Categ	Term	Cour	Count i	P-value	Gene	Title
GO	heart development	16	114	7E-05	10512	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (
GO	heart development	16	114	7E-05	1136	cholinergic receptor, nicotinic, alpha 3
GO	heart development	16	114	7E-05	2736	GLI family zinc finger 2
GO	heart development	16	114	7E-05	4763	neurofibromin 1
GO	heart development	16	114	7E-05	5021	oxytocin receptor
GO	heart development	16	114	7E-05	5125	proprotein convertase subtilisin/kexin type 5
GO	heart development	16	114	7E-05	55803	ArfGAP with dual PH domains 2
GO	heart development	16	114	7E-05	5795	protein tyrosine phosphatase, receptor type, J
GO	heart development	16	114	7E-05	6299	sal-like 1 (Drosophila)
GO	heart development	16	114	7E-05	6474	short stature homeobox 2
GO	heart development	16	114	7E-05	6659	SRY (sex determining region Y)-box 4
GO	heart development	16	114	7E-05	6662	SRY (sex determining region Y)-box 9
GO	heart development	16	114	7E-05	6899	T-box 1
GO	heart development	16	114	7E-05	7046	transforming growth factor, beta receptor 1
GO	heart development	16	114	7E-05	7137	troponin I type 3 (cardiac)
GO	heart development	16	114	7E-05	7490	Wilms tumor 1
GO	maternal process involved in parturitior	3	3	1E-04	1543	cytochrome P450, family 1, subfamily A, polypeptide 1
GO	maternal process involved in parturitior	3	3	1E-04	5021	oxytocin receptor
GO	maternal process involved in parturitior	3	3	1E-04	6347	chemokine (C-C motif) ligand 2
GO	cytoplasm	247	4355	2E-04	10000	v-akt murine thymoma viral oncogene homolog 3 (protein kinase B, gamma
GO	cytoplasm	247	4355	2E-04	1E+08	forkhead box O6
GO	cytoplasm	247	4355	2E-04	10051	structural maintenance of chromosomes 4
GO	cytoplasm	247	4355	2E-04	10056	phenylalanyl-tRNA synthetase, beta subunit
GO	cytoplasm	247	4355	2E-04	10096	ARP3 actin-related protein 3 homolog (yeast)
GO	cytoplasm	247	4355	2E-04	10097	ARP2 actin-related protein 2 homolog (yeast)
GO	cytoplasm	247	4355	2E-04	10189	THO complex 4
GO	cytoplasm	247	4355	2E-04	10202	dehydrogenase/reductase (SDR family) member 2
GO	cytoplasm	247	4355	2E-04	10254	signal transducing adaptor molecule (SH3 domain and ITAM motif) 2
GO	cytoplasm	247	4355	2E-04	1026	cyclin-dependent kinase inhibitor 1A (p21, Cip1)
GO	cytoplasm	247	4355	2E-04	10293	TRAF interacting protein
GO	cytoplasm	247	4355	2E-04	10391	coronin, actin binding protein, 2B
GO	cytoplasm	247	4355	2E-04	10395	deleted in liver cancer 1
GO	cytoplasm	247	4355	2E-04	10465	peptidylprolyl isomerase H (cyclophilin H)
GO	cytoplasm	247	4355	2E-04	10492	synaptotagmin binding, cytoplasmic RNA interacting protein
GO	cytoplasm	247	4355	2E-04	10539	glutaredoxin 3

GO	cytoplasm	247	4355	2E-04	10612	tripartite motif-containing 3
GO	cytoplasm	247	4355	2E-04	10656	KH domain containing, RNA binding, signal transduction associated 3
GO	cytoplasm	247	4355	2E-04	10777	cyclic AMP-regulated phosphoprotein, 21 kD
GO	cytoplasm	247	4355	2E-04	10785	WD repeat domain 4
GO	cytoplasm	247	4355	2E-04	10808	heat shock 105kDa/110kDa protein 1
GO	cytoplasm	247	4355	2E-04	11169	WD repeat and HMG-box DNA binding protein 1
GO	cytoplasm	247	4355	2E-04	11259	filamin A interacting protein 1-like
GO	cytoplasm	247	4355	2E-04	113130	cell division cycle associated 5
GO	cytoplasm	247	4355	2E-04	114088	tripartite motif-containing 9
GO	cytoplasm	247	4355	2E-04	114757	cytoglobin
GO	cytoplasm	247	4355	2E-04	116362	retinol binding protein 7, cellular
GO	cytoplasm	247	4355	2E-04	118788	phosphoinositide-3-kinase adaptor protein 1
GO	cytoplasm	247	4355	2E-04	121268	Ras homolog enriched in brain like 1
GO	cytoplasm	247	4355	2E-04	122786	FERM domain containing 6
GO	cytoplasm	247	4355	2E-04	124540	musashi homolog 2 (Drosophila)
GO	cytoplasm	247	4355	2E-04	128853	dual specificity phosphatase 15
GO	cytoplasm	247	4355	2E-04	132158	glycerate kinase
GO	cytoplasm	247	4355	2E-04	132625	zinc finger protein 42 homolog (mouse)
GO	cytoplasm	247	4355	2E-04	132671	spermatogenesis associated 18 homolog (rat)
GO	cytoplasm	247	4355	2E-04	132851	spermatogenesis associated 4
GO	cytoplasm	247	4355	2E-04	135114	histidine triad nucleotide binding protein 3
GO	cytoplasm	247	4355	2E-04	1379	complement component (3b/4b) receptor 1-like
GO	cytoplasm	247	4355	2E-04	1496	catenin (cadherin-associated protein), alpha 2
GO	cytoplasm	247	4355	2E-04	150684	copper metabolism (Murr1) domain containing 1
GO	cytoplasm	247	4355	2E-04	1543	cytochrome P450, family 1, subfamily A, polypeptide 1
GO	cytoplasm	247	4355	2E-04	158	adenylosuccinate lyase
GO	cytoplasm	247	4355	2E-04	166336	prickle homolog 2 (Drosophila)
GO	cytoplasm	247	4355	2E-04	1716	deoxyguanosine kinase
GO	cytoplasm	247	4355	2E-04	1730	diaphanous homolog 2 (Drosophila)
GO	cytoplasm	247	4355	2E-04	1781	dynein, cytoplasmic 1, intermediate chain 2
GO	cytoplasm	247	4355	2E-04	1788	DNA (cytosine-5-)-methyltransferase 3 alpha
GO	cytoplasm	247	4355	2E-04	1983	eukaryotic translation initiation factor 5
GO	cytoplasm	247	4355	2E-04	1984	eukaryotic translation initiation factor 5A
GO	cytoplasm	247	4355	2E-04	201299	RAD52 motif 1
GO	cytoplasm	247	4355	2E-04	2027	enolase 3 (beta, muscle)
GO	cytoplasm	247	4355	2E-04	203	adenylate kinase 1

GO	cytoplasm	247	4355	2E-04	2037	erythrocyte membrane protein band 4.1-like 2
GO	cytoplasm	247	4355	2E-04	2139	eyes absent homolog 2 (Drosophila)
GO	cytoplasm	247	4355	2E-04	2171	fatty acid binding protein 5 (psoriasis-associated)
GO	cytoplasm	247	4355	2E-04	2172	fatty acid binding protein 6, ileal
GO	cytoplasm	247	4355	2E-04	219736	storkhead box 1
GO	cytoplasm	247	4355	2E-04	220	aldehyde dehydrogenase 1 family, member A3
GO	cytoplasm	247	4355	2E-04	220042	chromosome 11 open reading frame 82
GO	cytoplasm	247	4355	2E-04	220134	spindle and kinetochore associated complex subunit 1
GO	cytoplasm	247	4355	2E-04	221357	glutathione S-transferase alpha 5
GO	cytoplasm	247	4355	2E-04	2273	four and a half LIM domains 1
GO	cytoplasm	247	4355	2E-04	2281	FK506 binding protein 1B, 12.6 kDa
GO	cytoplasm	247	4355	2E-04	23057	nicotinamide nucleotide adenylyltransferase 2
GO	cytoplasm	247	4355	2E-04	23136	erythrocyte membrane protein band 4.1-like 3
GO	cytoplasm	247	4355	2E-04	23138	Nedd4 binding protein 3
GO	cytoplasm	247	4355	2E-04	23157	septin 6
GO	cytoplasm	247	4355	2E-04	23171	glycerol-3-phosphate dehydrogenase 1-like
GO	cytoplasm	247	4355	2E-04	23189	KN motif and ankyrin repeat domains 1
GO	cytoplasm	247	4355	2E-04	2321	fms-related tyrosine kinase 1 (vascular endothelial growth factor/vascular
GO	cytoplasm	247	4355	2E-04	2533	FYN binding protein (FYB-120/130)
GO	cytoplasm	247	4355	2E-04	254528	chromosome 16 open reading frame 73
GO	cytoplasm	247	4355	2E-04	25758	chromosome 11 open reading frame 41
GO	cytoplasm	247	4355	2E-04	25780	RAS guanyl releasing protein 3 (calcium and DAG-regulated)
GO	cytoplasm	247	4355	2E-04	25827	F-box and leucine-rich repeat protein 2
GO	cytoplasm	247	4355	2E-04	25884	chordin-like 2
GO	cytoplasm	247	4355	2E-04	25953	paroxysmal nonkinesigenic dyskinesia
GO	cytoplasm	247	4355	2E-04	26019	UPF2 regulator of nonsense transcripts homolog (yeast)
GO	cytoplasm	247	4355	2E-04	26059	ELKS/RAB6-interacting/CAST family member 2
GO	cytoplasm	247	4355	2E-04	26127	FGFR1 oncogene partner 2
GO	cytoplasm	247	4355	2E-04	2618	phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide
GO	cytoplasm	247	4355	2E-04	26207	phosphatidylinositol transfer protein, cytoplasmic 1
GO	cytoplasm	247	4355	2E-04	26230	T-cell lymphoma invasion and metastasis 2
GO	cytoplasm	247	4355	2E-04	2628	glycine amidinotransferase (L-arginine:glycine amidinotransferase)
GO	cytoplasm	247	4355	2E-04	26499	pleckstrin 2
GO	cytoplasm	247	4355	2E-04	26586	cytoskeleton associated protein 2
GO	cytoplasm	247	4355	2E-04	26999	cytoplasmic FMR1 interacting protein 2
GO	cytoplasm	247	4355	2E-04	27065	DNA segment on chromosome 4 (unique) 234 expressed sequence

GO	cytoplasm	247	4355	2E-04	27241	Bardet-Biedl syndrome 9
GO	cytoplasm	247	4355	2E-04	27289	Rho family GTPase 1
GO	cytoplasm	247	4355	2E-04	2736	GLI family zinc finger 2
GO	cytoplasm	247	4355	2E-04	283455	kinase suppressor of ras 2
GO	cytoplasm	247	4355	2E-04	287	ankyrin 2, neuronal
GO	cytoplasm	247	4355	2E-04	28984	chromosome 13 open reading frame 15
GO	cytoplasm	247	4355	2E-04	29767	tropomodulin 2 (neuronal)
GO	cytoplasm	247	4355	2E-04	29842	transcription factor CP2-like 1
GO	cytoplasm	247	4355	2E-04	29995	LIM and cysteine-rich domains 1
GO	cytoplasm	247	4355	2E-04	30011	SH3-domain kinase binding protein 1
GO	cytoplasm	247	4355	2E-04	3028	hydroxysteroid (17-beta) dehydrogenase 10
GO	cytoplasm	247	4355	2E-04	309	annexin A6
GO	cytoplasm	247	4355	2E-04	3157	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 (soluble)
GO	cytoplasm	247	4355	2E-04	3248	hydroxyprostaglandin dehydrogenase 15-(NAD)
GO	cytoplasm	247	4355	2E-04	3276	protein arginine methyltransferase 1
GO	cytoplasm	247	4355	2E-04	332	baculoviral IAP repeat-containing 5
GO	cytoplasm	247	4355	2E-04	3336	heat shock 10kDa protein 1 (chaperonin 10)
GO	cytoplasm	247	4355	2E-04	348	apolipoprotein E
GO	cytoplasm	247	4355	2E-04	3557	interleukin 1 receptor antagonist
GO	cytoplasm	247	4355	2E-04	3763	potassium inwardly-rectifying channel, subfamily J, member 6
GO	cytoplasm	247	4355	2E-04	3800	kinesin family member 5C
GO	cytoplasm	247	4355	2E-04	3836	karyopherin alpha 1 (importin alpha 5)
GO	cytoplasm	247	4355	2E-04	3838	karyopherin alpha 2 (RAG cohort 1, importin alpha 1)
GO	cytoplasm	247	4355	2E-04	389421	lin-28 homolog B (C. elegans)
GO	cytoplasm	247	4355	2E-04	3932	lymphocyte-specific protein tyrosine kinase
GO	cytoplasm	247	4355	2E-04	3936	lymphocyte cytosolic protein 1 (L-plastin)
GO	cytoplasm	247	4355	2E-04	400954	echinoderm microtubule associated protein like 6
GO	cytoplasm	247	4355	2E-04	409	arrestin, beta 2
GO	cytoplasm	247	4355	2E-04	4287	ataxin 3
GO	cytoplasm	247	4355	2E-04	4291	myeloid leukemia factor 1
GO	cytoplasm	247	4355	2E-04	4734	neural precursor cell expressed, developmentally down-regulated 4
GO	cytoplasm	247	4355	2E-04	4763	neurofibromin 1
GO	cytoplasm	247	4355	2E-04	4830	non-metastatic cells 1, protein (NM23A) expressed in
GO	cytoplasm	247	4355	2E-04	50940	phosphodiesterase 11A
GO	cytoplasm	247	4355	2E-04	5110	protein-L-isoaspartate (D-aspartate) O-methyltransferase
GO	cytoplasm	247	4355	2E-04	51177	pleckstrin homology domain containing, family O member 1

GO	cytoplasm	247	4355	2E-04	51191	hect domain and RLD 5
GO	cytoplasm	247	4355	2E-04	51339	dapper, antagonist of beta-catenin, homolog 1 (Xenopus laevis)
GO	cytoplasm	247	4355	2E-04	51499	TP53 regulated inhibitor of apoptosis 1
GO	cytoplasm	247	4355	2E-04	5216	profilin 1
GO	cytoplasm	247	4355	2E-04	528	ATPase, H+ transporting, lysosomal 42kDa, V1 subunit C1
GO	cytoplasm	247	4355	2E-04	5303	protein (peptidylprolyl cis/trans isomerase) NIMA-interacting, 4 (parvulin)
GO	cytoplasm	247	4355	2E-04	5341	pleckstrin
GO	cytoplasm	247	4355	2E-04	5420	podocalyxin-like
GO	cytoplasm	247	4355	2E-04	54332	ganglioside-induced differentiation-associated protein 1
GO	cytoplasm	247	4355	2E-04	54756	interleukin 17 receptor D
GO	cytoplasm	247	4355	2E-04	54839	leucine rich repeat containing 49
GO	cytoplasm	247	4355	2E-04	54843	synaptotagmin-like 2
GO	cytoplasm	247	4355	2E-04	55012	protein phosphatase 2 (formerly 2A), regulatory subunit B'', gamma
GO	cytoplasm	247	4355	2E-04	55135	WD repeat containing, antisense to TP53
GO	cytoplasm	247	4355	2E-04	55165	centrosomal protein 55kDa
GO	cytoplasm	247	4355	2E-04	55207	ADP-ribosylation factor-like 8B
GO	cytoplasm	247	4355	2E-04	55283	mucolipin 3
GO	cytoplasm	247	4355	2E-04	55323	La ribonucleoprotein domain family, member 6
GO	cytoplasm	247	4355	2E-04	55521	tripartite motif-containing 36
GO	cytoplasm	247	4355	2E-04	5569	protein kinase (cAMP-dependent, catalytic) inhibitor alpha
GO	cytoplasm	247	4355	2E-04	55752	septin 11
GO	cytoplasm	247	4355	2E-04	55803	ArfGAP with dual PH domains 2
GO	cytoplasm	247	4355	2E-04	55854	zinc finger CCCH-type containing 15
GO	cytoplasm	247	4355	2E-04	5588	protein kinase C, theta
GO	cytoplasm	247	4355	2E-04	55916	nuclear transport factor 2-like export factor 2
GO	cytoplasm	247	4355	2E-04	56062	kelch-like 4 (Drosophila)
GO	cytoplasm	247	4355	2E-04	5702	proteasome (prosome, macropain) 26S subunit, ATPase, 3
GO	cytoplasm	247	4355	2E-04	5744	parathyroid hormone-like hormone
GO	cytoplasm	247	4355	2E-04	57560	intraflagellar transport 80 homolog (Chlamydomonas)
GO	cytoplasm	247	4355	2E-04	57599	WD repeat domain 48
GO	cytoplasm	247	4355	2E-04	57650	KIAA1524
GO	cytoplasm	247	4355	2E-04	57817	hepcidin antimicrobial peptide
GO	cytoplasm	247	4355	2E-04	581	BCL2-associated X protein
GO	cytoplasm	247	4355	2E-04	586	branched chain aminotransferase 1, cytosolic
GO	cytoplasm	247	4355	2E-04	59	actin, alpha 2, smooth muscle, aorta
GO	cytoplasm	247	4355	2E-04	5924	Ras protein-specific guanine nucleotide-releasing factor 2

GO	cytoplasm	247	4355	2E-04	5947	retinol binding protein 1, cellular
GO	cytoplasm	247	4355	2E-04	597	BCL2-related protein A1
GO	cytoplasm	247	4355	2E-04	6133	ribosomal protein L9
GO	cytoplasm	247	4355	2E-04	6204	ribosomal protein S10
GO	cytoplasm	247	4355	2E-04	6241	ribonucleotide reductase M2
GO	cytoplasm	247	4355	2E-04	6299	sal-like 1 (Drosophila)
GO	cytoplasm	247	4355	2E-04	6347	chemokine (C-C motif) ligand 2
GO	cytoplasm	247	4355	2E-04	641	Bloom syndrome, RecQ helicase-like
GO	cytoplasm	247	4355	2E-04	64151	non-SMC condensin I complex, subunit G
GO	cytoplasm	247	4355	2E-04	6442	sarcoglycan, alpha (50kDa dystrophin-associated glycoprotein)
GO	cytoplasm	247	4355	2E-04	6444	sarcoglycan, delta (35kDa dystrophin-associated glycoprotein)
GO	cytoplasm	247	4355	2E-04	65009	NDRG family member 4
GO	cytoplasm	247	4355	2E-04	65055	receptor accessory protein 1
GO	cytoplasm	247	4355	2E-04	6525	smoothelin
GO	cytoplasm	247	4355	2E-04	6657	SRY (sex determining region Y)-box 2
GO	cytoplasm	247	4355	2E-04	6659	SRY (sex determining region Y)-box 4
GO	cytoplasm	247	4355	2E-04	667	dystonin
GO	cytoplasm	247	4355	2E-04	6672	SP100 nuclear antigen
GO	cytoplasm	247	4355	2E-04	6683	spastin
GO	cytoplasm	247	4355	2E-04	6711	spectrin, beta, non-erythrocytic 1
GO	cytoplasm	247	4355	2E-04	672	breast cancer 1, early onset
GO	cytoplasm	247	4355	2E-04	6741	Sjogren syndrome antigen B (autoantigen La)
GO	cytoplasm	247	4355	2E-04	6820	sulfotransferase family, cytosolic, 2B, member 1
GO	cytoplasm	247	4355	2E-04	70	actin, alpha, cardiac muscle 1
GO	cytoplasm	247	4355	2E-04	7078	TIMP metallopeptidase inhibitor 3
GO	cytoplasm	247	4355	2E-04	7113	transmembrane protease, serine 2
GO	cytoplasm	247	4355	2E-04	7137	troponin I type 3 (cardiac)
GO	cytoplasm	247	4355	2E-04	7168	tropomyosin 1 (alpha)
GO	cytoplasm	247	4355	2E-04	7171	tropomyosin 4
GO	cytoplasm	247	4355	2E-04	7220	transient receptor potential cation channel, subfamily C, member 1
GO	cytoplasm	247	4355	2E-04	729230	chemokine (C-C motif) receptor 2
GO	cytoplasm	247	4355	2E-04	7341	SMT3 suppressor of mif two 3 homolog 1 (S. cerevisiae)
GO	cytoplasm	247	4355	2E-04	7347	ubiquitin carboxyl-terminal esterase L3 (ubiquitin thiolesterase)
GO	cytoplasm	247	4355	2E-04	7353	ubiquitin fusion degradation 1 like (yeast)
GO	cytoplasm	247	4355	2E-04	7389	uroporphyrinogen decarboxylase
GO	cytoplasm	247	4355	2E-04	7456	WAS/WASL interacting protein family, member 1

GO	cytoplasm	247	4355	2E-04	7490	Wilms tumor 1
GO	cytoplasm	247	4355	2E-04	767	carbonic anhydrase VIII
GO	cytoplasm	247	4355	2E-04	7711	zinc finger protein 155
GO	cytoplasm	247	4355	2E-04	773	calcium channel, voltage-dependent, P/Q type, alpha 1A subunit
GO	cytoplasm	247	4355	2E-04	7840	Alstrom syndrome 1
GO	cytoplasm	247	4355	2E-04	79187	fibronectin type III and SPRY domain containing 1
GO	cytoplasm	247	4355	2E-04	79646	pantothenate kinase 3
GO	cytoplasm	247	4355	2E-04	79682	MLF1 interacting protein
GO	cytoplasm	247	4355	2E-04	79805	vasohibin 2
GO	cytoplasm	247	4355	2E-04	79833	gem (nuclear organelle) associated protein 6
GO	cytoplasm	247	4355	2E-04	79929	MAP6 domain containing 1
GO	cytoplasm	247	4355	2E-04	80712	ESX homeobox 1
GO	cytoplasm	247	4355	2E-04	81606	limb bud and heart development homolog (mouse)
GO	cytoplasm	247	4355	2E-04	81706	protein phosphatase 1, regulatory (inhibitor) subunit 14C
GO	cytoplasm	247	4355	2E-04	81786	tripartite motif-containing 7
GO	cytoplasm	247	4355	2E-04	8193	D4, zinc and double PHD fingers family 1
GO	cytoplasm	247	4355	2E-04	83871	RAB34, member RAS oncogene family
GO	cytoplasm	247	4355	2E-04	8409	ubiquitously-expressed transcript
GO	cytoplasm	247	4355	2E-04	84206	mex-3 homolog B (C. elegans)
GO	cytoplasm	247	4355	2E-04	84296	GINS complex subunit 4 (Sld5 homolog)
GO	cytoplasm	247	4355	2E-04	84365	MKI67 (FHA domain) interacting nucleolar phosphoprotein
GO	cytoplasm	247	4355	2E-04	84518	cornifelin
GO	cytoplasm	247	4355	2E-04	84552	par-6 partitioning defective 6 homolog gamma (C. elegans)
GO	cytoplasm	247	4355	2E-04	8458	transcription termination factor, RNA polymerase II
GO	cytoplasm	247	4355	2E-04	84665	myopalladin
GO	cytoplasm	247	4355	2E-04	84668	family with sequence similarity 126, member A
GO	cytoplasm	247	4355	2E-04	84959	ubiquitin associated and SH3 domain containing, B
GO	cytoplasm	247	4355	2E-04	8520	histone acetyltransferase 1
GO	cytoplasm	247	4355	2E-04	8533	COP9 constitutive photomorphogenic homolog subunit 3 (Arabidopsis)
GO	cytoplasm	247	4355	2E-04	8536	calcium/calmodulin-dependent protein kinase I
GO	cytoplasm	247	4355	2E-04	8563	THO complex 5
GO	cytoplasm	247	4355	2E-04	8626	tumor protein p63
GO	cytoplasm	247	4355	2E-04	8835	suppressor of cytokine signaling 2
GO	cytoplasm	247	4355	2E-04	8872	cell division cycle 123 homolog (S. cerevisiae)
GO	cytoplasm	247	4355	2E-04	890	cyclin A2
GO	cytoplasm	247	4355	2E-04	898	cyclin E1

GO	cytoplasm	247	4355	2E-04	8997	kalirin, RhoGEF kinase
GO	cytoplasm	247	4355	2E-04	9053	microtubule-associated protein 7
GO	cytoplasm	247	4355	2E-04	91624	nexilin (F actin binding protein)
GO	cytoplasm	247	4355	2E-04	91801	alkB, alkylation repair homolog 8 (E. coli)
GO	cytoplasm	247	4355	2E-04	92312	mex-3 homolog A (C. elegans)
GO	cytoplasm	247	4355	2E-04	9260	PDZ and LIM domain 7 (enigma)
GO	cytoplasm	247	4355	2E-04	92675	D-tyrosyl-tRNA deacylase 1 homolog (S. cerevisiae)
GO	cytoplasm	247	4355	2E-04	93323	HAUS augmin-like complex, subunit 8
GO	cytoplasm	247	4355	2E-04	93474	zinc finger protein 670
GO	cytoplasm	247	4355	2E-04	9419	cysteine-rich PDZ-binding protein
GO	cytoplasm	247	4355	2E-04	9455	homer homolog 2 (Drosophila)
GO	cytoplasm	247	4355	2E-04	9568	gamma-aminobutyric acid (GABA) B receptor, 2
GO	cytoplasm	247	4355	2E-04	9805	secernin 1
GO	cytoplasm	247	4355	2E-04	9833	maternal embryonic leucine zipper kinase
GO	cytoplasm	247	4355	2E-04	9882	TBC1 domain family, member 4
GO	actin binding	27	278	2E-04	10096	ARP3 actin-related protein 3 homolog (yeast)
GO	actin binding	27	278	2E-04	10097	ARP2 actin-related protein 2 homolog (yeast)
GO	actin binding	27	278	2E-04	10391	coronin, actin binding protein, 2B
GO	actin binding	27	278	2E-04	10788	IQ motif containing GTPase activating protein 2
GO	actin binding	27	278	2E-04	1264	calponin 1, basic, smooth muscle
GO	actin binding	27	278	2E-04	1730	diaphanous homolog 2 (Drosophila)
GO	actin binding	27	278	2E-04	2037	erythrocyte membrane protein band 4.1-like 2
GO	actin binding	27	278	2E-04	23136	erythrocyte membrane protein band 4.1-like 3
GO	actin binding	27	278	2E-04	29767	tropomodulin 2 (neuronal)
GO	actin binding	27	278	2E-04	3778	potassium large conductance calcium-activated channel, subfamily M, alph
GO	actin binding	27	278	2E-04	3936	lymphocyte cytosolic protein 1 (L-plastin)
GO	actin binding	27	278	2E-04	4430	myosin IB
GO	actin binding	27	278	2E-04	4651	myosin X
GO	actin binding	27	278	2E-04	5216	profilin 1
GO	actin binding	27	278	2E-04	54822	transient receptor potential cation channel, subfamily M, member 7
GO	actin binding	27	278	2E-04	56062	kelch-like 4 (Drosophila)
GO	actin binding	27	278	2E-04	6525	smoothelin
GO	actin binding	27	278	2E-04	667	dystonin
GO	actin binding	27	278	2E-04	6711	spectrin, beta, non-erythrocytic 1
GO	actin binding	27	278	2E-04	7137	troponin I type 3 (cardiac)
GO	actin binding	27	278	2E-04	7168	tropomyosin 1 (alpha)

GO	actin binding	27	278	2E-04	7171	tropomyosin 4
GO	actin binding	27	278	2E-04	7456	WAS/WASL interacting protein family, member 1
GO	actin binding	27	278	2E-04	81624	diaphanous homolog 3 (Drosophila)
GO	actin binding	27	278	2E-04	84665	myopalladin
GO	actin binding	27	278	2E-04	9455	homer homolog 2 (Drosophila)
GO	actin binding	27	278	2E-04	9535	glia maturation factor, gamma
GO	collagen	6	22	4E-04	1282	collagen, type IV, alpha 1
GO	collagen	6	22	4E-04	1284	collagen, type IV, alpha 2
GO	collagen	6	22	4E-04	1288	collagen, type IV, alpha 6
GO	collagen	6	22	4E-04	1289	collagen, type V, alpha 1
GO	collagen	6	22	4E-04	1290	collagen, type V, alpha 2
GO	collagen	6	22	4E-04	1301	collagen, type XI, alpha 1
GO	synapse assembly	7	33	7E-04	1000	cadherin 2, type 1, N-cadherin (neuronal)
GO	synapse assembly	7	33	7E-04	23705	cell adhesion molecule 1
GO	synapse assembly	7	33	7E-04	4897	neuronal cell adhesion molecule
GO	synapse assembly	7	33	7E-04	56126	protocadherin beta 10
GO	synapse assembly	7	33	7E-04	56133	protocadherin beta 2
GO	synapse assembly	7	33	7E-04	773	calcium channel, voltage-dependent, P/Q type, alpha 1A subunit
GO	synapse assembly	7	33	7E-04	92737	delta/notch-like EGF repeat containing
GO	positive regulation of Wnt receptor sign	4	10	8E-04	5494	protein phosphatase, Mg2+/Mn2+ dependent, 1A
GO	positive regulation of Wnt receptor sign	4	10	8E-04	6299	sal-like 1 (Drosophila)
GO	positive regulation of Wnt receptor sign	4	10	8E-04	6659	SRY (sex determining region Y)-box 4
GO	positive regulation of Wnt receptor sign	4	10	8E-04	9839	zinc finger E-box binding homeobox 2
GO	thrombin receptor activity	3	5	9E-04	2149	coagulation factor II (thrombin) receptor
GO	thrombin receptor activity	3	5	9E-04	2150	coagulation factor II (thrombin) receptor-like 1
GO	thrombin receptor activity	3	5	9E-04	2151	coagulation factor II (thrombin) receptor-like 2
GO	negative regulation of chondrocyte diffe	3	5	9E-04	2736	GLI family zinc finger 2
GO	negative regulation of chondrocyte diffe	3	5	9E-04	5744	parathyroid hormone-like hormone
GO	negative regulation of chondrocyte diffe	3	5	9E-04	6662	SRY (sex determining region Y)-box 9
GO	negative regulation of DNA recombinati	3	5	9E-04	4436	mutS homolog 2, colon cancer, nonpolyposis type 1 (E. coli)
GO	negative regulation of DNA recombinati	3	5	9E-04	56852	RAD18 homolog (S. cerevisiae)
GO	negative regulation of DNA recombinati	3	5	9E-04	641	Bloom syndrome, RecQ helicase-like
GO	collagen fibril organization	6	26	0.001	1289	collagen, type V, alpha 1
GO	collagen fibril organization	6	26	0.001	1290	collagen, type V, alpha 2
GO	collagen fibril organization	6	26	0.001	1301	collagen, type XI, alpha 1
GO	collagen fibril organization	6	26	0.001	4060	lumican

GO	collagen fibril organization	6	26	0.001	4763	neurofibromin 1
GO	collagen fibril organization	6	26	0.001	7046	transforming growth factor, beta receptor 1
GO	nucleoplasm	36	455	0.001	1026	cyclin-dependent kinase inhibitor 1A (p21, Cip1)
GO	nucleoplasm	36	455	0.001	10492	synaptotagmin binding, cytoplasmic RNA interacting protein
GO	nucleoplasm	36	455	0.001	10785	WD repeat domain 4
GO	nucleoplasm	36	455	0.001	11169	WD repeat and HMG-box DNA binding protein 1
GO	nucleoplasm	36	455	0.001	1161	excision repair cross-complementing rodent repair deficiency, complement
GO	nucleoplasm	36	455	0.001	135295	splicing factor, arginine/serine-rich 13B
GO	nucleoplasm	36	455	0.001	1643	damage-specific DNA binding protein 2, 48kDa
GO	nucleoplasm	36	455	0.001	1763	DNA replication helicase 2 homolog (yeast)
GO	nucleoplasm	36	455	0.001	23594	origin recognition complex, subunit 6 like (yeast)
GO	nucleoplasm	36	455	0.001	25885	polymerase (RNA) I polypeptide A, 194kDa
GO	nucleoplasm	36	455	0.001	27330	ribosomal protein S6 kinase, 90kDa, polypeptide 6
GO	nucleoplasm	36	455	0.001	2965	general transcription factor IIH, polypeptide 1, 62kDa
GO	nucleoplasm	36	455	0.001	3836	karyopherin alpha 1 (importin alpha 5)
GO	nucleoplasm	36	455	0.001	3838	karyopherin alpha 2 (RAG cohort 1, importin alpha 1)
GO	nucleoplasm	36	455	0.001	4171	minichromosome maintenance complex component 2
GO	nucleoplasm	36	455	0.001	4287	ataxin 3
GO	nucleoplasm	36	455	0.001	4928	nucleoporin 98kDa
GO	nucleoplasm	36	455	0.001	4968	8-oxoguanine DNA glycosylase
GO	nucleoplasm	36	455	0.001	5000	origin recognition complex, subunit 4-like (yeast)
GO	nucleoplasm	36	455	0.001	5245	prohibitin
GO	nucleoplasm	36	455	0.001	5440	polymerase (RNA) II (DNA directed) polypeptide K, 7.0kDa
GO	nucleoplasm	36	455	0.001	55215	Fanconi anemia, complementation group I
GO	nucleoplasm	36	455	0.001	5558	primase, DNA, polypeptide 2 (58kDa)
GO	nucleoplasm	36	455	0.001	55759	WD repeat domain 12
GO	nucleoplasm	36	455	0.001	56339	methyltransferase like 3
GO	nucleoplasm	36	455	0.001	64782	apoptosis enhancing nuclease
GO	nucleoplasm	36	455	0.001	6637	small nuclear ribonucleoprotein polypeptide G
GO	nucleoplasm	36	455	0.001	672	breast cancer 1, early onset
GO	nucleoplasm	36	455	0.001	7324	ubiquitin-conjugating enzyme E2E 1 (UBC4/5 homolog, yeast)
GO	nucleoplasm	36	455	0.001	7490	Wilms tumor 1
GO	nucleoplasm	36	455	0.001	79075	defective in sister chromatid cohesion 1 homolog (S. cerevisiae)
GO	nucleoplasm	36	455	0.001	79833	gem (nuclear organelle) associated protein 6
GO	nucleoplasm	36	455	0.001	84172	polymerase (RNA) I polypeptide B, 128kDa
GO	nucleoplasm	36	455	0.001	84365	MKI67 (FHA domain) interacting nucleolar phosphoprotein

GO	nucleoplasm	36	455	0.001	890	cyclin A2
GO	nucleoplasm	36	455	0.001	898	cyclin E1
GO	actomyosin structure organization	3	6	0.002	1264	calponin 1, basic, smooth muscle
GO	actomyosin structure organization	3	6	0.002	54822	transient receptor potential cation channel, subfamily M, member 7
GO	actomyosin structure organization	3	6	0.002	70	actin, alpha, cardiac muscle 1
GO	collagen type IV	3	6	0.002	1282	collagen, type IV, alpha 1
GO	collagen type IV	3	6	0.002	1284	collagen, type IV, alpha 2
GO	collagen type IV	3	6	0.002	1288	collagen, type IV, alpha 6
GO	negative regulation of protein import in	2	2	0.002	11142	protein kinase (cAMP-dependent, catalytic) inhibitor gamma
GO	negative regulation of protein import in	2	2	0.002	5569	protein kinase (cAMP-dependent, catalytic) inhibitor alpha
GO	regulation of acetylcholine secretion	2	2	0.002	1136	cholinergic receptor, nicotinic, alpha 3
GO	regulation of acetylcholine secretion	2	2	0.002	773	calcium channel, voltage-dependent, P/Q type, alpha 1A subunit
GO	DNA replication, removal of RNA primer	2	2	0.002	1763	DNA replication helicase 2 homolog (yeast)
GO	DNA replication, removal of RNA primer	2	2	0.002	2237	flap structure-specific endonuclease 1
GO	negative regulation of mitotic recombin	2	2	0.002	4292	mutL homolog 1, colon cancer, nonpolyposis type 2 (E. coli)
GO	negative regulation of mitotic recombin	2	2	0.002	641	Bloom syndrome, RecQ helicase-like
GO	CCR2 chemokine receptor binding	2	2	0.002	6347	chemokine (C-C motif) ligand 2
GO	CCR2 chemokine receptor binding	2	2	0.002	729230	chemokine (C-C motif) receptor 2
GO	ectoderm and mesoderm interaction	2	2	0.002	6591	snail homolog 2 (Drosophila)
GO	ectoderm and mesoderm interaction	2	2	0.002	8626	tumor protein p63
GO	regulation of smooth muscle contractio	4	13	0.002	1136	cholinergic receptor, nicotinic, alpha 3
GO	regulation of smooth muscle contractio	4	13	0.002	1264	calponin 1, basic, smooth muscle
GO	regulation of smooth muscle contractio	4	13	0.002	2321	fms-related tyrosine kinase 1 (vascular endothelial growth factor/vascular
GO	regulation of smooth muscle contractio	4	13	0.002	7137	troponin I type 3 (cardiac)
GO	DNA recombination	8	52	0.003	201299	RAD52 motif 1
GO	DNA recombination	8	52	0.003	29893	PSMC3 interacting protein
GO	DNA recombination	8	52	0.003	3149	high-mobility group box 3
GO	DNA recombination	8	52	0.003	3516	recombination signal binding protein for immunoglobulin kappa J region
GO	DNA recombination	8	52	0.003	5889	RAD51 homolog C (S. cerevisiae)
GO	DNA recombination	8	52	0.003	5965	RecQ protein-like (DNA helicase Q1-like)
GO	DNA recombination	8	52	0.003	641	Bloom syndrome, RecQ helicase-like
GO	DNA recombination	8	52	0.003	79677	structural maintenance of chromosomes 6
GO	proximal/distal pattern formation	5	22	0.003	1746	distal-less homeobox 2
GO	proximal/distal pattern formation	5	22	0.003	2736	GLI family zinc finger 2
GO	proximal/distal pattern formation	5	22	0.003	3236	homeobox D10
GO	proximal/distal pattern formation	5	22	0.003	3237	homeobox D11

