, light chain 4, alkali; atrial, embryonic	5.86	regulation of the force of heart contraction	myosin complex	ATP binding
1,6	AB035305	CDH8	cadherin 8, type 2	5.72	cell adhesion	plasma membrane	calcium ion binding
5467	BC,2715	PPARD	peroxisome proliferator-activated receptor delta	3.12	negative regulation of transcription	nucleus	DNA binding, NF-kappaB binding
8942	BC,879	KYNU	kynureninase	3.49	tryptophan catabolic process	cytoplasm,mitochondrion	catalytic activity
56134	AF152308	PCDHA1	protocadherin alpha 1 subfamily C, 2	0.21	cell adhesion	extracellular region,membrane,	calcium ion binding
84658	AF239764	EMR3	egf-like module containing, mucin-like, hormone receptor-like 3	18.04	signal transduction	extracellular region,membrane	,signal transducer activity
10395	AF026219	DLC1	deleted in liver cancer 1	3.01	,neural tube closure,heart morphogenesis	nucleus,cytoplasm	Rho GTPase activator activity,SH2 domain binding
4771	BC,3112	NF2	neurofibromin 2 (merlin)	11.23	negative regulation of cell-matrix adhesion	ruffle,nucleus	cytoskeletal protein binding
9194	AF049608	SLC16A7	solute carrier family 16, member 7 (monocarboxylic acid transporter 2)	0.30	pyruvate transport	membrane fraction	symporter activity
5,1	AF081459	ORC5L	origin recognition complex, subunit 5-like (yeast)	5.50	DNA replication	nucleus	DNA replication origin binding

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6,5	AF031549	RHAG	Rh-associated glycoprotein	5.19	ammonium transport	plasma membrane	ammonium transmembrane transporter activity
140597	AF063606	TCEAL2	transcription elongation factor A (SII)-like 2	8.96	transcription	nucleus	
2145	AB,4818	EZH1	enhancer of zeste homolog 1 (Drosophila)	4.52	transcription,chromatin modification	nucleus	DNA binding,chromatin binding
25840	AF113,7	METTL7A	methyltransferase like 7A	22.20	metabolic process		methyltransferase activity
64816	AF280110	CYP3A43	cytochrome P450, family 3, subfamily A, polypeptide 43	0.09	oxidation reduction	endoplasmic reticulum	monooxygenase activity
6819	AF186255	SULT1C2	sulfotransferase family, cytosolic, 1C, member 2	0.32	amine metabolic process	cytoplasm	sulfotransferase activity
51343	AB013463	FZR1	fizzy/cell division cycle 20 related 1 (Drosophila)	0.25	mitotic cell cycle	nucleus	enzyme activator activity
56114	AF152507	PCDHGA1	protocadherin gamma subfamily A, 1	0.04	homophilic cell adhesion	membrane	calcium ion binding
10461	L08961	MERTK	c-mer proto-oncogene tyrosine kinase	8.65	phosphorylation,visual perception	photoreceptor outer segment	ATP binding
161	AA994666	AP2A2	adaptor-related protein complex 2, alpha 2 subunit	0.08	endocytosis	cytosol	protein binding
10410	BF338947	IFITM3	interferon induced transmembrane protein 3 (1-8U)	0.30	immune response	Golgi apparatus,membrane	
3934	NM_,5564	LCN2	lipocalin 2	0.16	response to virus	extracellular region	transporter activity
158471	AL138349	PRUNE2	prune homolog 2 (Drosophila)	0.25	apoptosis	cytoplasm	oxidoreductase activity
57,7	AI817041	CXCR7	chemokine (C-X-C motif) receptor 7	5.83	signal transduction	membrane	receptor activity
112464	AI088622	PRKCDBP	protein kinase C, delta binding protein	11.70	negative regulation of cell cycle		protein kinase C binding

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1117	U58515	CHI3L2	chitinase 3-like 2	0.12	carbohydrate metabolic process	extracellular space,mitochondrion	hydrolase activity
1028	N95363	CDKN1C	Cyclin-dependent kinase inhibitor 1C (p57, Kip2)	0.13	cell cycle	nucleus	cyclin-dependent protein kinase inhibitor activity
3851	X07695	KRT4	keratin 4	0.32	epithelial cell differentiation	intermediate filament	structural molecule activity
23098	AJ290445	SARM1	sterile alpha and TIR motif containing 1	0.21	immune response	microtubule	transmembrane receptor activity
3676	BG532690	ITGA4	integrin, alpha 4 (antigen CD49D, alpha 4 subunit of VLA-4 receptor)	12.46	cell adhesion	integrin complex	fibronectin binding
7329	AA910614	UBE2I	Ubiquitin-conjugating enzyme E2I (UBC9 homolog, yeast)	0.25	cell cycle,mitosis	synaptonemal complex	specific transcriptional repressor activity,ligase activity
5134	AA764988	PDCD2	Programmed cell death 2	0.33	apoptosis	nucleus	DNA binding
29896	AW978896	TRA2A	transformer 2 alpha homolog (Drosophila)	0.31	nuclear mRNA splicing	nucleus	RNA binding
10114	AW291829	HIPK3	homeodomain interacting protein kinase 3	0.15	transcription	nucleus	DNA binding,ATP binding
131566	D29810	DCBLD2	discoidin, CUB and LCCL domain containing 2	9.51	cell adhesion,negative regulation of cell growth	membrane	protein binding
2012	BF445047	EMP1	epithelial membrane protein 1	0.30	cell proliferation	membrane	
54474	AI732381	KRT20	keratin 20	0.28	apoptosis	cytoplasm	structural molecule activity
5789	BF062299	PTPRD	protein tyrosine phosphatase, receptor type, D	0.18	dephosphorylation	membrane	phosphoprotein phosphatase activity
9046	AI828929	DOK2	docking protein 2, 56kDa	3.43	Ras protein signal transduction		tyrosine kinase signaling
11238	AW,3516	CA5B	carbonic anhydrase VB, mitochondrial	0.15	one-carbon compound metabolic process	mitochondrion	carbonate dehydratase activity