GO	proximal/distal pattern formation	5	22	0.003	8626	tumor protein p63
GO	positive regulation of filopodium assem	3	7	0.003	10096	ARP3 actin-related protein 3 homolog (yeast)
GO	positive regulation of filopodium assem	3	7	0.003	5588	protein kinase C, theta
GO	positive regulation of filopodium assem	3	7	0.003	7046	transforming growth factor, beta receptor 1
GO	positive regulation of Notch signaling pa	3	7	0.003	182	jagged 1 (Alagille syndrome)
GO	positive regulation of Notch signaling pa	3	7	0.003	6657	SRY (sex determining region Y)-box 2
GO	positive regulation of Notch signaling pa	3	7	0.003	8626	tumor protein p63
GO	DNA replication	15	146	0.003	2237	flap structure-specific endonuclease 1
GO	DNA replication	15	146	0.003	23594	origin recognition complex, subunit 6 like (yeast)
GO	DNA replication	15	146	0.003	4171	minichromosome maintenance complex component 2
GO	DNA replication	15	146	0.003	4928	nucleoporin 98kDa
GO	DNA replication	15	146	0.003	5000	origin recognition complex, subunit 4-like (yeast)
GO	DNA replication	15	146	0.003	5245	prohibitin
GO	DNA replication	15	146	0.003	5469	mediator complex subunit 1
GO	DNA replication	15	146	0.003	5558	primase, DNA, polypeptide 2 (58kDa)
GO	DNA replication	15	146	0.003	5965	RecQ protein-like (DNA helicase Q1-like)
GO	DNA replication	15	146	0.003	6241	ribonucleotide reductase M2
GO	DNA replication	15	146	0.003	641	Bloom syndrome, RecQ helicase-like
GO	DNA replication	15	146	0.003	64785	GINS complex subunit 3 (Psf3 homolog)
GO	DNA replication	15	146	0.003	7298	thymidylate synthetase
GO	DNA replication	15	146	0.003	79075	defective in sister chromatid cohesion 1 homolog (S. cerevisiae)
GO	DNA replication	15	146	0.003	84296	GINS complex subunit 4 (Sld5 homolog)
GO	damaged DNA binding	7	44	0.004	157570	establishment of cohesion 1 homolog 2 (S. cerevisiae)
GO	damaged DNA binding	7	44	0.004	1643	damage-specific DNA binding protein 2, 48kDa
GO	damaged DNA binding	7	44	0.004	2237	flap structure-specific endonuclease 1
GO	damaged DNA binding	7	44	0.004	4436	mutS homolog 2, colon cancer, nonpolyposis type 1 (E. coli)
GO	damaged DNA binding	7	44	0.004	4968	8-oxoguanine DNA glycosylase
GO	damaged DNA binding	7	44	0.004	56852	RAD18 homolog (S. cerevisiae)
GO	damaged DNA binding	7	44	0.004	8626	tumor protein p63
GO	cell projection	11	94	0.004	10097	ARP2 actin-related protein 2 homolog (yeast)
GO	cell projection	11	94	0.004	26499	pleckstrin 2
GO	cell projection	11	94	0.004	3751	potassium voltage-gated channel, Shal-related subfamily, member 2
GO	cell projection	11	94	0.004	51062	atlastin GTPase 1
GO	cell projection	11	94	0.004	55752	septin 11
GO	cell projection	11	94	0.004	57560	intraflagellar transport 80 homolog (Chlamydomonas)
GO	cell projection	11	94	0.004	773	calcium channel, voltage-dependent, P/Q type, alpha 1A subunit

GO	cell projection	11	94	0.004	84168	anthrax toxin receptor 1
GO	cell projection	11	94	0.004	8777	multiple PDZ domain protein
GO	cell projection	11	94	0.004	9419	cysteine-rich PDZ-binding protein
GO	cell projection	11	94	0.004	9497	solute carrier family 4, sodium bicarbonate cotransporter, member 7
GO	response to drug	20	225	0.004	1026	cyclin-dependent kinase inhibitor 1A (p21, Cip1)
GO	response to drug	20	225	0.004	10512	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (
GO	response to drug	20	225	0.004	1136	cholinergic receptor, nicotinic, alpha 3
GO	response to drug	20	225	0.004	1503	CTP synthase
GO	response to drug	20	225	0.004	1543	cytochrome P450, family 1, subfamily A, polypeptide 1
GO	response to drug	20	225	0.004	2027	enolase 3 (beta, muscle)
GO	response to drug	20	225	0.004	220	aldehyde dehydrogenase 1 family, member A3
GO	response to drug	20	225	0.004	2878	glutathione peroxidase 3 (plasma)
GO	response to drug	20	225	0.004	3157	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 (soluble)
GO	response to drug	20	225	0.004	3932	lymphocyte-specific protein tyrosine kinase
GO	response to drug	20	225	0.004	4436	mutS homolog 2, colon cancer, nonpolyposis type 1 (E. coli)
GO	response to drug	20	225	0.004	4830	non-metastatic cells 1, protein (NM23A) expressed in
GO	response to drug	20	225	0.004	5021	oxytocin receptor
GO	response to drug	20	225	0.004	5228	placental growth factor
GO	response to drug	20	225	0.004	590	butyrylcholinesterase
GO	response to drug	20	225	0.004	6347	chemokine (C-C motif) ligand 2
GO	response to drug	20	225	0.004	6546	solute carrier family 8 (sodium/calcium exchanger), member 1
GO	response to drug	20	225	0.004	70	actin, alpha, cardiac muscle 1
GO	response to drug	20	225	0.004	898	cyclin E1
GO	response to drug	20	225	0.004	9420	cytochrome P450, family 7, subfamily B, polypeptide 1
GO	cell junction	30	387	0.004	10052	gap junction protein, gamma 1, 45kDa
GO	cell junction	30	387	0.004	11149	blood vessel epicardial substance
GO	cell junction	30	387	0.004	1136	cholinergic receptor, nicotinic, alpha 3
GO	cell junction	30	387	0.004	1138	cholinergic receptor, nicotinic, alpha 5
GO	cell junction	30	387	0.004	126374	Wilms tumor 1 interacting protein
GO	cell junction	30	387	0.004	127534	gap junction protein, beta 4, 30.3kDa
GO	cell junction	30	387	0.004	1496	catenin (cadherin-associated protein), alpha 2
GO	cell junction	30	387	0.004	1830	desmoglein 3 (pemphigus vulgaris antigen)
GO	cell junction	30	387	0.004	200959	gamma-aminobutyric acid (GABA) receptor, rho 3
GO	cell junction	30	387	0.004	23562	claudin 14
GO	cell junction	30	387	0.004	2558	gamma-aminobutyric acid (GABA) A receptor, alpha 5
GO	cell junction	30	387	0.004	26059	ELKS/RAB6-interacting/CAST family member 2

GO	cell junction	30	387	0.004	26999	cytoplasmic FMR1 interacting protein 2
GO	cell junction	30	387	0.004	27445	piccolo (presynaptic cytomatrix protein)
GO	cell junction	30	387	0.004	2898	glutamate receptor, ionotropic, kainate 2
GO	cell junction	30	387	0.004	2906	glutamate receptor, ionotropic, N-methyl D-aspartate 2D
GO	cell junction	30	387	0.004	30011	SH3-domain kinase binding protein 1
GO	cell junction	30	387	0.004	3936	lymphocyte cytosolic protein 1 (L-plastin)
GO	cell junction	30	387	0.004	4867	nephronophthisis 1 (juvenile)
GO	cell junction	30	387	0.004	55752	septin 11
GO	cell junction	30	387	0.004	5795	protein tyrosine phosphatase, receptor type, J
GO	cell junction	30	387	0.004	84552	par-6 partitioning defective 6 homolog gamma (C. elegans)
GO	cell junction	30	387	0.004	8777	multiple PDZ domain protein
GO	cell junction	30	387	0.004	9076	claudin 1
GO	cell junction	30	387	0.004	91624	nexilin (F actin binding protein)
GO	cell junction	30	387	0.004	9260	PDZ and LIM domain 7 (enigma)
GO	cell junction	30	387	0.004	9419	cysteine-rich PDZ-binding protein
GO	cell junction	30	387	0.004	9455	homer homolog 2 (Drosophila)
GO	cell junction	30	387	0.004	9568	gamma-aminobutyric acid (GABA) B receptor, 2
GO	cell junction	30	387	0.004	9635	chloride channel accessory 2
GO	DNA repair	17	182	0.005	157570	establishment of cohesion 1 homolog 2 (S. cerevisiae)
GO	DNA repair	17	182	0.005	1643	damage-specific DNA binding protein 2, 48kDa
GO	DNA repair	17	182	0.005	201299	RAD52 motif 1
GO	DNA repair	17	182	0.005	2139	eyes absent homolog 2 (Drosophila)
GO	DNA repair	17	182	0.005	2237	flap structure-specific endonuclease 1
GO	DNA repair	17	182	0.005	29128	ubiquitin-like with PHD and ring finger domains 1
GO	DNA repair	17	182	0.005	2965	general transcription factor IIH, polypeptide 1, 62kDa
GO	DNA repair	17	182	0.005	4436	mutS homolog 2, colon cancer, nonpolyposis type 1 (E. coli)
GO	DNA repair	17	182	0.005	55215	Fanconi anemia, complementation group I
GO	DNA repair	17	182	0.005	56852	RAD18 homolog (S. cerevisiae)
GO	DNA repair	17	182	0.005	5889	RAD51 homolog C (S. cerevisiae)
GO	DNA repair	17	182	0.005	5965	RecQ protein-like (DNA helicase Q1-like)
GO	DNA repair	17	182	0.005	641	Bloom syndrome, RecQ helicase-like
GO	DNA repair	17	182	0.005	7298	thymidylate synthetase
GO	DNA repair	17	182	0.005	7341	SMT3 suppressor of mif two 3 homolog 1 (S. cerevisiae)
GO	DNA repair	17	182	0.005	79677	structural maintenance of chromosomes 6
GO	DNA repair	17	182	0.005	91442	chromosome 19 open reading frame 40
GO	organ regeneration	6	35	0.005	1026	cyclin-dependent kinase inhibitor 1A (p21, Cip1)

GO	organ regeneration	6	35	0.005	558	AXL receptor tyrosine kinase
GO	organ regeneration	6	35	0.005	6347	chemokine (C-C motif) ligand 2
GO	organ regeneration	6	35	0.005	7046	transforming growth factor, beta receptor 1
GO	organ regeneration	6	35	0.005	890	cyclin A2
GO	organ regeneration	6	35	0.005	898	cyclin E1
GO	fat cell differentiation	5	25	0.005	27241	Bardet-Biedl syndrome 9
GO	fat cell differentiation	5	25	0.005	3589	interleukin 11
GO	fat cell differentiation	5	25	0.005	5469	mediator complex subunit 1
GO	fat cell differentiation	5	25	0.005	64318	nucleolar complex associated 3 homolog (S. cerevisiae)
GO	fat cell differentiation	5	25	0.005	81029	wingless-type MMTV integration site family, member 5B
GO	muscle contraction	11	97	0.005	10052	gap junction protein, gamma 1, 45kDa
GO	muscle contraction	11	97	0.005	2281	FK506 binding protein 1B, 12.6 kDa
GO	muscle contraction	11	97	0.005	4637	myosin, light chain 6, alkali, smooth muscle and non-muscle
GO	muscle contraction	11	97	0.005	5021	oxytocin receptor
GO	muscle contraction	11	97	0.005	59	actin, alpha 2, smooth muscle, aorta
GO	muscle contraction	11	97	0.005	6442	sarcoglycan, alpha (50kDa dystrophin-associated glycoprotein)
GO	muscle contraction	11	97	0.005	6546	solute carrier family 8 (sodium/calcium exchanger), member 1
GO	muscle contraction	11	97	0.005	70	actin, alpha, cardiac muscle 1
GO	muscle contraction	11	97	0.005	7168	tropomyosin 1 (alpha)
GO	muscle contraction	11	97	0.005	7171	tropomyosin 4
GO	muscle contraction	11	97	0.005	9172	myomesin (M-protein) 2, 165kDa
GO	induction of apoptosis	16	170	0.006	10293	TRAF interacting protein
GO	induction of apoptosis	16	170	0.006	10395	deleted in liver cancer 1
GO	induction of apoptosis	16	170	0.006	1984	eukaryotic translation initiation factor 5A
GO	induction of apoptosis	16	170	0.006	348	apolipoprotein E
GO	induction of apoptosis	16	170	0.006	355	Fas (TNF receptor superfamily, member 6)
GO	induction of apoptosis	16	170	0.006	3624	inhibin, beta A
GO	induction of apoptosis	16	170	0.006	3932	lymphocyte-specific protein tyrosine kinase
GO	induction of apoptosis	16	170	0.006	581	BCL2-associated X protein
GO	induction of apoptosis	16	170	0.006	64393	zinc finger, matrin type 3
GO	induction of apoptosis	16	170	0.006	666	BCL2-related ovarian killer
GO	induction of apoptosis	16	170	0.006	7046	transforming growth factor, beta receptor 1
GO	induction of apoptosis	16	170	0.006	7490	Wilms tumor 1
GO	induction of apoptosis	16	170	0.006	8193	D4, zinc and double PHD fingers family 1
GO	induction of apoptosis	16	170	0.006	8626	tumor protein p63
GO	induction of apoptosis	16	170	0.006	9262	serine/threonine kinase 17b

GO	induction of apoptosis	16	170	0.006	94241	tumor protein p53 inducible nuclear protein 1
GO	collagen type V	2	3	0.006	1289	collagen, type V, alpha 1
GO	collagen type V	2	3	0.006	1290	collagen, type V, alpha 2
GO	branching morphogenesis of a nerve	2	3	0.006	1746	distal-less homeobox 2
GO	branching morphogenesis of a nerve	2	3	0.006	2045	EPH receptor A7
GO	5'-flap endonuclease activity	2	3	0.006	1763	DNA replication helicase 2 homolog (yeast)
GO	5'-flap endonuclease activity	2	3	0.006	2237	flap structure-specific endonuclease 1
GO	positive regulation of myeloid cell differ	2	3	0.006	182	jagged 1 (Alagille syndrome)
GO	positive regulation of myeloid cell differ	2	3	0.006	3952	leptin
GO	positive regulation of muscle cell differe	2	3	0.006	1984	eukaryotic translation initiation factor 5A
GO	positive regulation of muscle cell differe	2	3	0.006	8536	calcium/calmodulin-dependent protein kinase I
GO	guanyl-nucleotide exchange factor com	2	3	0.006	25780	RAS guanyl releasing protein 3 (calcium and DAG-regulated)
GO	guanyl-nucleotide exchange factor com	2	3	0.006	5140	phosphodiesterase 3B, cGMP-inhibited
GO	prostatic bud formation	2	3	0.006	2736	GLI family zinc finger 2
GO	prostatic bud formation	2	3	0.006	8626	tumor protein p63
GO	very-low-density lipoprotein particle cle	2	3	0.006	341	apolipoprotein C-I
GO	very-low-density lipoprotein particle cle	2	3	0.006	348	apolipoprotein E
GO	negative regulation of cell adhesion me	2	3	0.006	5054	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor t
GO	negative regulation of cell adhesion me	2	3	0.006	5140	phosphodiesterase 3B, cGMP-inhibited
GO	regulation of cyclin-dependent protein	6	37	0.007	1026	cyclin-dependent kinase inhibitor 1A (p21, Cip1)
GO	regulation of cyclin-dependent protein	6	37	0.007	1164	CDC28 protein kinase regulatory subunit 2
GO	regulation of cyclin-dependent protein	6	37	0.007	28984	chromosome 13 open reading frame 15
GO	regulation of cyclin-dependent protein	6	37	0.007	2965	general transcription factor IIH, polypeptide 1, 62kDa
GO	regulation of cyclin-dependent protein	6	37	0.007	51191	hect domain and RLD 5
GO	regulation of cyclin-dependent protein	6	37	0.007	641	Bloom syndrome, RecQ helicase-like
GO	mitochondrial large ribosomal subunit	4	17	0.007	11222	mitochondrial ribosomal protein L3
GO	mitochondrial large ribosomal subunit	4	17	0.007	28998	mitochondrial ribosomal protein L13
GO	mitochondrial large ribosomal subunit	4	17	0.007	65003	mitochondrial ribosomal protein L11
GO	mitochondrial large ribosomal subunit	4	17	0.007	65008	mitochondrial ribosomal protein L1
GO	Notch binding	3	9	0.007	10683	delta-like 3 (Drosophila)
GO	Notch binding	3	9	0.007	182	jagged 1 (Alagille syndrome)
GO	Notch binding	3	9	0.007	92737	delta/notch-like EGF repeat containing
GO	auditory receptor cell differentiation	3	9	0.007	182	jagged 1 (Alagille syndrome)
GO	auditory receptor cell differentiation	3	9	0.007	3778	potassium large conductance calcium-activated channel, subfamily M, alph
GO	auditory receptor cell differentiation	3	9	0.007	55283	mucolipin 3
GO	female pregnancy	8	61	0.007	2321	fms-related tyrosine kinase 1 (vascular endothelial growth factor/vascular

GO	female pregnancy	8	61	0.007	2878	glutathione peroxidase 3 (plasma)
GO	female pregnancy	8	61	0.007	29842	transcription factor CP2-like 1
GO	female pregnancy	8	61	0.007	3248	hydroxyprostaglandin dehydrogenase 15-(NAD)
GO	female pregnancy	8	61	0.007	5021	oxytocin receptor
GO	female pregnancy	8	61	0.007	5228	placental growth factor
GO	female pregnancy	8	61	0.007	5744	parathyroid hormone-like hormone
GO	female pregnancy	8	61	0.007	6019	relaxin 2
GO	DNA-dependent ATPase activity	5	27	0.007	1161	excision repair cross-complementing rodent repair deficiency, complement
GO	DNA-dependent ATPase activity	5	27	0.007	2965	general transcription factor IIH, polypeptide 1, 62kDa
GO	DNA-dependent ATPase activity	5	27	0.007	50485	SWI/SNF related, matrix associated, actin dependent regulator of chromati
GO	DNA-dependent ATPase activity	5	27	0.007	5889	RAD51 homolog C (S. cerevisiae)
GO	DNA-dependent ATPase activity	5	27	0.007	8458	transcription termination factor, RNA polymerase II
GO	sarcomere	5	27	0.007	70	actin, alpha, cardiac muscle 1
GO	sarcomere	5	27	0.007	7137	troponin I type 3 (cardiac)
GO	sarcomere	5	27	0.007	7168	tropomyosin 1 (alpha)
GO	sarcomere	5	27	0.007	7220	transient receptor potential cation channel, subfamily C, member 1
GO	sarcomere	5	27	0.007	84665	myopalladin
GO	polypeptide N-acetylgalactosaminyltran	4	18	0.008	11226	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltr
GO	polypeptide N-acetylgalactosaminyltran	4	18	0.008	11227	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltr
GO	polypeptide N-acetylgalactosaminyltran	4	18	0.008	114805	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltr
GO	polypeptide N-acetylgalactosaminyltran	4	18	0.008	79623	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltr
GO	pituitary gland development	4	18	0.008	220	aldehyde dehydrogenase 1 family, member A3
GO	pituitary gland development	4	18	0.008	2736	GLI family zinc finger 2
GO	pituitary gland development	4	18	0.008	6299	sal-like 1 (Drosophila)
GO	pituitary gland development	4	18	0.008	6657	SRY (sex determining region Y)-box 2
GO	actin filament	5	28	0.009	10096	ARP3 actin-related protein 3 homolog (yeast)
GO	actin filament	5	28	0.009	10395	deleted in liver cancer 1
GO	actin filament	5	28	0.009	3936	lymphocyte cytosolic protein 1 (L-plastin)
GO	actin filament	5	28	0.009	70	actin, alpha, cardiac muscle 1
GO	actin filament	5	28	0.009	7456	WAS/WASL interacting protein family, member 1
GO	CTP biosynthetic process	3	10	0.009	1503	CTP synthase
GO	CTP biosynthetic process	3	10	0.009	29922	non-metastatic cells 7, protein expressed in (nucleoside-diphosphate kinas
GO	CTP biosynthetic process	3	10	0.009	4830	non-metastatic cells 1, protein (NM23A) expressed in
GO	embryonic digestive tract development	3	10	0.009	2736	GLI family zinc finger 2
GO	embryonic digestive tract development	3	10	0.009	5125	proprotein convertase subtilisin/kexin type 5
GO	embryonic digestive tract development	3	10	0.009	6299	sal-like 1 (Drosophila)

GO	negative regulation of blood coagulatio	3	10	0.009	348	apolipoprotein E
GO	negative regulation of blood coagulatio	3	10	0.009	5054	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor t
GO	negative regulation of blood coagulatio	3	10	0.009	5624	protein C (inactivator of coagulation factors Va and VIIIa)
GO	actin cytoskeleton	13	134	0.01	10096	ARP3 actin-related protein 3 homolog (yeast)
GO	actin cytoskeleton	13	134	0.01	10097	ARP2 actin-related protein 2 homolog (yeast)
GO	actin cytoskeleton	13	134	0.01	10391	coronin, actin binding protein, 2B
GO	actin cytoskeleton	13	134	0.01	10788	IQ motif containing GTPase activating protein 2
GO	actin cytoskeleton	13	134	0.01	1496	catenin (cadherin-associated protein), alpha 2
GO	actin cytoskeleton	13	134	0.01	5216	profilin 1
GO	actin cytoskeleton	13	134	0.01	59	actin, alpha 2, smooth muscle, aorta
GO	actin cytoskeleton	13	134	0.01	6525	smoothelin
GO	actin cytoskeleton	13	134	0.01	7168	tropomyosin 1 (alpha)
GO	actin cytoskeleton	13	134	0.01	7456	WAS/WASL interacting protein family, member 1
GO	actin cytoskeleton	13	134	0.01	8997	kalirin, RhoGEF kinase
GO	actin cytoskeleton	13	134	0.01	9260	PDZ and LIM domain 7 (enigma)
GO	actin cytoskeleton	13	134	0.01	9262	serine/threonine kinase 17b
GO	mRNA export from nucleus	5	29	0.01	10189	THO complex 4
GO	mRNA export from nucleus	5	29	0.01	10212	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39
GO	mRNA export from nucleus	5	29	0.01	1984	eukaryotic translation initiation factor 5A
GO	mRNA export from nucleus	5	29	0.01	26019	UPF2 regulator of nonsense transcripts homolog (yeast)
GO	mRNA export from nucleus	5	29	0.01	8563	THO complex 5
GO	chromosome	13	135	0.01	10051	structural maintenance of chromosomes 4
GO	chromosome	13	135	0.01	3149	high-mobility group box 3
GO	chromosome	13	135	0.01	387103	centromere protein W
GO	chromosome	13	135	0.01	55215	Fanconi anemia, complementation group I
GO	chromosome	13	135	0.01	55506	H2A histone family, member Y2
GO	chromosome	13	135	0.01	6672	SP100 nuclear antigen
GO	chromosome	13	135	0.01	79172	centromere protein O
GO	chromosome	13	135	0.01	79677	structural maintenance of chromosomes 6
GO	chromosome	13	135	0.01	79682	MLF1 interacting protein
GO	chromosome	13	135	0.01	8091	high mobility group AT-hook 2
GO	chromosome	13	135	0.01	8348	histone cluster 1, H2bo
GO	chromosome	13	135	0.01	8349	histone cluster 2, H2be
GO	chromosome	13	135	0.01	8970	histone cluster 1, H2bj
GO	methyltransferase activity	11	106	0.01	131965	methyltransferase like 6
GO	methyltransferase activity	11	106	0.01	149281	methyltransferase like 11B

GO	methyltransferase activity	11	106	0.01	1787	tRNA aspartic acid methyltransferase 1
GO	methyltransferase activity	11	106	0.01	1788	DNA (cytosine-5-)-methyltransferase 3 alpha
GO	methyltransferase activity	11	106	0.01	2618	phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide
GO	methyltransferase activity	11	106	0.01	3276	protein arginine methyltransferase 1
GO	methyltransferase activity	11	106	0.01	345630	fibrillarin-like 1
GO	methyltransferase activity	11	106	0.01	5110	protein-L-isoaspartate (D-aspartate) O-methyltransferase
GO	methyltransferase activity	11	106	0.01	56339	methyltransferase like 3
GO	methyltransferase activity	11	106	0.01	7298	thymidylate synthetase
GO	methyltransferase activity	11	106	0.01	91801	alkB, alkylation repair homolog 8 (E. coli)
GO	heterophilic cell-cell adhesion	4	19	0.01	1000	cadherin 2, type 1, N-cadherin (neuronal)
GO	heterophilic cell-cell adhesion	4	19	0.01	1002	cadherin 4, type 1, R-cadherin (retinal)
GO	heterophilic cell-cell adhesion	4	19	0.01	23705	cell adhesion molecule 1
GO	heterophilic cell-cell adhesion	4	19	0.01	347902	adhesion molecule with Ig-like domain 2
GO	collagen catabolic process	4	19	0.01	4312	matrix metallopeptidase 1 (interstitial collagenase)
GO	collagen catabolic process	4	19	0.01	4318	matrix metallopeptidase 9 (gelatinase B, 92kDa gelatinase, 92kDa type IV c
GO	collagen catabolic process	4	19	0.01	4319	matrix metallopeptidase 10 (stromelysin 2)
GO	collagen catabolic process	4	19	0.01	5184	peptidase D
GO	basolateral plasma membrane	11	107	0.011	1496	catenin (cadherin-associated protein), alpha 2
GO	basolateral plasma membrane	11	107	0.011	23705	cell adhesion molecule 1
GO	basolateral plasma membrane	11	107	0.011	287	ankyrin 2, neuronal
GO	basolateral plasma membrane	11	107	0.011	5028	purinergic receptor P2Y, G-protein coupled, 1
GO	basolateral plasma membrane	11	107	0.011	5031	pyrimidinergic receptor P2Y, G-protein coupled, 6
GO	basolateral plasma membrane	11	107	0.011	6580	solute carrier family 22 (organic cation transporter), member 1
GO	basolateral plasma membrane	11	107	0.011	7010	TEK tyrosine kinase, endothelial
GO	basolateral plasma membrane	11	107	0.011	7046	transforming growth factor, beta receptor 1
GO	basolateral plasma membrane	11	107	0.011	7220	transient receptor potential cation channel, subfamily C, member 1
GO	basolateral plasma membrane	11	107	0.011	9053	microtubule-associated protein 7
GO	basolateral plasma membrane	11	107	0.011	9497	solute carrier family 4, sodium bicarbonate cotransporter, member 7
GO	eye morphogenesis	2	4	0.012	1289	collagen, type V, alpha 1
GO	eye morphogenesis	2	4	0.012	1290	collagen, type V, alpha 2
GO	apicolateral plasma membrane	2	4	0.012	166336	prickle homolog 2 (Drosophila)
GO	apicolateral plasma membrane	2	4	0.012	4734	neural precursor cell expressed, developmentally down-regulated 4
GO	DNA (cytosine-5-)-methyltransferase ac	2	4	0.012	1787	tRNA aspartic acid methyltransferase 1
GO	DNA (cytosine-5-)-methyltransferase ac	2	4	0.012	1788	DNA (cytosine-5-)-methyltransferase 3 alpha
GO	lipoxygenase pathway	2	4	0.012	241	arachidonate 5-lipoxygenase-activating protein
GO	lipoxygenase pathway	2	4	0.012	3248	hydroxyprostaglandin dehydrogenase 15-(NAD)

GO	DNA-directed RNA polymerase I comple	2	4	0.012	25885	polymerase (RNA) I polypeptide A, 194kDa
GO	DNA-directed RNA polymerase I comple	2	4	0.012	84172	polymerase (RNA) I polypeptide B, 128kDa
GO	chylomicron remnant clearance	2	4	0.012	341	apolipoprotein C-I
GO	chylomicron remnant clearance	2	4	0.012	348	apolipoprotein E
GO	regulation of axon extension	2	4	0.012	348	apolipoprotein E
GO	regulation of axon extension	2	4	0.012	4897	neuronal cell adhesion molecule
GO	saliva secretion	2	4	0.012	3778	potassium large conductance calcium-activated channel, subfamily M, alph
GO	saliva secretion	2	4	0.012	7220	transient receptor potential cation channel, subfamily C, member 1
GO	regulation of DNA recombination	2	4	0.012	3836	karyopherin alpha 1 (importin alpha 5)
GO	regulation of DNA recombination	2	4	0.012	3838	karyopherin alpha 2 (RAG cohort 1, importin alpha 1)
GO	response to methylmercury	2	4	0.012	411	arylsulfatase B
GO	response to methylmercury	2	4	0.012	898	cyclin E1
GO	guanine/thymine mispair binding	2	4	0.012	4292	mutL homolog 1, colon cancer, nonpolyposis type 2 (E. coli)
GO	guanine/thymine mispair binding	2	4	0.012	4436	mutS homolog 2, colon cancer, nonpolyposis type 1 (E. coli)
GO	regulation of G2/M transition of mitotic	2	4	0.012	5569	protein kinase (cAMP-dependent, catalytic) inhibitor alpha
GO	regulation of G2/M transition of mitotic	2	4	0.012	5588	protein kinase C, theta
GO	ATP-dependent 3'-5' DNA helicase activ	2	4	0.012	5965	RecQ protein-like (DNA helicase Q1-like)
GO	ATP-dependent 3'-5' DNA helicase activ	2	4	0.012	641	Bloom syndrome, RecQ helicase-like
GO	DNA strand annealing activity	2	4	0.012	5965	RecQ protein-like (DNA helicase Q1-like)
GO	DNA strand annealing activity	2	4	0.012	641	Bloom syndrome, RecQ helicase-like
GO	muscle thin filament tropomyosin	2	4	0.012	7168	tropomyosin 1 (alpha)
GO	muscle thin filament tropomyosin	2	4	0.012	7171	tropomyosin 4
GO	gamma-aminobutyric acid signaling patl	4	20	0.012	200959	gamma-aminobutyric acid (GABA) receptor, rho 3
GO	gamma-aminobutyric acid signaling patl	4	20	0.012	2558	gamma-aminobutyric acid (GABA) A receptor, alpha 5
GO	gamma-aminobutyric acid signaling patl	4	20	0.012	773	calcium channel, voltage-dependent, P/Q type, alpha 1A subunit
GO	gamma-aminobutyric acid signaling patl	4	20	0.012	9568	gamma-aminobutyric acid (GABA) B receptor, 2
GO	tissue regeneration	4	20	0.012	2628	glycine amidinotransferase (L-arginine:glycine amidinotransferase)
GO	tissue regeneration	4	20	0.012	5054	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor t
GO	tissue regeneration	4	20	0.012	5588	protein kinase C, theta
GO	tissue regeneration	4	20	0.012	7078	TIMP metallopeptidase inhibitor 3
GO	transforming growth factor beta recept	3	11	0.012	4052	latent transforming growth factor beta binding protein 1
GO	transforming growth factor beta recept	3	11	0.012	659	bone morphogenetic protein receptor, type II (serine/threonine kinase)
GO	transforming growth factor beta recept	3	11	0.012	7046	transforming growth factor, beta receptor 1
GO	negative regulation of DNA binding	3	11	0.012	58499	zinc finger protein 462
GO	negative regulation of DNA binding	3	11	0.012	6672	SP100 nuclear antigen
GO	negative regulation of DNA binding	3	11	0.012	7341	SMT3 suppressor of mif two 3 homolog 1 (S. cerevisiae)

GO	positive regulation of endothelial cell pr	5	31	0.013	5228	placental growth factor
GO	positive regulation of endothelial cell pr	5	31	0.013	6347	chemokine (C-C motif) ligand 2
GO	positive regulation of endothelial cell pr	5	31	0.013	659	bone morphogenetic protein receptor, type II (serine/threonine kinase)
GO	positive regulation of endothelial cell pr	5	31	0.013	7857	secretogranin II (chromogranin C)
GO	positive regulation of endothelial cell pr	5	31	0.013	79805	vasohibin 2
GO	protein binding	321	6249	0.014	1000	cadherin 2, type 1, N-cadherin (neuronal)
GO	protein binding	321	6249	0.014	10000	v-akt murine thymoma viral oncogene homolog 3 (protein kinase B, gamma
GO	protein binding	321	6249	0.014	10051	structural maintenance of chromosomes 4
GO	protein binding	321	6249	0.014	10052	gap junction protein, gamma 1, 45kDa
GO	protein binding	321	6249	0.014	10055	SUMO1 activating enzyme subunit 1
GO	protein binding	321	6249	0.014	10096	ARP3 actin-related protein 3 homolog (yeast)
GO	protein binding	321	6249	0.014	10097	ARP2 actin-related protein 2 homolog (yeast)
GO	protein binding	321	6249	0.014	10189	THO complex 4
GO	protein binding	321	6249	0.014	10190	thioredoxin domain containing 9
GO	protein binding	321	6249	0.014	10199	M-phase phosphoprotein 10 (U3 small nucleolar ribonucleoprotein)
GO	protein binding	321	6249	0.014	10212	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39
GO	protein binding	321	6249	0.014	10213	proteasome (prosome, macropain) 26S subunit, non-ATPase, 14
GO	protein binding	321	6249	0.014	10254	signal transducing adaptor molecule (SH3 domain and ITAM motif) 2
GO	protein binding	321	6249	0.014	1026	cyclin-dependent kinase inhibitor 1A (p21, Cip1)
GO	protein binding	321	6249	0.014	10293	TRAF interacting protein
GO	protein binding	321	6249	0.014	10395	deleted in liver cancer 1
GO	protein binding	321	6249	0.014	1045	caudal type homeobox 2
GO	protein binding	321	6249	0.014	10465	peptidylprolyl isomerase H (cyclophilin H)
GO	protein binding	321	6249	0.014	10474	transcriptional adaptor 3
GO	protein binding	321	6249	0.014	10492	synaptotagmin binding, cytoplasmic RNA interacting protein
GO	protein binding	321	6249	0.014	10528	NOP56 ribonucleoprotein homolog (yeast)
GO	protein binding	321	6249	0.014	10539	glutaredoxin 3
GO	protein binding	321	6249	0.014	10612	tripartite motif-containing 3
GO	protein binding	321	6249	0.014	10656	KH domain containing, RNA binding, signal transduction associated 3
GO	protein binding	321	6249	0.014	10672	guanine nucleotide binding protein (G protein), alpha 13
GO	protein binding	321	6249	0.014	10683	delta-like 3 (Drosophila)
GO	protein binding	321	6249	0.014	10785	WD repeat domain 4
GO	protein binding	321	6249	0.014	10788	IQ motif containing GTPase activating protein 2
GO	protein binding	321	6249	0.014	10799	ribonuclease P/MRP 40kDa subunit
GO	protein binding	321	6249	0.014	10890	RAB10, member RAS oncogene family
GO	protein binding	321	6249	0.014	11142	protein kinase (cAMP-dependent, catalytic) inhibitor gamma

GO	protein binding	321	6249	0.014	11154	adaptor-related protein complex 4, sigma 1 subunit
GO	protein binding	321	6249	0.014	1121	choroideremia (Rab escort protein 1)
GO	protein binding	321	6249	0.014	1123	chimerin (chimaerin) 1
GO	protein binding	321	6249	0.014	114088	tripartite motif-containing 9
GO	protein binding	321	6249	0.014	114804	ring finger protein 157
GO	protein binding	321	6249	0.014	115290	F-box protein 17
GO	protein binding	321	6249	0.014	1161	excision repair cross-complementing rodent repair deficiency, complement
GO	protein binding	321	6249	0.014	118788	phosphoinositide-3-kinase adaptor protein 1
GO	protein binding	321	6249	0.014	118924	chromosome 10 open reading frame 4
GO	protein binding	321	6249	0.014	12	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), me
GO	protein binding	321	6249	0.014	121268	Ras homolog enriched in brain like 1
GO	protein binding	321	6249	0.014	1282	collagen, type IV, alpha 1
GO	protein binding	321	6249	0.014	1284	collagen, type IV, alpha 2
GO	protein binding	321	6249	0.014	1288	collagen, type IV, alpha 6
GO	protein binding	321	6249	0.014	128853	dual specificity phosphatase 15
GO	protein binding	321	6249	0.014	1289	collagen, type V, alpha 1
GO	protein binding	321	6249	0.014	132158	glycerate kinase
GO	protein binding	321	6249	0.014	140739	ubiquitin-conjugating enzyme E2F (putative)
GO	protein binding	321	6249	0.014	146760	reticulon 4 receptor-like 1
GO	protein binding	321	6249	0.014	1496	catenin (cadherin-associated protein), alpha 2
GO	protein binding	321	6249	0.014	1503	CTP synthase
GO	protein binding	321	6249	0.014	150684	copper metabolism (Murr1) domain containing 1
GO	protein binding	321	6249	0.014	151188	ADP-ribosylation-like factor 6 interacting protein 6
GO	protein binding	321	6249	0.014	157773	chromosome 8 open reading frame 48
GO	protein binding	321	6249	0.014	1643	damage-specific DNA binding protein 2, 48kDa
GO	protein binding	321	6249	0.014	1687	deafness, autosomal dominant 5
GO	protein binding	321	6249	0.014	170082	transcription elongation factor A (SII) N-terminal and central domain contai
GO	protein binding	321	6249	0.014	1746	distal-less homeobox 2
GO	protein binding	321	6249	0.014	1775	deoxyribonuclease I-like 2
GO	protein binding	321	6249	0.014	1781	dynein, cytoplasmic 1, intermediate chain 2
GO	protein binding	321	6249	0.014	1788	DNA (cytosine-5-)-methyltransferase 3 alpha
GO	protein binding	321	6249	0.014	182	jagged 1 (Alagille syndrome)
GO	protein binding	321	6249	0.014	1984	eukaryotic translation initiation factor 5A
GO	protein binding	321	6249	0.014	203	adenylate kinase 1
GO	protein binding	321	6249	0.014	2037	erythrocyte membrane protein band 4.1-like 2
GO	protein binding	321	6249	0.014	2045	EPH receptor A7

GO	protein binding	321	6249	0.014	2139	eyes absent homolog 2 (Drosophila)
GO	protein binding	321	6249	0.014	2149	coagulation factor II (thrombin) receptor
GO	protein binding	321	6249	0.014	2151	coagulation factor II (thrombin) receptor-like 2
GO	protein binding	321	6249	0.014	2171	fatty acid binding protein 5 (psoriasis-associated)
GO	protein binding	321	6249	0.014	220134	spindle and kinetochore associated complex subunit 1
GO	protein binding	321	6249	0.014	221687	ring finger protein 182
GO	protein binding	321	6249	0.014	2232	ferredoxin reductase
GO	protein binding	321	6249	0.014	2237	flap structure-specific endonuclease 1
GO	protein binding	321	6249	0.014	2242	feline sarcoma oncogene
GO	protein binding	321	6249	0.014	2264	fibroblast growth factor receptor 4
GO	protein binding	321	6249	0.014	2273	four and a half LIM domains 1
GO	protein binding	321	6249	0.014	2281	FK506 binding protein 1B, 12.6 kDa
GO	protein binding	321	6249	0.014	22891	zinc finger protein 365
GO	protein binding	321	6249	0.014	2305	forkhead box M1
GO	protein binding	321	6249	0.014	23136	erythrocyte membrane protein band 4.1-like 3
GO	protein binding	321	6249	0.014	23157	septin 6
GO	protein binding	321	6249	0.014	23194	F-box and leucine-rich repeat protein 7
GO	protein binding	321	6249	0.014	23305	acyl-CoA synthetase long-chain family member 6
GO	protein binding	321	6249	0.014	23594	origin recognition complex, subunit 6 like (yeast)
GO	protein binding	321	6249	0.014	23658	LSM5 homolog, U6 small nuclear RNA associated (S. cerevisiae)
GO	protein binding	321	6249	0.014	241	arachidonate 5-lipoxygenase-activating protein
GO	protein binding	321	6249	0.014	2533	FYN binding protein (FYB-120/130)
GO	protein binding	321	6249	0.014	2534	FYN oncogene related to SRC, FGR, YES
GO	protein binding	321	6249	0.014	25780	RAS guanyl releasing protein 3 (calcium and DAG-regulated)
GO	protein binding	321	6249	0.014	25827	F-box and leucine-rich repeat protein 2
GO	protein binding	321	6249	0.014	25885	polymerase (RNA) I polypeptide A, 194kDa
GO	protein binding	321	6249	0.014	26019	UPF2 regulator of nonsense transcripts homolog (yeast)
GO	protein binding	321	6249	0.014	26059	ELKS/RAB6-interacting/CAST family member 2
GO	protein binding	321	6249	0.014	2618	phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide
GO	protein binding	321	6249	0.014	26207	phosphatidylinositol transfer protein, cytoplasmic 1
GO	protein binding	321	6249	0.014	26230	T-cell lymphoma invasion and metastasis 2
GO	protein binding	321	6249	0.014	26275	3-hydroxyisobutyryl-Coenzyme A hydrolase
GO	protein binding	321	6249	0.014	2628	glycine amidinotransferase (L-arginine:glycine amidinotransferase)
GO	protein binding	321	6249	0.014	26519	translocase of inner mitochondrial membrane 10 homolog (yeast)
GO	protein binding	321	6249	0.014	26521	translocase of inner mitochondrial membrane 8 homolog B (yeast)
GO	protein binding	321	6249	0.014	26577	procollagen C-endopeptidase enhancer 2

GO	protein binding	321	6249	0.014	26999	cytoplasmic FMR1 interacting protein 2
GO	protein binding	321	6249	0.014	27258	LSM3 homolog, U6 small nuclear RNA associated (S. cerevisiae)
GO	protein binding	321	6249	0.014	27289	Rho family GTPase 1
GO	protein binding	321	6249	0.014	2736	GLI family zinc finger 2
GO	protein binding	321	6249	0.014	27429	HtrA serine peptidase 2
GO	protein binding	321	6249	0.014	287	ankyrin 2, neuronal
GO	protein binding	321	6249	0.014	28984	chromosome 13 open reading frame 15
GO	protein binding	321	6249	0.014	2906	glutamate receptor, ionotropic, N-methyl D-aspartate 2D
GO	protein binding	321	6249	0.014	29128	ubiquitin-like with PHD and ring finger domains 1
GO	protein binding	321	6249	0.014	2965	general transcription factor IIH, polypeptide 1, 62kDa
GO	protein binding	321	6249	0.014	29887	sorting nexin 10
GO	protein binding	321	6249	0.014	29995	LIM and cysteine-rich domains 1
GO	protein binding	321	6249	0.014	30011	SH3-domain kinase binding protein 1
GO	protein binding	321	6249	0.014	3028	hydroxysteroid (17-beta) dehydrogenase 10
GO	protein binding	321	6249	0.014	309	annexin A6
GO	protein binding	321	6249	0.014	3183	heterogeneous nuclear ribonucleoprotein C (C1/C2)
GO	protein binding	321	6249	0.014	3224	homeobox C8
GO	protein binding	321	6249	0.014	3236	homeobox D10
GO	protein binding	321	6249	0.014	3276	protein arginine methyltransferase 1
GO	protein binding	321	6249	0.014	332	baculoviral IAP repeat-containing 5
GO	protein binding	321	6249	0.014	3336	heat shock 10kDa protein 1 (chaperonin 10)
GO	protein binding	321	6249	0.014	344805	transmembrane protease, serine 7
GO	protein binding	321	6249	0.014	347902	adhesion molecule with Ig-like domain 2
GO	protein binding	321	6249	0.014	348	apolipoprotein E
GO	protein binding	321	6249	0.014	3516	recombination signal binding protein for immunoglobulin kappa J region
GO	protein binding	321	6249	0.014	353091	retinoic acid early transcript 1G
GO	protein binding	321	6249	0.014	355	Fas (TNF receptor superfamily, member 6)
GO	protein binding	321	6249	0.014	3557	interleukin 1 receptor antagonist
GO	protein binding	321	6249	0.014	3624	inhibin, beta A
GO	protein binding	321	6249	0.014	3685	integrin, alpha V (vitronectin receptor, alpha polypeptide, antigen CD51)
GO	protein binding	321	6249	0.014	3751	potassium voltage-gated channel, Shal-related subfamily, member 2
GO	protein binding	321	6249	0.014	3754	potassium voltage-gated channel, subfamily F, member 1
GO	protein binding	321	6249	0.014	3763	potassium inwardly-rectifying channel, subfamily J, member 6
GO	protein binding	321	6249	0.014	3778	potassium large conductance calcium-activated channel, subfamily M, alph
GO	protein binding	321	6249	0.014	3800	kinesin family member 5C
GO	protein binding	321	6249	0.014	3836	karyopherin alpha 1 (importin alpha 5)

GO	protein binding	321	6249	0.014	3838	karyopherin alpha 2 (RAG cohort 1, importin alpha 1)
GO	protein binding	321	6249	0.014	3883	keratin 33A
GO	protein binding	321	6249	0.014	3887	keratin 81
GO	protein binding	321	6249	0.014	389421	lin-28 homolog B (C. elegans)
GO	protein binding	321	6249	0.014	3932	lymphocyte-specific protein tyrosine kinase
GO	protein binding	321	6249	0.014	3936	lymphocyte cytosolic protein 1 (L-plastin)
GO	protein binding	321	6249	0.014	3952	leptin
GO	protein binding	321	6249	0.014	3975	LIM homeobox 1
GO	protein binding	321	6249	0.014	401265	kelch-like 31 (Drosophila)
GO	protein binding	321	6249	0.014	406	aryl hydrocarbon receptor nuclear translocator-like
GO	protein binding	321	6249	0.014	409	arrestin, beta 2
GO	protein binding	321	6249	0.014	4158	melanocortin 2 receptor (adrenocorticotropic hormone)
GO	protein binding	321	6249	0.014	4171	minichromosome maintenance complex component 2
GO	protein binding	321	6249	0.014	4287	ataxin 3
GO	protein binding	321	6249	0.014	4291	myeloid leukemia factor 1
GO	protein binding	321	6249	0.014	4292	mutL homolog 1, colon cancer, nonpolyposis type 2 (E. coli)
GO	protein binding	321	6249	0.014	4318	matrix metallopeptidase 9 (gelatinase B, 92kDa gelatinase, 92kDa type IV c
GO	protein binding	321	6249	0.014	4430	myosin IB
GO	protein binding	321	6249	0.014	4436	mutS homolog 2, colon cancer, nonpolyposis type 1 (E. coli)
GO	protein binding	321	6249	0.014	4734	neural precursor cell expressed, developmentally down-regulated 4
GO	protein binding	321	6249	0.014	4763	neurofibromin 1
GO	protein binding	321	6249	0.014	4830	non-metastatic cells 1, protein (NM23A) expressed in
GO	protein binding	321	6249	0.014	4867	nephronophthisis 1 (juvenile)
GO	protein binding	321	6249	0.014	4893	neuroblastoma RAS viral (v-ras) oncogene homolog
GO	protein binding	321	6249	0.014	4928	nucleoporin 98kDa
GO	protein binding	321	6249	0.014	4968	8-oxoguanine DNA glycosylase
GO	protein binding	321	6249	0.014	5000	origin recognition complex, subunit 4-like (yeast)
GO	protein binding	321	6249	0.014	5021	oxytocin receptor
GO	protein binding	321	6249	0.014	5054	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor t
GO	protein binding	321	6249	0.014	5081	paired box 7
GO	protein binding	321	6249	0.014	51003	mediator complex subunit 31
GO	protein binding	321	6249	0.014	5101	protocadherin 9
GO	protein binding	321	6249	0.014	51062	atlastin GTPase 1
GO	protein binding	321	6249	0.014	5110	protein-L-isoaspartate (D-aspartate) O-methyltransferase
GO	protein binding	321	6249	0.014	51136	ring finger protein, transmembrane 1
GO	protein binding	321	6249	0.014	51382	ATPase, H+ transporting, lysosomal 34kDa, V1 subunit D

GO	protein binding	321	6249	0.014	5140	phosphodiesterase 3B, cGMP-inhibited
GO	protein binding	321	6249	0.014	51499	TP53 regulated inhibitor of apoptosis 1
GO	protein binding	321	6249	0.014	5245	prohibitin
GO	protein binding	321	6249	0.014	5264	phytanoyl-CoA 2-hydroxylase
GO	protein binding	321	6249	0.014	528	ATPase, H+ transporting, lysosomal 42kDa, V1 subunit C1
GO	protein binding	321	6249	0.014	5341	pleckstrin
GO	protein binding	321	6249	0.014	53981	cleavage and polyadenylation specific factor 2, 100kDa
GO	protein binding	321	6249	0.014	5420	podocalyxin-like
GO	protein binding	321	6249	0.014	5469	mediator complex subunit 1
GO	protein binding	321	6249	0.014	54726	OTU domain containing 4
GO	protein binding	321	6249	0.014	54839	leucine rich repeat containing 49
GO	protein binding	321	6249	0.014	54843	synaptotagmin-like 2
GO	protein binding	321	6249	0.014	54849	differentially expressed in FDCP 8 homolog (mouse)
GO	protein binding	321	6249	0.014	5494	protein phosphatase, Mg2+/Mn2+ dependent, 1A
GO	protein binding	321	6249	0.014	54951	COMM domain containing 8
GO	protein binding	321	6249	0.014	54984	PIN2-interacting protein 1
GO	protein binding	321	6249	0.014	55012	protein phosphatase 2 (formerly 2A), regulatory subunit B'', gamma
GO	protein binding	321	6249	0.014	55135	WD repeat containing, antisense to TP53
GO	protein binding	321	6249	0.014	55215	Fanconi anemia, complementation group I
GO	protein binding	321	6249	0.014	55521	tripartite motif-containing 36
GO	protein binding	321	6249	0.014	55577	N-acetylglucosamine kinase
GO	protein binding	321	6249	0.014	55752	septin 11
GO	protein binding	321	6249	0.014	55759	WD repeat domain 12
GO	protein binding	321	6249	0.014	558	AXL receptor tyrosine kinase
GO	protein binding	321	6249	0.014	55803	ArfGAP with dual PH domains 2
GO	protein binding	321	6249	0.014	5588	protein kinase C, theta
GO	protein binding	321	6249	0.014	55916	nuclear transport factor 2-like export factor 2
GO	protein binding	321	6249	0.014	56062	kelch-like 4 (Drosophila)
GO	protein binding	321	6249	0.014	5624	protein C (inactivator of coagulation factors Va and VIIIa)
GO	protein binding	321	6249	0.014	56241	sushi domain containing 2
GO	protein binding	321	6249	0.014	56655	polymerase (DNA-directed), epsilon 4 (p12 subunit)
GO	protein binding	321	6249	0.014	56852	RAD18 homolog (S. cerevisiae)
GO	protein binding	321	6249	0.014	5702	proteasome (prosome, macropain) 26S subunit, ATPase, 3
GO	protein binding	321	6249	0.014	57099	apoptosis, caspase activation inhibitor
GO	protein binding	321	6249	0.014	57144	p21 protein (Cdc42/Rac)-activated kinase 7
GO	protein binding	321	6249	0.014	5717	proteasome (prosome, macropain) 26S subunit, non-ATPase, 11

GO	protein binding	321	6249	0.014	57333	reticulocalbin 3, EF-hand calcium binding domain
GO	protein binding	321	6249	0.014	57484	ring finger protein 150
GO	protein binding	321	6249	0.014	5754	PTK7 protein tyrosine kinase 7
GO	protein binding	321	6249	0.014	57599	WD repeat domain 48
GO	protein binding	321	6249	0.014	57650	KIAA1524
GO	protein binding	321	6249	0.014	5795	protein tyrosine phosphatase, receptor type, J
GO	protein binding	321	6249	0.014	581	BCL2-associated X protein
GO	protein binding	321	6249	0.014	59	actin, alpha 2, smooth muscle, aorta
GO	protein binding	321	6249	0.014	5924	Ras protein-specific guanine nucleotide-releasing factor 2
GO	protein binding	321	6249	0.014	5965	RecQ protein-like (DNA helicase Q1-like)
GO	protein binding	321	6249	0.014	597	BCL2-related protein A1
GO	protein binding	321	6249	0.014	6000	regulator of G-protein signaling 7
GO	protein binding	321	6249	0.014	6120	ribulose-5-phosphate-3-epimerase
GO	protein binding	321	6249	0.014	6154	ribosomal protein L26
GO	protein binding	321	6249	0.014	6204	ribosomal protein S10
GO	protein binding	321	6249	0.014	6241	ribonucleotide reductase M2
GO	protein binding	321	6249	0.014	6242	rhotekin
GO	protein binding	321	6249	0.014	6251	Ras suppressor protein 1
GO	protein binding	321	6249	0.014	6299	sal-like 1 (Drosophila)
GO	protein binding	321	6249	0.014	6347	chemokine (C-C motif) ligand 2
GO	protein binding	321	6249	0.014	641	Bloom syndrome, RecQ helicase-like
GO	protein binding	321	6249	0.014	64151	non-SMC condensin I complex, subunit G
GO	protein binding	321	6249	0.014	6442	sarcoglycan, alpha (50kDa dystrophin-associated glycoprotein)
GO	protein binding	321	6249	0.014	6444	sarcoglycan, delta (35kDa dystrophin-associated glycoprotein)
GO	protein binding	321	6249	0.014	65062	amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 4
GO	protein binding	321	6249	0.014	6580	solute carrier family 22 (organic cation transporter), member 1
GO	protein binding	321	6249	0.014	6586	slit homolog 3 (Drosophila)
GO	protein binding	321	6249	0.014	659	bone morphogenetic protein receptor, type II (serine/threonine kinase)
GO	protein binding	321	6249	0.014	6615	snail homolog 1 (Drosophila)
GO	protein binding	321	6249	0.014	6637	small nuclear ribonucleoprotein polypeptide G
GO	protein binding	321	6249	0.014	6657	SRY (sex determining region Y)-box 2
GO	protein binding	321	6249	0.014	6659	SRY (sex determining region Y)-box 4
GO	protein binding	321	6249	0.014	6662	SRY (sex determining region Y)-box 9
GO	protein binding	321	6249	0.014	667	dystonin
GO	protein binding	321	6249	0.014	6672	SP100 nuclear antigen
GO	protein binding	321	6249	0.014	6683	spastin

GO	protein binding	321	6249	0.014	6711	spectrin, beta, non-erythrocytic 1
GO	protein binding	321	6249	0.014	672	breast cancer 1, early onset
GO	protein binding	321	6249	0.014	6741	Sjogren syndrome antigen B (autoantigen La)
GO	protein binding	321	6249	0.014	6820	sulfotransferase family, cytosolic, 2B, member 1
GO	protein binding	321	6249	0.014	70	actin, alpha, cardiac muscle 1
GO	protein binding	321	6249	0.014	7010	TEK tyrosine kinase, endothelial
GO	protein binding	321	6249	0.014	7021	transcription factor AP-2 beta (activating enhancer binding protein 2 beta)
GO	protein binding	321	6249	0.014	7046	transforming growth factor, beta receptor 1
GO	protein binding	321	6249	0.014	7058	thrombospondin 2
GO	protein binding	321	6249	0.014	7078	TIMP metallopeptidase inhibitor 3
GO	protein binding	321	6249	0.014	7137	troponin I type 3 (cardiac)
GO	protein binding	321	6249	0.014	7220	transient receptor potential cation channel, subfamily C, member 1
GO	protein binding	321	6249	0.014	7324	ubiquitin-conjugating enzyme E2E 1 (UBC4/5 homolog, yeast)
GO	protein binding	321	6249	0.014	7341	SMT3 suppressor of mif two 3 homolog 1 (S. cerevisiae)
GO	protein binding	321	6249	0.014	7347	ubiquitin carboxyl-terminal esterase L3 (ubiquitin thiolesterase)
GO	protein binding	321	6249	0.014	7353	ubiquitin fusion degradation 1 like (yeast)
GO	protein binding	321	6249	0.014	7456	WAS/WASL interacting protein family, member 1
GO	protein binding	321	6249	0.014	7490	Wilms tumor 1
GO	protein binding	321	6249	0.014	767	carbonic anhydrase VIII
GO	protein binding	321	6249	0.014	773	calcium channel, voltage-dependent, P/Q type, alpha 1A subunit
GO	protein binding	321	6249	0.014	7857	secretogranin II (chromogranin C)
GO	protein binding	321	6249	0.014	79075	defective in sister chromatid cohesion 1 homolog (S. cerevisiae)
GO	protein binding	321	6249	0.014	79172	centromere protein O
GO	protein binding	321	6249	0.014	79682	MLF1 interacting protein
GO	protein binding	321	6249	0.014	79780	coiled-coil domain containing 82
GO	protein binding	321	6249	0.014	79833	gem (nuclear organelle) associated protein 6
GO	protein binding	321	6249	0.014	80304	chromosome 2 open reading frame 44
GO	protein binding	321	6249	0.014	80342	TRAF3 interacting protein 3
GO	protein binding	321	6249	0.014	8091	high mobility group AT-hook 2
GO	protein binding	321	6249	0.014	81706	protein phosphatase 1, regulatory (inhibitor) subunit 14C
GO	protein binding	321	6249	0.014	81786	tripartite motif-containing 7
GO	protein binding	321	6249	0.014	8193	D4, zinc and double PHD fingers family 1
GO	protein binding	321	6249	0.014	8349	histone cluster 2, H2be
GO	protein binding	321	6249	0.014	8409	ubiquitously-expressed transcript
GO	protein binding	321	6249	0.014	84125	leucine-rich repeats and IQ motif containing 1
GO	protein binding	321	6249	0.014	84168	anthrax toxin receptor 1

GO	protein binding	321	6249	0.014	84172	polymerase (RNA) I polypeptide B, 128kDa
GO	protein binding	321	6249	0.014	84189	SLIT and NTRK-like family, member 6
GO	protein binding	321	6249	0.014	84206	mex-3 homolog B (C. elegans)
GO	protein binding	321	6249	0.014	84230	leucine rich repeat containing 8 family, member C
GO	protein binding	321	6249	0.014	84296	GINS complex subunit 4 (Sld5 homolog)
GO	protein binding	321	6249	0.014	84365	MKI67 (FHA domain) interacting nucleolar phosphoprotein
GO	protein binding	321	6249	0.014	84541	kelch repeat and BTB (POZ) domain containing 8
GO	protein binding	321	6249	0.014	84552	par-6 partitioning defective 6 homolog gamma (C. elegans)
GO	protein binding	321	6249	0.014	8458	transcription termination factor, RNA polymerase II
GO	protein binding	321	6249	0.014	8482	semaphorin 7A, GPI membrane anchor (John Milton Hagen blood group)
GO	protein binding	321	6249	0.014	84878	zinc finger and BTB domain containing 45
GO	protein binding	321	6249	0.014	8520	histone acetyltransferase 1
GO	protein binding	321	6249	0.014	8533	COP9 constitutive photomorphogenic homolog subunit 3 (Arabidopsis)
GO	protein binding	321	6249	0.014	8563	THO complex 5
GO	protein binding	321	6249	0.014	8604	solute carrier family 25 (mitochondrial carrier, Aralar), member 12
GO	protein binding	321	6249	0.014	8626	tumor protein p63
GO	protein binding	321	6249	0.014	8777	multiple PDZ domain protein
GO	protein binding	321	6249	0.014	8788	delta-like 1 homolog (Drosophila)
GO	protein binding	321	6249	0.014	8835	suppressor of cytokine signaling 2
GO	protein binding	321	6249	0.014	890	cyclin A2
GO	protein binding	321	6249	0.014	8905	adaptor-related protein complex 1, sigma 2 subunit
GO	protein binding	321	6249	0.014	8970	histone cluster 1, H2bj
GO	protein binding	321	6249	0.014	898	cyclin E1
GO	protein binding	321	6249	0.014	8997	kalirin, RhoGEF kinase
GO	protein binding	321	6249	0.014	91442	chromosome 19 open reading frame 40
GO	protein binding	321	6249	0.014	91801	alkB, alkylation repair homolog 8 (E. coli)
GO	protein binding	321	6249	0.014	92312	mex-3 homolog A (C. elegans)
GO	protein binding	321	6249	0.014	9260	PDZ and LIM domain 7 (enigma)
GO	protein binding	321	6249	0.014	9262	serine/threonine kinase 17b
GO	protein binding	321	6249	0.014	92737	delta/notch-like EGF repeat containing
GO	protein binding	321	6249	0.014	93649	myocardin
GO	protein binding	321	6249	0.014	9455	homer homolog 2 (Drosophila)
GO	protein binding	321	6249	0.014	9497	solute carrier family 4, sodium bicarbonate cotransporter, member 7
GO	protein binding	321	6249	0.014	9568	gamma-aminobutyric acid (GABA) B receptor, 2
GO	protein binding	321	6249	0.014	9688	nucleoporin 93kDa
GO	protein binding	321	6249	0.014	9732	dedicator of cytokinesis 4

GO	protein binding	321	6249	0.014	9744	ArfGAP with coiled-coil, ankyrin repeat and PH domains 1
GO	protein binding	321	6249	0.014	9833	maternal embryonic leucine zipper kinase
GO	cell cycle	32	458	0.014	10051	structural maintenance of chromosomes 4
GO	cell cycle	32	458	0.014	113130	cell division cycle associated 5
GO	cell cycle	32	458	0.014	1164	CDC28 protein kinase regulatory subunit 2
GO	cell cycle	32	458	0.014	157570	establishment of cohesion 1 homolog 2 (S. cerevisiae)
GO	cell cycle	32	458	0.014	1841	deoxythymidylate kinase (thymidylate kinase)
GO	cell cycle	32	458	0.014	220042	chromosome 11 open reading frame 82
GO	cell cycle	32	458	0.014	220134	spindle and kinetochore associated complex subunit 1
GO	cell cycle	32	458	0.014	2305	forkhead box M1
GO	cell cycle	32	458	0.014	23157	septin 6
GO	cell cycle	32	458	0.014	26586	cytoskeleton associated protein 2
GO	cell cycle	32	458	0.014	28984	chromosome 13 open reading frame 15
GO	cell cycle	32	458	0.014	29128	ubiquitin-like with PHD and ring finger domains 1
GO	cell cycle	32	458	0.014	332	baculoviral IAP repeat-containing 5
GO	cell cycle	32	458	0.014	4171	minichromosome maintenance complex component 2
GO	cell cycle	32	458	0.014	4291	myeloid leukemia factor 1
GO	cell cycle	32	458	0.014	4292	mutL homolog 1, colon cancer, nonpolyposis type 2 (E. coli)
GO	cell cycle	32	458	0.014	55165	centrosomal protein 55kDa
GO	cell cycle	32	458	0.014	55207	ADP-ribosylation factor-like 8B
GO	cell cycle	32	458	0.014	55215	Fanconi anemia, complementation group I
GO	cell cycle	32	458	0.014	55752	septin 11
GO	cell cycle	32	458	0.014	64151	non-SMC condensin I complex, subunit G
GO	cell cycle	32	458	0.014	6683	spastin
GO	cell cycle	32	458	0.014	672	breast cancer 1, early onset
GO	cell cycle	32	458	0.014	7029	transcription factor Dp-2 (E2F dimerization partner 2)
GO	cell cycle	32	458	0.014	79075	defective in sister chromatid cohesion 1 homolog (S. cerevisiae)
GO	cell cycle	32	458	0.014	79187	fibronectin type III and SPRY domain containing 1
GO	cell cycle	32	458	0.014	8091	high mobility group AT-hook 2
GO	cell cycle	32	458	0.014	84552	par-6 partitioning defective 6 homolog gamma (C. elegans)
GO	cell cycle	32	458	0.014	8872	cell division cycle 123 homolog (S. cerevisiae)
GO	cell cycle	32	458	0.014	890	cyclin A2
GO	cell cycle	32	458	0.014	898	cyclin E1
GO	cell cycle	32	458	0.014	93323	HAUS augmin-like complex, subunit 8
GO	protein kinase inhibitor activity	4	21	0.015	1026	cyclin-dependent kinase inhibitor 1A (p21, Cip1)
GO	protein kinase inhibitor activity	4	21	0.015	11142	protein kinase (cAMP-dependent, catalytic) inhibitor gamma

GO	protein kinase inhibitor activity	4	21	0.015	5569	protein kinase (cAMP-dependent, catalytic) inhibitor alpha
GO	protein kinase inhibitor activity	4	21	0.015	9535	glia maturation factor, gamma
GO	mitotic chromosome condensation	3	12	0.016	10051	structural maintenance of chromosomes 4
GO	mitotic chromosome condensation	3	12	0.016	113130	cell division cycle associated 5
GO	mitotic chromosome condensation	3	12	0.016	64151	non-SMC condensin I complex, subunit G
GO	blastocyst development	3	12	0.016	1045	caudal type homeobox 2
GO	blastocyst development	3	12	0.016	5702	proteasome (prosome, macropain) 26S subunit, ATPase, 3
GO	blastocyst development	3	12	0.016	7046	transforming growth factor, beta receptor 1
GO	NLS-bearing substrate import into nucle	3	12	0.016	2533	FYN binding protein (FYB-120/130)
GO	NLS-bearing substrate import into nucle	3	12	0.016	3836	karyopherin alpha 1 (importin alpha 5)
GO	NLS-bearing substrate import into nucle	3	12	0.016	3838	karyopherin alpha 2 (RAG cohort 1, importin alpha 1)
GO	rRNA transcription	3	12	0.016	25885	polymerase (RNA) I polypeptide A, 194kDa
GO	rRNA transcription	3	12	0.016	84172	polymerase (RNA) I polypeptide B, 128kDa
GO	rRNA transcription	3	12	0.016	84365	MKI67 (FHA domain) interacting nucleolar phosphoprotein
GO	adrenal gland development	3	12	0.016	4763	neurofibromin 1
GO	adrenal gland development	3	12	0.016	6299	sal-like 1 (Drosophila)
GO	adrenal gland development	3	12	0.016	7490	Wilms tumor 1
GO	dendrite	12	128	0.016	1136	cholinergic receptor, nicotinic, alpha 3
GO	dendrite	12	128	0.016	1138	cholinergic receptor, nicotinic, alpha 5
GO	dendrite	12	128	0.016	1984	eukaryotic translation initiation factor 5A
GO	dendrite	12	128	0.016	2045	EPH receptor A7
GO	dendrite	12	128	0.016	23705	cell adhesion molecule 1
GO	dendrite	12	128	0.016	348	apolipoprotein E
GO	dendrite	12	128	0.016	3763	potassium inwardly-rectifying channel, subfamily J, member 6
GO	dendrite	12	128	0.016	4763	neurofibromin 1
GO	dendrite	12	128	0.016	773	calcium channel, voltage-dependent, P/Q type, alpha 1A subunit
GO	dendrite	12	128	0.016	8626	tumor protein p63
GO	dendrite	12	128	0.016	8777	multiple PDZ domain protein
GO	dendrite	12	128	0.016	92737	delta/notch-like EGF repeat containing
GO	isomerase activity	10	99	0.017	10465	peptidylprolyl isomerase H (cyclophilin H)
GO	isomerase activity	10	99	0.017	150962	pseudouridylate synthase 10
GO	isomerase activity	10	99	0.017	2281	FK506 binding protein 1B, 12.6 kDa
GO	isomerase activity	10	99	0.017	22934	ribose 5-phosphate isomerase A
GO	isomerase activity	10	99	0.017	283209	phosphoglucomutase 2-like 1
GO	isomerase activity	10	99	0.017	29940	dermatan sulfate epimerase
GO	isomerase activity	10	99	0.017	51645	peptidylprolyl isomerase (cyclophilin)-like 1

GO	isomerase activity	10	99	0.017	5303	protein (peptidylprolyl cis/trans isomerase) NIMA-interacting, 4 (parvulin)
GO	isomerase activity	10	99	0.017	6120	ribulose-5-phosphate-3-epimerase
GO	isomerase activity	10	99	0.017	669	2,3-bisphosphoglycerate mutase
GO	actin cytoskeleton organization	11	114	0.017	10391	coronin, actin binding protein, 2B
GO	actin cytoskeleton organization	11	114	0.017	10395	deleted in liver cancer 1
GO	actin cytoskeleton organization	11	114	0.017	1730	diaphanous homolog 2 (Drosophila)
GO	actin cytoskeleton organization	11	114	0.017	26499	pleckstrin 2
GO	actin cytoskeleton organization	11	114	0.017	4763	neurofibromin 1
GO	actin cytoskeleton organization	11	114	0.017	4867	nephronophthisis 1 (juvenile)
GO	actin cytoskeleton organization	11	114	0.017	4893	neuroblastoma RAS viral (v-ras) oncogene homolog
GO	actin cytoskeleton organization	11	114	0.017	5216	profilin 1
GO	actin cytoskeleton organization	11	114	0.017	7456	WAS/WASL interacting protein family, member 1
GO	actin cytoskeleton organization	11	114	0.017	81624	diaphanous homolog 3 (Drosophila)
GO	actin cytoskeleton organization	11	114	0.017	9260	PDZ and LIM domain 7 (enigma)
GO	positive regulation of neuron differentia	4	22	0.017	10096	ARP3 actin-related protein 3 homolog (yeast)
GO	positive regulation of neuron differentia	4	22	0.017	2736	GLI family zinc finger 2
GO	positive regulation of neuron differentia	4	22	0.017	4897	neuronal cell adhesion molecule
GO	positive regulation of neuron differentia	4	22	0.017	6657	SRY (sex determining region Y)-box 2
GO	condensin complex	2	5	0.02	10051	structural maintenance of chromosomes 4
GO	condensin complex	2	5	0.02	64151	non-SMC condensin I complex, subunit G
GO	hemidesmosome	2	5	0.02	10096	ARP3 actin-related protein 3 homolog (yeast)
GO	hemidesmosome	2	5	0.02	667	dystonin
GO	cAMP-dependent protein kinase inhibit	2	5	0.02	11142	protein kinase (cAMP-dependent, catalytic) inhibitor gamma
GO	cAMP-dependent protein kinase inhibit	2	5	0.02	5569	protein kinase (cAMP-dependent, catalytic) inhibitor alpha
GO	negative regulation of oligodendrocyte	2	5	0.02	1746	distal-less homeobox 2
GO	negative regulation of oligodendrocyte	2	5	0.02	4763	neurofibromin 1
GO	positive regulation of triglyceride biosy	2	5	0.02	23305	acyl-CoA synthetase long-chain family member 6
GO	positive regulation of triglyceride biosy	2	5	0.02	57678	glycerol-3-phosphate acyltransferase, mitochondrial
GO	nuclear origin of replication recognition	2	5	0.02	23594	origin recognition complex, subunit 6 like (yeast)
GO	nuclear origin of replication recognition	2	5	0.02	4171	minichromosome maintenance complex component 2
GO	activated T cell proliferation	2	5	0.02	23705	cell adhesion molecule 1
GO	activated T cell proliferation	2	5	0.02	2534	FYN oncogene related to SRC, FGR, YES
GO	spinal cord association neuron different	2	5	0.02	266727	MAM domain containing glycosylphosphatidylinositol anchor 1
GO	spinal cord association neuron different	2	5	0.02	5081	paired box 7
GO	profilin binding	2	5	0.02	27445	piccolo (presynaptic cytomatrix protein)
GO	profilin binding	2	5	0.02	7456	WAS/WASL interacting protein family, member 1

GO	phosphatidylcholine-sterol O-acyltransf	2	5	0.02	341	apolipoprotein C-I
GO	phosphatidylcholine-sterol O-acyltransf	2	5	0.02	348	apolipoprotein E
GO	lysosomal transport	2	5	0.02	411	arylsulfatase B
GO	lysosomal transport	2	5	0.02	4734	neural precursor cell expressed, developmentally down-regulated 4
GO	positive regulation of penile erection	2	5	0.02	5021	oxytocin receptor
GO	positive regulation of penile erection	2	5	0.02	5028	purinergic receptor P2Y, G-protein coupled, 1
GO	pattern recognition receptor activity	2	5	0.02	81035	collectin sub-family member 12
GO	pattern recognition receptor activity	2	5	0.02	8685	macrophage receptor with collagenous structure
GO	regulation of cell proliferation	8	73	0.02	182	jagged 1 (Alagille syndrome)
GO	regulation of cell proliferation	8	73	0.02	2305	forkhead box M1
GO	regulation of cell proliferation	8	73	0.02	5054	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor t
GO	regulation of cell proliferation	8	73	0.02	659	bone morphogenetic protein receptor, type II (serine/threonine kinase)
GO	regulation of cell proliferation	8	73	0.02	6662	SRY (sex determining region Y)-box 9
GO	regulation of cell proliferation	8	73	0.02	672	breast cancer 1, early onset
GO	regulation of cell proliferation	8	73	0.02	7010	TEK tyrosine kinase, endothelial
GO	regulation of cell proliferation	8	73	0.02	83879	cell division cycle associated 7
GO	cortical actin cytoskeleton organization	3	13	0.02	2037	erythrocyte membrane protein band 4.1-like 2
GO	cortical actin cytoskeleton organization	3	13	0.02	23136	erythrocyte membrane protein band 4.1-like 3
GO	cortical actin cytoskeleton organization	3	13	0.02	5341	pleckstrin
GO	positive regulation of smooth muscle cc	3	13	0.02	2149	coagulation factor II (thrombin) receptor
GO	positive regulation of smooth muscle cc	3	13	0.02	60675	prokineticin 2
GO	positive regulation of smooth muscle cc	3	13	0.02	93649	myocardin
GO	negative regulation of Wnt receptor sig	3	13	0.02	6422	secreted frizzled-related protein 1
GO	negative regulation of Wnt receptor sig	3	13	0.02	6657	SRY (sex determining region Y)-box 2
GO	negative regulation of Wnt receptor sig	3	13	0.02	81029	wingless-type MMTV integration site family, member 5B
GO	embryonic skeletal system developmen	4	23	0.02	1746	distal-less homeobox 2
GO	embryonic skeletal system developmen	4	23	0.02	5081	paired box 7
GO	embryonic skeletal system developmen	4	23	0.02	5125	proprotein convertase subtilisin/kexin type 5
GO	embryonic skeletal system developmen	4	23	0.02	8788	delta-like 1 homolog (Drosophila)
GO	growth factor binding	4	23	0.02	2321	fms-related tyrosine kinase 1 (vascular endothelial growth factor/vascular
GO	growth factor binding	4	23	0.02	4052	latent transforming growth factor beta binding protein 1
GO	growth factor binding	4	23	0.02	659	bone morphogenetic protein receptor, type II (serine/threonine kinase)
GO	growth factor binding	4	23	0.02	7046	transforming growth factor, beta receptor 1
GO	structural molecule activity	16	196	0.021	11149	blood vessel epicardial substance
GO	structural molecule activity	16	196	0.021	182	jagged 1 (Alagille syndrome)
GO	structural molecule activity	16	196	0.021	2037	erythrocyte membrane protein band 4.1-like 2

GO	structural molecule activity	16	196	0.021	23136	erythrocyte membrane protein band 4.1-like 3
GO	structural molecule activity	16	196	0.021	23562	claudin 14
GO	structural molecule activity	16	196	0.021	347733	tubulin, beta 2B
GO	structural molecule activity	16	196	0.021	3883	keratin 33A
GO	structural molecule activity	16	196	0.021	3887	keratin 81
GO	structural molecule activity	16	196	0.021	4867	nephronophthisis 1 (juvenile)
GO	structural molecule activity	16	196	0.021	57642	collagen, type XX, alpha 1
GO	structural molecule activity	16	196	0.021	7058	thrombospondin 2
GO	structural molecule activity	16	196	0.021	7348	uroplakin 1B
GO	structural molecule activity	16	196	0.021	7846	tubulin, alpha 1a
GO	structural molecule activity	16	196	0.021	79861	tubulin, alpha-like 3
GO	structural molecule activity	16	196	0.021	9053	microtubule-associated protein 7
GO	structural molecule activity	16	196	0.021	9076	claudin 1
GO	RNA binding	37	562	0.021	10056	phenylalanyl-tRNA synthetase, beta subunit
GO	RNA binding	37	562	0.021	10189	THO complex 4
GO	RNA binding	37	562	0.021	10492	synaptotagmin binding, cytoplasmic RNA interacting protein
GO	RNA binding	37	562	0.021	10528	NOP56 ribonucleoprotein homolog (yeast)
GO	RNA binding	37	562	0.021	11022	tudor and KH domain containing
GO	RNA binding	37	562	0.021	11056	DEAD (Asp-Glu-Ala-Asp) box polypeptide 52
GO	RNA binding	37	562	0.021	11222	mitochondrial ribosomal protein L3
GO	RNA binding	37	562	0.021	132430	poly(A) binding protein, cytoplasmic 4-like
GO	RNA binding	37	562	0.021	135295	splicing factor, arginine/serine-rich 13B
GO	RNA binding	37	562	0.021	1787	tRNA aspartic acid methyltransferase 1
GO	RNA binding	37	562	0.021	1984	eukaryotic translation initiation factor 5A
GO	RNA binding	37	562	0.021	201299	RAD52 motif 1
GO	RNA binding	37	562	0.021	23658	LSM5 homolog, U6 small nuclear RNA associated (S. cerevisiae)
GO	RNA binding	37	562	0.021	26019	UPF2 regulator of nonsense transcripts homolog (yeast)
GO	RNA binding	37	562	0.021	27258	LSM3 homolog, U6 small nuclear RNA associated (S. cerevisiae)
GO	RNA binding	37	562	0.021	3183	heterogeneous nuclear ribonucleoprotein C (C1/C2)
GO	RNA binding	37	562	0.021	345630	fibrillarin-like 1
GO	RNA binding	37	562	0.021	389421	lin-28 homolog B (C. elegans)
GO	RNA binding	37	562	0.021	53981	cleavage and polyadenylation specific factor 2, 100kDa
GO	RNA binding	37	562	0.021	55135	WD repeat containing, antisense to TP53
GO	RNA binding	37	562	0.021	55323	La ribonucleoprotein domain family, member 6
GO	RNA binding	37	562	0.021	56339	methyltransferase like 3
GO	RNA binding	37	562	0.021	56902	partner of NOB1 homolog (S. cerevisiae)

GO	RNA binding	37	562	0.021	58155	polypyrimidine tract binding protein 2
GO	RNA binding	37	562	0.021	6133	ribosomal protein L9
GO	RNA binding	37	562	0.021	6154	ribosomal protein L26
GO	RNA binding	37	562	0.021	64393	zinc finger, matrin type 3
GO	RNA binding	37	562	0.021	65008	mitochondrial ribosomal protein L1
GO	RNA binding	37	562	0.021	6637	small nuclear ribonucleoprotein polypeptide G
GO	RNA binding	37	562	0.021	672	breast cancer 1, early onset
GO	RNA binding	37	562	0.021	7490	Wilms tumor 1
GO	RNA binding	37	562	0.021	81892	chromosome 14 open reading frame 156
GO	RNA binding	37	562	0.021	84206	mex-3 homolog B (C. elegans)
GO	RNA binding	37	562	0.021	84365	MKI67 (FHA domain) interacting nucleolar phosphoprotein
GO	RNA binding	37	562	0.021	8563	THO complex 5
GO	RNA binding	37	562	0.021	91801	alkB, alkylation repair homolog 8 (E. coli)
GO	RNA binding	37	562	0.021	92312	mex-3 homolog A (C. elegans)
GO	interspecies interaction between organi	21	280	0.021	10189	THO complex 4
GO	interspecies interaction between organi	21	280	0.021	10492	synaptotagmin binding, cytoplasmic RNA interacting protein
GO	interspecies interaction between organi	21	280	0.021	131450	CD200 receptor 1
GO	interspecies interaction between organi	21	280	0.021	23157	septin 6
GO	interspecies interaction between organi	21	280	0.021	2534	FYN oncogene related to SRC, FGR, YES
GO	interspecies interaction between organi	21	280	0.021	3685	integrin, alpha V (vitronectin receptor, alpha polypeptide, antigen CD51)
GO	interspecies interaction between organi	21	280	0.021	3694	integrin, beta 6
GO	interspecies interaction between organi	21	280	0.021	3836	karyopherin alpha 1 (importin alpha 5)
GO	interspecies interaction between organi	21	280	0.021	3838	karyopherin alpha 2 (RAG cohort 1, importin alpha 1)
GO	interspecies interaction between organi	21	280	0.021	3932	lymphocyte-specific protein tyrosine kinase
GO	interspecies interaction between organi	21	280	0.021	4312	matrix metallopeptidase 1 (interstitial collagenase)
GO	interspecies interaction between organi	21	280	0.021	4734	neural precursor cell expressed, developmentally down-regulated 4
GO	interspecies interaction between organi	21	280	0.021	4928	nucleoporin 98kDa
GO	interspecies interaction between organi	21	280	0.021	5702	proteasome (prosome, macropain) 26S subunit, ATPase, 3
GO	interspecies interaction between organi	21	280	0.021	57599	WD repeat domain 48
GO	interspecies interaction between organi	21	280	0.021	6672	SP100 nuclear antigen
GO	interspecies interaction between organi	21	280	0.021	7037	transferrin receptor (p90, CD71)
GO	interspecies interaction between organi	21	280	0.021	729230	chemokine (C-C motif) receptor 2
GO	interspecies interaction between organi	21	280	0.021	79682	MLF1 interacting protein
GO	interspecies interaction between organi	21	280	0.021	8777	multiple PDZ domain protein
GO	interspecies interaction between organi	21	280	0.021	9076	claudin 1
GO	postsynaptic membrane	13	149	0.022	1136	cholinergic receptor, nicotinic, alpha 3