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7205	BE964082	TRIP6	thyroid hormone receptor interactor 6	4.53	release of cytoplasmic sequestered NF-kappaB	interleukin-1 receptor complex	interleukin-1 receptor binding
9260	AW206786	PDLIM7	PDZ and LIM domain 7 (enigma)	0.33	endocytosis	cytoskeleton	protein binding,zinc ion binding
22924	AI885178	MAPRE3	microtubule-associated protein, RP/EB family, member 3	4.25	cell cycle,mitosis	microtubule	small GTPase regulator activity
131185 / 5887	T93562	LOC131185 / RAD23B	similar to RAD23B protein / RAD23 homolog B (S. cerevisiae)	0.24	DNA damage removal	nucleus	damaged DNA binding
23522	NM_012330	MYST4	MYST histone acetyltransferase (monocytic leukemia) 4	4.37	nucleosome assembly	nucleosome	DNA binding
797	AA747379	CALCB	calcitonin-related polypeptide beta	11.07	,cellular calcium ion homeostasis	extracellular region	neuropeptide hormone activity
3205	U41813	HOXA9	homeobox A9	17.11	transcription	nucleus	DNA binding
23086	AB014524	EXPH5	exophilin 5	0.14	protein transport		protein binding,Rab GTPase binding
90333	BE541042	ZNF468	zinc finger protein 468	8.61	transcription	nucleus	DNA binding
149076	AK021842	ZNF362	Zinc finger protein 362	0.06	transcription	nucleus	DNA binding
26032	BF977837	SUSD5	sushi domain containing 5	5.36	cell adhesion	membrane	hyaluronic acid binding
6480	X17247	ST6GAL1	ST6 beta-galactosamide alpha-2,6-sialyltransferase 1	5.62	glycosylation,humoral immune response	,extracellular region,Golgi apparatus,membrane	beta-galactoside alpha-2,6-sialyltransferase activity
23020	AK021418	SNRNP2,	small nuclear ribonucleoprotein 2,kDa (U5)	3.34	nuclear mRNA splicing, via spliceosome	nucleus,spliceosome	ATP binding
2549	AL049449	GAB1	GRB2-associated binding protein 1	0.08	activation of MAPK activity	cytosol	SH3/SH2 adaptor activity
158586 / 7789	BF509566	ZXDA / ZXDB	zinc finger, X-linked, duplicated A	0.05	transcription	nucleus	nucleic acid binding

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4703	R78299	NEB	nebulin	7.65	regulation of actin filament length	cytoskeleton	actin binding
9699	AF,7156	RIMS2	regulating synaptic membrane exocytosis 2	0.30	intracellular protein transport	membrane	Rab GTPase binding
27352	AI081779	SGSM3	small G protein signaling modulator 3	3.00	cell cycle	cytoplasm	,Rab GTPase activator activity
23304	AK,1118	UBR2	Ubiquitin protein ligase E3 component n-recognin 2	0.22	ubiquitin-dependent protein catabolic process	ubiquitin ligase complex	ubiquitin-protein ligase activity
54516	AU145135	MTRF1L	Mitochondrial translational release factor 1-like	3.58	translational termination	mitochondrion	translation release factor activity
1,133748 / 389524 / 84163	AC,4883	GTF2IRD2 / GTF2IRD2B / LOC1,133748	GTF2I repeat domain containing 2 / GTF2I repeat domain containing 2B / similar to GTF2IRD2 protein	3.67	transcription	nucleus	DNA binding
22987	AB028977	SV2C	synaptic vesicle glycoprotein 2C	0.09	neurotransmitter transport	synaptic vesicle,membrane	transporter activity
6964	AA284903	TRD	T cell receptor delta locus	3.19	immune response	plasma membrane	MHC protein binding
2710 / 2713	X78713	GK / GK3P	glycerol kinase / glycerol kinase 3 pseudogene	0.31	glycerol metabolic process	,mitochondrial outer membrane	glycerol kinase activity
1,128,701	AL390738	HNRNPA1 / LOC643033	heterogeneous nuclear ribonucleoprotein A1	3.65	nuclear mRNA splicing	spliceosom	single-stranded DNA binding,RNA binding
2683	U10473	B4GALT1	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase , polypeptide 1	0.04	acute inflammatory response	Golgi apparatus	beta-N-acetylglucosaminylglycopeptide
5618	S78505	PRLR	prolactin receptor	4.04	steroid biosynthetic process,anti-apoptosis	extracellular region,membrane	cytokine receptor activity
54532	AK025301	USP53	ubiquitin specific peptidase 53	0.06	ubiquitin-dependent protein catabolic process		ubiquitin thiolesterase activity
91807	BF114815	MYLK3	myosin light chain kinase 3	14.31	phosphorylation		,ATP binding,transferase activity