GO	postsynaptic membrane	13	149	0.022	1138	cholinergic receptor, nicotinic, alpha 5
GO	postsynaptic membrane	13	149	0.022	200959	gamma-aminobutyric acid (GABA) receptor, rho 3
GO	postsynaptic membrane	13	149	0.022	2045	EPH receptor A7
GO	postsynaptic membrane	13	149	0.022	2149	coagulation factor II (thrombin) receptor
GO	postsynaptic membrane	13	149	0.022	2558	gamma-aminobutyric acid (GABA) A receptor, alpha 5
GO	postsynaptic membrane	13	149	0.022	2898	glutamate receptor, ionotropic, kainate 2
GO	postsynaptic membrane	13	149	0.022	2906	glutamate receptor, ionotropic, N-methyl D-aspartate 2D
GO	postsynaptic membrane	13	149	0.022	3778	potassium large conductance calcium-activated channel, subfamily M, alph
GO	postsynaptic membrane	13	149	0.022	8777	multiple PDZ domain protein
GO	postsynaptic membrane	13	149	0.022	9419	cysteine-rich PDZ-binding protein
GO	postsynaptic membrane	13	149	0.022	9455	homer homolog 2 (Drosophila)
GO	postsynaptic membrane	13	149	0.022	9568	gamma-aminobutyric acid (GABA) B receptor, 2
GO	transmembrane receptor protein tyrosi	5	35	0.022	2045	EPH receptor A7
GO	transmembrane receptor protein tyrosi	5	35	0.022	2321	fms-related tyrosine kinase 1 (vascular endothelial growth factor/vascular
GO	transmembrane receptor protein tyrosi	5	35	0.022	558	AXL receptor tyrosine kinase
GO	transmembrane receptor protein tyrosi	5	35	0.022	5754	PTK7 protein tyrosine kinase 7
GO	transmembrane receptor protein tyrosi	5	35	0.022	7010	TEK tyrosine kinase, endothelial
GO	kidney development	7	61	0.022	220	aldehyde dehydrogenase 1 family, member A3
GO	kidney development	7	61	0.022	2736	GLI family zinc finger 2
GO	kidney development	7	61	0.022	3975	LIM homeobox 1
GO	kidney development	7	61	0.022	5125	proprotein convertase subtilisin/kexin type 5
GO	kidney development	7	61	0.022	6299	sal-like 1 (Drosophila)
GO	kidney development	7	61	0.022	7046	transforming growth factor, beta receptor 1
GO	kidney development	7	61	0.022	7490	Wilms tumor 1
GO	homophilic cell adhesion	12	135	0.023	1000	cadherin 2, type 1, N-cadherin (neuronal)
GO	homophilic cell adhesion	12	135	0.023	1002	cadherin 4, type 1, R-cadherin (retinal)
GO	homophilic cell adhesion	12	135	0.023	1008	cadherin 10, type 2 (T2-cadherin)
GO	homophilic cell adhesion	12	135	0.023	120114	FAT tumor suppressor homolog 3 (Drosophila)
GO	homophilic cell adhesion	12	135	0.023	1830	desmoglein 3 (pemphigus vulgaris antigen)
GO	homophilic cell adhesion	12	135	0.023	23705	cell adhesion molecule 1
GO	homophilic cell adhesion	12	135	0.023	347902	adhesion molecule with Ig-like domain 2
GO	homophilic cell adhesion	12	135	0.023	5101	protocadherin 9
GO	homophilic cell adhesion	12	135	0.023	56104	protocadherin gamma subfamily B, 1
GO	homophilic cell adhesion	12	135	0.023	56126	protocadherin beta 10
GO	homophilic cell adhesion	12	135	0.023	56133	protocadherin beta 2
GO	homophilic cell adhesion	12	135	0.023	57575	protocadherin 10

GO	G-protein-coupled receptor binding	4	24	0.023	10672	guanine nucleotide binding protein (G protein), alpha 13
GO	G-protein-coupled receptor binding	4	24	0.023	409	arrestin, beta 2
GO	G-protein-coupled receptor binding	4	24	0.023	60675	prokineticin 2
GO	G-protein-coupled receptor binding	4	24	0.023	6347	chemokine (C-C motif) ligand 2
GO	single-stranded RNA binding	3	14	0.025	10656	KH domain containing, RNA binding, signal transduction associated 3
GO	single-stranded RNA binding	3	14	0.025	124540	musashi homolog 2 (Drosophila)
GO	single-stranded RNA binding	3	14	0.025	1746	distal-less homeobox 2
GO	response to X-ray	3	14	0.025	1161	excision repair cross-complementing rodent repair deficiency, complement
GO	response to X-ray	3	14	0.025	4436	mutS homolog 2, colon cancer, nonpolyposis type 1 (E. coli)
GO	response to X-ray	3	14	0.025	641	Bloom syndrome, RecQ helicase-like
GO	tubulin binding	3	14	0.025	2534	FYN oncogene related to SRC, FGR, YES
GO	tubulin binding	3	14	0.025	332	baculoviral IAP repeat-containing 5
GO	tubulin binding	3	14	0.025	672	breast cancer 1, early onset
GO	artery morphogenesis	3	14	0.025	348	apolipoprotein E
GO	artery morphogenesis	3	14	0.025	4763	neurofibromin 1
GO	artery morphogenesis	3	14	0.025	7046	transforming growth factor, beta receptor 1
GO	anatomical structure formation involve	3	14	0.025	3975	LIM homeobox 1
GO	anatomical structure formation involve	3	14	0.025	6657	SRY (sex determining region Y)-box 2
GO	anatomical structure formation involve	3	14	0.025	8626	tumor protein p63
GO	identical protein binding	24	338	0.026	113130	cell division cycle associated 5
GO	identical protein binding	24	338	0.026	150684	copper metabolism (Murr1) domain containing 1
GO	identical protein binding	24	338	0.026	23562	claudin 14
GO	identical protein binding	24	338	0.026	2534	FYN oncogene related to SRC, FGR, YES
GO	identical protein binding	24	338	0.026	26019	UPF2 regulator of nonsense transcripts homolog (yeast)
GO	identical protein binding	24	338	0.026	26061	2-hydroxyacyl-CoA lyase 1
GO	identical protein binding	24	338	0.026	283518	potassium channel regulator
GO	identical protein binding	24	338	0.026	3028	hydroxysteroid (17-beta) dehydrogenase 10
GO	identical protein binding	24	338	0.026	3183	heterogeneous nuclear ribonucleoprotein C (C1/C2)
GO	identical protein binding	24	338	0.026	332	baculoviral IAP repeat-containing 5
GO	identical protein binding	24	338	0.026	348	apolipoprotein E
GO	identical protein binding	24	338	0.026	355	Fas (TNF receptor superfamily, member 6)
GO	identical protein binding	24	338	0.026	3624	inhibin, beta A
GO	identical protein binding	24	338	0.026	3936	lymphocyte cytosolic protein 1 (L-plastin)
GO	identical protein binding	24	338	0.026	4436	mutS homolog 2, colon cancer, nonpolyposis type 1 (E. coli)
GO	identical protein binding	24	338	0.026	4830	non-metastatic cells 1, protein (NM23A) expressed in
GO	identical protein binding	24	338	0.026	51062	atlastin GTPase 1

GO	identical protein binding	24	338	0.026	5110	protein-L-isoaspartate (D-aspartate) O-methyltransferase
GO	identical protein binding	24	338	0.026	581	BCL2-associated X protein
GO	identical protein binding	24	338	0.026	586	branched chain aminotransferase 1, cytosolic
GO	identical protein binding	24	338	0.026	6672	SP100 nuclear antigen
GO	identical protein binding	24	338	0.026	672	breast cancer 1, early onset
GO	identical protein binding	24	338	0.026	8626	tumor protein p63
GO	identical protein binding	24	338	0.026	9076	claudin 1
GO	stress fiber	4	25	0.027	10395	deleted in liver cancer 1
GO	stress fiber	4	25	0.027	55752	septin 11
GO	stress fiber	4	25	0.027	7168	tropomyosin 1 (alpha)
GO	stress fiber	4	25	0.027	9260	PDZ and LIM domain 7 (enigma)
GO	osteoblast differentiation	4	25	0.027	10457	glycoprotein (transmembrane) nmb
GO	osteoblast differentiation	4	25	0.027	2736	GLI family zinc finger 2
GO	osteoblast differentiation	4	25	0.027	4763	neurofibromin 1
GO	osteoblast differentiation	4	25	0.027	6657	SRY (sex determining region Y)-box 2
GO	heterotrimeric G-protein complex	4	25	0.027	10672	guanine nucleotide binding protein (G protein), alpha 13
GO	heterotrimeric G-protein complex	4	25	0.027	2786	guanine nucleotide binding protein (G protein), gamma 4
GO	heterotrimeric G-protein complex	4	25	0.027	54331	guanine nucleotide binding protein (G protein), gamma 2
GO	heterotrimeric G-protein complex	4	25	0.027	6000	regulator of G-protein signaling 7
GO	response to DNA damage stimulus	8	78	0.028	1026	cyclin-dependent kinase inhibitor 1A (p21, Cip1)
GO	response to DNA damage stimulus	8	78	0.028	1161	excision repair cross-complementing rodent repair deficiency, complement
GO	response to DNA damage stimulus	8	78	0.028	27244	sestrin 1
GO	response to DNA damage stimulus	8	78	0.028	641	Bloom syndrome, RecQ helicase-like
GO	response to DNA damage stimulus	8	78	0.028	64393	zinc finger, matrin type 3
GO	response to DNA damage stimulus	8	78	0.028	64782	apoptosis enhancing nuclease
GO	response to DNA damage stimulus	8	78	0.028	672	breast cancer 1, early onset
GO	response to DNA damage stimulus	8	78	0.028	91801	alkB, alkylation repair homolog 8 (E. coli)
GO	intronless viral mRNA export from host	2	6	0.029	10189	THO complex 4
GO	intronless viral mRNA export from host	2	6	0.029	8563	THO complex 5
GO	transcription export complex	2	6	0.029	10189	THO complex 4
GO	transcription export complex	2	6	0.029	8563	THO complex 5
GO	behavioral response to nicotine	2	6	0.029	1136	cholinergic receptor, nicotinic, alpha 3
GO	behavioral response to nicotine	2	6	0.029	1138	cholinergic receptor, nicotinic, alpha 5
GO	thyroid hormone generation	2	6	0.029	1733	deiodinase, iodothyronine, type I
GO	thyroid hormone generation	2	6	0.029	5469	mediator complex subunit 1
GO	forebrain neuron differentiation	2	6	0.029	1746	distal-less homeobox 2

GO	forebrain neuron differentiation	2	6	0.029	6657	SRY (sex determining region Y)-box 2
GO	deoxyribonuclease activity	2	6	0.029	1775	deoxyribonuclease I-like 2
GO	deoxyribonuclease activity	2	6	0.029	4830	non-metastatic cells 1, protein (NM23A) expressed in
GO	regulation of blood coagulation	2	6	0.029	2149	coagulation factor II (thrombin) receptor
GO	regulation of blood coagulation	2	6	0.029	2150	coagulation factor II (thrombin) receptor-like 1
GO	mitochondrial intermembrane space pr	2	6	0.029	26519	translocase of inner mitochondrial membrane 10 homolog (yeast)
GO	mitochondrial intermembrane space pr	2	6	0.029	26521	translocase of inner mitochondrial membrane 8 homolog B (yeast)
GO	protein import into mitochondrial inner	2	6	0.029	26519	translocase of inner mitochondrial membrane 10 homolog (yeast)
GO	protein import into mitochondrial inner	2	6	0.029	26521	translocase of inner mitochondrial membrane 8 homolog B (yeast)
GO	response to dietary excess	2	6	0.029	348	apolipoprotein E
GO	response to dietary excess	2	6	0.029	3952	leptin
GO	cerebellar Purkinje cell differentiation	2	6	0.029	3975	LIM homeobox 1
GO	cerebellar Purkinje cell differentiation	2	6	0.029	773	calcium channel, voltage-dependent, P/Q type, alpha 1A subunit
GO	DNA replication origin binding	2	6	0.029	4171	minichromosome maintenance complex component 2
GO	DNA replication origin binding	2	6	0.029	5000	origin recognition complex, subunit 4-like (yeast)
GO	somatic hypermutation of immunoglob	2	6	0.029	4292	mutL homolog 1, colon cancer, nonpolyposis type 2 (E. coli)
GO	somatic hypermutation of immunoglob	2	6	0.029	4436	mutS homolog 2, colon cancer, nonpolyposis type 1 (E. coli)
GO	response to folic acid	2	6	0.029	590	butyrylcholinesterase
GO	response to folic acid	2	6	0.029	7078	TIMP metallopeptidase inhibitor 3
GO	sarcoglycan complex	2	6	0.029	6442	sarcoglycan, alpha (50kDa dystrophin-associated glycoprotein)
GO	sarcoglycan complex	2	6	0.029	6444	sarcoglycan, delta (35kDa dystrophin-associated glycoprotein)
GO	parathyroid gland development	2	6	0.029	6899	T-box 1
GO	parathyroid gland development	2	6	0.029	7046	transforming growth factor, beta receptor 1
GO	heart contraction	2	6	0.029	70	actin, alpha, cardiac muscle 1
GO	heart contraction	2	6	0.029	7137	troponin I type 3 (cardiac)
GO	cell cycle arrest	10	108	0.029	1026	cyclin-dependent kinase inhibitor 1A (p21, Cip1)
GO	cell cycle arrest	10	108	0.029	220042	chromosome 11 open reading frame 82
GO	cell cycle arrest	10	108	0.029	27244	sestrin 1
GO	cell cycle arrest	10	108	0.029	3624	inhibin, beta A
GO	cell cycle arrest	10	108	0.029	4291	myeloid leukemia factor 1
GO	cell cycle arrest	10	108	0.029	4436	mutS homolog 2, colon cancer, nonpolyposis type 1 (E. coli)
GO	cell cycle arrest	10	108	0.029	6657	SRY (sex determining region Y)-box 2
GO	cell cycle arrest	10	108	0.029	667	dystonin
GO	cell cycle arrest	10	108	0.029	8872	cell division cycle 123 homolog (S. cerevisiae)
GO	cell cycle arrest	10	108	0.029	94241	tumor protein p53 inducible nuclear protein 1
GO	induction of apoptosis by intracellular si	3	15	0.03	1026	cyclin-dependent kinase inhibitor 1A (p21, Cip1)

GO	induction of apoptosis by intracellular si	3	15	0.03	27429	HtrA serine peptidase 2
GO	induction of apoptosis by intracellular si	3	15	0.03	581	BCL2-associated X protein
GO	digestive tract development	3	15	0.03	1543	cytochrome P450, family 1, subfamily A, polypeptide 1
GO	digestive tract development	3	15	0.03	5021	oxytocin receptor
GO	digestive tract development	3	15	0.03	7046	transforming growth factor, beta receptor 1
GO	N-acetylglucosamine metabolic process	3	15	0.03	2135	exostoses (multiple)-like 2
GO	N-acetylglucosamine metabolic process	3	15	0.03	55577	N-acetylglucosamine kinase
GO	N-acetylglucosamine metabolic process	3	15	0.03	9215	like-glycosyltransferase
GO	forebrain development	6	51	0.03	10395	deleted in liver cancer 1
GO	forebrain development	6	51	0.03	2534	FYN oncogene related to SRC, FGR, YES
GO	forebrain development	6	51	0.03	27429	HtrA serine peptidase 2
GO	forebrain development	6	51	0.03	5015	orthodenticle homeobox 2
GO	forebrain development	6	51	0.03	5101	protocadherin 9
GO	forebrain development	6	51	0.03	6657	SRY (sex determining region Y)-box 2
GO	nucleotide-excision repair	4	26	0.031	1161	excision repair cross-complementing rodent repair deficiency, complement
GO	nucleotide-excision repair	4	26	0.031	1643	damage-specific DNA binding protein 2, 48kDa
GO	nucleotide-excision repair	4	26	0.031	4287	ataxin 3
GO	nucleotide-excision repair	4	26	0.031	4968	8-oxoguanine DNA glycosylase
GO	triglyceride metabolic process	4	26	0.031	23305	acyl-CoA synthetase long-chain family member 6
GO	triglyceride metabolic process	4	26	0.031	341	apolipoprotein C-I
GO	triglyceride metabolic process	4	26	0.031	348	apolipoprotein E
GO	triglyceride metabolic process	4	26	0.031	7840	Alstrom syndrome 1
GO	branching involved in ureteric bud morp	4	26	0.031	3237	homeobox D11
GO	branching involved in ureteric bud morp	4	26	0.031	5228	placental growth factor
GO	branching involved in ureteric bud morp	4	26	0.031	6299	sal-like 1 (Drosophila)
GO	branching involved in ureteric bud morp	4	26	0.031	7490	Wilms tumor 1
GO	skeletal system development	11	125	0.031	10683	delta-like 3 (Drosophila)
GO	skeletal system development	11	125	0.031	1290	collagen, type V, alpha 2
GO	skeletal system development	11	125	0.031	2736	GLI family zinc finger 2
GO	skeletal system development	11	125	0.031	3236	homeobox D10
GO	skeletal system development	11	125	0.031	3237	homeobox D11
GO	skeletal system development	11	125	0.031	4318	matrix metallopeptidase 9 (gelatinase B, 92kDa gelatinase, 92kDa type IV c
GO	skeletal system development	11	125	0.031	5744	parathyroid hormone-like hormone
GO	skeletal system development	11	125	0.031	6474	short stature homeobox 2
GO	skeletal system development	11	125	0.031	7046	transforming growth factor, beta receptor 1
GO	skeletal system development	11	125	0.031	7353	ubiquitin fusion degradation 1 like (yeast)

GO	skeletal system development	11	125	0.031	8626	tumor protein p63
GO	cytoskeleton	40	635	0.032	122786	FERM domain containing 6
GO	cytoskeleton	40	635	0.032	1264	calponin 1, basic, smooth muscle
GO	cytoskeleton	40	635	0.032	2037	erythrocyte membrane protein band 4.1-like 2
GO	cytoskeleton	40	635	0.032	220134	spindle and kinetochore associated complex subunit 1
GO	cytoskeleton	40	635	0.032	23136	erythrocyte membrane protein band 4.1-like 3
GO	cytoskeleton	40	635	0.032	23157	septin 6
GO	cytoskeleton	40	635	0.032	26059	ELKS/RAB6-interacting/CAST family member 2
GO	cytoskeleton	40	635	0.032	26499	pleckstrin 2
GO	cytoskeleton	40	635	0.032	27241	Bardet-Biedl syndrome 9
GO	cytoskeleton	40	635	0.032	27289	Rho family GTPase 1
GO	cytoskeleton	40	635	0.032	27445	piccolo (presynaptic cytomatrix protein)
GO	cytoskeleton	40	635	0.032	287	ankyrin 2, neuronal
GO	cytoskeleton	40	635	0.032	28984	chromosome 13 open reading frame 15
GO	cytoskeleton	40	635	0.032	29767	tropomodulin 2 (neuronal)
GO	cytoskeleton	40	635	0.032	30011	SH3-domain kinase binding protein 1
GO	cytoskeleton	40	635	0.032	332	baculoviral IAP repeat-containing 5
GO	cytoskeleton	40	635	0.032	3936	lymphocyte cytosolic protein 1 (L-plastin)
GO	cytoskeleton	40	635	0.032	4651	myosin X
GO	cytoskeleton	40	635	0.032	5303	protein (peptidylprolyl cis/trans isomerase) NIMA-interacting, 4 (parvulin)
GO	cytoskeleton	40	635	0.032	54839	leucine rich repeat containing 49
GO	cytoskeleton	40	635	0.032	55165	centrosomal protein 55kDa
GO	cytoskeleton	40	635	0.032	55207	ADP-ribosylation factor-like 8B
GO	cytoskeleton	40	635	0.032	55521	tripartite motif-containing 36
GO	cytoskeleton	40	635	0.032	55531	ELMO/CED-12 domain containing 1
GO	cytoskeleton	40	635	0.032	55752	septin 11
GO	cytoskeleton	40	635	0.032	56062	kelch-like 4 (Drosophila)
GO	cytoskeleton	40	635	0.032	57560	intraflagellar transport 80 homolog (Chlamydomonas)
GO	cytoskeleton	40	635	0.032	6442	sarcoglycan, alpha (50kDa dystrophin-associated glycoprotein)
GO	cytoskeleton	40	635	0.032	6444	sarcoglycan, delta (35kDa dystrophin-associated glycoprotein)
GO	cytoskeleton	40	635	0.032	6525	smoothelin
GO	cytoskeleton	40	635	0.032	667	dystonin
GO	cytoskeleton	40	635	0.032	70	actin, alpha, cardiac muscle 1
GO	cytoskeleton	40	635	0.032	7168	tropomyosin 1 (alpha)
GO	cytoskeleton	40	635	0.032	7171	tropomyosin 4
GO	cytoskeleton	40	635	0.032	7840	Alstrom syndrome 1

GO	cytoskeleton	40	635	0.032	79187	fibronectin type III and SPRY domain containing 1
GO	cytoskeleton	40	635	0.032	79929	MAP6 domain containing 1
GO	cytoskeleton	40	635	0.032	8409	ubiquitously-expressed transcript
GO	cytoskeleton	40	635	0.032	91624	nexilin (F actin binding protein)
GO	cytoskeleton	40	635	0.032	93323	HAUS augmin-like complex, subunit 8
GO	ureteric bud development	5	39	0.033	3975	LIM homeobox 1
GO	ureteric bud development	5	39	0.033	6299	sal-like 1 (Drosophila)
GO	ureteric bud development	5	39	0.033	6422	secreted frizzled-related protein 1
GO	ureteric bud development	5	39	0.033	7490	Wilms tumor 1
GO	ureteric bud development	5	39	0.033	9244	cytokine receptor-like factor 1
GO	adherens junction	4	27	0.035	126374	Wilms tumor 1 interacting protein
GO	adherens junction	4	27	0.035	1496	catenin (cadherin-associated protein), alpha 2
GO	adherens junction	4	27	0.035	27289	Rho family GTPase 1
GO	adherens junction	4	27	0.035	4867	nephronophthisis 1 (juvenile)
GO	response to wounding	6	53	0.035	1543	cytochrome P450, family 1, subfamily A, polypeptide 1
GO	response to wounding	6	53	0.035	2149	coagulation factor II (thrombin) receptor
GO	response to wounding	6	53	0.035	2151	coagulation factor II (thrombin) receptor-like 2
GO	response to wounding	6	53	0.035	26127	FGFR1 oncogene partner 2
GO	response to wounding	6	53	0.035	6657	SRY (sex determining region Y)-box 2
GO	response to wounding	6	53	0.035	729230	chemokine (C-C motif) receptor 2
GO	lateral plasma membrane	3	16	0.036	11149	blood vessel epicardial substance
GO	lateral plasma membrane	3	16	0.036	166336	prickle homolog 2 (Drosophila)
GO	lateral plasma membrane	3	16	0.036	9076	claudin 1
GO	negative regulation of endothelial cell p	3	16	0.036	348	apolipoprotein E
GO	negative regulation of endothelial cell p	3	16	0.036	4763	neurofibromin 1
GO	negative regulation of endothelial cell p	3	16	0.036	7857	secretogranin II (chromogranin C)
GO	mismatch repair	3	16	0.036	4292	mutL homolog 1, colon cancer, nonpolyposis type 2 (E. coli)
GO	mismatch repair	3	16	0.036	4436	mutS homolog 2, colon cancer, nonpolyposis type 1 (E. coli)
GO	mismatch repair	3	16	0.036	5378	PMS1 postmeiotic segregation increased 1 (S. cerevisiae)
GO	neuron fate commitment	3	16	0.036	5081	paired box 7
GO	neuron fate commitment	3	16	0.036	6657	SRY (sex determining region Y)-box 2
GO	neuron fate commitment	3	16	0.036	7046	transforming growth factor, beta receptor 1
GO	blood vessel development	5	40	0.037	1045	caudal type homeobox 2
GO	blood vessel development	5	40	0.037	1121	choroideremia (Rab escort protein 1)
GO	blood vessel development	5	40	0.037	1289	collagen, type V, alpha 1
GO	blood vessel development	5	40	0.037	3685	integrin, alpha V (vitronectin receptor, alpha polypeptide, antigen CD51)

GO	blood vessel development	5	40	0.037	80712	ESX homeobox 1
GO	anti-apoptosis	14	178	0.038	332	baculoviral IAP repeat-containing 5
GO	anti-apoptosis	14	178	0.038	347902	adhesion molecule with Ig-like domain 2
GO	anti-apoptosis	14	178	0.038	348	apolipoprotein E
GO	anti-apoptosis	14	178	0.038	355	Fas (TNF receptor superfamily, member 6)
GO	anti-apoptosis	14	178	0.038	5081	paired box 7
GO	anti-apoptosis	14	178	0.038	51499	TP53 regulated inhibitor of apoptosis 1
GO	anti-apoptosis	14	178	0.038	57099	apoptosis, caspase activation inhibitor
GO	anti-apoptosis	14	178	0.038	57144	p21 protein (Cdc42/Rac)-activated kinase 7
GO	anti-apoptosis	14	178	0.038	597	BCL2-related protein A1
GO	anti-apoptosis	14	178	0.038	60675	prokineticin 2
GO	anti-apoptosis	14	178	0.038	6347	chemokine (C-C motif) ligand 2
GO	anti-apoptosis	14	178	0.038	6422	secreted frizzled-related protein 1
GO	anti-apoptosis	14	178	0.038	8626	tumor protein p63
GO	anti-apoptosis	14	178	0.038	8835	suppressor of cytokine signaling 2
GO	cell division	18	246	0.039	10051	structural maintenance of chromosomes 4
GO	cell division	18	246	0.039	113130	cell division cycle associated 5
GO	cell division	18	246	0.039	1164	CDC28 protein kinase regulatory subunit 2
GO	cell division	18	246	0.039	220134	spindle and kinetochore associated complex subunit 1
GO	cell division	18	246	0.039	332	baculoviral IAP repeat-containing 5
GO	cell division	18	246	0.039	55165	centrosomal protein 55kDa
GO	cell division	18	246	0.039	55207	ADP-ribosylation factor-like 8B
GO	cell division	18	246	0.039	55752	septin 11
GO	cell division	18	246	0.039	64151	non-SMC condensin I complex, subunit G
GO	cell division	18	246	0.039	6683	spastin
GO	cell division	18	246	0.039	79172	centromere protein O
GO	cell division	18	246	0.039	79187	fibronectin type III and SPRY domain containing 1
GO	cell division	18	246	0.039	8091	high mobility group AT-hook 2
GO	cell division	18	246	0.039	84552	par-6 partitioning defective 6 homolog gamma (C. elegans)
GO	cell division	18	246	0.039	8872	cell division cycle 123 homolog (S. cerevisiae)
GO	cell division	18	246	0.039	890	cyclin A2
GO	cell division	18	246	0.039	898	cyclin E1
GO	cell division	18	246	0.039	93323	HAUS augmin-like complex, subunit 8
GO	aging	8	83	0.039	1984	eukaryotic translation initiation factor 5A
GO	aging	8	83	0.039	2027	enolase 3 (beta, muscle)
GO	aging	8	83	0.039	5028	purinergic receptor P2Y, G-protein coupled, 1

GO	aging	8	83	0.039	5588	protein kinase C, theta
GO	aging	8	83	0.039	7037	transferrin receptor (p90, CD71)
GO	aging	8	83	0.039	7046	transforming growth factor, beta receptor 1
GO	aging	8	83	0.039	7078	TIMP metallopeptidase inhibitor 3
GO	aging	8	83	0.039	8835	suppressor of cytokine signaling 2
GO	Arp2/3 protein complex	2	7	0.039	10096	ARP3 actin-related protein 3 homolog (yeast)
GO	Arp2/3 protein complex	2	7	0.039	10097	ARP2 actin-related protein 2 homolog (yeast)
GO	small nucleolar ribonucleoprotein comp	2	7	0.039	10199	M-phase phosphoprotein 10 (U3 small nucleolar ribonucleoprotein)
GO	small nucleolar ribonucleoprotein comp	2	7	0.039	10528	NOP56 ribonucleoprotein homolog (yeast)
GO	DNA damage response, signal transduct	2	7	0.039	1026	cyclin-dependent kinase inhibitor 1A (p21, Cip1)
GO	DNA damage response, signal transduct	2	7	0.039	51499	TP53 regulated inhibitor of apoptosis 1
GO	regulation of transcription from RNA po	2	7	0.039	10622	polymerase (RNA) III (DNA directed) polypeptide G (32kD)
GO	regulation of transcription from RNA po	2	7	0.039	672	breast cancer 1, early onset
GO	tRNA modification	2	7	0.039	10785	WD repeat domain 4
GO	tRNA modification	2	7	0.039	6741	Sjogren syndrome antigen B (autoantigen La)
GO	detection of mechanical stimulus involv	2	7	0.039	1301	collagen, type XI, alpha 1
GO	detection of mechanical stimulus involv	2	7	0.039	6657	SRY (sex determining region Y)-box 2
GO	suckling behavior	2	7	0.039	130507	ubiquitin protein ligase E3 component n-recognin 3 (putative)
GO	suckling behavior	2	7	0.039	5021	oxytocin receptor
GO	positive regulation of blood coagulation	2	7	0.039	2149	coagulation factor II (thrombin) receptor
GO	positive regulation of blood coagulation	2	7	0.039	5054	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor t
GO	protein heterotetramerization	2	7	0.039	23590	prenyl (decaprenyl) diphosphate synthase, subunit 1
GO	protein heterotetramerization	2	7	0.039	6241	ribonucleotide reductase M2
GO	branched chain family amino acid catab	2	7	0.039	26275	3-hydroxyisobutyryl-Coenzyme A hydrolase
GO	branched chain family amino acid catab	2	7	0.039	586	branched chain aminotransferase 1, cytosolic
GO	receptor clustering	2	7	0.039	2898	glutamate receptor, ionotropic, kainate 2
GO	receptor clustering	2	7	0.039	773	calcium channel, voltage-dependent, P/Q type, alpha 1A subunit
GO	negative regulation of fatty acid biosynt	2	7	0.039	341	apolipoprotein C-I
GO	negative regulation of fatty acid biosynt	2	7	0.039	672	breast cancer 1, early onset
GO	positive regulation of cholesterol esteri	2	7	0.039	341	apolipoprotein C-I
GO	positive regulation of cholesterol esteri	2	7	0.039	348	apolipoprotein E
GO	response to reactive oxygen species	2	7	0.039	348	apolipoprotein E
GO	response to reactive oxygen species	2	7	0.039	5054	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor t
GO	negative regulation of smooth muscle c	2	7	0.039	3516	recombination signal binding protein for immunoglobulin kappa J region
GO	negative regulation of smooth muscle c	2	7	0.039	5054	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor t
GO	G2 phase of mitotic cell cycle	2	7	0.039	3838	karyopherin alpha 2 (RAG cohort 1, importin alpha 1)

GO	G2 phase of mitotic cell cycle	2	7	0.039	641	Bloom syndrome, RecQ helicase-like
GO	postreplication repair	2	7	0.039	4436	mutS homolog 2, colon cancer, nonpolyposis type 1 (E. coli)
GO	postreplication repair	2	7	0.039	672	breast cancer 1, early onset
GO	spinal cord development	2	7	0.039	4763	neurofibromin 1
GO	spinal cord development	2	7	0.039	6586	slit homolog 3 (Drosophila)
GO	sympathetic nervous system developme	2	7	0.039	4763	neurofibromin 1
GO	sympathetic nervous system developme	2	7	0.039	8626	tumor protein p63
GO	3',5'-cyclic-GMP phosphodiesterase acti	2	7	0.039	50940	phosphodiesterase 11A
GO	3',5'-cyclic-GMP phosphodiesterase acti	2	7	0.039	5145	phosphodiesterase 6A, cGMP-specific, rod, alpha
GO	cAMP catabolic process	2	7	0.039	50940	phosphodiesterase 11A
GO	cAMP catabolic process	2	7	0.039	5140	phosphodiesterase 3B, cGMP-inhibited
GO	signal peptide processing	2	7	0.039	5125	proprotein convertase subtilisin/kexin type 5
GO	signal peptide processing	2	7	0.039	90701	SEC11 homolog C (S. cerevisiae)
GO	transcription	7	69	0.041	10622	polymerase (RNA) III (DNA directed) polypeptide G (32kD)
GO	transcription	7	69	0.041	170082	transcription elongation factor A (SII) N-terminal and central domain contai
GO	transcription	7	69	0.041	25885	polymerase (RNA) I polypeptide A, 194kDa
GO	transcription	7	69	0.041	4291	myeloid leukemia factor 1
GO	transcription	7	69	0.041	5440	polymerase (RNA) II (DNA directed) polypeptide K, 7.0kDa
GO	transcription	7	69	0.041	5558	primase, DNA, polypeptide 2 (58kDa)
GO	transcription	7	69	0.041	84172	polymerase (RNA) I polypeptide B, 128kDa
GO	extracellular matrix structural constitue	7	69	0.041	1282	collagen, type IV, alpha 1
GO	extracellular matrix structural constitue	7	69	0.041	1284	collagen, type IV, alpha 2
GO	extracellular matrix structural constitue	7	69	0.041	1288	collagen, type IV, alpha 6
GO	extracellular matrix structural constitue	7	69	0.041	1289	collagen, type V, alpha 1
GO	extracellular matrix structural constitue	7	69	0.041	1290	collagen, type V, alpha 2
GO	extracellular matrix structural constitue	7	69	0.041	1301	collagen, type XI, alpha 1
GO	extracellular matrix structural constitue	7	69	0.041	4060	lumican
GO	fatty acid binding	3	17	0.042	2171	fatty acid binding protein 5 (psoriasis-associated)
GO	fatty acid binding	3	17	0.042	2172	fatty acid binding protein 6, ileal
GO	fatty acid binding	3	17	0.042	341	apolipoprotein C-I
GO	cardiac muscle contraction	3	17	0.042	70	actin, alpha, cardiac muscle 1
GO	cardiac muscle contraction	3	17	0.042	7137	troponin I type 3 (cardiac)
GO	cardiac muscle contraction	3	17	0.042	7168	tropomyosin 1 (alpha)
GO	lipid binding	10	116	0.044	116362	retinol binding protein 7, cellular
GO	lipid binding	10	116	0.044	1622	diazepam binding inhibitor (GABA receptor modulator, acyl-Coenzyme A bi
GO	lipid binding	10	116	0.044	2171	fatty acid binding protein 5 (psoriasis-associated)

GO	lipid binding	10	116	0.044	2172	fatty acid binding protein 6, ileal
GO	lipid binding	10	116	0.044	26207	phosphatidylinositol transfer protein, cytoplasmic 1
GO	lipid binding	10	116	0.044	348	apolipoprotein E
GO	lipid binding	10	116	0.044	516	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit C1 (subu
GO	lipid binding	10	116	0.044	5360	phospholipid transfer protein
GO	lipid binding	10	116	0.044	581	BCL2-associated X protein
GO	lipid binding	10	116	0.044	5947	retinol binding protein 1, cellular
GO	G1/S transition of mitotic cell cycle	5	42	0.044	1026	cyclin-dependent kinase inhibitor 1A (p21, Cip1)
GO	G1/S transition of mitotic cell cycle	5	42	0.044	113130	cell division cycle associated 5
GO	G1/S transition of mitotic cell cycle	5	42	0.044	3624	inhibin, beta A
GO	G1/S transition of mitotic cell cycle	5	42	0.044	586	branched chain aminotransferase 1, cytosolic
GO	G1/S transition of mitotic cell cycle	5	42	0.044	898	cyclin E1
GO	chromosome segregation	5	42	0.044	220134	spindle and kinetochore associated complex subunit 1
GO	chromosome segregation	5	42	0.044	332	baculoviral IAP repeat-containing 5
GO	chromosome segregation	5	42	0.044	55207	ADP-ribosylation factor-like 8B
GO	chromosome segregation	5	42	0.044	672	breast cancer 1, early onset
GO	chromosome segregation	5	42	0.044	79172	centromere protein O
GO	RNA splicing	18	251	0.045	10189	THO complex 4
GO	RNA splicing	18	251	0.045	10199	M-phase phosphoprotein 10 (U3 small nucleolar ribonucleoprotein)
GO	RNA splicing	18	251	0.045	10212	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39
GO	RNA splicing	18	251	0.045	10465	peptidylprolyl isomerase H (cyclophilin H)
GO	RNA splicing	18	251	0.045	10492	synaptotagmin binding, cytoplasmic RNA interacting protein
GO	RNA splicing	18	251	0.045	135295	splicing factor, arginine/serine-rich 13B
GO	RNA splicing	18	251	0.045	23658	LSM5 homolog, U6 small nuclear RNA associated (S. cerevisiae)
GO	RNA splicing	18	251	0.045	27258	LSM3 homolog, U6 small nuclear RNA associated (S. cerevisiae)
GO	RNA splicing	18	251	0.045	3183	heterogeneous nuclear ribonucleoprotein C (C1/C2)
GO	RNA splicing	18	251	0.045	51645	peptidylprolyl isomerase (cyclophilin)-like 1
GO	RNA splicing	18	251	0.045	53981	cleavage and polyadenylation specific factor 2, 100kDa
GO	RNA splicing	18	251	0.045	5440	polymerase (RNA) II (DNA directed) polypeptide K, 7.0kDa
GO	RNA splicing	18	251	0.045	58155	polypyrimidine tract binding protein 2
GO	RNA splicing	18	251	0.045	6637	small nuclear ribonucleoprotein polypeptide G
GO	RNA splicing	18	251	0.045	7490	Wilms tumor 1
GO	RNA splicing	18	251	0.045	79833	gem (nuclear organelle) associated protein 6
GO	RNA splicing	18	251	0.045	8458	transcription termination factor, RNA polymerase II
GO	RNA splicing	18	251	0.045	8563	THO complex 5
GO	cell adhesion	33	522	0.046	1000	cadherin 2, type 1, N-cadherin (neuronal)