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563 / 646282	AC_4522	AZGP1 / AZGP1P1	zinc-binding / alpha-2-glycoprotein 1, zinc-binding pseudogene 1	5.28	immune response, cell adhesion	extracellular region	ribonuclease activity
9282	AK023368	MED14	mediator complex subunit 14	5.18	transcription	mediator complex	RNA polymerase II transcription mediator activity
5369	S64288	PMCHL1	pro-melanin-concentrating hormone-like 1	24.99	synaptic transmission	extracellular region	melanin-concentrating hormone activity
164022	AL022240	PPIAL4A	peptidylprolyl isomerase A (cyclophilin A)-like 4A	3.38	protein folding	cytoplasm	isomerase activity
7142	X63759	TNP2	transition protein 2 (during histone to protamine replacement)	0.01	multicellular organismal development	chromosome	DNA binding
6556	AI346187	SLC11A1	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 1	0.12	iron ion transport, immune response	membrane	iron ion binding
1373	W80357	CPS1	carbamoyl-phosphate synthetase 1, mitochondrial	0.30	glutamine metabolic process	mitochondrion	carbamoyl-phosphate synthase activity
11333	AA464753	PDAP1	PDGFA associated protein 1	8.65	signal transduction, cell proliferation		
9123	AA853175	SLC16A3	Solute carrier family 16, member 3 (monocarboxylic acid transporter 4)	0.26	monocarboxylic acid transport	plasma membrane	monocarboxylic acid transmembrane transporter activity
23469	AL050329	PHF3	PHD finger protein 3	5.37	transcription	nucleus	zinc ion binding
116496	AF288391	FAM129A	family with sequence similarity 129, member A	3.46	phosphorylation	cytoplasm	
56949	NM_020196	XAB2	XPA binding protein 2	0.23	DNA repair, RNA splicing	nucleus	protein binding

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65982	NM_023926	ZSCAN18	zinc finger and SCAN domain containing 18	3.91	transcription	nucleus	transcription factor activity
26585	NM_013372	GREM1	gremlin 1, cysteine knot superfamily, homolog (Xenopus laevis)	3.88	organ morphogenesis	extracellular region	cytokine activity
7227	NM_014112	TRPS1	trichorhinophalangeal syndrome I	16.19	transcription	nucleus	transcription factor activity
408	NM_,4041	ARRB1	arrestin, beta 1	0.04	phototransduction	membrane fraction	enzyme inhibitor activity
57134	NM_020379	MAN1C1	mannosidase, alpha, class 1C, member 1	0.33	protein glycosylation	Golgi apparatus	mannosyl-oligosaccharide 1,2-alpha-mannosidase activity
9388	NM_,6033	LIPG	lipase, endothelial	15.10	lipid metabolic process	extracellular region	catalytic activity, lipoprotein lipase activity
10891	NM_013261	PPARGC1A	peroxisome proliferator-activated receptor gamma, coactivator 1 alpha	0.03	transcription	nucleus	DNA binding
79977	NM_024915	GRHL2	grainyhead-like 2 (Drosophila)	7.76	transcription	nucleus	DNA binding
3773	NM_018658	KCNJ16	potassium inwardly-rectifying channel, subfamily J, member 16	0.17	potassium ion transport	membrane	ion channel activity
81545	NM_024862	FBXO38	F-box protein 38	7.08	protein modification	nucleus	
2266	NM_,509	FGG	fibrinogen gamma chain	0.26	platelet activation	extracellular region	calcium ion binding
10734	NM_012447	STAG3	stromal antigen 3	13.99	meiosis	nucleus	binding
4883	AI628360	NPR3	natriuretic peptide receptor C/guanylate cyclase C (atrionatriuretic peptide receptor C)	3.69	inhibition of adenylate cyclase activity	membrane	receptor activity
59349	NM_021633	KLHL12	kelch-like 12 (Drosophila)	0.33	Wnt receptor signaling pathway		protein binding

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50856	NM_016184	CLEC4A	C-type lectin domain family 4, member A	4.23	immune response	nucleus,cytoplasm,membrane	sugar binding
23746	NM_014336	AIPL1	aryl hydrocarbon receptor interacting protein-like 1	3.72	visual perception	photoreceptor inner segment,nucleus	farnesylated protein binding
56605	NM_019891	ERO1LB	ERO1-like beta (S. cerevisiae)	0.30	electron transport chain	endoplasmic reticulum	electron carrier activity
57716	NM_020956	PRX	periaxin	0.22	axon ensheathment	nucleus,cytoplasm	protein binding
64097	NM_022140	EPB41L4A	erythrocyte membrane protein band 4.1 like 4A	0.20		cytoplasm	cytoskeletal protein binding
55762	NM_018260	ZNF701	zinc finger protein 701	3.56	transcription	nucleus	DNA binding
9227	NM_,4744	LRAT	lecithin retinol acyltransferase (phosphatidylcholine-retinol O-acyltransferase)	0.23	vitamin A metabolic process	endoplasmic reticulum	acyltransferase activity
641,	NM_022142	ELSPBP1	epididymal sperm binding protein 1	0.19	single fertilization	extracellular region	
11095	NM_,7037	ADAMTS8	ADAM metalloproteinase with thrombospondin type 1 motif, 8	0.27	negative regulation of cell proliferation	extracellular matrix	metalloendopeptidase activity
63971	NM_022113	KIF13A	kinesin family member 13A	13.15	microtubule-based movement	microtubule	microtubule motor activity,ATP binding
25879	NM_014156	WDSOF1	WD repeats and SOF1 domain containing	11.41	ribosome biogenesis	ribonucleoprotein complex	
29072	NM_014159	SETD2	SET domain containing 2	3.18	transcription	nucleus	transferase activity
81033	NM_030779	KCNH6	potassium voltage-gated channel, subfamily H (eag-related), member 6	4.48	transcription,potassium ion transport	membrane	ion channel activity
11132	NM_023089	CAPN10	calpain 10	9.73	egulation of intracellular transport	cytosol,membrane	cysteine-type endopeptidase activity