GO	cell adhesion	33	522	0.046	1002	cadherin 4, type 1, R-cadherin (retinal)
GO	cell adhesion	33	522	0.046	10457	glycoprotein (transmembrane) nmb
GO	cell adhesion	33	522	0.046	11149	blood vessel epicardial substance
GO	cell adhesion	33	522	0.046	120114	FAT tumor suppressor homolog 3 (Drosophila)
GO	cell adhesion	33	522	0.046	1288	collagen, type IV, alpha 6
GO	cell adhesion	33	522	0.046	1289	collagen, type V, alpha 1
GO	cell adhesion	33	522	0.046	1301	collagen, type XI, alpha 1
GO	cell adhesion	33	522	0.046	145864	hyaluronan and proteoglycan link protein 3
GO	cell adhesion	33	522	0.046	1830	desmoglein 3 (pemphigus vulgaris antigen)
GO	cell adhesion	33	522	0.046	22801	integrin, alpha 11
GO	cell adhesion	33	522	0.046	23705	cell adhesion molecule 1
GO	cell adhesion	33	522	0.046	23768	fibronectin leucine rich transmembrane protein 2
GO	cell adhesion	33	522	0.046	26032	sushi domain containing 5
GO	cell adhesion	33	522	0.046	285761	discoidin, CUB and LCCL domain containing 1
GO	cell adhesion	33	522	0.046	347902	adhesion molecule with Ig-like domain 2
GO	cell adhesion	33	522	0.046	3685	integrin, alpha V (vitronectin receptor, alpha polypeptide, antigen CD51)
GO	cell adhesion	33	522	0.046	3694	integrin, beta 6
GO	cell adhesion	33	522	0.046	3918	laminin, gamma 2
GO	cell adhesion	33	522	0.046	5101	protocadherin 9
GO	cell adhesion	33	522	0.046	56104	protocadherin gamma subfamily B, 1
GO	cell adhesion	33	522	0.046	56126	protocadherin beta 10
GO	cell adhesion	33	522	0.046	56133	protocadherin beta 2
GO	cell adhesion	33	522	0.046	5754	PTK7 protein tyrosine kinase 7
GO	cell adhesion	33	522	0.046	57575	protocadherin 10
GO	cell adhesion	33	522	0.046	57642	collagen, type XX, alpha 1
GO	cell adhesion	33	522	0.046	6347	chemokine (C-C motif) ligand 2
GO	cell adhesion	33	522	0.046	667	dystonin
GO	cell adhesion	33	522	0.046	6695	sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 1
GO	cell adhesion	33	522	0.046	7058	thrombospondin 2
GO	cell adhesion	33	522	0.046	9076	claudin 1
GO	cell adhesion	33	522	0.046	953	ectonucleoside triphosphate diphosphohydrolase 1
GO	cell adhesion	33	522	0.046	9635	chloride channel accessory 2
GO	regulation of myelination	1	1	0.046	1000	cadherin 2, type 1, N-cadherin (neuronal)
GO	regulation of myosin II filament assemb	1	1	0.046	10096	ARP3 actin-related protein 3 homolog (yeast)
GO	D5 dopamine receptor binding	1	1	0.046	10672	guanine nucleotide binding protein (G protein), alpha 13
GO	positive regulation of locomotion	1	1	0.046	11149	blood vessel epicardial substance

GO	D-ribose catabolic process	1	1	0.046	11164	nudix (nucleoside diphosphate linked moiety X)-type motif 5
GO	ribonucleoside diphosphate catabolic pı	1	1	0.046	11164	nudix (nucleoside diphosphate linked moiety X)-type motif 5
GO	meiosis I	1	1	0.046	1164	CDC28 protein kinase regulatory subunit 2
GO	stem cell development	1	1	0.046	124540	musashi homolog 2 (Drosophila)
GO	integrin biosynthetic process	1	1	0.046	1289	collagen, type V, alpha 1
GO	glycerate kinase activity	1	1	0.046	132158	glycerate kinase
GO	nuclear mRNA 5'-splice site recognition	1	1	0.046	135295	splicing factor, arginine/serine-rich 13B
GO	coumarin metabolic process	1	1	0.046	1543	cytochrome P450, family 1, subfamily A, polypeptide 1
GO	dibenzo-p-dioxin catabolic process	1	1	0.046	1543	cytochrome P450, family 1, subfamily A, polypeptide 1
GO	flavonoid 3'-monooxygenase activity	1	1	0.046	1543	cytochrome P450, family 1, subfamily A, polypeptide 1
GO	flavonoid metabolic process	1	1	0.046	1543	cytochrome P450, family 1, subfamily A, polypeptide 1
GO	insecticide metabolic process	1	1	0.046	1543	cytochrome P450, family 1, subfamily A, polypeptide 1
GO	oxidoreductase activity, acting on diphe	1	1	0.046	1543	cytochrome P450, family 1, subfamily A, polypeptide 1
GO	response to herbicide	1	1	0.046	1543	cytochrome P450, family 1, subfamily A, polypeptide 1
GO	response to iron(III) ion	1	1	0.046	1543	cytochrome P450, family 1, subfamily A, polypeptide 1
GO	(S)-2-(5-amino-1-(5-phospho-D-ribosyl)i	1	1	0.046	158	adenylosuccinate lyase
GO	N6-(1,2-dicarboxyethyl)AMP AMP-lyase	1	1	0.046	158	adenylosuccinate lyase
GO	deoxyguanosine kinase activity	1	1	0.046	1716	deoxyguanosine kinase
GO	dGTP metabolic process	1	1	0.046	1716	deoxyguanosine kinase
GO	guanosine metabolic process	1	1	0.046	1716	deoxyguanosine kinase
GO	site-specific endodeoxyribonuclease act	1	1	0.046	1763	DNA replication helicase 2 homolog (yeast)
GO	euchromatin	1	1	0.046	1788	DNA (cytosine-5-)-methyltransferase 3 alpha
GO	dTDP biosynthetic process	1	1	0.046	1841	deoxythymidylate kinase (thymidylate kinase)
GO	nucleoside phosphate kinase activity	1	1	0.046	1841	deoxythymidylate kinase (thymidylate kinase)
GO	thymidylate kinase activity	1	1	0.046	1841	deoxythymidylate kinase (thymidylate kinase)
GO	alpha-1,4-N-acetylgalactosaminyltransfe	1	1	0.046	2135	exostoses (multiple)-like 2
GO	mesodermal cell fate specification	1	1	0.046	2139	eyes absent homolog 2 (Drosophila)
GO	nucleus accumbens development	1	1	0.046	220	aldehyde dehydrogenase 1 family, member A3
GO	optic cup morphogenesis involved in caı	1	1	0.046	220	aldehyde dehydrogenase 1 family, member A3
GO	ferredoxin-NADP+ reductase activity	1	1	0.046	2232	ferredoxin reductase
GO	double-stranded DNA specific exodeoxy	1	1	0.046	2237	flap structure-specific endonuclease 1
GO	regulation of calcium ion transport via s	1	1	0.046	2281	FK506 binding protein 1B, 12.6 kDa
GO	ribose-5-phosphate isomerase activity	1	1	0.046	22934	ribose 5-phosphate isomerase A
GO	regulation of cell cycle arrest	1	1	0.046	2305	forkhead box M1
GO	phosphoribosylamine-glycine ligase acti	1	1	0.046	2618	phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide
GO	phosphoribosylformylglycinamidine cyc	1	1	0.046	2618	phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide

GO	phosphoribosylglycinamide formyltrans	1	1	0.046	2618	phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide
GO	3-hydroxyisobutyryl-CoA hydrolase activ	1	1	0.046	26275	3-hydroxyisobutyryl-Coenzyme A hydrolase
GO	glycine amidinotransferase activity	1	1	0.046	2628	glycine amidinotransferase (L-arginine:glycine amidinotransferase)
GO	glycine decarboxylation via glycine cleav	1	1	0.046	2653	glycine cleavage system protein H (aminomethyl carrier)
GO	cochlea morphogenesis	1	1	0.046	2736	GLI family zinc finger 2
GO	floor plate formation	1	1	0.046	2736	GLI family zinc finger 2
GO	ventral spinal cord development	1	1	0.046	2736	GLI family zinc finger 2
GO	glucose-1,6-bisphosphate synthase activ	1	1	0.046	283209	phosphoglucomutase 2-like 1
GO	intramolecular transferase activity, pho:	1	1	0.046	283209	phosphoglucomutase 2-like 1
GO	induction of programmed cell death in r	1	1	0.046	2898	glutamate receptor, ionotropic, kainate 2
GO	chondroitin-glucuronate 5-epimerase ac	1	1	0.046	29940	dermatan sulfate epimerase
GO	positive regulation of calcineurin-NFAT :	1	1	0.046	29995	LIM and cysteine-rich domains 1
GO	regulation of cardiac muscle hypertroph	1	1	0.046	29995	LIM and cysteine-rich domains 1
GO	3-hydroxy-2-methylbutyryl-CoA dehydro	1	1	0.046	3028	hydroxysteroid (17-beta) dehydrogenase 10
GO	7-alpha-hydroxysteroid dehydrogenase	1	1	0.046	3028	hydroxysteroid (17-beta) dehydrogenase 10
GO	acetoacetyl-CoA reductase activity	1	1	0.046	3028	hydroxysteroid (17-beta) dehydrogenase 10
GO	interphase microtubule organizing cent	1	1	0.046	332	baculoviral IAP repeat-containing 5
GO	spindle checkpoint	1	1	0.046	332	baculoviral IAP repeat-containing 5
GO	negative regulation of phosphatidylchol	1	1	0.046	341	apolipoprotein C-I
GO	plasma lipoprotein particle remodeling	1	1	0.046	341	apolipoprotein C-I
GO	regulation of lipid transport	1	1	0.046	341	apolipoprotein C-I
GO	maintenance of location in cell	1	1	0.046	348	apolipoprotein E
GO	metal chelating activity	1	1	0.046	348	apolipoprotein E
GO	positive regulation of low-density lipopr	1	1	0.046	348	apolipoprotein E
GO	recombinase activity	1	1	0.046	3516	recombination signal binding protein for immunoglobulin kappa J region
GO	interleukin-11 receptor binding	1	1	0.046	3589	interleukin 11
GO	activin A complex	1	1	0.046	3624	inhibin, beta A
GO	cellular potassium ion homeostasis	1	1	0.046	3778	potassium large conductance calcium-activated channel, subfamily M, alph
GO	eye blink reflex	1	1	0.046	3778	potassium large conductance calcium-activated channel, subfamily M, alph
GO	large conductance calcium-activated po	1	1	0.046	3778	potassium large conductance calcium-activated channel, subfamily M, alph
GO	micturition	1	1	0.046	3778	potassium large conductance calcium-activated channel, subfamily M, alph
GO	negative regulation of cell volume	1	1	0.046	3778	potassium large conductance calcium-activated channel, subfamily M, alph
GO	regulation of aldosterone metabolic prc	1	1	0.046	3778	potassium large conductance calcium-activated channel, subfamily M, alph
GO	response to carbon monoxide	1	1	0.046	3778	potassium large conductance calcium-activated channel, subfamily M, alph
GO	CD8 receptor binding	1	1	0.046	3932	lymphocyte-specific protein tyrosine kinase
GO	regulation of lymphocyte activation	1	1	0.046	3932	lymphocyte-specific protein tyrosine kinase

GO	regulation of intracellular protein trans	1	1	0.046	3936	lymphocyte cytosolic protein 1 (L-plastin)
GO	negative regulation of metabolic proces	1	1	0.046	3952	leptin
GO	fibrillar collagen	1	1	0.046	4060	lumican
GO	negative regulation of natural killer cell	1	1	0.046	409	arrestin, beta 2
GO	adrenocorticotropin receptor activity	1	1	0.046	4158	melanocortin 2 receptor (adrenocorticotropic hormone)
GO	male meiosis chromosome segregation	1	1	0.046	4292	mutL homolog 1, colon cancer, nonpolyposis type 2 (E. coli)
GO	meiotic metaphase I plate congression	1	1	0.046	4292	mutL homolog 1, colon cancer, nonpolyposis type 2 (E. coli)
GO	nuclear-transcribed mRNA poly(A) tail s	1	1	0.046	4292	mutL homolog 1, colon cancer, nonpolyposis type 2 (E. coli)
GO	resolution of meiotic recombination int	1	1	0.046	4292	mutL homolog 1, colon cancer, nonpolyposis type 2 (E. coli)
GO	spindle midzone assembly involved in m	1	1	0.046	4292	mutL homolog 1, colon cancer, nonpolyposis type 2 (E. coli)
GO	development during symbiotic interacti	1	1	0.046	4734	neural precursor cell expressed, developmentally down-regulated 4
GO	negative regulation of sodium ion trans	1	1	0.046	4734	neural precursor cell expressed, developmentally down-regulated 4
GO	negative regulation of transcription fro	1	1	0.046	4734	neural precursor cell expressed, developmentally down-regulated 4
GO	positive regulation of nucleocytoplasmi	1	1	0.046	4734	neural precursor cell expressed, developmentally down-regulated 4
GO	sodium channel inhibitor activity	1	1	0.046	4734	neural precursor cell expressed, developmentally down-regulated 4
GO	transmission of virus	1	1	0.046	4734	neural precursor cell expressed, developmentally down-regulated 4
GO	forebrain astrocyte development	1	1	0.046	4763	neurofibromin 1
GO	negative regulation of transcription fact	1	1	0.046	4763	neurofibromin 1
GO	regulation of glial cell differentiation	1	1	0.046	4763	neurofibromin 1
GO	negative regulation of myeloid leukocyt	1	1	0.046	4830	non-metastatic cells 1, protein (NM23A) expressed in
GO	nucleoside diphosphate phosphorylatio	1	1	0.046	4830	non-metastatic cells 1, protein (NM23A) expressed in
GO	oxidized purine base lesion DNA N-glyc	1	1	0.046	4968	8-oxoguanine DNA glycosylase
GO	oxytocin receptor activity	1	1	0.046	5021	oxytocin receptor
GO	negative regulation of vascular wound	1	1	0.046	5054	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor t
GO	negative regulation of wound healing	1	1	0.046	5054	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor t
GO	positive regulation of leukotriene produ	1	1	0.046	5054	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor t
GO	satellite cell commitment	1	1	0.046	5081	paired box 7
GO	cyclic-nucleotide phosphodiesterase act	1	1	0.046	50940	phosphodiesterase 11A
GO	renin secretion into blood stream	1	1	0.046	5125	proprotein convertase subtilisin/kexin type 5
GO	negative regulation of cAMP-mediated	1	1	0.046	5140	phosphodiesterase 3B, cGMP-inhibited
GO	phytanoyl-CoA dioxygenase activity	1	1	0.046	5264	phytanoyl-CoA 2-hydroxylase
GO	bent DNA binding	1	1	0.046	5303	protein (peptidylprolyl cis/trans isomerase) NIMA-interacting, 4 (parvulin)
GO	preribosome	1	1	0.046	5303	protein (peptidylprolyl cis/trans isomerase) NIMA-interacting, 4 (parvulin)
GO	inhibition of phospholipase C activity in	1	1	0.046	5341	pleckstrin
GO	negative regulation of inositol phosphat	1	1	0.046	5341	pleckstrin
GO	positive regulation of inositol-polyphos	1	1	0.046	5341	pleckstrin

GO	protein secretion by platelet	1	1	0.046	5341	pleckstrin
GO	regulation of cell diameter	1	1	0.046	5341	pleckstrin
GO	epithelial tube formation	1	1	0.046	5420	podocalyxin-like
GO	positive regulation of cell-cell adhesion	1	1	0.046	5420	podocalyxin-like
GO	regulation of microvillus assembly	1	1	0.046	5420	podocalyxin-like
GO	positive regulation of mammary gland e	1	1	0.046	5469	mediator complex subunit 1
GO	positive regulation of mucus secretion	1	1	0.046	54843	synaptotagmin-like 2
GO	regulation of telomerase activity	1	1	0.046	54984	PIN2-interacting protein 1
GO	N-acetylglucosamine kinase activity	1	1	0.046	55577	N-acetylglucosamine kinase
GO	N-acetylmannosamine metabolic proce	1	1	0.046	55577	N-acetylglucosamine kinase
GO	negative regulation of activation-induce	1	1	0.046	57678	glycerol-3-phosphate acyltransferase, mitochondrial
GO	regulation of cytokine secretion	1	1	0.046	57678	glycerol-3-phosphate acyltransferase, mitochondrial
GO	induction of retinal programmed cell de	1	1	0.046	581	BCL2-associated X protein
GO	mitochondrial permeability transition p	1	1	0.046	581	BCL2-associated X protein
GO	release of matrix enzymes from mitoch	1	1	0.046	581	BCL2-associated X protein
GO	ethanolamine-phosphate cytidylyltrans	1	1	0.046	5833	phosphate cytidylyltransferase 2, ethanolamine
GO	smooth muscle contractile fiber	1	1	0.046	59	actin, alpha 2, smooth muscle, aorta
GO	vascular smooth muscle contraction	1	1	0.046	59	actin, alpha 2, smooth muscle, aorta
GO	cocaine metabolic process	1	1	0.046	590	butyrylcholinesterase
GO	deoxynucleotide transmembrane trans	1	1	0.046	60386	solute carrier family 25 (mitochondrial thiamine pyrophosphate carrier), m
GO	deoxynucleotide transport	1	1	0.046	60386	solute carrier family 25 (mitochondrial thiamine pyrophosphate carrier), m
GO	ribulose-phosphate 3-epimerase activity	1	1	0.046	6120	ribulose-5-phosphate-3-epimerase
GO	inductive cell-cell signaling	1	1	0.046	6299	sal-like 1 (Drosophila)
GO	kidney epithelium development	1	1	0.046	6299	sal-like 1 (Drosophila)
GO	olfactory bulb mitral cell layer developm	1	1	0.046	6299	sal-like 1 (Drosophila)
GO	ureteric bud invasion	1	1	0.046	6299	sal-like 1 (Drosophila)
GO	chemokine-mediated signaling pathway	1	1	0.046	6347	chemokine (C-C motif) ligand 2
GO	D-ribose metabolic process	1	1	0.046	64080	ribokinase
GO	ribokinase activity	1	1	0.046	64080	ribokinase
GO	negative regulation of cell division	1	1	0.046	641	Bloom syndrome, RecQ helicase-like
GO	Wnt receptor signaling pathway, planar	1	1	0.046	6422	secreted frizzled-related protein 1
GO	negative regulation of systemic arterial	1	1	0.046	659	bone morphogenetic protein receptor, type II (serine/threonine kinase)
GO	regulation of lung blood pressure	1	1	0.046	659	bone morphogenetic protein receptor, type II (serine/threonine kinase)
GO	detection of mechanical stimulus involv	1	1	0.046	6657	SRY (sex determining region Y)-box 2
GO	diencephalon morphogenesis	1	1	0.046	6657	SRY (sex determining region Y)-box 2
GO	glial cell fate commitment	1	1	0.046	6657	SRY (sex determining region Y)-box 2

GO	pigment biosynthetic process	1	1	0.046	6657	SRY (sex determining region Y)-box 2
GO	endochondral bone morphogenesis	1	1	0.046	6662	SRY (sex determining region Y)-box 9
GO	epithelial cell proliferation involved in p	1	1	0.046	6662	SRY (sex determining region Y)-box 9
GO	male germ-line sex determination	1	1	0.046	6662	SRY (sex determining region Y)-box 9
GO	microtubule plus end	1	1	0.046	667	dystonin
GO	interferon-gamma-mediated signaling p	1	1	0.046	6672	SP100 nuclear antigen
GO	response to type I interferon	1	1	0.046	6672	SP100 nuclear antigen
GO	type I interferon-mediated signaling pat	1	1	0.046	6672	SP100 nuclear antigen
GO	negative regulation of centriole replicat	1	1	0.046	672	breast cancer 1, early onset
GO	histone mRNA metabolic process	1	1	0.046	6741	Sjogren syndrome antigen B (autoantigen La)
GO	actomyosin, actin part	1	1	0.046	70	actin, alpha, cardiac muscle 1
GO	plasma membrane part	1	1	0.046	7046	transforming growth factor, beta receptor 1
GO	regulation of systemic arterial blood pre	1	1	0.046	7137	troponin I type 3 (cardiac)
GO	positive regulation of heart rate by epin	1	1	0.046	7168	tropomyosin 1 (alpha)
GO	deoxyribonucleoside monophosphate b	1	1	0.046	7298	thymidylate synthetase
GO	dTMP biosynthetic process	1	1	0.046	7298	thymidylate synthetase
GO	dUMP metabolic process	1	1	0.046	7298	thymidylate synthetase
GO	thymidylate synthase activity	1	1	0.046	7298	thymidylate synthetase
GO	uroporphyrinogen decarboxylase activit	1	1	0.046	7389	uroporphyrinogen decarboxylase
GO	uroporphyrinogen III metabolic process	1	1	0.046	7389	uroporphyrinogen decarboxylase
GO	cerebellar molecular layer development	1	1	0.046	773	calcium channel, voltage-dependent, P/Q type, alpha 1A subunit
GO	cerebellum maturation	1	1	0.046	773	calcium channel, voltage-dependent, P/Q type, alpha 1A subunit
GO	negative regulation of hormone biosynt	1	1	0.046	773	calcium channel, voltage-dependent, P/Q type, alpha 1A subunit
GO	rhythmic synaptic transmission	1	1	0.046	773	calcium channel, voltage-dependent, P/Q type, alpha 1A subunit
GO	vestibular nucleus development	1	1	0.046	773	calcium channel, voltage-dependent, P/Q type, alpha 1A subunit
GO	eosinophil chemotaxis	1	1	0.046	7857	secretogranin II (chromogranin C)
GO	fatty acid elongation	1	1	0.046	79071	ELOVL family member 6, elongation of long chain fatty acids (FEN1/Elo2, SU
GO	agmatinase activity	1	1	0.046	79814	agmatine ureohydrolase (agmatinase)
GO	putrescine biosynthetic process	1	1	0.046	79814	agmatine ureohydrolase (agmatinase)
GO	N-terminal peptidyl-L-cysteine N-palmit	1	1	0.046	79929	MAP6 domain containing 1
GO	nucleologenesis	1	1	0.046	84172	polymerase (RNA) I polypeptide B, 128kDa
GO	rRNA metabolic process	1	1	0.046	84365	MKI67 (FHA domain) interacting nucleolar phosphoprotein
GO	RNA polymerase II transcription termina	1	1	0.046	8458	transcription termination factor, RNA polymerase II
GO	polarized epithelial cell differentiation	1	1	0.046	8626	tumor protein p63
GO	squamous basal epithelial stem cell diffe	1	1	0.046	8626	tumor protein p63
GO	1-pyrroline-5-carboxylate dehydrogena	1	1	0.046	8659	aldehyde dehydrogenase 4 family, member A1

GO	tRNA (uracil) methyltransferase activity	1	1	0.046	91801	alkB, alkylation repair homolog 8 (E. coli)
GO	25-hydroxycholesterol 7alpha-hydroxyla	1	1	0.046	9420	cytochrome P450, family 7, subfamily B, polypeptide 1
GO	metabotropic glutamate receptor bindi	1	1	0.046	9455	homer homolog 2 (Drosophila)
GO	heparan sulfate 2-O-sulfotransferase ac	1	1	0.046	9653	heparan sulfate 2-O-sulfotransferase 1
GO	heparin metabolic process	1	1	0.046	9653	heparan sulfate 2-O-sulfotransferase 1
GO	synaptic transmission	13	167	0.048	10052	gap junction protein, gamma 1, 45kDa
GO	synaptic transmission	13	167	0.048	1138	cholinergic receptor, nicotinic, alpha 5
GO	synaptic transmission	13	167	0.048	200959	gamma-aminobutyric acid (GABA) receptor, rho 3
GO	synaptic transmission	13	167	0.048	2558	gamma-aminobutyric acid (GABA) A receptor, alpha 5
GO	synaptic transmission	13	167	0.048	2898	glutamate receptor, ionotropic, kainate 2
GO	synaptic transmission	13	167	0.048	3751	potassium voltage-gated channel, Shal-related subfamily, member 2
GO	synaptic transmission	13	167	0.048	3778	potassium large conductance calcium-activated channel, subfamily M, alph
GO	synaptic transmission	13	167	0.048	4287	ataxin 3
GO	synaptic transmission	13	167	0.048	4884	neuronal pentraxin I
GO	synaptic transmission	13	167	0.048	56126	protocadherin beta 10
GO	synaptic transmission	13	167	0.048	56133	protocadherin beta 2
GO	synaptic transmission	13	167	0.048	56479	potassium voltage-gated channel, KQT-like subfamily, member 5
GO	synaptic transmission	13	167	0.048	9568	gamma-aminobutyric acid (GABA) B receptor, 2
GO	structural constituent of muscle	5	43	0.048	4637	myosin, light chain 6, alkali, smooth muscle and non-muscle
GO	structural constituent of muscle	5	43	0.048	6525	smoothelin
GO	structural constituent of muscle	5	43	0.048	7168	tropomyosin 1 (alpha)
GO	structural constituent of muscle	5	43	0.048	7171	tropomyosin 4
GO	structural constituent of muscle	5	43	0.048	9172	myomesin (M-protein) 2, 165kDa
GO	tRNA processing	6	57	0.048	10799	ribonuclease P/MRP 40kDa subunit
GO	tRNA processing	6	57	0.048	134637	adenosine deaminase, tRNA-specific 2, TAD2 homolog (S. cerevisiae)
GO	tRNA processing	6	57	0.048	150962	pseudouridylate synthase 10
GO	tRNA processing	6	57	0.048	1787	tRNA aspartic acid methyltransferase 1
GO	tRNA processing	6	57	0.048	3028	hydroxysteroid (17-beta) dehydrogenase 10
GO	tRNA processing	6	57	0.048	345630	fibrillarin-like 1
GO	neuron migration	6	57	0.048	2534	FYN oncogene related to SRC, FGR, YES
GO	neuron migration	6	57	0.048	266727	MAM domain containing glycosylphosphatidylinositol anchor 1
GO	neuron migration	6	57	0.048	347733	tubulin, beta 2B
GO	neuron migration	6	57	0.048	4897	neuronal cell adhesion molecule
GO	neuron migration	6	57	0.048	51473	doublecortin domain containing 2
GO	neuron migration	6	57	0.048	92737	delta/notch-like EGF repeat containing
GO	regulation of protein localization	3	18	0.048	1000	cadherin 2, type 1, N-cadherin (neuronal)

GO	regulation of protein localization	3	18	0.048	7341	SMT3 suppressor of mif two 3 homolog 1 (S. cerevisiae)
GO	regulation of protein localization	3	18	0.048	9910	RAB GTPase activating protein 1-like
GO	response to corticosterone stimulus	3	18	0.048	1026	cyclin-dependent kinase inhibitor 1A (p21, Cip1)
GO	response to corticosterone stimulus	3	18	0.048	2878	glutathione peroxidase 3 (plasma)
GO	response to corticosterone stimulus	3	18	0.048	898	cyclin E1
GO	response to inorganic substance	3	18	0.048	1136	cholinergic receptor, nicotinic, alpha 3
GO	response to inorganic substance	3	18	0.048	2618	phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide
GO	response to inorganic substance	3	18	0.048	7037	transferrin receptor (p90, CD71)
GO	DNA helicase activity	3	18	0.048	1161	excision repair cross-complementing rodent repair deficiency, complement
GO	DNA helicase activity	3	18	0.048	50485	SWI/SNF related, matrix associated, actin dependent regulator of chromati
GO	DNA helicase activity	3	18	0.048	5965	RecQ protein-like (DNA helicase Q1-like)
GO	beta-amyloid binding	3	18	0.048	3028	hydroxysteroid (17-beta) dehydrogenase 10
GO	beta-amyloid binding	3	18	0.048	348	apolipoprotein E
GO	beta-amyloid binding	3	18	0.048	590	butyrylcholinesterase
GO	beta-tubulin binding	3	18	0.048	55207	ADP-ribosylation factor-like 8B
GO	beta-tubulin binding	3	18	0.048	6683	spastin
GO	beta-tubulin binding	3	18	0.048	8409	ubiquitously-expressed transcript
GO	response to UV	4	30	0.049	1026	cyclin-dependent kinase inhibitor 1A (p21, Cip1)
GO	response to UV	4	30	0.049	1161	excision repair cross-complementing rodent repair deficiency, complement
GO	response to UV	4	30	0.049	1643	damage-specific DNA binding protein 2, 48kDa
GO	response to UV	4	30	0.049	56852	RAD18 homolog (S. cerevisiae)
GO	response to arsenic	2	8	0.05	1026	cyclin-dependent kinase inhibitor 1A (p21, Cip1)
GO	response to arsenic	2	8	0.05	1543	cytochrome P450, family 1, subfamily A, polypeptide 1
GO	response to hyperoxia	2	8	0.05	1026	cyclin-dependent kinase inhibitor 1A (p21, Cip1)
GO	response to hyperoxia	2	8	0.05	1543	cytochrome P450, family 1, subfamily A, polypeptide 1
GO	nucleotide biosynthetic process	2	8	0.05	1841	deoxythymidylate kinase (thymidylate kinase)
GO	nucleotide biosynthetic process	2	8	0.05	7298	thymidylate synthetase
GO	determination of adult lifespan	2	8	0.05	29842	transcription factor CP2-like 1
GO	determination of adult lifespan	2	8	0.05	4436	mutS homolog 2, colon cancer, nonpolyposis type 1 (E. coli)
GO	hemopoietic progenitor cell differentiat	2	8	0.05	3624	inhibin, beta A
GO	hemopoietic progenitor cell differentiat	2	8	0.05	5341	pleckstrin
GO	nuclear localization sequence binding	2	8	0.05	3836	karyopherin alpha 1 (importin alpha 5)
GO	nuclear localization sequence binding	2	8	0.05	3838	karyopherin alpha 2 (RAG cohort 1, importin alpha 1)
GO	mismatched DNA binding	2	8	0.05	4436	mutS homolog 2, colon cancer, nonpolyposis type 1 (E. coli)
GO	mismatched DNA binding	2	8	0.05	5378	PMS1 postmeiotic segregation increased 1 (S. cerevisiae)
GO	proline-rich region binding	2	8	0.05	4734	neural precursor cell expressed, developmentally down-regulated 4

GO	proline-rich region binding	2	8	0.05	5216	profilin 1
GO	pharyngeal system development	2	8	0.05	6899	T-box 1
GO	pharyngeal system development	2	8	0.05	7046	transforming growth factor, beta receptor 1
GO	positive regulation of MAPKKK cascade	4	31	0.054	2149	coagulation factor II (thrombin) receptor
GO	positive regulation of MAPKKK cascade	4	31	0.054	3589	interleukin 11
GO	positive regulation of MAPKKK cascade	4	31	0.054	3952	leptin
GO	positive regulation of MAPKKK cascade	4	31	0.054	6657	SRY (sex determining region Y)-box 2
GO	heparin binding	9	105	0.055	10457	glycoprotein (transmembrane) nmb
GO	heparin binding	9	105	0.055	1289	collagen, type V, alpha 1
GO	heparin binding	9	105	0.055	143282	fibroblast growth factor binding protein 3
GO	heparin binding	9	105	0.055	26577	procollagen C-endopeptidase enhancer 2
GO	heparin binding	9	105	0.055	348	apolipoprotein E
GO	heparin binding	9	105	0.055	3918	laminin, gamma 2
GO	heparin binding	9	105	0.055	5228	placental growth factor
GO	heparin binding	9	105	0.055	6347	chemokine (C-C motif) ligand 2
GO	heparin binding	9	105	0.055	7058	thrombospondin 2
GO	DNA metabolic process	3	19	0.056	1775	deoxyribonuclease I-like 2
GO	DNA metabolic process	3	19	0.056	3838	karyopherin alpha 2 (RAG cohort 1, importin alpha 1)
GO	DNA metabolic process	3	19	0.056	50485	SWI/SNF related, matrix associated, actin dependent regulator of chromati
GO	nucleocytoplasmic transport	3	19	0.056	1984	eukaryotic translation initiation factor 5A
GO	nucleocytoplasmic transport	3	19	0.056	4928	nucleoporin 98kDa
GO	nucleocytoplasmic transport	3	19	0.056	8536	calcium/calmodulin-dependent protein kinase I
GO	high-density lipoprotein particle	3	19	0.056	341	apolipoprotein C-I
GO	high-density lipoprotein particle	3	19	0.056	348	apolipoprotein E
GO	high-density lipoprotein particle	3	19	0.056	79135	apolipoprotein O
GO	very-low-density lipoprotein particle	3	19	0.056	341	apolipoprotein C-I
GO	very-low-density lipoprotein particle	3	19	0.056	348	apolipoprotein E
GO	very-low-density lipoprotein particle	3	19	0.056	79135	apolipoprotein O
GO	response to amino acid stimulus	3	19	0.056	4436	mutS homolog 2, colon cancer, nonpolyposis type 1 (E. coli)
GO	response to amino acid stimulus	3	19	0.056	6347	chemokine (C-C motif) ligand 2
GO	response to amino acid stimulus	3	19	0.056	7078	TIMP metallopeptidase inhibitor 3
GO	neuron projection	6	60	0.059	114757	cytoglobin
GO	neuron projection	6	60	0.059	3800	kinesin family member 5C
GO	neuron projection	6	60	0.059	4897	neuronal cell adhesion molecule
GO	neuron projection	6	60	0.059	5494	protein phosphatase, Mg2+/Mn2+ dependent, 1A
GO	neuron projection	6	60	0.059	8997	kalirin, RhoGEF kinase

GO	neuron projection	6	60	0.059	9568	gamma-aminobutyric acid (GABA) B receptor, 2
GO	nuclear pore	6	60	0.059	1984	eukaryotic translation initiation factor 5A
GO	nuclear pore	6	60	0.059	3836	karyopherin alpha 1 (importin alpha 5)
GO	nuclear pore	6	60	0.059	3838	karyopherin alpha 2 (RAG cohort 1, importin alpha 1)
GO	nuclear pore	6	60	0.059	4928	nucleoporin 98kDa
GO	nuclear pore	6	60	0.059	7341	SMT3 suppressor of mif two 3 homolog 1 (S. cerevisiae)
GO	nuclear pore	6	60	0.059	9688	nucleoporin 93kDa
GO	peptidyl-prolyl cis-trans isomerase activ	4	32	0.059	10465	peptidylprolyl isomerase H (cyclophilin H)
GO	peptidyl-prolyl cis-trans isomerase activ	4	32	0.059	2281	FK506 binding protein 1B, 12.6 kDa
GO	peptidyl-prolyl cis-trans isomerase activ	4	32	0.059	51645	peptidylprolyl isomerase (cyclophilin)-like 1
GO	peptidyl-prolyl cis-trans isomerase activ	4	32	0.059	5303	protein (peptidylprolyl cis/trans isomerase) NIMA-interacting, 4 (parvulin)
GO	manganese ion binding	4	32	0.059	147699	protein phosphatase, Mg2+/Mn2+ dependent, 1N (putative)
GO	manganese ion binding	4	32	0.059	2237	flap structure-specific endonuclease 1
GO	manganese ion binding	4	32	0.059	5184	peptidase D
GO	manganese ion binding	4	32	0.059	5494	protein phosphatase, Mg2+/Mn2+ dependent, 1A
GO	sensory perception of sound	8	91	0.061	1301	collagen, type XI, alpha 1
GO	sensory perception of sound	8	91	0.061	1687	deafness, autosomal dominant 5
GO	sensory perception of sound	8	91	0.061	1690	coagulation factor C homolog, cochlin (Limulus polyphemus)
GO	sensory perception of sound	8	91	0.061	26519	translocase of inner mitochondrial membrane 10 homolog (yeast)
GO	sensory perception of sound	8	91	0.061	26521	translocase of inner mitochondrial membrane 8 homolog B (yeast)
GO	sensory perception of sound	8	91	0.061	3778	potassium large conductance calcium-activated channel, subfamily M, alph
GO	sensory perception of sound	8	91	0.061	55084	sine oculis binding protein homolog (Drosophila)
GO	sensory perception of sound	8	91	0.061	7840	Alstrom syndrome 1
GO	response to hypoxia	11	140	0.062	1543	cytochrome P450, family 1, subfamily A, polypeptide 1
GO	response to hypoxia	11	140	0.062	2321	fms-related tyrosine kinase 1 (vascular endothelial growth factor/vascular
GO	response to hypoxia	11	140	0.062	23305	acyl-CoA synthetase long-chain family member 6
GO	response to hypoxia	11	140	0.062	3778	potassium large conductance calcium-activated channel, subfamily M, alph
GO	response to hypoxia	11	140	0.062	4763	neurofibromin 1
GO	response to hypoxia	11	140	0.062	5228	placental growth factor
GO	response to hypoxia	11	140	0.062	5588	protein kinase C, theta
GO	response to hypoxia	11	140	0.062	6347	chemokine (C-C motif) ligand 2
GO	response to hypoxia	11	140	0.062	6546	solute carrier family 8 (sodium/calcium exchanger), member 1
GO	response to hypoxia	11	140	0.062	7037	transferrin receptor (p90, CD71)
GO	response to hypoxia	11	140	0.062	7046	transforming growth factor, beta receptor 1
GO	Rac GTPase activator activity	2	9	0.062	10395	deleted in liver cancer 1
GO	Rac GTPase activator activity	2	9	0.062	9732	dedicator of cytokinesis 4

GO	retinal binding	2	9	0.062	116362	retinol binding protein 7, cellular
GO	retinal binding	2	9	0.062	5947	retinol binding protein 1, cellular
GO	female gonad development	2	9	0.062	132625	zinc finger protein 42 homolog (mouse)
GO	female gonad development	2	9	0.062	431707	LIM homeobox 8
GO	skeletal muscle tissue regeneration	2	9	0.062	2027	enolase 3 (beta, muscle)
GO	skeletal muscle tissue regeneration	2	9	0.062	5081	paired box 7
GO	spectrin	2	9	0.062	2037	erythrocyte membrane protein band 4.1-like 2
GO	spectrin	2	9	0.062	6711	spectrin, beta, non-erythrocytic 1
GO	aldehyde dehydrogenase (NAD) activity	2	9	0.062	220	aldehyde dehydrogenase 1 family, member A3
GO	aldehyde dehydrogenase (NAD) activity	2	9	0.062	8659	aldehyde dehydrogenase 4 family, member A1
GO	lamellipodium membrane	2	9	0.062	26499	pleckstrin 2
GO	lamellipodium membrane	2	9	0.062	84168	anthrax toxin receptor 1
GO	regulation of smoothened signaling patl	2	9	0.062	2736	GLI family zinc finger 2
GO	regulation of smoothened signaling patl	2	9	0.062	5015	orthodenticle homeobox 2
GO	M band	2	9	0.062	287	ankyrin 2, neuronal
GO	M band	2	9	0.062	6711	spectrin, beta, non-erythrocytic 1
GO	positive regulation of synaptic transmis:	2	9	0.062	2898	glutamate receptor, ionotropic, kainate 2
GO	positive regulation of synaptic transmis:	2	9	0.062	6347	chemokine (C-C motif) ligand 2
GO	GTP biosynthetic process	2	9	0.062	29922	non-metastatic cells 7, protein expressed in (nucleoside-diphosphate kinas
GO	GTP biosynthetic process	2	9	0.062	4830	non-metastatic cells 1, protein (NM23A) expressed in
GO	nucleoside diphosphate kinase activity	2	9	0.062	29922	non-metastatic cells 7, protein expressed in (nucleoside-diphosphate kinas
GO	nucleoside diphosphate kinase activity	2	9	0.062	4830	non-metastatic cells 1, protein (NM23A) expressed in
GO	UTP biosynthetic process	2	9	0.062	29922	non-metastatic cells 7, protein expressed in (nucleoside-diphosphate kinas
GO	UTP biosynthetic process	2	9	0.062	4830	non-metastatic cells 1, protein (NM23A) expressed in
GO	phospholipid efflux	2	9	0.062	341	apolipoprotein C-I
GO	phospholipid efflux	2	9	0.062	348	apolipoprotein E
GO	muscle filament sliding	2	9	0.062	4637	myosin, light chain 6, alkali, smooth muscle and non-muscle
GO	muscle filament sliding	2	9	0.062	7168	tropomyosin 1 (alpha)
GO	smooth muscle tissue development	2	9	0.062	4763	neurofibromin 1
GO	smooth muscle tissue development	2	9	0.062	8626	tumor protein p63
GO	response to growth factor stimulus	2	9	0.062	5028	purinergic receptor P2Y, G-protein coupled, 1
GO	response to growth factor stimulus	2	9	0.062	6657	SRY (sex determining region Y)-box 2
GO	ruffle organization	2	9	0.062	5341	pleckstrin
GO	ruffle organization	2	9	0.062	7168	tropomyosin 1 (alpha)
GO	DNA damage response, signal transduct	2	9	0.062	6672	SP100 nuclear antigen
GO	DNA damage response, signal transduct	2	9	0.062	672	breast cancer 1, early onset