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7099	NM_,3266	TLR4	toll-like receptor 4	5.42	immune response	plasma membrane	lipopolysaccharide binding
64377	NM_022467	CHST8	carbohydrate (N-acetylgalactosamine 4-O) sulfotransferase 8	0.15	central nervous system development	,Golgi membrane	sulfotransferase activity
9132	NM_,47,	KCNQ4	potassium voltage-gated channel, KQT-like subfamily, member 4	0.20	potassium ion transport	potassium channel complex	,ion channel activity
55584	NM_017581	CHRNA9	cholinergic receptor, nicotinic, alpha 9	3.87	calcium ion transport	membrane	ion channel activity
54848	NM_0177,	FLJ20184	hypothetical protein FLJ20184	4.08	Rho protein signal transduction	intracellular	Rho guanyl-nucleotide exchange factor activity
79366	NM_030763	NSBP1	nucleosomal binding protein 1	0.13	transcription	nucleus	chromatin binding
54575	NM_019076	UGT1A10	UDP glucuronosyltransferase 1 family	7.15	xenobiotic metabolic process	endoplasmic reticulum	UDP-glycosyltransferase activity
80329	NM_025218	ULBP1	UL16 binding protein 1	4.93	immune response	endoplasmic reticulum	MHC class I receptor activity
7145	AL046979	TNS1	tensin 1	11.08	cell migration	cytoplasm	actin binding
73,51	AK022663	ZNF814	zinc finger protein 814	15.73	transcription	nucleus	DNA binding,zinc ion binding
342538	AJ278883	NACA2	nascent polypeptide-associated complex alpha subunit 2	3.80	protein transport	nucleus,cytoplasm	
25818	AF243527	KLK5	kallikrein-related peptidase 5	3.54	proteolysis	extracellular region	serine-type endopeptidase activity,peptidase activity
56893	AK023354	UBQLN4	ubiquilin 4	0.29	protein modification process	nucleus,cytoplasm	protein binding
3268	H07885	AGFG2	ArfGAP with FG repeats 2	0.18	ARF GTPase activity		ARF GTPase activator activity
28988	AF077353	DBNL	drebrin-like	0.14	endocytosis,immune responses	ruffle,intracellular,cytoplasm	actin binding
22801	AF109681	ITGA11	integrin, alpha 11	19.61	cell adhesion	integrin complex	magnesium ion binding

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57733	AW235567	GBA3	glucosidase, beta, acid 3 (cytosolic)	3.26	glycoside catabolic process	cytoplasm	beta-galactosidase activity,hydrolase activity
8708	AF117222	B3GALT1	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase , polypeptide 1	3.42	protein glycosylation	Golgi's organs	UDP-galactose:beta-N-acetylglucosamine beta-1,3-galactosyltransferase activity
25930	BF057506	PTPN23	protein tyrosine phosphatase, non-receptor type 23	0.23	dephosphorylation	cytoplasmic vesicle	phosphoprotein phosphatase activity
55964	AF285109	41520	septin 3	0.05	cell cycle	nucleus,cytoplasm	GTP binding
90592	AL136732	ZNF7,	zinc finger protein 7,	0.13	transcription	nucleus	DNA binding,zinc ion binding
27010	AB028138	TPK1	thiamin pyrophosphokinase 1	0.30	thiamin metabolic process		ATP binding,kinase activity
26166	AY,9106	RGS22	regulator of G-protein signaling 22	14.49	negative regulation of signal transduction		signal transducer activity
56126	AF131761	PCDHB10	protocadherin beta 10	0.25	cell adhesion	plasma membrane	calcium ion binding
56670	AF348078	SUCNR1	succinate receptor 1	0.09	signal transduction	plasma membrane	signal transducer activity
9818	BC,1104	NUPL1	nucleoporin like 1	3.23	protein transport,mRNA transport	nuclear	
57380	BC,1028	MRS2	MRS2 magnesium homeostasis factor homolog (S. cerevisiae)	3.05	ion transport	mitochondrial	magnesium ion binding
27198	AF345568	GPR81	G protein-coupled receptor 81	0.14	signal transduction	plasma membrane	signal transducer activity
56995	AF288480	TULP4	tubby like protein 4	0.20	transcription	nucleus	transcription factor activity
50940	AB038041	PDE11A	phosphodiesterase 11A	5.79	signal transduction	cytoplasm	catalytic activity
56163	AF285603	RNF17	ring finger protein 17	0.16	multicellular organismal development	nucleus,cytoplasm	nucleic acid binding
150696	NM_144707	PROM2	prominin 2	3.37		membrane	

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140803	AF350881	TRPM6	transient receptor potential cation channel, subfamily M, member 6	3.36	phosphorylation,calcium ion transport	Golgi apparatus	protein serine/threonine kinase activity
6542	AA876372	SLC7A2	solute carrier family 7 (cationic amino acid transporter, y+ system), member 2	0.31	production of nitric oxide	cytoplasm,membrane	L-ornithine transmembrane transporter activity
26298	AI763378	EHF	Ets homologous factor	0.23	transcription	nucleus	DNA binding
6850	BF593625	SYK	spleen tyrosine kinase	0.06	activation of MAPK activity,serotonin secretion	nucleolus,cytoplasm	nucleotide binding,protein kinase activity
134111	H17038	FLJ25076	probable ubiquitin-conjugating enzyme E2 FLJ25076	3.72	post-translational protein modification		ubiquitin-protein ligase activity
117	AW451961	ADCYAP1R1	Adenylate cyclase activating polypeptide 1 (pituitary) receptor type I	3.78	receptor linked signal transduction	plasma membrane	signal transducer activity
34	AV646610	ID4	Inhibitor of DNA binding 4, dominant negative helix-loop-helix protein	0.30	,G1/S transition of mitotic cell cycle,transcription	nucleus	transcription corepressor activity
222171	AI347918	PRR15	proline rich 15	0.31	organismal development		
9953	AA78,67	HS3ST3B1	heparan sulfate (glucosamine) 3-O-sulfotransferase 3B1	0.31	heparan sulfate proteoglycan biosynthetic process	Golgi apparatus	sulfotransferase activity
1958	AI459194	EGR1	Early growth response 1	0.14	negative regulation of transcription	,nucleus	transcription factor activity
157506	AV697515	RDH10	retinol dehydrogenase 10 (all-trans)	0.32	visual perception	endoplasmic reticulum	retinol dehydrogenase activity
4907	AI086864	NT5E	5'-nucleotidase, ecto (CD73)	5.14	DNA metabolic process	plasma membrane	5'-nucleotidase activity
138050	BF433,5	HGSNAT	heparan-alpha-glucosaminide N-acetyltransferase	0.10	glycosaminoglycan metabolic process	lysosomal membrane	acyltransferase activity