GO	positive regulation of neuron apoptosis	3	20	0.063	2045	EPH receptor A7
GO	positive regulation of neuron apoptosis	3	20	0.063	4763	neurofibromin 1
GO	positive regulation of neuron apoptosis	3	20	0.063	581	BCL2-associated X protein
GO	adult walking behavior	3	20	0.063	27429	HtrA serine peptidase 2
GO	adult walking behavior	3	20	0.063	3778	potassium large conductance calcium-activated channel, subfamily M, alph
GO	adult walking behavior	3	20	0.063	773	calcium channel, voltage-dependent, P/Q type, alpha 1A subunit
GO	response to organic cyclic substance	8	92	0.064	1026	cyclin-dependent kinase inhibitor 1A (p21, Cip1)
GO	response to organic cyclic substance	8	92	0.064	1543	cytochrome P450, family 1, subfamily A, polypeptide 1
GO	response to organic cyclic substance	8	92	0.064	2878	glutathione peroxidase 3 (plasma)
GO	response to organic cyclic substance	8	92	0.064	4436	mutS homolog 2, colon cancer, nonpolyposis type 1 (E. coli)
GO	response to organic cyclic substance	8	92	0.064	5021	oxytocin receptor
GO	response to organic cyclic substance	8	92	0.064	5588	protein kinase C, theta
GO	response to organic cyclic substance	8	92	0.064	7046	transforming growth factor, beta receptor 1
GO	response to organic cyclic substance	8	92	0.064	7078	TIMP metallopeptidase inhibitor 3
GO	elevation of cytosolic calcium ion conce	8	92	0.064	10672	guanine nucleotide binding protein (G protein), alpha 13
GO	elevation of cytosolic calcium ion conce	8	92	0.064	2150	coagulation factor II (thrombin) receptor-like 1
GO	elevation of cytosolic calcium ion conce	8	92	0.064	5021	oxytocin receptor
GO	elevation of cytosolic calcium ion conce	8	92	0.064	5028	purinergic receptor P2Y, G-protein coupled, 1
GO	elevation of cytosolic calcium ion conce	8	92	0.064	60675	prokineticin 2
GO	elevation of cytosolic calcium ion conce	8	92	0.064	6546	solute carrier family 8 (sodium/calcium exchanger), member 1
GO	elevation of cytosolic calcium ion conce	8	92	0.064	729230	chemokine (C-C motif) receptor 2
GO	elevation of cytosolic calcium ion conce	8	92	0.064	773	calcium channel, voltage-dependent, P/Q type, alpha 1A subunit
GO	negative regulation of transcription fror	16	227	0.064	1045	caudal type homeobox 2
GO	negative regulation of transcription fror	16	227	0.064	11142	protein kinase (cAMP-dependent, catalytic) inhibitor gamma
GO	negative regulation of transcription fror	16	227	0.064	11278	Kruppel-like factor 12
GO	negative regulation of transcription fror	16	227	0.064	1746	distal-less homeobox 2
GO	negative regulation of transcription fror	16	227	0.064	1788	DNA (cytosine-5-)-methyltransferase 3 alpha
GO	negative regulation of transcription fror	16	227	0.064	2736	GLI family zinc finger 2
GO	negative regulation of transcription fror	16	227	0.064	29842	transcription factor CP2-like 1
GO	negative regulation of transcription fror	16	227	0.064	29995	LIM and cysteine-rich domains 1
GO	negative regulation of transcription fror	16	227	0.064	3224	homeobox C8
GO	negative regulation of transcription fror	16	227	0.064	5569	protein kinase (cAMP-dependent, catalytic) inhibitor alpha
GO	negative regulation of transcription fror	16	227	0.064	6299	sal-like 1 (Drosophila)
GO	negative regulation of transcription fror	16	227	0.064	6591	snail homolog 2 (Drosophila)
GO	negative regulation of transcription fror	16	227	0.064	6657	SRY (sex determining region Y)-box 2
GO	negative regulation of transcription fror	16	227	0.064	6672	SP100 nuclear antigen

GO	negative regulation of transcription fror	16	227	0.064	7490	Wilms tumor 1
GO	negative regulation of transcription fror	16	227	0.064	8626	tumor protein p63
GO	phosphoinositide-mediated signaling	4	33	0.065	1164	CDC28 protein kinase regulatory subunit 2
GO	phosphoinositide-mediated signaling	4	33	0.065	2237	flap structure-specific endonuclease 1
GO	phosphoinositide-mediated signaling	4	33	0.065	7298	thymidylate synthetase
GO	phosphoinositide-mediated signaling	4	33	0.065	767	carbonic anhydrase VIII
GO	apical plasma membrane	12	159	0.067	2151	coagulation factor II (thrombin) receptor-like 2
GO	apical plasma membrane	12	159	0.067	287	ankyrin 2, neuronal
GO	apical plasma membrane	12	159	0.067	309	annexin A6
GO	apical plasma membrane	12	159	0.067	3778	potassium large conductance calcium-activated channel, subfamily M, alph
GO	apical plasma membrane	12	159	0.067	5021	oxytocin receptor
GO	apical plasma membrane	12	159	0.067	5028	purinergic receptor P2Y, G-protein coupled, 1
GO	apical plasma membrane	12	159	0.067	5031	pyrimidinergic receptor P2Y, G-protein coupled, 6
GO	apical plasma membrane	12	159	0.067	5420	podocalyxin-like
GO	apical plasma membrane	12	159	0.067	7010	TEK tyrosine kinase, endothelial
GO	apical plasma membrane	12	159	0.067	7046	transforming growth factor, beta receptor 1
GO	apical plasma membrane	12	159	0.067	8777	multiple PDZ domain protein
GO	apical plasma membrane	12	159	0.067	9497	solute carrier family 4, sodium bicarbonate cotransporter, member 7
GO	negative regulation of signal transductic	5	48	0.071	409	arrestin, beta 2
GO	negative regulation of signal transductic	5	48	0.071	55003	PAK1 interacting protein 1
GO	negative regulation of signal transductic	5	48	0.071	6000	regulator of G-protein signaling 7
GO	negative regulation of signal transductic	5	48	0.071	8490	regulator of G-protein signaling 5
GO	negative regulation of signal transductic	5	48	0.071	8835	suppressor of cytokine signaling 2
GO	collagen binding	4	34	0.071	22801	integrin, alpha 11
GO	collagen binding	4	34	0.071	4060	lumican
GO	collagen binding	4	34	0.071	4318	matrix metallopeptidase 9 (gelatinase B, 92kDa gelatinase, 92kDa type IV c
GO	collagen binding	4	34	0.071	84168	anthrax toxin receptor 1
GO	response to retinoic acid	4	34	0.071	54332	ganglioside-induced differentiation-associated protein 1
GO	response to retinoic acid	4	34	0.071	6657	SRY (sex determining region Y)-box 2
GO	response to retinoic acid	4	34	0.071	6672	SP100 nuclear antigen
GO	response to retinoic acid	4	34	0.071	7037	transferrin receptor (p90, CD71)
GO	ATP binding	78	1426	0.073	10000	v-akt murine thymoma viral oncogene homolog 3 (protein kinase B, gamma
GO	ATP binding	78	1426	0.073	10051	structural maintenance of chromosomes 4
GO	ATP binding	78	1426	0.073	10056	phenylalanyl-tRNA synthetase, beta subunit
GO	ATP binding	78	1426	0.073	10096	ARP3 actin-related protein 3 homolog (yeast)
GO	ATP binding	78	1426	0.073	10097	ARP2 actin-related protein 2 homolog (yeast)

GO	ATP binding	78	1426	0.073	10212	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39
GO	ATP binding	78	1426	0.073	10808	heat shock 105kDa/110kDa protein 1
GO	ATP binding	78	1426	0.073	11056	DEAD (Asp-Glu-Ala-Asp) box polypeptide 52
GO	ATP binding	78	1426	0.073	132158	glycerate kinase
GO	ATP binding	78	1426	0.073	140739	ubiquitin-conjugating enzyme E2F (putative)
GO	ATP binding	78	1426	0.073	1503	CTP synthase
GO	ATP binding	78	1426	0.073	1716	deoxyguanosine kinase
GO	ATP binding	78	1426	0.073	1763	DNA replication helicase 2 homolog (yeast)
GO	ATP binding	78	1426	0.073	1841	deoxythymidylate kinase (thymidylate kinase)
GO	ATP binding	78	1426	0.073	203	adenylate kinase 1
GO	ATP binding	78	1426	0.073	2045	EPH receptor A7
GO	ATP binding	78	1426	0.073	2242	feline sarcoma oncogene
GO	ATP binding	78	1426	0.073	2264	fibroblast growth factor receptor 4
GO	ATP binding	78	1426	0.073	22868	FAST kinase domains 2
GO	ATP binding	78	1426	0.073	23057	nicotinamide nucleotide adenylyltransferase 2
GO	ATP binding	78	1426	0.073	2321	fms-related tyrosine kinase 1 (vascular endothelial growth factor/vascular
GO	ATP binding	78	1426	0.073	23305	acyl-CoA synthetase long-chain family member 6
GO	ATP binding	78	1426	0.073	2534	FYN oncogene related to SRC, FGR, YES
GO	ATP binding	78	1426	0.073	26154	ATP-binding cassette, sub-family A (ABC1), member 12
GO	ATP binding	78	1426	0.073	2618	phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide
GO	ATP binding	78	1426	0.073	27330	ribosomal protein S6 kinase, 90kDa, polypeptide 6
GO	ATP binding	78	1426	0.073	283455	kinase suppressor of ras 2
GO	ATP binding	78	1426	0.073	29922	non-metastatic cells 7, protein expressed in (nucleoside-diphosphate kinas
GO	ATP binding	78	1426	0.073	3336	heat shock 10kDa protein 1 (chaperonin 10)
GO	ATP binding	78	1426	0.073	340273	ATP-binding cassette, sub-family B (MDR/TAP), member 5
GO	ATP binding	78	1426	0.073	3797	kinesin family member 3C
GO	ATP binding	78	1426	0.073	3800	kinesin family member 5C
GO	ATP binding	78	1426	0.073	3932	lymphocyte-specific protein tyrosine kinase
GO	ATP binding	78	1426	0.073	4171	minichromosome maintenance complex component 2
GO	ATP binding	78	1426	0.073	4292	mutL homolog 1, colon cancer, nonpolyposis type 2 (E. coli)
GO	ATP binding	78	1426	0.073	4430	myosin IB
GO	ATP binding	78	1426	0.073	4436	mutS homolog 2, colon cancer, nonpolyposis type 1 (E. coli)
GO	ATP binding	78	1426	0.073	4651	myosin X
GO	ATP binding	78	1426	0.073	479	ATPase, H+/K+ transporting, nongastric, alpha polypeptide
GO	ATP binding	78	1426	0.073	4830	non-metastatic cells 1, protein (NM23A) expressed in
GO	ATP binding	78	1426	0.073	5000	origin recognition complex, subunit 4-like (yeast)

GO	ATP binding	78	1426	0.073	5026	purinergic receptor P2X, ligand-gated ion channel, 5
GO	ATP binding	78	1426	0.073	5028	purinergic receptor P2Y, G-protein coupled, 1
GO	ATP binding	78	1426	0.073	50485	SWI/SNF related, matrix associated, actin dependent regulator of chromati
GO	ATP binding	78	1426	0.073	5378	PMS1 postmeiotic segregation increased 1 (S. cerevisiae)
GO	ATP binding	78	1426	0.073	54822	transient receptor potential cation channel, subfamily M, member 7
GO	ATP binding	78	1426	0.073	55137	fidgetin
GO	ATP binding	78	1426	0.073	55577	N-acetylglucosamine kinase
GO	ATP binding	78	1426	0.073	558	AXL receptor tyrosine kinase
GO	ATP binding	78	1426	0.073	5588	protein kinase C, theta
GO	ATP binding	78	1426	0.073	5702	proteasome (prosome, macropain) 26S subunit, ATPase, 3
GO	ATP binding	78	1426	0.073	57144	p21 protein (Cdc42/Rac)-activated kinase 7
GO	ATP binding	78	1426	0.073	5754	PTK7 protein tyrosine kinase 7
GO	ATP binding	78	1426	0.073	5889	RAD51 homolog C (S. cerevisiae)
GO	ATP binding	78	1426	0.073	59	actin, alpha 2, smooth muscle, aorta
GO	ATP binding	78	1426	0.073	5965	RecQ protein-like (DNA helicase Q1-like)
GO	ATP binding	78	1426	0.073	64080	ribokinase
GO	ATP binding	78	1426	0.073	641	Bloom syndrome, RecQ helicase-like
GO	ATP binding	78	1426	0.073	659	bone morphogenetic protein receptor, type II (serine/threonine kinase)
GO	ATP binding	78	1426	0.073	6683	spastin
GO	ATP binding	78	1426	0.073	6833	ATP-binding cassette, sub-family C (CFTR/MRP), member 8
GO	ATP binding	78	1426	0.073	70	actin, alpha, cardiac muscle 1
GO	ATP binding	78	1426	0.073	7010	TEK tyrosine kinase, endothelial
GO	ATP binding	78	1426	0.073	7046	transforming growth factor, beta receptor 1
GO	ATP binding	78	1426	0.073	7324	ubiquitin-conjugating enzyme E2E 1 (UBC4/5 homolog, yeast)
GO	ATP binding	78	1426	0.073	79646	pantothenate kinase 3
GO	ATP binding	78	1426	0.073	79677	structural maintenance of chromosomes 6
GO	ATP binding	78	1426	0.073	79710	MORC family CW-type zinc finger 4
GO	ATP binding	78	1426	0.073	84083	zinc finger, RAN-binding domain containing 3
GO	ATP binding	78	1426	0.073	84319	chromosome 3 open reading frame 26
GO	ATP binding	78	1426	0.073	8458	transcription termination factor, RNA polymerase II
GO	ATP binding	78	1426	0.073	8536	calcium/calmodulin-dependent protein kinase I
GO	ATP binding	78	1426	0.073	89797	neuron navigator 2
GO	ATP binding	78	1426	0.073	8997	kalirin, RhoGEF kinase
GO	ATP binding	78	1426	0.073	9262	serine/threonine kinase 17b
GO	ATP binding	78	1426	0.073	9448	mitogen-activated protein kinase kinase kinase kinase 4
GO	ATP binding	78	1426	0.073	953	ectonucleoside triphosphate diphosphohydrolase 1

GO	ATP binding	78	1426	0.073	9833	maternal embryonic leucine zipper kinase
GO	Ras GTPase activator activity	2	10	0.076	10788	IQ motif containing GTPase activating protein 2
GO	Ras GTPase activator activity	2	10	0.076	4763	neurofibromin 1
GO	substrate adhesion-dependent cell spre	2	10	0.076	11149	blood vessel epicardial substance
GO	substrate adhesion-dependent cell spre	2	10	0.076	84168	anthrax toxin receptor 1
GO	NAD binding	2	10	0.076	220	aldehyde dehydrogenase 1 family, member A3
GO	NAD binding	2	10	0.076	3248	hydroxyprostaglandin dehydrogenase 15-(NAD)
GO	general transcriptional repressor activit	2	10	0.076	29842	transcription factor CP2-like 1
GO	general transcriptional repressor activit	2	10	0.076	6672	SP100 nuclear antigen
GO	limb morphogenesis	2	10	0.076	344191	even-skipped homeobox 2
GO	limb morphogenesis	2	10	0.076	5125	proprotein convertase subtilisin/kexin type 5
GO	receptor internalization	2	10	0.076	409	arrestin, beta 2
GO	receptor internalization	2	10	0.076	4734	neural precursor cell expressed, developmentally down-regulated 4
GO	isotype switching	2	10	0.076	4292	mutL homolog 1, colon cancer, nonpolyposis type 2 (E. coli)
GO	isotype switching	2	10	0.076	4436	mutS homolog 2, colon cancer, nonpolyposis type 1 (E. coli)
GO	prefoldin complex	2	10	0.076	5203	prefoldin subunit 4
GO	prefoldin complex	2	10	0.076	8409	ubiquitously-expressed transcript
GO	ribosomal large subunit biogenesis	2	10	0.076	55759	WD repeat domain 12
GO	ribosomal large subunit biogenesis	2	10	0.076	6154	ribosomal protein L26
GO	vascular endothelial growth factor rece	2	10	0.076	6347	chemokine (C-C motif) ligand 2
GO	vascular endothelial growth factor rece	2	10	0.076	659	bone morphogenetic protein receptor, type II (serine/threonine kinase)
GO	G2/M transition DNA damage checkpoi	2	10	0.076	641	Bloom syndrome, RecQ helicase-like
GO	G2/M transition DNA damage checkpoi	2	10	0.076	672	breast cancer 1, early onset
GO	acetylglucosaminyltransferase activity	2	10	0.076	64131	xylosyltransferase I
GO	acetylglucosaminyltransferase activity	2	10	0.076	9215	like-glycosyltransferase
GO	caveola	5	49	0.076	10395	deleted in liver cancer 1
GO	caveola	5	49	0.076	2149	coagulation factor II (thrombin) receptor
GO	caveola	5	49	0.076	3778	potassium large conductance calcium-activated channel, subfamily M, alph
GO	caveola	5	49	0.076	6546	solute carrier family 8 (sodium/calcium exchanger), member 1
GO	caveola	5	49	0.076	659	bone morphogenetic protein receptor, type II (serine/threonine kinase)
GO	calcium ion binding	36	605	0.077	1000	cadherin 2, type 1, N-cadherin (neuronal)
GO	calcium ion binding	36	605	0.077	1002	cadherin 4, type 1, R-cadherin (retinal)
GO	calcium ion binding	36	605	0.077	1008	cadherin 10, type 2 (T2-cadherin)
GO	calcium ion binding	36	605	0.077	1047	calmegin
GO	calcium ion binding	36	605	0.077	10893	matrix metallopeptidase 24 (membrane-inserted)
GO	calcium ion binding	36	605	0.077	120114	FAT tumor suppressor homolog 3 (Drosophila)

GO	calcium ion binding	36	605	0.077	162494	rhomboid, veinlet-like 3 (Drosophila)
GO	calcium ion binding	36	605	0.077	1775	deoxyribonuclease I-like 2
GO	calcium ion binding	36	605	0.077	182	jagged 1 (Alagille syndrome)
GO	calcium ion binding	36	605	0.077	1830	desmoglein 3 (pemphigus vulgaris antigen)
GO	calcium ion binding	36	605	0.077	25780	RAS guanyl releasing protein 3 (calcium and DAG-regulated)
GO	calcium ion binding	36	605	0.077	27445	piccolo (presynaptic cytomatrix protein)
GO	calcium ion binding	36	605	0.077	309	annexin A6
GO	calcium ion binding	36	605	0.077	3936	lymphocyte cytosolic protein 1 (L-plastin)
GO	calcium ion binding	36	605	0.077	4052	latent transforming growth factor beta binding protein 1
GO	calcium ion binding	36	605	0.077	4312	matrix metallopeptidase 1 (interstitial collagenase)
GO	calcium ion binding	36	605	0.077	4319	matrix metallopeptidase 10 (stromelysin 2)
GO	calcium ion binding	36	605	0.077	4637	myosin, light chain 6, alkali, smooth muscle and non-muscle
GO	calcium ion binding	36	605	0.077	5101	protocadherin 9
GO	calcium ion binding	36	605	0.077	55012	protein phosphatase 2 (formerly 2A), regulatory subunit B'', gamma
GO	calcium ion binding	36	605	0.077	56104	protocadherin gamma subfamily B, 1
GO	calcium ion binding	36	605	0.077	56126	protocadherin beta 10
GO	calcium ion binding	36	605	0.077	56133	protocadherin beta 2
GO	calcium ion binding	36	605	0.077	5624	protein C (inactivator of coagulation factors Va and VIIIa)
GO	calcium ion binding	36	605	0.077	57333	reticulocalbin 3, EF-hand calcium binding domain
GO	calcium ion binding	36	605	0.077	57575	protocadherin 10
GO	calcium ion binding	36	605	0.077	6442	sarcoglycan, alpha (50kDa dystrophin-associated glycoprotein)
GO	calcium ion binding	36	605	0.077	6586	slit homolog 3 (Drosophila)
GO	calcium ion binding	36	605	0.077	667	dystonin
GO	calcium ion binding	36	605	0.077	6695	sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 1
GO	calcium ion binding	36	605	0.077	7058	thrombospondin 2
GO	calcium ion binding	36	605	0.077	7171	tropomyosin 4
GO	calcium ion binding	36	605	0.077	84206	mex-3 homolog B (C. elegans)
GO	calcium ion binding	36	605	0.077	8604	solute carrier family 25 (mitochondrial carrier, Aralar), member 12
GO	calcium ion binding	36	605	0.077	90141	chromosome 14 open reading frame 143
GO	calcium ion binding	36	605	0.077	92737	delta/notch-like EGF repeat containing
GO	circadian rhythm	4	35	0.078	3778	potassium large conductance calcium-activated channel, subfamily M, alph
GO	circadian rhythm	4	35	0.078	406	aryl hydrocarbon receptor nuclear translocator-like
GO	circadian rhythm	4	35	0.078	60675	prokineticin 2
GO	circadian rhythm	4	35	0.078	9420	cytochrome P450, family 7, subfamily B, polypeptide 1
GO	calcium-independent cell-cell adhesion	3	22	0.08	23562	claudin 14
GO	calcium-independent cell-cell adhesion	3	22	0.08	23705	cell adhesion molecule 1

GO	calcium-independent cell-cell adhesion	3	22	0.08	9076	claudin 1
GO	eating behavior	3	22	0.08	3952	leptin
GO	eating behavior	3	22	0.08	5021	oxytocin receptor
GO	eating behavior	3	22	0.08	5028	purinergic receptor P2Y, G-protein coupled, 1
GO	protein heterodimerization activity	14	199	0.081	10051	structural maintenance of chromosomes 4
GO	protein heterodimerization activity	14	199	0.081	10055	SUMO1 activating enzyme subunit 1
GO	protein heterodimerization activity	14	199	0.081	2027	enolase 3 (beta, muscle)
GO	protein heterodimerization activity	14	199	0.081	23590	prenyl (decaprenyl) diphosphate synthase, subunit 1
GO	protein heterodimerization activity	14	199	0.081	241	arachidonate 5-lipoxygenase-activating protein
GO	protein heterodimerization activity	14	199	0.081	332	baculoviral IAP repeat-containing 5
GO	protein heterodimerization activity	14	199	0.081	348	apolipoprotein E
GO	protein heterodimerization activity	14	199	0.081	3624	inhibin, beta A
GO	protein heterodimerization activity	14	199	0.081	3751	potassium voltage-gated channel, Shal-related subfamily, member 2
GO	protein heterodimerization activity	14	199	0.081	5228	placental growth factor
GO	protein heterodimerization activity	14	199	0.081	581	BCL2-associated X protein
GO	protein heterodimerization activity	14	199	0.081	666	BCL2-related ovarian killer
GO	protein heterodimerization activity	14	199	0.081	7046	transforming growth factor, beta receptor 1
GO	protein heterodimerization activity	14	199	0.081	83851	synaptotagmin XVI
GO	activation of caspase activity	5	50	0.081	10395	deleted in liver cancer 1
GO	activation of caspase activity	5	50	0.081	2149	coagulation factor II (thrombin) receptor
GO	activation of caspase activity	5	50	0.081	3336	heat shock 10kDa protein 1 (chaperonin 10)
GO	activation of caspase activity	5	50	0.081	3932	lymphocyte-specific protein tyrosine kinase
GO	activation of caspase activity	5	50	0.081	581	BCL2-associated X protein
GO	anterior/posterior pattern formation	7	81	0.082	1045	caudal type homeobox 2
GO	anterior/posterior pattern formation	7	81	0.082	3224	homeobox C8
GO	anterior/posterior pattern formation	7	81	0.082	3236	homeobox D10
GO	anterior/posterior pattern formation	7	81	0.082	3237	homeobox D11
GO	anterior/posterior pattern formation	7	81	0.082	5125	proprotein convertase subtilisin/kexin type 5
GO	anterior/posterior pattern formation	7	81	0.082	659	bone morphogenetic protein receptor, type II (serine/threonine kinase)
GO	anterior/posterior pattern formation	7	81	0.082	7046	transforming growth factor, beta receptor 1
GO	nervous system development	24	382	0.083	10612	tripartite motif-containing 3
GO	nervous system development	24	382	0.083	1136	cholinergic receptor, nicotinic, alpha 3
GO	nervous system development	24	382	0.083	182	jagged 1 (Alagille syndrome)
GO	nervous system development	24	382	0.083	266727	MAM domain containing glycosylphosphatidylinositol anchor 1
GO	nervous system development	24	382	0.083	29767	tropomodulin 2 (neuronal)
GO	nervous system development	24	382	0.083	3624	inhibin, beta A

GO	nervous system development	24	382	0.083	3975	LIM homeobox 1
GO	nervous system development	24	382	0.083	4287	ataxin 3
GO	nervous system development	24	382	0.083	4830	non-metastatic cells 1, protein (NM23A) expressed in
GO	nervous system development	24	382	0.083	5026	purinergic receptor P2X, ligand-gated ion channel, 5
GO	nervous system development	24	382	0.083	5264	phytanoyl-CoA 2-hydroxylase
GO	nervous system development	24	382	0.083	56133	protocadherin beta 2
GO	nervous system development	24	382	0.083	6474	short stature homeobox 2
GO	nervous system development	24	382	0.083	6586	slit homolog 3 (Drosophila)
GO	nervous system development	24	382	0.083	6683	spastin
GO	nervous system development	24	382	0.083	6695	sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 1
GO	nervous system development	24	382	0.083	7021	transcription factor AP-2 beta (activating enhancer binding protein 2 beta)
GO	nervous system development	24	382	0.083	8193	D4, zinc and double PHD fingers family 1
GO	nervous system development	24	382	0.083	8482	semaphorin 7A, GPI membrane anchor (John Milton Hagen blood group)
GO	nervous system development	24	382	0.083	8536	calcium/calmodulin-dependent protein kinase I
GO	nervous system development	24	382	0.083	89797	neuron navigator 2
GO	nervous system development	24	382	0.083	8997	kalirin, RhoGEF kinase
GO	nervous system development	24	382	0.083	91584	plexin A4
GO	nervous system development	24	382	0.083	9839	zinc finger E-box binding homeobox 2
GO	transporter activity	19	290	0.083	11154	adaptor-related protein complex 4, sigma 1 subunit
GO	transporter activity	19	290	0.083	116362	retinol binding protein 7, cellular
GO	transporter activity	19	290	0.083	1836	solute carrier family 26 (sulfate transporter), member 2
GO	transporter activity	19	290	0.083	2171	fatty acid binding protein 5 (psoriasis-associated)
GO	transporter activity	19	290	0.083	2172	fatty acid binding protein 6, ileal
GO	transporter activity	19	290	0.083	2558	gamma-aminobutyric acid (GABA) A receptor, alpha 5
GO	transporter activity	19	290	0.083	27445	piccolo (presynaptic cytomatrix protein)
GO	transporter activity	19	290	0.083	2906	glutamate receptor, ionotropic, N-methyl D-aspartate 2D
GO	transporter activity	19	290	0.083	4928	nucleoporin 98kDa
GO	transporter activity	19	290	0.083	516	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit C1 (subu
GO	transporter activity	19	290	0.083	528	ATPase, H+ transporting, lysosomal 42kDa, V1 subunit C1
GO	transporter activity	19	290	0.083	5947	retinol binding protein 1, cellular
GO	transporter activity	19	290	0.083	60386	solute carrier family 25 (mitochondrial thiamine pyrophosphate carrier), m
GO	transporter activity	19	290	0.083	6518	solute carrier family 2 (facilitated glucose/fructose transporter), member 5
GO	transporter activity	19	290	0.083	6527	solute carrier family 5 (low affinity glucose cotransporter), member 4
GO	transporter activity	19	290	0.083	6580	solute carrier family 22 (organic cation transporter), member 1
GO	transporter activity	19	290	0.083	729025	solute carrier family 15, member 5
GO	transporter activity	19	290	0.083	8604	solute carrier family 25 (mitochondrial carrier, Aralar), member 12

GO	transporter activity	19	290	0.083	9497	solute carrier family 4, sodium bicarbonate cotransporter, member 7
GO	somitogenesis	4	36	0.084	10512	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (
GO	somitogenesis	4	36	0.084	10683	delta-like 3 (Drosophila)
GO	somitogenesis	4	36	0.084	6422	secreted frizzled-related protein 1
GO	somitogenesis	4	36	0.084	9839	zinc finger E-box binding homeobox 2
GO	DNA-directed RNA polymerase activity	4	36	0.084	10622	polymerase (RNA) III (DNA directed) polypeptide G (32kD)
GO	DNA-directed RNA polymerase activity	4	36	0.084	25885	polymerase (RNA) I polypeptide A, 194kDa
GO	DNA-directed RNA polymerase activity	4	36	0.084	5440	polymerase (RNA) II (DNA directed) polypeptide K, 7.0kDa
GO	DNA-directed RNA polymerase activity	4	36	0.084	84172	polymerase (RNA) I polypeptide B, 128kDa
GO	odontogenesis of dentine-containing to	4	36	0.084	1746	distal-less homeobox 2
GO	odontogenesis of dentine-containing to	4	36	0.084	2736	GLI family zinc finger 2
GO	odontogenesis of dentine-containing to	4	36	0.084	431707	LIM homeobox 8
GO	odontogenesis of dentine-containing to	4	36	0.084	8626	tumor protein p63
GO	lipid transport	6	66	0.085	114880	oxysterol binding protein-like 6
GO	lipid transport	6	66	0.085	26154	ATP-binding cassette, sub-family A (ABC1), member 12
GO	lipid transport	6	66	0.085	26207	phosphatidylinositol transfer protein, cytoplasmic 1
GO	lipid transport	6	66	0.085	348	apolipoprotein E
GO	lipid transport	6	66	0.085	5360	phospholipid transfer protein
GO	lipid transport	6	66	0.085	79135	apolipoprotein O
GO	synapse	17	255	0.086	1000	cadherin 2, type 1, N-cadherin (neuronal)
GO	synapse	17	255	0.086	1136	cholinergic receptor, nicotinic, alpha 3
GO	synapse	17	255	0.086	1138	cholinergic receptor, nicotinic, alpha 5
GO	synapse	17	255	0.086	200959	gamma-aminobutyric acid (GABA) receptor, rho 3
GO	synapse	17	255	0.086	23705	cell adhesion molecule 1
GO	synapse	17	255	0.086	2558	gamma-aminobutyric acid (GABA) A receptor, alpha 5
GO	synapse	17	255	0.086	26059	ELKS/RAB6-interacting/CAST family member 2
GO	synapse	17	255	0.086	26999	cytoplasmic FMR1 interacting protein 2
GO	synapse	17	255	0.086	27445	piccolo (presynaptic cytomatrix protein)
GO	synapse	17	255	0.086	2898	glutamate receptor, ionotropic, kainate 2
GO	synapse	17	255	0.086	2906	glutamate receptor, ionotropic, N-methyl D-aspartate 2D
GO	synapse	17	255	0.086	30011	SH3-domain kinase binding protein 1
GO	synapse	17	255	0.086	55752	septin 11
GO	synapse	17	255	0.086	8777	multiple PDZ domain protein
GO	synapse	17	255	0.086	9419	cysteine-rich PDZ-binding protein
GO	synapse	17	255	0.086	9455	homer homolog 2 (Drosophila)
GO	synapse	17	255	0.086	9568	gamma-aminobutyric acid (GABA) B receptor, 2

GO	negative regulation of neuron apoptosis	5	51	0.087	2149	coagulation factor II (thrombin) receptor
GO	negative regulation of neuron apoptosis	5	51	0.087	2898	glutamate receptor, ionotropic, kainate 2
GO	negative regulation of neuron apoptosis	5	51	0.087	4436	mutS homolog 2, colon cancer, nonpolyposis type 1 (E. coli)
GO	negative regulation of neuron apoptosis	5	51	0.087	4893	neuroblastoma RAS viral (v-ras) oncogene homolog
GO	negative regulation of neuron apoptosis	5	51	0.087	773	calcium channel, voltage-dependent, P/Q type, alpha 1A subunit
GO	ATP-dependent DNA helicase activity	3	23	0.089	1763	DNA replication helicase 2 homolog (yeast)
GO	ATP-dependent DNA helicase activity	3	23	0.089	5965	RecQ protein-like (DNA helicase Q1-like)
GO	ATP-dependent DNA helicase activity	3	23	0.089	641	Bloom syndrome, RecQ helicase-like
GO	activation of MAPKK activity	3	23	0.089	2149	coagulation factor II (thrombin) receptor
GO	activation of MAPKK activity	3	23	0.089	2321	fms-related tyrosine kinase 1 (vascular endothelial growth factor/vascular
GO	activation of MAPKK activity	3	23	0.089	7046	transforming growth factor, beta receptor 1
GO	negative regulation of cell adhesion	3	23	0.089	27289	Rho family GTPase 1
GO	negative regulation of cell adhesion	3	23	0.089	5140	phosphodiesterase 3B, cGMP-inhibited
GO	negative regulation of cell adhesion	3	23	0.089	5420	podocalyxin-like
GO	developmental growth	3	23	0.089	2736	GLI family zinc finger 2
GO	developmental growth	3	23	0.089	3237	homeobox D11
GO	developmental growth	3	23	0.089	7840	Alstrom syndrome 1
GO	nuclear chromosome	3	23	0.089	332	baculoviral IAP repeat-containing 5
GO	nuclear chromosome	3	23	0.089	54984	PIN2-interacting protein 1
GO	nuclear chromosome	3	23	0.089	642636	RAD21-like 1 (S. pombe)
GO	somatic stem cell maintenance	2	11	0.09	1045	caudal type homeobox 2
GO	somatic stem cell maintenance	2	11	0.09	6657	SRY (sex determining region Y)-box 2
GO	GTPase inhibitor activity	2	11	0.09	10788	IQ motif containing GTPase activating protein 2
GO	GTPase inhibitor activity	2	11	0.09	6242	rhotekin
GO	glycosaminoglycan biosynthetic process	2	11	0.09	11227	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminylt
GO	glycosaminoglycan biosynthetic process	2	11	0.09	64131	xylosyltransferase I
GO	mitotic metaphase plate congression	2	11	0.09	113130	cell division cycle associated 5
GO	mitotic metaphase plate congression	2	11	0.09	54984	PIN2-interacting protein 1
GO	retinol binding	2	11	0.09	116362	retinol binding protein 7, cellular
GO	retinol binding	2	11	0.09	5947	retinol binding protein 1, cellular
GO	platelet-derived growth factor binding	2	11	0.09	1282	collagen, type IV, alpha 1
GO	platelet-derived growth factor binding	2	11	0.09	1289	collagen, type V, alpha 1
GO	fibroblast growth factor binding	2	11	0.09	143282	fibroblast growth factor binding protein 3
GO	fibroblast growth factor binding	2	11	0.09	2264	fibroblast growth factor receptor 4
GO	chylomicron	2	11	0.09	341	apolipoprotein C-I
GO	chylomicron	2	11	0.09	348	apolipoprotein E

GO	negative regulation of lipid catabolic pr	2	11	0.09	341	apolipoprotein C-I
GO	negative regulation of lipid catabolic pr	2	11	0.09	5140	phosphodiesterase 3B, cGMP-inhibited
GO	vasodilation	2	11	0.09	348	apolipoprotein E
GO	vasodilation	2	11	0.09	3778	potassium large conductance calcium-activated channel, subfamily M, alph
GO	3',5'-cyclic-nucleotide phosphodiesteras	2	11	0.09	50940	phosphodiesterase 11A
GO	3',5'-cyclic-nucleotide phosphodiesteras	2	11	0.09	5140	phosphodiesterase 3B, cGMP-inhibited
GO	large ribosomal subunit	2	11	0.09	51121	ribosomal protein L26-like 1
GO	large ribosomal subunit	2	11	0.09	65008	mitochondrial ribosomal protein L1
GO	dipeptidase activity	2	11	0.09	5184	peptidase D
GO	dipeptidase activity	2	11	0.09	9805	secernin 1
GO	phosphatidylinositol-3,4-bisphosphate b	2	11	0.09	5341	pleckstrin
GO	phosphatidylinositol-3,4-bisphosphate b	2	11	0.09	55803	ArfGAP with dual PH domains 2
GO	replication fork	2	11	0.09	56852	RAD18 homolog (S. cerevisiae)
GO	replication fork	2	11	0.09	641	Bloom syndrome, RecQ helicase-like
GO	ubiquitin activating enzyme activity	1	2	0.091	10055	SUMO1 activating enzyme subunit 1
GO	C21-steroid hormone metabolic process	1	2	0.091	10202	dehydrogenase/reductase (SDR family) member 2
GO	cardiac right ventricle morphogenesis	1	2	0.091	10512	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (
GO	pulmonary myocardium development	1	2	0.091	10512	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (
GO	semaphorin receptor binding	1	2	0.091	10512	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (
GO	activation of phospholipase D activity	1	2	0.091	10672	guanine nucleotide binding protein (G protein), alpha 13
GO	tRNA (guanine-N7-)-methyltransferase a	1	2	0.091	10785	WD repeat domain 4
GO	ADP-sugar diphosphatase activity	1	2	0.091	11164	nudix (nucleoside diphosphate linked moiety X)-type motif 5
GO	Rab-protein geranylgeranyltransferase c	1	2	0.091	1121	choroideremia (Rab escort protein 1)
GO	regulation of cellular component organi	1	2	0.091	1289	collagen, type V, alpha 1
GO	deacetylase activity	1	2	0.091	13	arylacetamide deacetylase (esterase)
GO	collagen type XI	1	2	0.091	1301	collagen, type XI, alpha 1
GO	cytoplasmic transport	1	2	0.091	135295	splicing factor, arginine/serine-rich 13B
GO	radial glia guided migration of Purkinje c	1	2	0.091	1496	catenin (cadherin-associated protein), alpha 2
GO	regulation of synapse structural plasticit	1	2	0.091	1496	catenin (cadherin-associated protein), alpha 2
GO	CTP synthase activity	1	2	0.091	1503	CTP synthase
GO	demethylase activity	1	2	0.091	1543	cytochrome P450, family 1, subfamily A, polypeptide 1
GO	developmental process	1	2	0.091	1543	cytochrome P450, family 1, subfamily A, polypeptide 1
GO	vitamin D 24-hydroxylase activity	1	2	0.091	1543	cytochrome P450, family 1, subfamily A, polypeptide 1
GO	benzodiazepine receptor binding	1	2	0.091	1622	diazepam binding inhibitor (GABA receptor modulator, acyl-Coenzyme A bi
GO	cerebral cortex GABAergic interneuron	1	2	0.091	1746	distal-less homeobox 2
GO	regulation of transcription from RNA po	1	2	0.091	1746	distal-less homeobox 2