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56849	BF591534	TCEAL7	transcription elongation factor A (SII)-like 7	0.07	transcription	nucleus	translation elongation factor activity
4093	AA934610	SMAD9	SMAD family member 9	7.48	transcription	nucleus	transcription factor activity
59352	AA524536	LGR6	leucine-rich repeat-containing G protein-coupled receptor 6	0.22	signal transduction	plasma membrane	signal transducer activity
644538	AW242,9	LOC644538	hypothetical protein LOC644538	0.06	negative regulation of complement activation	extracellular region	serine-type endopeptidase inhibitor activity
10160	BF725250	FARP1	FERM, RhoGEF (ARHGEF) and pleckstrin domain protein 1 (chondrocyte-derived)	0.08	Rho protein signal transduction	cytoskeleton	Rho guanyl-nucleotide exchange factor activity
6657	AI669815	SOX2	SRY (sex determining region Y)-box 2	0.07	negative regulation of transcription	nucleus	DNA bindin
65975	AI703417	STK33	serine/threonine kinase 33	10.64	phosphorylation	cytoplasm	nucleotide binding,protein serine/threonine kinase activity
1356	AI684991	CP	ceruloplasmin (ferroxidase)	0.26	copper ion transport	extracellular region	ferroxidase activity
3778	AI832576	KCNMA1	potassium large conductance calcium-activated channel, subfamily M, alpha member 1	3.29	response to hypoxia	potassium channel complex	ion channel activity
51477	AI675636	ISYNA1	inositol-3-phosphate synthase 1	4.27	inositol biosynthetic process	cytoplasm	inositol-3-phosphate synthase activity
931	AI862674	MS4A1	membrane-spanning 4-domains, subfamily A, member 1	0.07	immune response	membrane	receptor activity
137075	BF11,53	CLDN23	claudin 23	3.99	calcium-independent cell-cell adhesion	membrane	structural molecule activity
170261	AV725825	ZCCHC12	zinc finger, CCHC domain containing 12	19.42	transcription		nucleic acid binding
63035	N57931	BCORL1	BCL6 co-repressor-like 1	5.17	transcription	nucleus	

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80115	AA532851	BAIAP2L2	BAI1-associated protein 2-like 2	3.74	signal transduction	nucleus,mitochondrion	SH3 domain binding
65266	AW082836	WNK4	WNK lysine deficient protein kinase 4	0.07	phosphorylation,chloride transport	cytoplasm	nucleotide binding,protein serine/threonine kinase activity
57158	AA716165	JPH2	junctionophilin 2	0.07	elevation of cytosolic calcium ion concentration	membrane fraction	protein binding
144132	AL040892	DNHD1	dynein heavy chain domain 1	0.10	protein targeting to mitochondrion transport	mitochondrion	microtubule motor activity
55752	AI333326	41528	septin 11	3.98	cell cycle	nucleus,cytoplasm	nucleotide binding
116442	AV724323	RAB39B	RAB39B, member RAS oncogene family	3.26	small GTPase mediated signal transduction	cytoplasm,membrane	GTP binding
345557	AI694325	PLCXD3	phosphatidylinositol-specific phospholipase C, X domain containing 3	0.17	intracellular signaling cascade,lipid catabolic process		phospholipase C activity,signal transducer activity
2151	AI378647	F2RL2	coagulation factor II (thrombin) receptor-like 2	3.80	signal transduction	plasma membrane	phosphoinositide phospholipase C activity
286436 / 767811	H09657	H2BFM / H2BFXP	H2B histone family, member M / H2B histone family, member X, pseudogene	0.14	nucleosome assembly	chromosome	DNA binding
4036	R73030	LRP2	low density lipoprotein-related protein 2	0.30	glycosylation,vitamin metabolic process	endosome,endoplasmic reticulum,Golgi apparatus	receptor activity,SH3 domain binding
64321	AI821669	SOX17	SRY (sex determining region Y)-box 17	0.18	vasculogenesis,transcription	nucleus	DNA binding
6635	AU144102	SNRPE	small nuclear ribonucleoprotein polypeptide E	0.23	RNA splicing	ribonucleoprotein complex	RNA binding
79365	R93946	BHLHE41	basic helix-loop-helix family, member e41	8.84	transcription	nucleus	transcription regulator activity
359787	AI066520	DPPA3	developmental pluripotency associated 3	0.06		nucleus,cytoplasm	