GO	gamma DNA polymerase complex	1	2	0.091	1763	DNA replication helicase 2 homolog (yeast)
GO	tRNA (cytosine-5-)-methyltransferase a	1	2	0.091	1787	tRNA aspartic acid methyltransferase 1
GO	DNA (cytosine-5-)-methyltransferase ac	1	2	0.091	1788	DNA (cytosine-5-)-methyltransferase 3 alpha
GO	DNA methylation on cytosine within a C	1	2	0.091	1788	DNA (cytosine-5-)-methyltransferase 3 alpha
GO	annulate lamellae	1	2	0.091	1984	eukaryotic translation initiation factor 5A
GO	PH domain binding	1	2	0.091	2037	erythrocyte membrane protein band 4.1-like 2
GO	glucuronyl-galactosyl-proteoglycan 4-al	1	2	0.091	2135	exostoses (multiple)-like 2
GO	establishment of synaptic specificity at	1	2	0.091	2149	coagulation factor II (thrombin) receptor
GO	platelet dense tubular network	1	2	0.091	2149	coagulation factor II (thrombin) receptor
GO	olfactory pit development	1	2	0.091	220	aldehyde dehydrogenase 1 family, member A3
GO	retinoic acid biosynthetic process	1	2	0.091	220	aldehyde dehydrogenase 1 family, member A3
GO	de novo' protein folding	1	2	0.091	2281	FK506 binding protein 1B, 12.6 kDa
GO	negative regulation of protein phosphat	1	2	0.091	2281	FK506 binding protein 1B, 12.6 kDa
GO	regulation of cardiac muscle contractio	1	2	0.091	2281	FK506 binding protein 1B, 12.6 kDa
GO	release of sequestered calcium ion into	1	2	0.091	2281	FK506 binding protein 1B, 12.6 kDa
GO	pentose-phosphate shunt, non-oxidativ	1	2	0.091	22934	ribose 5-phosphate isomerase A
GO	glycerol-3-phosphate catabolic process	1	2	0.091	23171	glycerol-3-phosphate dehydrogenase 1-like
GO	negative regulation of actin filament po	1	2	0.091	23189	KN motif and ankyrin repeat domains 1
GO	positive regulation of plasma membran	1	2	0.091	23305	acyl-CoA synthetase long-chain family member 6
GO	trans-hexaprenyltranstransferase activit	1	2	0.091	23590	prenyl (decaprenyl) diphosphate synthase, subunit 1
GO	trans-octaprenyltranstransferase activit	1	2	0.091	23590	prenyl (decaprenyl) diphosphate synthase, subunit 1
GO	detection of stimulus	1	2	0.091	23705	cell adhesion molecule 1
GO	T cell mediated cytotoxicity	1	2	0.091	23705	cell adhesion molecule 1
GO	arachidonate 5-lipoxygenase activity	1	2	0.091	241	arachidonate 5-lipoxygenase-activating protein
GO	hydroxyacylglutathione hydrolase activi	1	2	0.091	25953	paroxysmal nonkinesigenic dyskinesia
GO	carbon-carbon lyase activity	1	2	0.091	26061	2-hydroxyacyl-CoA lyase 1
GO	creatine biosynthetic process	1	2	0.091	2628	glycine amidinotransferase (L-arginine:glycine amidinotransferase)
GO	glycine cleavage complex	1	2	0.091	2653	glycine cleavage system protein H (aminomethyl carrier)
GO	notochord regression	1	2	0.091	2736	GLI family zinc finger 2
GO	smoothened signaling pathway involve	1	2	0.091	2736	GLI family zinc finger 2
GO	smoothened signaling pathway involve	1	2	0.091	2736	GLI family zinc finger 2
GO	specification of segmental identity, max	1	2	0.091	2736	GLI family zinc finger 2
GO	spinal cord ventral commissure morpho	1	2	0.091	2736	GLI family zinc finger 2
GO	response to lipid hydroperoxide	1	2	0.091	2878	glutathione peroxidase 3 (plasma)
GO	kainate selective glutamate receptor co	1	2	0.091	2898	glutamate receptor, ionotropic, kainate 2
GO	voltage-gated cation channel activity	1	2	0.091	2906	glutamate receptor, ionotropic, N-methyl D-aspartate 2D

GO	cytoplasm organization	1	2	0.091	29842	transcription factor CP2-like 1
GO	positive regulation of growth	1	2	0.091	29842	transcription factor CP2-like 1
GO	dermatan sulfate biosynthetic process	1	2	0.091	29940	dermatan sulfate epimerase
GO	hydroxymethylglutaryl-CoA synthase ac	1	2	0.091	3157	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 (soluble)
GO	positive regulation of cell development	1	2	0.091	3237	homeobox D11
GO	15-hydroxyprostaglandin dehydrogenas	1	2	0.091	3248	hydroxyprostaglandin dehydrogenase 15-(NAD)
GO	N-methyltransferase activity	1	2	0.091	3276	protein arginine methyltransferase 1
GO	establishment of chromosome localizati	1	2	0.091	332	baculoviral IAP repeat-containing 5
GO	follistatin binding	1	2	0.091	3624	inhibin, beta A
GO	inhibin A complex	1	2	0.091	3624	inhibin, beta A
GO	negative regulation of lipoprotein metal	1	2	0.091	3685	integrin, alpha V (vitronectin receptor, alpha polypeptide, antigen CD51)
GO	neuronal cell body membrane	1	2	0.091	3763	potassium inwardly-rectifying channel, subfamily J, member 6
GO	smooth muscle contraction involved in	1	2	0.091	3778	potassium large conductance calcium-activated channel, subfamily M, alph
GO	M phase specific microtubule process	1	2	0.091	3838	karyopherin alpha 2 (RAG cohort 1, importin alpha 1)
GO	CD4 receptor binding	1	2	0.091	3932	lymphocyte-specific protein tyrosine kinase
GO	leptin-mediated signaling pathway	1	2	0.091	3952	leptin
GO	cerebellar Purkinje cell-granule cell prec	1	2	0.091	3975	LIM homeobox 1
GO	ectoderm formation	1	2	0.091	3975	LIM homeobox 1
GO	forebrain regionalization	1	2	0.091	3975	LIM homeobox 1
GO	head development	1	2	0.091	3975	LIM homeobox 1
GO	angiotensin receptor binding	1	2	0.091	409	arrestin, beta 2
GO	N-acetylgalactosamine-4-sulfatase activ	1	2	0.091	411	arylsulfatase B
GO	chiasma	1	2	0.091	4292	mutL homolog 1, colon cancer, nonpolyposis type 2 (E. coli)
GO	MutLalpha complex	1	2	0.091	4292	mutL homolog 1, colon cancer, nonpolyposis type 2 (E. coli)
GO	B cell mediated immunity	1	2	0.091	4436	mutS homolog 2, colon cancer, nonpolyposis type 1 (E. coli)
GO	dinucleotide repeat insertion binding	1	2	0.091	4436	mutS homolog 2, colon cancer, nonpolyposis type 1 (E. coli)
GO	MutSalpha complex	1	2	0.091	4436	mutS homolog 2, colon cancer, nonpolyposis type 1 (E. coli)
GO	MutSbeta complex	1	2	0.091	4436	mutS homolog 2, colon cancer, nonpolyposis type 1 (E. coli)
GO	single thymine insertion binding	1	2	0.091	4436	mutS homolog 2, colon cancer, nonpolyposis type 1 (E. coli)
GO	beta-2 adrenergic receptor binding	1	2	0.091	4734	neural precursor cell expressed, developmentally down-regulated 4
GO	phosphothreonine binding	1	2	0.091	4734	neural precursor cell expressed, developmentally down-regulated 4
GO	regulation of Ras GTPase activity	1	2	0.091	4763	neurofibromin 1
GO	Schwann cell development	1	2	0.091	4763	neurofibromin 1
GO	hydrogen:potassium-exchanging ATPase	1	2	0.091	479	ATPase, H+/K+ transporting, nongastric, alpha polypeptide
GO	protein import into nucleus, docking	1	2	0.091	4928	nucleoporin 98kDa
GO	regulation of fibroblast growth factor re	1	2	0.091	5015	orthodenticle homeobox 2

GO	regulation of digestive system process	1	2	0.091	5021	oxytocin receptor
GO	response to anoxia	1	2	0.091	5021	oxytocin receptor
GO	negative regulation of norepinephrine s	1	2	0.091	5028	purinergic receptor P2Y, G-protein coupled, 1
GO	UDP-activated nucleotide receptor activ	1	2	0.091	5031	pyrimidinergic receptor P2Y, G-protein coupled, 6
GO	chronological cell aging	1	2	0.091	5054	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor t
GO	viral assembly, maturation, egress, and	1	2	0.091	5125	proprotein convertase subtilisin/kexin type 5
GO	cGMP-inhibited cyclic-nucleotide phosp	1	2	0.091	5140	phosphodiesterase 3B, cGMP-inhibited
GO	regulation of morphogenesis of a branc	1	2	0.091	5228	placental growth factor
GO	negative regulation of calcium-mediate	1	2	0.091	5341	pleckstrin
GO	platelet degranulation	1	2	0.091	5341	pleckstrin
GO	positive regulation of actin filament de	1	2	0.091	5341	pleckstrin
GO	positive regulation of integrin activatio	1	2	0.091	5341	pleckstrin
GO	thrombin receptor signaling pathway	1	2	0.091	5341	pleckstrin
GO	calcium-dependent cell-matrix adhesio	1	2	0.091	54822	transient receptor potential cation channel, subfamily M, member 7
GO	telomeric RNA binding	1	2	0.091	54984	PIN2-interacting protein 1
GO	drug transmembrane transport	1	2	0.091	55244	solute carrier family 47, member 1
GO	oleoyl-[acyl-carrier-protein] hydrolase a	1	2	0.091	55301	oleoyl-ACP hydrolase
GO	dosage compensation	1	2	0.091	55506	H2A histone family, member Y2
GO	N-acylmannosamine kinase activity	1	2	0.091	55577	N-acetylglucosamine kinase
GO	maturation of 5.8S rRNA from tricistron	1	2	0.091	55759	WD repeat domain 12
GO	preribosome, large subunit precursor	1	2	0.091	55759	WD repeat domain 12
GO	mRNA (2'-O-methyladenosine-N6-)-met	1	2	0.091	56339	methyltransferase like 3
GO	interleukin-2 secretion	1	2	0.091	57678	glycerol-3-phosphate acyltransferase, mitochondrial
GO	BH3 domain binding	1	2	0.091	581	BCL2-associated X protein
GO	establishment or maintenance of trans	1	2	0.091	581	BCL2-associated X protein
GO	mitochondrial fragmentation involved i	1	2	0.091	581	BCL2-associated X protein
GO	nuclear fragmentation involved in apop	1	2	0.091	581	BCL2-associated X protein
GO	branched chain family amino acid biosy	1	2	0.091	586	branched chain aminotransferase 1, cytosolic
GO	branched-chain-amino-acid transamina	1	2	0.091	586	branched chain aminotransferase 1, cytosolic
GO	crossover junction endodeoxyribonucle	1	2	0.091	5889	RAD51 homolog C (S. cerevisiae)
GO	female meiosis sister chromatid cohesi	1	2	0.091	5889	RAD51 homolog C (S. cerevisiae)
GO	acetylcholinesterase activity	1	2	0.091	590	butyrylcholinesterase
GO	response to alkaloid	1	2	0.091	590	butyrylcholinesterase
GO	DNA strand renaturation	1	2	0.091	5965	RecQ protein-like (DNA helicase Q1-like)
GO	class I ribonucleotide reductase activity	1	2	0.091	6241	ribonucleotide reductase M2
GO	deoxyribonucleoside diphosphate meta	1	2	0.091	6241	ribonucleotide reductase M2

GO	olfactory bulb interneuron differentiatic	1	2	0.091	6299	sal-like 1 (Drosophila)
GO	olfactory nerve development	1	2	0.091	6299	sal-like 1 (Drosophila)
GO	regulation of vascular endothelial growt	1	2	0.091	6347	chemokine (C-C motif) ligand 2
GO	response to vitamin B3	1	2	0.091	6347	chemokine (C-C motif) ligand 2
GO	alpha-beta T cell differentiation	1	2	0.091	641	Bloom syndrome, RecQ helicase-like
GO	four-way junction helicase activity	1	2	0.091	641	Bloom syndrome, RecQ helicase-like
GO	replication fork processing	1	2	0.091	641	Bloom syndrome, RecQ helicase-like
GO	negative regulation of axon regeneratio	1	2	0.091	64131	xylosyltransferase I
GO	protein xylosyltransferase activity	1	2	0.091	64131	xylosyltransferase I
GO	fructose transmembrane transporter ac	1	2	0.091	6518	solute carrier family 2 (facilitated glucose/fructose transporter), member 5
GO	fructose transport	1	2	0.091	6518	solute carrier family 2 (facilitated glucose/fructose transporter), member 5
GO	cytosolic calcium ion transport	1	2	0.091	6546	solute carrier family 8 (sodium/calcium exchanger), member 1
GO	negative regulation of vasoconstriction	1	2	0.091	659	bone morphogenetic protein receptor, type II (serine/threonine kinase)
GO	negative regulation of viral transcriptior	1	2	0.091	6672	SP100 nuclear antigen
GO	nuclear periphery	1	2	0.091	6672	SP100 nuclear antigen
GO	cytokinesis, completion of separation	1	2	0.091	6683	spastin
GO	protein hexamerization	1	2	0.091	6683	spastin
GO	2,3-bisphospho-D-glycerate 2-phosphoh	1	2	0.091	669	2,3-bisphosphoglycerate mutase
GO	bisphosphoglycerate mutase activity	1	2	0.091	669	2,3-bisphosphoglycerate mutase
GO	phosphoglycerate mutase activity	1	2	0.091	669	2,3-bisphosphoglycerate mutase
GO	cuticular plate	1	2	0.091	6711	spectrin, beta, non-erythrocytic 1
GO	BRCA1-BARD1 complex	1	2	0.091	672	breast cancer 1, early onset
GO	alcohol sulfotransferase activity	1	2	0.091	6820	sulfotransferase family, cytosolic, 2B, member 1
GO	steroid sulfotransferase activity	1	2	0.091	6820	sulfotransferase family, cytosolic, 2B, member 1
GO	sulfonylurea receptor activity	1	2	0.091	6833	ATP-binding cassette, sub-family C (CFTR/MRP), member 8
GO	transferrin receptor activity	1	2	0.091	7037	transferrin receptor (p90, CD71)
GO	negative regulation of endothelial cell d	1	2	0.091	7046	transforming growth factor, beta receptor 1
GO	ISG15 ligase activity	1	2	0.091	7324	ubiquitin-conjugating enzyme E2E 1 (UBC4/5 homolog, yeast)
GO	musculoskeletal movement, spinal refle	1	2	0.091	773	calcium channel, voltage-dependent, P/Q type, alpha 1A subunit
GO	sulfur amino acid metabolic process	1	2	0.091	773	calcium channel, voltage-dependent, P/Q type, alpha 1A subunit
GO	regulation of fat cell differentiation	1	2	0.091	7840	Alstrom syndrome 1
GO	labyrinthine layer morphogenesis	1	2	0.091	80712	ESX homeobox 1
GO	carbohydrate mediated signaling	1	2	0.091	81035	collectin sub-family member 12
GO	beta-galactoside alpha-2,6-sialyltransfe	1	2	0.091	84620	ST6 beta-galactosamide alpha-2,6-sialyltranferase 2
GO	chromatin silencing at telomere	1	2	0.091	8520	histone acetyltransferase 1
GO	internal protein amino acid acetylation	1	2	0.091	8520	histone acetyltransferase 1

GO	cloacal septation	1	2	0.091	8626	tumor protein p63
GO	female genitalia morphogenesis	1	2	0.091	8626	tumor protein p63
GO	rough microsome	1	2	0.091	8626	tumor protein p63
GO	proline metabolic process	1	2	0.091	8659	aldehyde dehydrogenase 4 family, member A1
GO	JAK pathway signal transduction adapto	1	2	0.091	8835	suppressor of cytokine signaling 2
GO	prolactin receptor binding	1	2	0.091	8835	suppressor of cytokine signaling 2
GO	male pronucleus	1	2	0.091	890	cyclin A2
GO	antral ovarian follicle growth	1	2	0.091	898	cyclin E1
GO	response to purine	1	2	0.091	898	cyclin E1
GO	cell-substrate adherens junction	1	2	0.091	91624	nexilin (F actin binding protein)
GO	D-amino acid catabolic process	1	2	0.091	92675	D-tyrosyl-tRNA deacylase 1 homolog (S. cerevisiae)
GO	oxysterol 7-alpha-hydroxylase activity	1	2	0.091	9420	cytochrome P450, family 7, subfamily B, polypeptide 1
GO	GKAP/Homer scaffold activity	1	2	0.091	9455	homer homolog 2 (Drosophila)
GO	acylphosphatase activity	1	2	0.091	97	acylphosphatase 1, erythrocyte (common) type
GO	stereocilium bundle	1	2	0.091	9732	dedicator of cytokinesis 4
GO	phosphatase regulator activity	1	2	0.091	9839	zinc finger E-box binding homeobox 2
GO	central nervous system development	8	100	0.093	10683	delta-like 3 (Drosophila)
GO	central nervous system development	8	100	0.093	27330	ribosomal protein S6 kinase, 90kDa, polypeptide 6
GO	central nervous system development	8	100	0.093	411	arylsulfatase B
GO	central nervous system development	8	100	0.093	4884	neuronal pentraxin I
GO	central nervous system development	8	100	0.093	4897	neuronal cell adhesion molecule
GO	central nervous system development	8	100	0.093	7078	TIMP metallopeptidase inhibitor 3
GO	central nervous system development	8	100	0.093	92737	delta/notch-like EGF repeat containing
GO	central nervous system development	8	100	0.093	9839	zinc finger E-box binding homeobox 2
GO	protein domain specific binding	9	117	0.094	10474	transcriptional adaptor 3
GO	protein domain specific binding	9	117	0.094	4291	myeloid leukemia factor 1
GO	protein domain specific binding	9	117	0.094	4734	neural precursor cell expressed, developmentally down-regulated 4
GO	protein domain specific binding	9	117	0.094	6672	SP100 nuclear antigen
GO	protein domain specific binding	9	117	0.094	7029	transcription factor Dp-2 (E2F dimerization partner 2)
GO	protein domain specific binding	9	117	0.094	7137	troponin I type 3 (cardiac)
GO	protein domain specific binding	9	117	0.094	7846	tubulin, alpha 1a
GO	protein domain specific binding	9	117	0.094	8626	tumor protein p63
GO	protein domain specific binding	9	117	0.094	9419	cysteine-rich PDZ-binding protein
GO	ubiquitin thiolesterase activity	6	68	0.095	10213	proteasome (prosome, macropain) 26S subunit, non-ATPase, 14
GO	ubiquitin thiolesterase activity	6	68	0.095	373856	ubiquitin specific peptidase 41
GO	ubiquitin thiolesterase activity	6	68	0.095	4287	ataxin 3

GO	ubiquitin thiolesterase activity	6	68	0.095	57478	ubiquitin specific peptidase 31
GO	ubiquitin thiolesterase activity	6	68	0.095	7347	ubiquitin carboxyl-terminal esterase L3 (ubiquitin thiolesterase)
GO	ubiquitin thiolesterase activity	6	68	0.095	84101	ubiquitin specific peptidase 44
GO	calcium-dependent cell-cell adhesion	3	24	0.098	1000	cadherin 2, type 1, N-cadherin (neuronal)
GO	calcium-dependent cell-cell adhesion	3	24	0.098	56126	protocadherin beta 10
GO	calcium-dependent cell-cell adhesion	3	24	0.098	56133	protocadherin beta 2
GO	platelet activation	3	24	0.098	10672	guanine nucleotide binding protein (G protein), alpha 13
GO	platelet activation	3	24	0.098	2149	coagulation factor II (thrombin) receptor
GO	platelet activation	3	24	0.098	3589	interleukin 11
GO	regulation of membrane potential	3	24	0.098	1136	cholinergic receptor, nicotinic, alpha 3
GO	regulation of membrane potential	3	24	0.098	2898	glutamate receptor, ionotropic, kainate 2
GO	regulation of membrane potential	3	24	0.098	3778	potassium large conductance calcium-activated channel, subfamily M, alph
GO	neuromuscular junction	3	24	0.098	2045	EPH receptor A7
GO	neuromuscular junction	3	24	0.098	2149	coagulation factor II (thrombin) receptor
GO	neuromuscular junction	3	24	0.098	5588	protein kinase C, theta
GO	response to progesterone stimulus	3	24	0.098	5021	oxytocin receptor
GO	response to progesterone stimulus	3	24	0.098	6347	chemokine (C-C motif) ligand 2
GO	response to progesterone stimulus	3	24	0.098	898	cyclin E1
GO	negative regulation of cell migration	4	38	0.098	10395	deleted in liver cancer 1
GO	negative regulation of cell migration	4	38	0.098	4763	neurofibromin 1
GO	negative regulation of cell migration	4	38	0.098	5054	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor t
GO	negative regulation of cell migration	4	38	0.098	7168	tropomyosin 1 (alpha)
GO	spliceosomal complex	9	118	0.098	10189	THO complex 4
GO	spliceosomal complex	9	118	0.098	10465	peptidylprolyl isomerase H (cyclophilin H)
GO	spliceosomal complex	9	118	0.098	10492	synaptotagmin binding, cytoplasmic RNA interacting protein
GO	spliceosomal complex	9	118	0.098	27258	LSM3 homolog, U6 small nuclear RNA associated (S. cerevisiae)
GO	spliceosomal complex	9	118	0.098	3183	heterogeneous nuclear ribonucleoprotein C (C1/C2)
GO	spliceosomal complex	9	118	0.098	51645	peptidylprolyl isomerase (cyclophilin)-like 1
GO	spliceosomal complex	9	118	0.098	6637	small nuclear ribonucleoprotein polypeptide G
GO	spliceosomal complex	9	118	0.098	79833	gem (nuclear organelle) associated protein 6
GO	spliceosomal complex	9	118	0.098	8458	transcription termination factor, RNA polymerase II
GO	nucleotide binding	98	1859	0.099	10000	v-akt murine thymoma viral oncogene homolog 3 (protein kinase B, gamma
GO	nucleotide binding	98	1859	0.099	10051	structural maintenance of chromosomes 4
GO	nucleotide binding	98	1859	0.099	10056	phenylalanyl-tRNA synthetase, beta subunit
GO	nucleotide binding	98	1859	0.099	10096	ARP3 actin-related protein 3 homolog (yeast)
GO	nucleotide binding	98	1859	0.099	10097	ARP2 actin-related protein 2 homolog (yeast)

GO	nucleotide binding	98	1859	0.099	10123	ADP-ribosylation factor-like 4C
GO	nucleotide binding	98	1859	0.099	10189	THO complex 4
GO	nucleotide binding	98	1859	0.099	10212	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39
GO	nucleotide binding	98	1859	0.099	10492	synaptotagmin binding, cytoplasmic RNA interacting protein
GO	nucleotide binding	98	1859	0.099	10672	guanine nucleotide binding protein (G protein), alpha 13
GO	nucleotide binding	98	1859	0.099	10808	heat shock 105kDa/110kDa protein 1
GO	nucleotide binding	98	1859	0.099	10890	RAB10, member RAS oncogene family
GO	nucleotide binding	98	1859	0.099	11056	DEAD (Asp-Glu-Ala-Asp) box polypeptide 52
GO	nucleotide binding	98	1859	0.099	121268	Ras homolog enriched in brain like 1
GO	nucleotide binding	98	1859	0.099	124540	musashi homolog 2 (Drosophila)
GO	nucleotide binding	98	1859	0.099	132158	glycerate kinase
GO	nucleotide binding	98	1859	0.099	132430	poly(A) binding protein, cytoplasmic 4-like
GO	nucleotide binding	98	1859	0.099	135295	splicing factor, arginine/serine-rich 13B
GO	nucleotide binding	98	1859	0.099	140739	ubiquitin-conjugating enzyme E2F (putative)
GO	nucleotide binding	98	1859	0.099	1503	CTP synthase
GO	nucleotide binding	98	1859	0.099	1716	deoxyguanosine kinase
GO	nucleotide binding	98	1859	0.099	1763	DNA replication helicase 2 homolog (yeast)
GO	nucleotide binding	98	1859	0.099	1841	deoxythymidylate kinase (thymidylate kinase)
GO	nucleotide binding	98	1859	0.099	1983	eukaryotic translation initiation factor 5
GO	nucleotide binding	98	1859	0.099	201299	RAD52 motif 1
GO	nucleotide binding	98	1859	0.099	203	adenylate kinase 1
GO	nucleotide binding	98	1859	0.099	2045	EPH receptor A7
GO	nucleotide binding	98	1859	0.099	2242	feline sarcoma oncogene
GO	nucleotide binding	98	1859	0.099	2264	fibroblast growth factor receptor 4
GO	nucleotide binding	98	1859	0.099	23057	nicotinamide nucleotide adenylyltransferase 2
GO	nucleotide binding	98	1859	0.099	23157	septin 6
GO	nucleotide binding	98	1859	0.099	2321	fms-related tyrosine kinase 1 (vascular endothelial growth factor/vascular
GO	nucleotide binding	98	1859	0.099	23305	acyl-CoA synthetase long-chain family member 6
GO	nucleotide binding	98	1859	0.099	2534	FYN oncogene related to SRC, FGR, YES
GO	nucleotide binding	98	1859	0.099	26154	ATP-binding cassette, sub-family A (ABC1), member 12
GO	nucleotide binding	98	1859	0.099	2618	phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide
GO	nucleotide binding	98	1859	0.099	27289	Rho family GTPase 1
GO	nucleotide binding	98	1859	0.099	27330	ribosomal protein S6 kinase, 90kDa, polypeptide 6
GO	nucleotide binding	98	1859	0.099	2774	guanine nucleotide binding protein (G protein), alpha activating activity pol
GO	nucleotide binding	98	1859	0.099	29922	non-metastatic cells 7, protein expressed in (nucleoside-diphosphate kinas
GO	nucleotide binding	98	1859	0.099	3183	heterogeneous nuclear ribonucleoprotein C (C1/C2)

GO	nucleotide binding	98	1859	0.099	340273	ATP-binding cassette, sub-family B (MDR/TAP), member 5
GO	nucleotide binding	98	1859	0.099	347733	tubulin, beta 2B
GO	nucleotide binding	98	1859	0.099	348093	RNA binding protein with multiple splicing 2
GO	nucleotide binding	98	1859	0.099	3797	kinesin family member 3C
GO	nucleotide binding	98	1859	0.099	3800	kinesin family member 5C
GO	nucleotide binding	98	1859	0.099	3932	lymphocyte-specific protein tyrosine kinase
GO	nucleotide binding	98	1859	0.099	4171	minichromosome maintenance complex component 2
GO	nucleotide binding	98	1859	0.099	4430	myosin IB
GO	nucleotide binding	98	1859	0.099	4436	mutS homolog 2, colon cancer, nonpolyposis type 1 (E. coli)
GO	nucleotide binding	98	1859	0.099	4651	myosin X
GO	nucleotide binding	98	1859	0.099	479	ATPase, H+/K+ transporting, nongastric, alpha polypeptide
GO	nucleotide binding	98	1859	0.099	4830	non-metastatic cells 1, protein (NM23A) expressed in
GO	nucleotide binding	98	1859	0.099	4893	neuroblastoma RAS viral (v-ras) oncogene homolog
GO	nucleotide binding	98	1859	0.099	5000	origin recognition complex, subunit 4-like (yeast)
GO	nucleotide binding	98	1859	0.099	50485	SWI/SNF related, matrix associated, actin dependent regulator of chromati
GO	nucleotide binding	98	1859	0.099	51062	atlastin GTPase 1
GO	nucleotide binding	98	1859	0.099	54822	transient receptor potential cation channel, subfamily M, member 7
GO	nucleotide binding	98	1859	0.099	55137	fidgetin
GO	nucleotide binding	98	1859	0.099	55207	ADP-ribosylation factor-like 8B
GO	nucleotide binding	98	1859	0.099	55577	N-acetylglucosamine kinase
GO	nucleotide binding	98	1859	0.099	55752	septin 11
GO	nucleotide binding	98	1859	0.099	558	AXL receptor tyrosine kinase
GO	nucleotide binding	98	1859	0.099	5588	protein kinase C, theta
GO	nucleotide binding	98	1859	0.099	5702	proteasome (prosome, macropain) 26S subunit, ATPase, 3
GO	nucleotide binding	98	1859	0.099	57144	p21 protein (Cdc42/Rac)-activated kinase 7
GO	nucleotide binding	98	1859	0.099	58155	polypyrimidine tract binding protein 2
GO	nucleotide binding	98	1859	0.099	5889	RAD51 homolog C (S. cerevisiae)
GO	nucleotide binding	98	1859	0.099	59	actin, alpha 2, smooth muscle, aorta
GO	nucleotide binding	98	1859	0.099	5965	RecQ protein-like (DNA helicase Q1-like)
GO	nucleotide binding	98	1859	0.099	6242	rhotekin
GO	nucleotide binding	98	1859	0.099	64080	ribokinase
GO	nucleotide binding	98	1859	0.099	641	Bloom syndrome, RecQ helicase-like
GO	nucleotide binding	98	1859	0.099	659	bone morphogenetic protein receptor, type II (serine/threonine kinase)
GO	nucleotide binding	98	1859	0.099	6683	spastin
GO	nucleotide binding	98	1859	0.099	6741	Sjogren syndrome antigen B (autoantigen La)
GO	nucleotide binding	98	1859	0.099	6833	ATP-binding cassette, sub-family C (CFTR/MRP), member 8

GO	nucleotide binding	98	1859	0.099	70	actin, alpha, cardiac muscle 1
GO	nucleotide binding	98	1859	0.099	7010	TEK tyrosine kinase, endothelial
GO	nucleotide binding	98	1859	0.099	7046	transforming growth factor, beta receptor 1
GO	nucleotide binding	98	1859	0.099	7298	thymidylate synthetase
GO	nucleotide binding	98	1859	0.099	7324	ubiquitin-conjugating enzyme E2E 1 (UBC4/5 homolog, yeast)
GO	nucleotide binding	98	1859	0.099	7846	tubulin, alpha 1a
GO	nucleotide binding	98	1859	0.099	79646	pantothenate kinase 3
GO	nucleotide binding	98	1859	0.099	79677	structural maintenance of chromosomes 6
GO	nucleotide binding	98	1859	0.099	79861	tubulin, alpha-like 3
GO	nucleotide binding	98	1859	0.099	81892	chromosome 14 open reading frame 156
GO	nucleotide binding	98	1859	0.099	83871	RAB34, member RAS oncogene family
GO	nucleotide binding	98	1859	0.099	84083	zinc finger, RAN-binding domain containing 3
GO	nucleotide binding	98	1859	0.099	84365	MKI67 (FHA domain) interacting nucleolar phosphoprotein
GO	nucleotide binding	98	1859	0.099	8458	transcription termination factor, RNA polymerase II
GO	nucleotide binding	98	1859	0.099	8536	calcium/calmodulin-dependent protein kinase I
GO	nucleotide binding	98	1859	0.099	89797	neuron navigator 2
GO	nucleotide binding	98	1859	0.099	8997	kalirin, RhoGEF kinase
GO	nucleotide binding	98	1859	0.099	9262	serine/threonine kinase 17b
GO	nucleotide binding	98	1859	0.099	9448	mitogen-activated protein kinase kinase kinase kinase 4
GO	nucleotide binding	98	1859	0.099	953	ectonucleoside triphosphate diphosphohydrolase 1
GO	nucleotide binding	98	1859	0.099	9833	maternal embryonic leucine zipper kinase
GO	lipid metabolic process	14	206	0.1	2171	fatty acid binding protein 5 (psoriasis-associated)
GO	lipid metabolic process	14	206	0.1	2172	fatty acid binding protein 6, ileal
GO	lipid metabolic process	14	206	0.1	23305	acyl-CoA synthetase long-chain family member 6
GO	lipid metabolic process	14	206	0.1	26061	2-hydroxyacyl-CoA lyase 1
GO	lipid metabolic process	14	206	0.1	3028	hydroxysteroid (17-beta) dehydrogenase 10
GO	lipid metabolic process	14	206	0.1	3157	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 (soluble)
GO	lipid metabolic process	14	206	0.1	3248	hydroxyprostaglandin dehydrogenase 15-(NAD)
GO	lipid metabolic process	14	206	0.1	341	apolipoprotein C-I
GO	lipid metabolic process	14	206	0.1	348	apolipoprotein E
GO	lipid metabolic process	14	206	0.1	3952	leptin
GO	lipid metabolic process	14	206	0.1	5264	phytanoyl-CoA 2-hydroxylase
GO	lipid metabolic process	14	206	0.1	5360	phospholipid transfer protein
GO	lipid metabolic process	14	206	0.1	7840	Alstrom syndrome 1
GO	lipid metabolic process	14	206	0.1	9744	ArfGAP with coiled-coil, ankyrin repeat and PH domains 1
GO	voltage-gated potassium channel compl	7	85	0.1	283518	potassium channel regulator

GO	voltage-gated potassium channel compl	7	85	0.1	3751	potassium voltage-gated channel, Shal-related subfamily, member 2
GO	voltage-gated potassium channel compl	7	85	0.1	3754	potassium voltage-gated channel, subfamily F, member 1
GO	voltage-gated potassium channel compl	7	85	0.1	3756	potassium voltage-gated channel, subfamily H (eag-related), member 1
GO	voltage-gated potassium channel compl	7	85	0.1	3763	potassium inwardly-rectifying channel, subfamily J, member 6
GO	voltage-gated potassium channel compl	7	85	0.1	3778	potassium large conductance calcium-activated channel, subfamily M, alph
GO	voltage-gated potassium channel compl	7	85	0.1	56479	potassium voltage-gated channel, KQT-like subfamily, member 5
GO	ligand-dependent nuclear receptor bind	2	12	0.105	10474	transcriptional adaptor 3
GO	ligand-dependent nuclear receptor bind	2	12	0.105	5469	mediator complex subunit 1
GO	tissue development	2	12	0.105	10683	delta-like 3 (Drosophila)
GO	tissue development	2	12	0.105	7490	Wilms tumor 1
GO	dendrite morphogenesis	2	12	0.105	1496	catenin (cadherin-associated protein), alpha 2
GO	dendrite morphogenesis	2	12	0.105	773	calcium channel, voltage-dependent, P/Q type, alpha 1A subunit
GO	release of sequestered calcium ion into	2	12	0.105	2149	coagulation factor II (thrombin) receptor
GO	release of sequestered calcium ion into	2	12	0.105	3932	lymphocyte-specific protein tyrosine kinase
GO	smooth muscle contraction	2	12	0.105	2281	FK506 binding protein 1B, 12.6 kDa
GO	smooth muscle contraction	2	12	0.105	6525	smoothelin
GO	septin complex	2	12	0.105	23157	septin 6
GO	septin complex	2	12	0.105	55752	septin 11
GO	mitochondrial inner membrane presequ	2	12	0.105	26519	translocase of inner mitochondrial membrane 10 homolog (yeast)
GO	mitochondrial inner membrane presequ	2	12	0.105	26521	translocase of inner mitochondrial membrane 8 homolog B (yeast)
GO	regulation of muscle contraction	2	12	0.105	309	annexin A6
GO	regulation of muscle contraction	2	12	0.105	7168	tropomyosin 1 (alpha)
GO	caspase inhibitor activity	2	12	0.105	332	baculoviral IAP repeat-containing 5
GO	caspase inhibitor activity	2	12	0.105	51499	TP53 regulated inhibitor of apoptosis 1
GO	low-density lipoprotein particle	2	12	0.105	348	apolipoprotein E
GO	low-density lipoprotein particle	2	12	0.105	79135	apolipoprotein O
GO	response to electrical stimulus	2	12	0.105	3763	potassium inwardly-rectifying channel, subfamily J, member 6
GO	response to electrical stimulus	2	12	0.105	7046	transforming growth factor, beta receptor 1
GO	alpha-tubulin binding	2	12	0.105	55207	ADP-ribosylation factor-like 8B
GO	alpha-tubulin binding	2	12	0.105	6683	spastin
GO	response to chemical stimulus	2	12	0.105	6657	SRY (sex determining region Y)-box 2
GO	response to chemical stimulus	2	12	0.105	7353	ubiquitin fusion degradation 1 like (yeast)
GO	ubiquitin ligase complex	5	54	0.105	23194	F-box and leucine-rich repeat protein 7
GO	ubiquitin ligase complex	5	54	0.105	26223	F-box and leucine-rich repeat protein 21 (gene/pseudogene)
GO	ubiquitin ligase complex	5	54	0.105	4734	neural precursor cell expressed, developmentally down-regulated 4
GO	ubiquitin ligase complex	5	54	0.105	672	breast cancer 1, early onset

GO	ubiquitin ligase complex	5	54	0.105	7324	ubiquitin-conjugating enzyme E2E 1 (UBC4/5 homolog, yeast)
GO	androgen receptor signaling pathway	4	39	0.106	5469	mediator complex subunit 1
GO	androgen receptor signaling pathway	4	39	0.106	56937	prostate transmembrane protein, androgen induced 1
GO	androgen receptor signaling pathway	4	39	0.106	672	breast cancer 1, early onset
GO	androgen receptor signaling pathway	4	39	0.106	898	cyclin E1
GO	response to antibiotic	3	25	0.108	10096	ARP3 actin-related protein 3 homolog (yeast)
GO	response to antibiotic	3	25	0.108	1543	cytochrome P450, family 1, subfamily A, polypeptide 1
GO	response to antibiotic	3	25	0.108	6347	chemokine (C-C motif) ligand 2
GO	nucleotide metabolic process	3	25	0.108	11164	nudix (nucleoside diphosphate linked moiety X)-type motif 5
GO	nucleotide metabolic process	3	25	0.108	29922	non-metastatic cells 7, protein expressed in (nucleoside-diphosphate kinas
GO	nucleotide metabolic process	3	25	0.108	4830	non-metastatic cells 1, protein (NM23A) expressed in
GO	midbody	3	25	0.108	332	baculoviral IAP repeat-containing 5
GO	midbody	3	25	0.108	55207	ADP-ribosylation factor-like 8B
GO	midbody	3	25	0.108	6683	spastin
GO	protein polymerization	3	25	0.108	347733	tubulin, beta 2B
GO	protein polymerization	3	25	0.108	7846	tubulin, alpha 1a
GO	protein polymerization	3	25	0.108	79861	tubulin, alpha-like 3
GO	nucleotidyltransferase activity	6	71	0.112	23057	nicotinamide nucleotide adenylyltransferase 2
GO	nucleotidyltransferase activity	6	71	0.112	25885	polymerase (RNA) I polypeptide A, 194kDa
GO	nucleotidyltransferase activity	6	71	0.112	5558	primase, DNA, polypeptide 2 (58kDa)
GO	nucleotidyltransferase activity	6	71	0.112	56655	polymerase (DNA-directed), epsilon 4 (p12 subunit)
GO	nucleotidyltransferase activity	6	71	0.112	5833	phosphate cytidylyltransferase 2, ethanolamine
GO	nucleotidyltransferase activity	6	71	0.112	84172	polymerase (RNA) I polypeptide B, 128kDa
GO	ubiquitin-dependent protein catabolic p	10	139	0.113	10213	proteasome (prosome, macropain) 26S subunit, non-ATPase, 14
GO	ubiquitin-dependent protein catabolic p	10	139	0.113	130507	ubiquitin protein ligase E3 component n-recognin 3 (putative)
GO	ubiquitin-dependent protein catabolic p	10	139	0.113	23194	F-box and leucine-rich repeat protein 7
GO	ubiquitin-dependent protein catabolic p	10	139	0.113	26263	F-box protein 22
GO	ubiquitin-dependent protein catabolic p	10	139	0.113	373856	ubiquitin specific peptidase 41
GO	ubiquitin-dependent protein catabolic p	10	139	0.113	57478	ubiquitin specific peptidase 31
GO	ubiquitin-dependent protein catabolic p	10	139	0.113	7324	ubiquitin-conjugating enzyme E2E 1 (UBC4/5 homolog, yeast)
GO	ubiquitin-dependent protein catabolic p	10	139	0.113	7347	ubiquitin carboxyl-terminal esterase L3 (ubiquitin thiolesterase)
GO	ubiquitin-dependent protein catabolic p	10	139	0.113	7353	ubiquitin fusion degradation 1 like (yeast)
GO	ubiquitin-dependent protein catabolic p	10	139	0.113	84101	ubiquitin specific peptidase 44
GO	enzyme activator activity	4	40	0.113	10055	SUMO1 activating enzyme subunit 1
GO	enzyme activator activity	4	40	0.113	10893	matrix metallopeptidase 24 (membrane-inserted)
GO	enzyme activator activity	4	40	0.113	241	arachidonate 5-lipoxygenase-activating protein