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159963	AV7,405	SLC5A12	solute carrier family 5 (sodium/glucose cotransporter), member 12	0.10	sodium ion transport	membrane	transporter activity
130120	BF056837	REG3G	regenerating islet-derived 3 gamma	5.26	inflammatory response	extracellular region	sugar binding
55349	AJ272267	CHDH	choline dehydrogenase	0.23	alcohol metabolic process	mitochondrion	oxidoreductase activity
79674	AK022666	VEPH1	ventricular zone expressed PH domain homolog 1 (zebrafish)	0.04	inflammatory response	extracellular region	zymosan binding
57689	AW118214	LRRC4C	leucine rich repeat containing 4C	0.06	regulation of axonogenesis	membrane	protein binding
83891	AK026814	SNX25	sorting nexin 25	4.27	transport,cell communication		signal transducer activity,phosphoinositide binding
80725	BF062187	SNIP	SNAP25-interacting protein	0.09	exocytosis	cytoskeleton	protein binding
6689	AK025419	SPIB	Spi-B transcription factor (Spi-1/PU.1 related)	0.12	transcription	nucleus,cytoplasm	DNA binding
57,7	BE552368	CXCR7	Chemokine (C-X-C motif) receptor 7	3.82	signal transduction	membrane	receptor activity
7991	AK026149	TUSC3	tumor suppressor candidate 3	8.42	protein amino acid N-linked glycosylation	endoplasmic reticulum	dolichyl-diphosphooligosaccharide-protein glycotransferase activity
404734	AK024189	ANKHD1	ankyrin repeat and KH domain containing 1	4.02	negative regulation of translation	cytoplasm	RNA binding
26272	AF176703	FBXO4	F-box protein 4	0.17	protein ubiquitination	ubiquitin ligase complex	,ubiquitin-protein ligase activity
51083	AL556409	GAL	galanin prepropeptide	3.16	smooth muscle contraction,	extracellular region,Golgi apparatus	neuropeptide hormone activity
168850	AF218032	ZNF8,	zinc finger protein 8,	3.18	transcription	nucleus	DNA binding
79869	H96922	FLJ12529	Pre-mRNA cleavage factor I	0.21	nuclear mRNA splicin	nucleus	RNA binding

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55633	AK021840	TBC1D22B	TBC1 domain family, member 22B	0.30	regulation of Rab GTPase activity	intracellular	Rab GTPase activator activity
648	AB051459	EFCAB6	EF-hand calcium binding domain 6	0.07	transcription	nucleus	calcium ion binding
80274	Z82214	SCUBE1	signal peptide, CUB domain, EGF-like 1	8.44	inflammatory response	extracellular region	calcium ion binding
353274	AK026891	ZNF445	zinc finger protein 445	3.17	transcription	intracellular,nucleus	DNA binding
259291	AF264628	TAS2R45	taste receptor, type 2, member 45	6.35	sensory perception of taste	membrane	receptor activity
571	AF317902	BACH1	BTB and CNC homology 1, basic leucine zipper transcription factor 1	0.28	transcription	nucleus	transcription factor activity
51744	AJ245377	CD244	CD244 molecule, natural killer cell receptor 2B4	8.81	signal transduction	plasma membrane	receptor activity
83401	AF292387	ELOVL3	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 3	0.10	fatty acid biosynthetic process	endoplasmic reticulum	
81696	AL096770	OR5V1	olfactory receptor, family 5, subfamily V, member 1	0.10	sensory perception of smell	membrane	olfactory receptor activity
1337	U82486	COX6A1	cytochrome c oxidase subunit VIa polypeptide 1 human	0.16	generation of precursor metabolites and energy	,mitochondrion	cytochrome-c oxidase activity
59269	AI8,713	HIVEP3	immunodeficiency virus type I enhancer binding protein 3	0.32	transcription	nucleus,cytoplasm	transcription activator activity
121536	AI580966	AEBP2	AE binding protein 2	3.44	transcription,chromatin modification	nucleus	DNA binding,zinc ion binding
54941	AI969697	RNF125	ring finger protein 125	3.93	immune response	intracellular	zinc ion binding,ligase activity
84307	BG027325	ZNF397	zinc finger protein 397	0.04	transcription	nucleus,cytoplasm	transcription factor activity,zinc ion binding

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256435	AW963951	ST6GALNAC3	ST6 (alpha-N-acetylneuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminidase alpha-2,6-sialyltransferase 3	3.42	protein amino acid glycosylation	Golgi apparatus	transferase activity
132864	BE646645	CPEB2	Cytoplasmic polyadenylation element binding protein 2	4.50	translation	cytoplasm	RNA binding
77	AW272167	ZNF141	zinc finger protein 141	3.64	transcription	nucleus	specific RNA polymerase II transcription factor activity
9181	AW299534	ARHGEF2	Rho/rac guanine nucleotide exchange factor (GEF) 2	0.14	cell morphogenesis	cytoplasm,Golgi apparatus	guanyl-nucleotide exchange factor activity
284443	AI758697	ZNF493	zinc finger protein 493	3.37	transcription	nucleus	DNA binding,zinc ion binding
54796	AA843242	BNC2	basonuclin 2	5.83	transcription	nucleus	zinc ion binding
167681	AL574912	PRSS35	protease, serine, 35	3.06	proteolysis	extracellular region	serine-type endopeptidase activity
606495	AI928392	CYB5RL	cytochrome b5 reductase-like	8.47	oxidation reduction		electron carrier activity,
11228	BF979984	RASSF8	Ras association (RalGDS/AF-6) domain family (N-terminal) member 8	0.11	signal transduction		
84448	AI912773	ABLIM2	actin binding LIM protein family, member 2	0.23	cytoskeleton organization,transcription	cytoplasm,actin cytoskeleton	actin binding,zinc ion binding
4915	BE858459	NTRK2	neurotrophic tyrosine kinase, receptor, type 2	0.10	vasculogenesis, phosphorylation	cytosol,plasma membrane	nucleotide binding,,protein tyrosine kinase activity
124975	AI697028	GGT6	gamma-glutamyltransferase 6	8.79	glutathione biosynthetic process	membrane	gamma-glutamyltransferase activity
5581	AA626142	PRKCE	Protein kinase C, epsilon	3.85	phosphorylation, apoptosis	membrane fraction	nucleotide binding,protein kinase C activity
8663	AI377875	EIF3C	eukaryotic translation initiation factor 3	5.75	translation	cytoplasm	translation initiation factor activity

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79987	BF436117	SVEP1	sushi, von Willebrand factor type A, EGF and pentraxin domain containing 1	0.24	cell adhesion	extracellular region,cytoplasm,membrane	chromatin binding,calcium ion binding
55973	BF433093	BCAP29	B-cell receptor-associated protein 29	6.52	transport,apoptosis	endoplasmic reticulum	receptor activity
144453	AA878383	BEST3	bestrophin 3	3.80	ion transport	plasma membrane	ion channel activity
55251	BF509219	PCMTD2	protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 2	0.23	transcription	nucleus	transcription factor activity
152110	AI652681	NEK10	NIMA (never in mitosis gene a)-related kinase 10	6.56	phosphorylation		protein serine/threonine kinase activityATP binding
158880	AI341140	USP51	ubiquitin specific peptidase 51	3.33	ubiquitin-dependent protein catabolic process	nucleus,cytoplasm	ubiquitin thiolesterase activity
6428	AA702507	SFRS3	Splicing factor, arginine/serine-rich 3	4.89	nuclear mRNA splicing	nucleus	RNA binding
57092 / 729298	BE465316	LOC729298 / PCNP	similar to PEST proteolytic signal containing nuclear protein / PEST proteolytic signal containing nuclear protein	0.14	cell cycle,protein ubiquitination	nucleus	protein binding
55186	AW514168	SLC25A36	Solute carrier family 25, member 36	3.83	transport	mitochondrion	transporter activity
117584	AV660759	RFFL	Ring finger and FYVE-like domain containing 1	5.36	protein transport,apoptosis	cytoplasm,membrane	zinc ion binding,ligase activity
195814	AI440266	SDR16C5	short chain dehydrogenase/reductase family 16C, member 5	0.18	oxidation reduction	membrane	catalytic activity

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7170	AV713323	TPM3	tropomyosin 3	0.24	cell motion,regulation of muscle contraction	nucleus,cytoplasm	actin binding
390963	AI651641	ZNF818P	zinc finger protein 818 pseudogene	4.39	transcription	nucleus	DNA binding,zinc ion binding
84253	AI698,1	GARNL3	GTPase activating Rap/RanGAP domain-like 3	0.18	small GTPase mediated signal transduction	intracellular	small GTPase regulator activity
163081	BF061829	ZNF567	zinc finger protein 567	0.30	transcription	nucleus	DNA binding,zinc ion binding
149111	AI142850	CNIH3	Cornichon homolog 3 (Drosophila)	0.16	intracellular signaling cascade	membrane	
80264	AW954842	ZNF430	zinc finger protein 430	3.52	transcription	nucleus	DNA binding,zinc ion binding
8526	AI589594	DGKE	diacylglycerol kinase, epsilon 64kDa	0.33	activation of protein kinase C activity	membrane	diacylglycerol kinase activity
83852	AW977837	SETDB2	SET domain, bifurcated 2	4.86	chromatin modification	nucleus	methyltransferase activity
22862	AA452239	FNDC3A	Fibronectin type III domain containing 3A	0.29	spermatid development	acrosomal vesicle,endoplasmic reticulum	
388585	AW079166	HES5	hairy and enhancer of split 5 (Drosophila)	0.24	transcription	nucleus	transcription regulator activity
147947	BE966038	ZNF542	zinc finger protein 542	3.94	transcription	nucleus	DNA binding,zinc ion binding
7562	BF223715	ZNF708	zinc finger protein 708	6.07	transcription	nucleus	DNA binding,zinc ion binding
6129	AI984074	RPL7	ribosomal protein L7	5.25	rRNA processing	ribosome	DNA binding,RNA binding
79685	AW058652	SAP30L	SAP30-like	0.13	transcription	nucleus	
5675	AI394154	PSG6	pregnancy specific beta-1-glycoprotein 6 major	14.84	pregnancy	extracellular region	
3116	BF057731	HLA-DPB2	histocompatibility complex, class II, DP beta 2 (pseudogene)	0.02	immune response	MHC class II protein complex	
8825	BF062244	LIN7A	lin-7 homolog A (C. elegans)	3.30	protein complex assembly	membrane	protein binding

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134288	AI927971	TMEM174	transmembrane protein 174	0.13		membrane	
1773	AI692769	DNASE1	deoxyribonuclease I	6.04	DNA catabolic process,apoptosis	extracellular region,nucleus	actin binding,nuclease activity
6095	AW663525	RORA	RAR-related orphan receptor A	4.12	transcription	nucleus	transcription factor activity
8925	AW591969	HERC1	hect (homologous to the E6-AP (UBE3A) carboxyl terminus) domain and RCC1 (CHC1)-like domain (RLD) 1	17.14	protein modification process	Golgi apparatus	ARF guanyl-nucleotide exchange factor activity
284716	R44984	RIMKLA	ribosomal modification protein rimK-like family member A	0.15	protein modification process		ATP binding,manganese ion binding
55211	AV756594	DPPA4	developmental pluripotency associated 4	13.93		nucleus	protein binding
229	AV650426	ALDOB	Aldolase B, fructose-bisphosphate	0.11	NADH oxidation,metabolic process	nucleolus,microtubule organizing center	fructose-bisphosphate aldolase activity
162967	AI025436	ZNF320	zinc finger protein 320	5.32	transcription	nucleus	DNA binding,zinc ion binding
23504	AA889573	RIMBP2	RIMS binding protein 2	18.73		membrane	
22978	AA677629	NT5C2	5'-nucleotidase, cytosolic II	6.24	nucleotide metabolic process	cytosol	5'-nucleotidase activity
55183	BF666241	RIF1	RAP1 interacting factor homolog (yeast)	3.05	DNA damage stimulus	chromosome	binding
55332	AA724995	DRAM	Damage-regulated autophagy modulator	5.73	autophagy,apoptosis	lysosome	
3417	AA825652	IDH1	Isocitrate dehydrogenase 1 (NADP+), soluble	7.33	glyoxylate cycle	cytoplasm	isocitrate dehydrogenase (NADP+) activity
124411	AI741586	ZNF720	zinc finger protein 720	19.42	regulation of transcription	intracellular	nucleic acid binding,zinc ion binding
440552	AI535835	LOC440552	OK/SW-cl.16	3.17	proton transport	mitochondrial	nitrite reductase [NAD(P)H] activity

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7572	AA749167	ZNF24	Zinc finger protein 24	11.74	transcription	nucleus	transcription factor activity
6711	H29479	SPTBN1	spectrin, beta, non-erythrocytic 1	0.23	SMAD protein phosphorylation	nucleus,cytoskeleton	actin binding
146540	AI375066	ZNF785	zinc finger protein 785	8.90	transcription	nucleus	DNA binding,zinc ion binding
2752	AW665656	GLUL	glutamate-ammonia ligase (glutamine synthetase)	0.20	glutamine biosynthetic process	mitochondrion,Golgi apparatus	glutamate-ammonia ligase activity
162966	AI620827	ZNF6,	zinc finger protein 6,	13.73	transcription	nucleus	DNA binding,zinc ion binding
57798	H48897	GATAD1	GATA zinc finger domain containing 1	11.47	,regulation of transcription, DNA-dependent	,nucleus,nucleus	,transcription factor activity,zinc ion binding,sequence-specific DNA binding,metal ion binding
147923	AI061288	ZNF420	zinc finger protein 420	3.12	transcription	nucleus	DNA binding,zinc ion binding
115196	AI924872	ZNF554	zinc finger protein 554	0.22	transcription	nucleus	heme oxygenase (decyclizing) activity
283481	AI042341	LOC283481	hypothetical protein LOC283481	0.07			
10135	AA873350	NAMPT	Nicotinamide phosphoribosyltransferase	3.69	signal transduction	cytoplasm	transferase activity
80216	AA521086	ALPK1	alpha-kinase 1	4.10	phosphorylation		,protein serine/threonine kinase activity
257194	AA115106	NEGR1	neuronal growth regulator 1	3.33	cell adhesion	membrane	protein binding
127254	AI674786	C1orf173	chromosome 1 open reading frame 173	13.71			
1,129289 / 5218	AI026778	LOC1,129289 / PFTK1	similar to rCG41102 / PFTAIRE protein kinase 1	5.86	phosphorylation	nucleus	protein serine/threonine kinase activity
124790	N93663	HEXIM2	Hexamethylene bis-acetamide inducible 2	0.33	transcription	nucleus,cytoplasm	cyclin-dependent protein kinase inhibitor activity
201625	AI,5163	DNAH12	dynein, axonemal, heavy chain 12	0.20	microtubule-based movement	axonemal dynein complex,microtubule	microtubule motor activity

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339965	AA927934	CCDC158	coiled-coil domain containing 158	19.87			
23,2	AL043148	DAAM1	dishevelled associated activator of morphogenesis 1	0.15	actin cytoskeleton organization	cytoplasm	actin binding,Rho GTPase binding
55622	AI129850	TTC27	Tetratricopeptide repeat domain 27	4.86			protein binding
152831	AI668605	KLB	klotho beta	0.22	carbohydrate metabolic process	membrane	catalytic activity
375	AW139048	ARF1	ADP-ribosylation factor 1	0.22	Golgi to ER transport	,Golgi apparatus,cytosol	GTPase activity
56479	BF5138,	KCNQ5	potassium voltage-gated channel, KQT-like subfamily, member 5	4.04	potassium ion transport	voltage-gated potassium channel complex	inward rectifier potassium channel activity
6233	AW013893	RPS27A	ribosomal protein S27a	3.12	translational elongation	cytosol,ribosome	structural constituent of ribosome,zinc ion binding
80854	AI985614	SETD7	SET domain containing (lysine methyltransferase) 7	0.31	transcription	chromosome	methyltransferase activity
5229	AI432340	PGGT1B	geranylgeranyltransferase type I, beta subunit	9.69	protein amino acid geranylgeranylation	CAAX-protein geranylgeranyltransferase complex	CAAX-protein geranylgeranyltransferase activity
4881	X15357	NPR1	natriuretic peptide receptor A/guanylate cyclase A (atrionatriuretic peptide receptor A)	0.22	cGMP biosynthetic process,phosphorylation	membrane	guanylate cyclase activity
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203102	NM_145004	ADAM32	ADAM metallopeptidase domain 32	0.10	proteolysis , integrin-mediated signaling pathway	extracellular region , membrane	metalloendopeptidase activity,peptidase activity, zinc ion binding
85509	NM_145208	MBD3L1	methyl-CpG binding domain protein 3-like 1	0.20	transcription	nucleus	
85509	NM_145208	MBD3L1	methyl-CpG binding domain protein 3-like 1	0.20	transcription	nucleus	

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114836	NM_052931	SLAMF6	SLAM family member 6	3.67		membrane	receptor activity
157753	BC030710	TMEM74	transmembrane protein 74	0.33		membrane	
253559	NM_153184	CADM2	cell adhesion molecule 2	5.60		membrane	
147687	NM_152475	ZNF417	zinc finger protein 417	0.04	transcription	nucleus	DNA binding,zinc ion binding
22858	NM_173041	ICK	intestinal cell (MAK-like) kinase	0.10	protein amino acid phosphorylation	nucleus,cytoplasm,membrane-bounded organelle	nucleotide binding, magnesium ion binding