GO	enzyme activator activity	4	40	0.113	9535 glia maturation factor, gamma
GO	embryonic development	6	72	0.117	130507 ubiquitin protein ligase E3 component n-recognin 3 (putative)
GO	embryonic development	6	72	0.117	2628 glycine amidinotransferase (L-arginine:glycine amidinotransferase)
GO	embryonic development	6	72	0.117	7046 transforming growth factor, beta receptor 1
GO	embryonic development	6	72	0.117	84172 polymerase (RNA) I polypeptide B, 128kDa
GO	embryonic development	6	72	0.117	8788 delta-like 1 homolog (Drosophila)
GO	embryonic development	6	72	0.117	9542 neuregulin 2
GO	response to nutrient	6	72	0.117	23305 acyl-CoA synthetase long-chain family member 6
GO	response to nutrient	6	72	0.117	2628 glycine amidinotransferase (L-arginine:glycine amidinotransferase)
GO	response to nutrient	6	72	0.117	411 arylsulfatase B
GO	response to nutrient	6	72	0.117	590 butyrylcholinesterase
GO	response to nutrient	6	72	0.117	6546 solute carrier family 8 (sodium/calcium exchanger), member 1
GO	response to nutrient	6	72	0.117	7037 transferrin receptor (p90, CD71)
GO	embryo implantation	3	26	0.118	5125 proprotein convertase subtilisin/kexin type 5
GO	embryo implantation	3	26	0.118	7046 transforming growth factor, beta receptor 1
GO	embryo implantation	3	26	0.118	84172 polymerase (RNA) I polypeptide B, 128kDa
GO	cellular response to hormone stimulus	3	26	0.118	5228 placental growth factor
GO	cellular response to hormone stimulus	3	26	0.118	6586 slit homolog 3 (Drosophila)
GO	cellular response to hormone stimulus	3	26	0.118	8835 suppressor of cytokine signaling 2
GO	negative regulation of phosphorylation	2	13	0.12	1026 cyclin-dependent kinase inhibitor 1A (p21, Cip1)
GO	negative regulation of phosphorylation	2	13	0.12	3624 inhibin, beta A
GO	acetylcholine receptor activity	2	13	0.12	1136 cholinergic receptor, nicotinic, alpha 3
GO	acetylcholine receptor activity	2	13	0.12	1138 cholinergic receptor, nicotinic, alpha 5
GO	protein autoubiquitination	2	13	0.12	1161 excision repair cross-complementing rodent repair deficiency, complement
GO	protein autoubiquitination	2	13	0.12	1643 damage-specific DNA binding protein 2, 48kDa
GO	oogenesis	2	13	0.12	1730 diaphanous homolog 2 (Drosophila)
GO	oogenesis	2	13	0.12	4292 mutL homolog 1, colon cancer, nonpolyposis type 2 (E. coli)
GO	embryonic cranial skeleton morphogene	2	13	0.12	1746 distal-less homeobox 2
GO	embryonic cranial skeleton morphogene	2	13	0.12	7046 transforming growth factor, beta receptor 1
GO	synaptic transmission, glutamatergic	2	13	0.12	2906 glutamate receptor, ionotropic, N-methyl D-aspartate 2D
GO	synaptic transmission, glutamatergic	2	13	0.12	773 calcium channel, voltage-dependent, P/Q type, alpha 1A subunit
GO	high-density lipoprotein particle remode	2	13	0.12	341 apolipoprotein C-I
GO	high-density lipoprotein particle remode	2	13	0.12	348 apolipoprotein E
GO	hormone metabolic process	2	13	0.12	3952 leptin
GO	hormone metabolic process	2	13	0.12	773 calcium channel, voltage-dependent, P/Q type, alpha 1A subunit
GO	myosin binding	2	13	0.12	54822 transient receptor potential cation channel, subfamily M, member 7

GO	myosin binding	2	13	0.12	70	actin, alpha, cardiac muscle 1
GO	positive regulation of stress fiber assem	2	13	0.12	5588	protein kinase C, theta
GO	positive regulation of stress fiber assem	2	13	0.12	7168	tropomyosin 1 (alpha)
GO	centrosome organization	2	13	0.12	8409	ubiquitously-expressed transcript
GO	centrosome organization	2	13	0.12	93323	HAUS augmin-like complex, subunit 8
GO	coated pit	4	41	0.121	11154	adaptor-related protein complex 4, sigma 1 subunit
GO	coated pit	4	41	0.121	409	arrestin, beta 2
GO	coated pit	4	41	0.121	7037	transferrin receptor (p90, CD71)
GO	coated pit	4	41	0.121	8905	adaptor-related protein complex 1, sigma 2 subunit
GO	myosin complex	4	41	0.121	11259	filamin A interacting protein 1-like
GO	myosin complex	4	41	0.121	4430	myosin IB
GO	myosin complex	4	41	0.121	4637	myosin, light chain 6, alkali, smooth muscle and non-muscle
GO	myosin complex	4	41	0.121	4651	myosin X
GO	magnesium ion binding	11	159	0.122	10056	phenylalanyl-tRNA synthetase, beta subunit
GO	magnesium ion binding	11	159	0.122	11164	nudix (nucleoside diphosphate linked moiety X)-type motif 5
GO	magnesium ion binding	11	159	0.122	147699	protein phosphatase, Mg2+/Mn2+ dependent, 1N (putative)
GO	magnesium ion binding	11	159	0.122	2027	enolase 3 (beta, muscle)
GO	magnesium ion binding	11	159	0.122	2139	eyes absent homolog 2 (Drosophila)
GO	magnesium ion binding	11	159	0.122	2237	flap structure-specific endonuclease 1
GO	magnesium ion binding	11	159	0.122	26061	2-hydroxyacyl-CoA lyase 1
GO	magnesium ion binding	11	159	0.122	27330	ribosomal protein S6 kinase, 90kDa, polypeptide 6
GO	magnesium ion binding	11	159	0.122	4436	mutS homolog 2, colon cancer, nonpolyposis type 1 (E. coli)
GO	magnesium ion binding	11	159	0.122	4830	non-metastatic cells 1, protein (NM23A) expressed in
GO	magnesium ion binding	11	159	0.122	5494	protein phosphatase, Mg2+/Mn2+ dependent, 1A
GO	nucleolus	39	692	0.122	10189	THO complex 4
GO	nucleolus	39	692	0.122	10199	M-phase phosphoprotein 10 (U3 small nucleolar ribonucleoprotein)
GO	nucleolus	39	692	0.122	10528	NOP56 ribonucleoprotein homolog (yeast)
GO	nucleolus	39	692	0.122	10656	KH domain containing, RNA binding, signal transduction associated 3
GO	nucleolus	39	692	0.122	10799	ribonuclease P/MRP 40kDa subunit
GO	nucleolus	39	692	0.122	11056	DEAD (Asp-Glu-Ala-Asp) box polypeptide 52
GO	nucleolus	39	692	0.122	11169	WD repeat and HMG-box DNA binding protein 1
GO	nucleolus	39	692	0.122	201299	RAD52 motif 1
GO	nucleolus	39	692	0.122	219736	storkhead box 1
GO	nucleolus	39	692	0.122	25885	polymerase (RNA) I polypeptide A, 194kDa
GO	nucleolus	39	692	0.122	25926	nucleolar protein 11
GO	nucleolus	39	692	0.122	2842	G protein-coupled receptor 19

GO	nucleolus	39	692	0.122	30011	SH3-domain kinase binding protein 1
GO	nucleolus	39	692	0.122	3248	hydroxyprostaglandin dehydrogenase 15-(NAD)
GO	nucleolus	39	692	0.122	332	baculoviral IAP repeat-containing 5
GO	nucleolus	39	692	0.122	345630	fibrillarin-like 1
GO	nucleolus	39	692	0.122	3516	recombination signal binding protein for immunoglobulin kappa J region
GO	nucleolus	39	692	0.122	4291	myeloid leukemia factor 1
GO	nucleolus	39	692	0.122	4603	v-myb myeloblastosis viral oncogene homolog (avian)-like 1
GO	nucleolus	39	692	0.122	51339	dapper, antagonist of beta-catenin, homolog 1 (Xenopus laevis)
GO	nucleolus	39	692	0.122	51491	NOP16 nucleolar protein homolog (yeast)
GO	nucleolus	39	692	0.122	5303	protein (peptidylprolyl cis/trans isomerase) NIMA-interacting, 4 (parvulin)
GO	nucleolus	39	692	0.122	54984	PIN2-interacting protein 1
GO	nucleolus	39	692	0.122	55003	PAK1 interacting protein 1
GO	nucleolus	39	692	0.122	55759	WD repeat domain 12
GO	nucleolus	39	692	0.122	56902	partner of NOB1 homolog (S. cerevisiae)
GO	nucleolus	39	692	0.122	6133	ribosomal protein L9
GO	nucleolus	39	692	0.122	641	Bloom syndrome, RecQ helicase-like
GO	nucleolus	39	692	0.122	64318	nucleolar complex associated 3 homolog (S. cerevisiae)
GO	nucleolus	39	692	0.122	64393	zinc finger, matrin type 3
GO	nucleolus	39	692	0.122	64782	apoptosis enhancing nuclease
GO	nucleolus	39	692	0.122	6662	SRY (sex determining region Y)-box 9
GO	nucleolus	39	692	0.122	6672	SP100 nuclear antigen
GO	nucleolus	39	692	0.122	6711	spectrin, beta, non-erythrocytic 1
GO	nucleolus	39	692	0.122	6741	Sjogren syndrome antigen B (autoantigen La)
GO	nucleolus	39	692	0.122	84172	polymerase (RNA) I polypeptide B, 128kDa
GO	nucleolus	39	692	0.122	84365	MKI67 (FHA domain) interacting nucleolar phosphoprotein
GO	nucleolus	39	692	0.122	89797	neuron navigator 2
GO	nucleolus	39	692	0.122	898	cyclin E1
GO	integrin-mediated signaling pathway	5	57	0.124	22801	integrin, alpha 11
GO	integrin-mediated signaling pathway	5	57	0.124	3685	integrin, alpha V (vitronectin receptor, alpha polypeptide, antigen CD51)
GO	integrin-mediated signaling pathway	5	57	0.124	3694	integrin, beta 6
GO	integrin-mediated signaling pathway	5	57	0.124	5341	pleckstrin
GO	integrin-mediated signaling pathway	5	57	0.124	667	dystonin
GO	protein complex binding	7	90	0.125	1000	cadherin 2, type 1, N-cadherin (neuronal)
GO	protein complex binding	7	90	0.125	1026	cyclin-dependent kinase inhibitor 1A (p21, Cip1)
GO	protein complex binding	7	90	0.125	1161	excision repair cross-complementing rodent repair deficiency, complement
GO	protein complex binding	7	90	0.125	3516	recombination signal binding protein for immunoglobulin kappa J region

GO	protein complex binding	7	90	0.125	6711	spectrin, beta, non-erythrocytic 1
GO	protein complex binding	7	90	0.125	7046	transforming growth factor, beta receptor 1
GO	protein complex binding	7	90	0.125	898	cyclin E1
GO	neuron development	3	27	0.128	23305	acyl-CoA synthetase long-chain family member 6
GO	neuron development	3	27	0.128	2736	GLI family zinc finger 2
GO	neuron development	3	27	0.128	27429	HtrA serine peptidase 2
GO	kinase binding	3	27	0.128	25780	RAS guanyl releasing protein 3 (calcium and DAG-regulated)
GO	kinase binding	3	27	0.128	355	Fas (TNF receptor superfamily, member 6)
GO	kinase binding	3	27	0.128	6672	SP100 nuclear antigen
GO	ATP synthesis coupled proton transport	3	27	0.128	51382	ATPase, H+ transporting, lysosomal 34kDa, V1 subunit D
GO	ATP synthesis coupled proton transport	3	27	0.128	516	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit C1 (subu
GO	ATP synthesis coupled proton transport	3	27	0.128	528	ATPase, H+ transporting, lysosomal 42kDa, V1 subunit C1
GO	JAK-STAT cascade	3	27	0.128	6347	chemokine (C-C motif) ligand 2
GO	JAK-STAT cascade	3	27	0.128	729230	chemokine (C-C motif) receptor 2
GO	JAK-STAT cascade	3	27	0.128	8835	suppressor of cytokine signaling 2
GO	vasculogenesis	4	42	0.129	10052	gap junction protein, gamma 1, 45kDa
GO	vasculogenesis	4	42	0.129	5795	protein tyrosine phosphatase, receptor type, J
GO	vasculogenesis	4	42	0.129	7137	troponin I type 3 (cardiac)
GO	vasculogenesis	4	42	0.129	7490	Wilms tumor 1
GO	negative regulation of cell growth	7	91	0.13	1026	cyclin-dependent kinase inhibitor 1A (p21, Cip1)
GO	negative regulation of cell growth	7	91	0.13	2786	guanine nucleotide binding protein (G protein), gamma 4
GO	negative regulation of cell growth	7	91	0.13	3624	inhibin, beta A
GO	negative regulation of cell growth	7	91	0.13	6586	slit homolog 3 (Drosophila)
GO	negative regulation of cell growth	7	91	0.13	659	bone morphogenetic protein receptor, type II (serine/threonine kinase)
GO	negative regulation of cell growth	7	91	0.13	7490	Wilms tumor 1
GO	negative regulation of cell growth	7	91	0.13	8626	tumor protein p63
GO	synaptosome	7	91	0.13	23705	cell adhesion molecule 1
GO	synaptosome	7	91	0.13	26059	ELKS/RAB6-interacting/CAST family member 2
GO	synaptosome	7	91	0.13	26999	cytoplasmic FMR1 interacting protein 2
GO	synaptosome	7	91	0.13	2906	glutamate receptor, ionotropic, N-methyl D-aspartate 2D
GO	synaptosome	7	91	0.13	30011	SH3-domain kinase binding protein 1
GO	synaptosome	7	91	0.13	3751	potassium voltage-gated channel, Shal-related subfamily, member 2
GO	synaptosome	7	91	0.13	8777	multiple PDZ domain protein
GO	microtubule binding	5	58	0.131	220134	spindle and kinetochore associated complex subunit 1
GO	microtubule binding	5	58	0.131	332	baculoviral IAP repeat-containing 5
GO	microtubule binding	5	58	0.131	6683	spastin

GO	microtubule binding	5	58	0.131	79929	MAP6 domain containing 1
GO	microtubule binding	5	58	0.131	8409	ubiquitously-expressed transcript
GO	cholesterol metabolic process	5	58	0.131	2232	ferredoxin reductase
GO	cholesterol metabolic process	5	58	0.131	341	apolipoprotein C-I
GO	cholesterol metabolic process	5	58	0.131	348	apolipoprotein E
GO	cholesterol metabolic process	5	58	0.131	3952	leptin
GO	cholesterol metabolic process	5	58	0.131	9420	cytochrome P450, family 7, subfamily B, polypeptide 1
GO	positive regulation of lamellipodium ass	1	3	0.133	10096	ARP3 actin-related protein 3 homolog (yeast)
GO	carbonyl reductase (NADPH) activity	1	3	0.133	10202	dehydrogenase/reductase (SDR family) member 2
GO	negative regulation of stress fiber assen	1	3	0.133	10395	deleted in liver cancer 1
GO	U4/U6 snRNP	1	3	0.133	10465	peptidylprolyl isomerase H (cyclophilin H)
GO	limb bud formation	1	3	0.133	10512	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (
GO	regulation of Rac GTPase activity	1	3	0.133	11149	blood vessel epicardial substance
GO	ADP-ribose diphosphatase activity	1	3	0.133	11164	nudix (nucleoside diphosphate linked moiety X)-type motif 5
GO	cohesin complex	1	3	0.133	113130	cell division cycle associated 5
GO	interphase of mitotic cell cycle	1	3	0.133	113130	cell division cycle associated 5
GO	synaptic transmission involved in mictui	1	3	0.133	1136	cholinergic receptor, nicotinic, alpha 3
GO	nucleotide-excision repair complex	1	3	0.133	1161	excision repair cross-complementing rodent repair deficiency, complement
GO	proteoglycan binding	1	3	0.133	1289	collagen, type V, alpha 1
GO	lipase activity	1	3	0.133	13	arylacetamide deacetylase (esterase)
GO	serine hydrolase activity	1	3	0.133	13	arylacetamide deacetylase (esterase)
GO	negative regulation of nuclear mRNA sp	1	3	0.133	135295	splicing factor, arginine/serine-rich 13B
GO	NEDD8 ligase activity	1	3	0.133	140739	ubiquitin-conjugating enzyme E2F (putative)
GO	positive regulation of vascular permeab	1	3	0.133	143282	fibroblast growth factor binding protein 3
GO	porphyrin metabolic process	1	3	0.133	1543	cytochrome P450, family 1, subfamily A, polypeptide 1
GO	positive regulation of S phase of mitotic	1	3	0.133	1543	cytochrome P450, family 1, subfamily A, polypeptide 1
GO	response to nematode	1	3	0.133	1543	cytochrome P450, family 1, subfamily A, polypeptide 1
GO	AMP biosynthetic process	1	3	0.133	158	adenylosuccinate lyase
GO	thyroxine 5'-deiodinase activity	1	3	0.133	1733	deiodinase, iodothyronine, type I
GO	DNA methylation involved in embryonic	1	3	0.133	1788	DNA (cytosine-5-)-methyltransferase 3 alpha
GO	S-adenosylmethioninamine metabolic p	1	3	0.133	1788	DNA (cytosine-5-)-methyltransferase 3 alpha
GO	positive regulation of translational elon	1	3	0.133	1984	eukaryotic translation initiation factor 5A
GO	positive regulation of translational term	1	3	0.133	1984	eukaryotic translation initiation factor 5A
GO	translational frameshifting	1	3	0.133	1984	eukaryotic translation initiation factor 5A
GO	UDP-N-acetylgalactosamine metabolic p	1	3	0.133	2135	exostoses (multiple)-like 2
GO	histone dephosphorylation	1	3	0.133	2139	eyes absent homolog 2 (Drosophila)

GO	connective tissue replacement during ir	1	3	0.133	2149	coagulation factor II (thrombin) receptor
GO	regulation of interleukin-1 beta product	1	3	0.133	2149	coagulation factor II (thrombin) receptor
GO	STAT protein nuclear translocation	1	3	0.133	2149	coagulation factor II (thrombin) receptor
GO	tyrosine phosphorylation of STAT protei	1	3	0.133	2149	coagulation factor II (thrombin) receptor
GO	thyroid hormone binding	1	3	0.133	220	aldehyde dehydrogenase 1 family, member A3
GO	substrate-bound cell migration	1	3	0.133	22801	integrin, alpha 11
GO	negative regulation of heart rate	1	3	0.133	2281	FK506 binding protein 1B, 12.6 kDa
GO	negative regulation of stress-activated N	1	3	0.133	2305	forkhead box M1
GO	regulation of oxygen and reactive oxyge	1	3	0.133	2305	forkhead box M1
GO	nicotinamide-nucleotide adenylyltransf	1	3	0.133	23057	nicotinamide nucleotide adenylyltransferase 2
GO	nicotinate-nucleotide adenylyltransfera	1	3	0.133	23057	nicotinamide nucleotide adenylyltransferase 2
GO	glycerol-3-phosphate dehydrogenase (N	1	3	0.133	23171	glycerol-3-phosphate dehydrogenase 1-like
GO	glycerol-3-phosphate dehydrogenase cc	1	3	0.133	23171	glycerol-3-phosphate dehydrogenase 1-like
GO	intracellular receptor mediated signalin	1	3	0.133	2321	fms-related tyrosine kinase 1 (vascular endothelial growth factor/vascular
GO	susceptibility to natural killer cell media	1	3	0.133	23705	cell adhesion molecule 1
GO	cellular response to calcium ion	1	3	0.133	241	arachidonate 5-lipoxygenase-activating protein
GO	Rap GTPase activator activity	1	3	0.133	25780	RAS guanyl releasing protein 3 (calcium and DAG-regulated)
GO	de novo' IMP biosynthetic process	1	3	0.133	2618	phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide
GO	organ development	1	3	0.133	2618	phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide
GO	cerebellar cortex morphogenesis	1	3	0.133	2736	GLI family zinc finger 2
GO	epidermal cell differentiation	1	3	0.133	2736	GLI family zinc finger 2
GO	smoothened signaling pathway involvec	1	3	0.133	2736	GLI family zinc finger 2
GO	tube development	1	3	0.133	2736	GLI family zinc finger 2
GO	ventral midline development	1	3	0.133	2736	GLI family zinc finger 2
GO	response to molecule of fungal origin	1	3	0.133	2878	glutathione peroxidase 3 (plasma)
GO	salivary gland development	1	3	0.133	29842	transcription factor CP2-like 1
GO	hyaluronan synthase activity	1	3	0.133	3037	hyaluronan synthase 2
GO	peripheral nervous system neuron deve	1	3	0.133	3236	homeobox D10
GO	spinal cord motor neuron cell fate speci	1	3	0.133	3236	homeobox D10
GO	chromosome passenger complex	1	3	0.133	332	baculoviral IAP repeat-containing 5
GO	cobalt ion binding	1	3	0.133	332	baculoviral IAP repeat-containing 5
GO	lipase inhibitor activity	1	3	0.133	341	apolipoprotein C-I
GO	negative regulation of cholesterol trans	1	3	0.133	341	apolipoprotein C-I
GO	negative regulation of lipid metabolic pr	1	3	0.133	341	apolipoprotein C-I
GO	negative regulation of very-low-density	1	3	0.133	341	apolipoprotein C-I
GO	intermediate-density lipoprotein particl	1	3	0.133	348	apolipoprotein E

GO	negative regulation of cholesterol biosy	1	3	0.133	348	apolipoprotein E
GO	very-low-density lipoprotein receptor bi	1	3	0.133	348	apolipoprotein E
GO	negative regulation of smooth muscle c	1	3	0.133	3516	recombination signal binding protein for immunoglobulin kappa J region
GO	positive regulation of necrotic cell deat	1	3	0.133	355	Fas (TNF receptor superfamily, member 6)
GO	negative regulation of B cell differentiat	1	3	0.133	3624	inhibin, beta A
GO	negative regulation of interferon-gamm	1	3	0.133	3624	inhibin, beta A
GO	positive regulation of follicle-stimulatin	1	3	0.133	3624	inhibin, beta A
GO	negative regulation of low-density lipop	1	3	0.133	3685	integrin, alpha V (vitronectin receptor, alpha polypeptide, antigen CD51)
GO	A-type (transient outward) potassium c	1	3	0.133	3751	potassium voltage-gated channel, Shal-related subfamily, member 2
GO	locomotor rhythm	1	3	0.133	3778	potassium large conductance calcium-activated channel, subfamily M, alph
GO	relaxation of vascular smooth muscle	1	3	0.133	3778	potassium large conductance calcium-activated channel, subfamily M, alph
GO	miRNA catabolic process	1	3	0.133	389421	lin-28 homolog B (C. elegans)
GO	positive regulation of T cell receptor sig	1	3	0.133	3932	lymphocyte-specific protein tyrosine kinase
GO	phagocytic cup	1	3	0.133	3936	lymphocyte cytosolic protein 1 (L-plastin)
GO	T cell activation during immune respons	1	3	0.133	3936	lymphocyte cytosolic protein 1 (L-plastin)
GO	regulation of gluconeogenesis	1	3	0.133	3952	leptin
GO	aryl hydrocarbon receptor binding	1	3	0.133	406	aryl hydrocarbon receptor nuclear translocator-like
GO	desensitization of G-protein coupled re	1	3	0.133	409	arrestin, beta 2
GO	myeloid progenitor cell differentiation	1	3	0.133	4291	myeloid leukemia factor 1
GO	dinucleotide insertion or deletion bindi	1	3	0.133	4436	mutS homolog 2, colon cancer, nonpolyposis type 1 (E. coli)
GO	four-way junction DNA binding	1	3	0.133	4436	mutS homolog 2, colon cancer, nonpolyposis type 1 (E. coli)
GO	maintenance of DNA repeat elements	1	3	0.133	4436	mutS homolog 2, colon cancer, nonpolyposis type 1 (E. coli)
GO	oxidized purine DNA binding	1	3	0.133	4436	mutS homolog 2, colon cancer, nonpolyposis type 1 (E. coli)
GO	single guanine insertion binding	1	3	0.133	4436	mutS homolog 2, colon cancer, nonpolyposis type 1 (E. coli)
GO	negative regulation of vascular endothe	1	3	0.133	4734	neural precursor cell expressed, developmentally down-regulated 4
GO	phosphoserine binding	1	3	0.133	4734	neural precursor cell expressed, developmentally down-regulated 4
GO	positive regulation of Ras GTPase activit	1	3	0.133	4763	neurofibromin 1
GO	regulation of blood vessel endothelial c	1	3	0.133	4763	neurofibromin 1
GO	regulation of bone resorption	1	3	0.133	4763	neurofibromin 1
GO	hydrogen:potassium-exchanging ATPas	1	3	0.133	479	ATPase, H+/K+ transporting, nongastric, alpha polypeptide
GO	visual behavior	1	3	0.133	4867	nephronophthisis 1 (juvenile)
GO	clustering of voltage-gated sodium cha	1	3	0.133	4897	neuronal cell adhesion molecule
GO	nuclear pore organization	1	3	0.133	4928	nucleoporin 98kDa
GO	depurination	1	3	0.133	4968	8-oxoguanine DNA glycosylase
GO	origin recognition complex	1	3	0.133	5000	origin recognition complex, subunit 4-like (yeast)
GO	estrous cycle phase	1	3	0.133	5021	oxytocin receptor

GO	positive regulation of norepinephrine se	1	3	0.133	5021	oxytocin receptor
GO	negative regulation of endopeptidase a	1	3	0.133	5054	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor t
GO	negative regulation of plasminogen acti	1	3	0.133	5054	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor t
GO	positive regulation of monocyte chemot	1	3	0.133	5054	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor t
GO	cGMP catabolic process	1	3	0.133	50940	phosphodiesterase 11A
GO	protein-L-isoaspartate (D-aspartate) O-m	1	3	0.133	5110	protein-L-isoaspartate (D-aspartate) O-methyltransferase
GO	respiratory tube development	1	3	0.133	5125	proprotein convertase subtilisin/kexin type 5
GO	proton-transporting two-sector ATPase	1	3	0.133	51382	ATPase, H+ transporting, lysosomal 34kDa, V1 subunit D
GO	positive regulation of actin filament bur	1	3	0.133	5341	pleckstrin
GO	protein kinase C signaling cascade	1	3	0.133	5341	pleckstrin
GO	epithelial cell proliferation involved in m	1	3	0.133	5469	mediator complex subunit 1
GO	mammary gland branching involved in p	1	3	0.133	5469	mediator complex subunit 1
GO	telomerase inhibitor activity	1	3	0.133	54984	PIN2-interacting protein 1
GO	telomere formation via telomerase	1	3	0.133	55135	WD repeat containing, antisense to TP53
GO	maturation of LSU-rRNA from tricistroni	1	3	0.133	55759	WD repeat domain 12
GO	PeBoW complex	1	3	0.133	55759	WD repeat domain 12
GO	inositol 1,3,4,5 tetrakisphosphate bindin	1	3	0.133	55803	ArfGAP with dual PH domains 2
GO	RNA methylation	1	3	0.133	56339	methyltransferase like 3
GO	Y-form DNA binding	1	3	0.133	56852	RAD18 homolog (S. cerevisiae)
GO	peptidyl-amino acid modification	1	3	0.133	57168	aspartate beta-hydroxylase domain containing 2
GO	cAMP metabolic process	1	3	0.133	5744	parathyroid hormone-like hormone
GO	fatty acid homeostasis	1	3	0.133	57678	glycerol-3-phosphate acyltransferase, mitochondrial
GO	glycerophospholipid metabolic process	1	3	0.133	57678	glycerol-3-phosphate acyltransferase, mitochondrial
GO	B cell apoptosis	1	3	0.133	581	BCL2-associated X protein
GO	cleavage of lamin	1	3	0.133	581	BCL2-associated X protein
GO	transformed cell apoptosis	1	3	0.133	581	BCL2-associated X protein
GO	choline binding	1	3	0.133	590	butyrylcholinesterase
GO	cholinesterase activity	1	3	0.133	590	butyrylcholinesterase
GO	deoxyribonucleotide biosynthetic proce	1	3	0.133	6241	ribonucleotide reductase M2
GO	ribonucleoside-diphosphate reductase a	1	3	0.133	6241	ribonucleotide reductase M2
GO	regulation of anti-apoptosis	1	3	0.133	6242	rhotekin
GO	chromocenter	1	3	0.133	6299	sal-like 1 (Drosophila)
GO	G-quadruplex DNA binding	1	3	0.133	641	Bloom syndrome, RecQ helicase-like
GO	replication fork protection	1	3	0.133	641	Bloom syndrome, RecQ helicase-like
GO	olfactory receptor binding	1	3	0.133	65055	receptor accessory protein 1
GO	axon extension involved in axon guidanc	1	3	0.133	6586	slit homolog 3 (Drosophila)

GO	chemorepulsion involved in embryonic	1	3	0.133	6586	slit homolog 3 (Drosophila)
GO	negative regulation of chemokine-medi	1	3	0.133	6586	slit homolog 3 (Drosophila)
GO	response to cortisol stimulus	1	3	0.133	6586	slit homolog 3 (Drosophila)
GO	Roundabout signaling pathway	1	3	0.133	6586	slit homolog 3 (Drosophila)
GO	miRNA binding	1	3	0.133	6657	SRY (sex determining region Y)-box 2
GO	olfactory placode formation	1	3	0.133	6657	SRY (sex determining region Y)-box 2
GO	positive regulation of epithelial cell diff	1	3	0.133	6657	SRY (sex determining region Y)-box 2
GO	BH domain binding	1	3	0.133	666	BCL2-related ovarian killer
GO	prostate gland morphogenesis	1	3	0.133	6662	SRY (sex determining region Y)-box 9
GO	microtubule severing	1	3	0.133	6683	spastin
GO	common-partner SMAD protein phosph	1	3	0.133	6711	spectrin, beta, non-erythrocytic 1
GO	sulfate assimilation	1	3	0.133	6820	sulfotransferase family, cytosolic, 2B, member 1
GO	potassium ion transmembrane transpor	1	3	0.133	6833	ATP-binding cassette, sub-family C (CFTR/MRP), member 8
GO	positive regulation of transcription fro	1	3	0.133	7021	transcription factor AP-2 beta (activating enhancer binding protein 2 beta)
GO	transforming growth factor beta recept	1	3	0.133	7046	transforming growth factor, beta receptor 1
GO	transforming growth factor beta recept	1	3	0.133	7046	transforming growth factor, beta receptor 1
GO	bleb	1	3	0.133	7168	tropomyosin 1 (alpha)
GO	response to organophosphorus	1	3	0.133	7298	thymidylate synthetase
GO	mesenchymal to epithelial transition	1	3	0.133	7490	Wilms tumor 1
GO	calcium ion-dependent exocytosis of ne	1	3	0.133	773	calcium channel, voltage-dependent, P/Q type, alpha 1A subunit
GO	cellular chloride ion homeostasis	1	3	0.133	773	calcium channel, voltage-dependent, P/Q type, alpha 1A subunit
GO	cerebellar Purkinje cell layer developme	1	3	0.133	773	calcium channel, voltage-dependent, P/Q type, alpha 1A subunit
GO	gamma-aminobutyric acid secretion	1	3	0.133	773	calcium channel, voltage-dependent, P/Q type, alpha 1A subunit
GO	neurotransmitter metabolic process	1	3	0.133	773	calcium channel, voltage-dependent, P/Q type, alpha 1A subunit
GO	retinal rod cell development	1	3	0.133	7840	Alstrom syndrome 1
GO	transferase activity, transferring acyl gr	1	3	0.133	79071	ELOVL family member 6, elongation of long chain fatty acids (FEN1/Elo2, S
GO	maintenance of mitotic sister chromati	1	3	0.133	79075	defective in sister chromatid cohesion 1 homolog (S. cerevisiae)
GO	spermidine biosynthetic process	1	3	0.133	79814	agmatine ureohydrolase (agmatinase)
GO	phagocytosis, recognition	1	3	0.133	81035	collectin sub-family member 12
GO	ER to Golgi transport vesicle	1	3	0.133	81562	lectin, mannose-binding 2-like
GO	ribonucleoside binding	1	3	0.133	84172	polymerase (RNA) I polypeptide B, 128kDa
GO	malate-aspartate shuttle	1	3	0.133	8604	solute carrier family 25 (mitochondrial carrier, Aralar), member 12
GO	negative regulation of keratinocyte diff	1	3	0.133	8626	tumor protein p63
GO	replicative cell aging	1	3	0.133	8626	tumor protein p63
GO	response to tumor cell	1	3	0.133	8626	tumor protein p63
GO	proline catabolic process	1	3	0.133	8659	aldehyde dehydrogenase 4 family, member A1

GO	growth hormone receptor signaling pat	1	3	0.133	8835	suppressor of cytokine signaling 2
GO	female pronucleus	1	3	0.133	890	cyclin A2
GO	cellular response to nutrient	1	3	0.133	898	cyclin E1
GO	response to vitamin E	1	3	0.133	898	cyclin E1
GO	regulation of dendrite development	1	3	0.133	8997	kalirin, RhoGEF kinase
GO	Fanconi anaemia nuclear complex	1	3	0.133	91442	chromosome 19 open reading frame 40
GO	negative regulation of estrogen recepto	1	3	0.133	9420	cytochrome P450, family 7, subfamily B, polypeptide 1
GO	sodium:bicarbonate symporter activity	1	3	0.133	9497	solute carrier family 4, sodium bicarbonate cotransporter, member 7
GO	GABA-B receptor activity	1	3	0.133	9568	gamma-aminobutyric acid (GABA) B receptor, 2
GO	apoptosis	26	444	0.134	132851	spermatogenesis associated 4
GO	apoptosis	26	444	0.134	2139	eyes absent homolog 2 (Drosophila)
GO	apoptosis	26	444	0.134	220042	chromosome 11 open reading frame 82
GO	apoptosis	26	444	0.134	22868	FAST kinase domains 2
GO	apoptosis	26	444	0.134	23705	cell adhesion molecule 1
GO	apoptosis	26	444	0.134	26230	T-cell lymphoma invasion and metastasis 2
GO	apoptosis	26	444	0.134	26586	cytoskeleton associated protein 2
GO	apoptosis	26	444	0.134	26999	cytoplasmic FMR1 interacting protein 2
GO	apoptosis	26	444	0.134	2736	GLI family zinc finger 2
GO	apoptosis	26	444	0.134	30011	SH3-domain kinase binding protein 1
GO	apoptosis	26	444	0.134	332	baculoviral IAP repeat-containing 5
GO	apoptosis	26	444	0.134	355	Fas (TNF receptor superfamily, member 6)
GO	apoptosis	26	444	0.134	51499	TP53 regulated inhibitor of apoptosis 1
GO	apoptosis	26	444	0.134	57099	apoptosis, caspase activation inhibitor
GO	apoptosis	26	444	0.134	5924	Ras protein-specific guanine nucleotide-releasing factor 2
GO	apoptosis	26	444	0.134	6242	rhotekin
GO	apoptosis	26	444	0.134	64393	zinc finger, matrin type 3
GO	apoptosis	26	444	0.134	64782	apoptosis enhancing nuclease
GO	apoptosis	26	444	0.134	666	BCL2-related ovarian killer
GO	apoptosis	26	444	0.134	672	breast cancer 1, early onset
GO	apoptosis	26	444	0.134	70	actin, alpha, cardiac muscle 1
GO	apoptosis	26	444	0.134	7840	Alstrom syndrome 1
GO	apoptosis	26	444	0.134	8626	tumor protein p63
GO	apoptosis	26	444	0.134	8997	kalirin, RhoGEF kinase
GO	apoptosis	26	444	0.134	9262	serine/threonine kinase 17b
GO	apoptosis	26	444	0.134	94241	tumor protein p53 inducible nuclear protein 1
GO	double-stranded DNA binding	6	75	0.135	2237	flap structure-specific endonuclease 1

GO	double-stranded DNA binding	6	75	0.135	3149	high-mobility group box 3
GO	double-stranded DNA binding	6	75	0.135	4436	mutS homolog 2, colon cancer, nonpolyposis type 1 (E. coli)
GO	double-stranded DNA binding	6	75	0.135	5303	protein (peptidylprolyl cis/trans isomerase) NIMA-interacting, 4 (parvulin)
GO	double-stranded DNA binding	6	75	0.135	7490	Wilms tumor 1
GO	double-stranded DNA binding	6	75	0.135	8626	tumor protein p63
GO	regulation of axonogenesis	2	14	0.136	1000	cadherin 2, type 1, N-cadherin (neuronal)
GO	regulation of axonogenesis	2	14	0.136	773	calcium channel, voltage-dependent, P/Q type, alpha 1A subunit
GO	senescence	2	14	0.136	1026	cyclin-dependent kinase inhibitor 1A (p21, Cip1)
GO	senescence	2	14	0.136	2305	forkhead box M1
GO	synaptic transmission, cholinergic	2	14	0.136	1136	cholinergic receptor, nicotinic, alpha 3
GO	synaptic transmission, cholinergic	2	14	0.136	348	apolipoprotein E
GO	selenium binding	2	14	0.136	1733	deiodinase, iodothyronine, type I
GO	selenium binding	2	14	0.136	2878	glutathione peroxidase 3 (plasma)
GO	DNA methylation	2	14	0.136	1787	tRNA aspartic acid methyltransferase 1
GO	DNA methylation	2	14	0.136	1788	DNA (cytosine-5-)-methyltransferase 3 alpha
GO	regulation of sensory perception of pair	2	14	0.136	2149	coagulation factor II (thrombin) receptor
GO	regulation of sensory perception of pair	2	14	0.136	2906	glutamate receptor, ionotropic, N-methyl D-aspartate 2D
GO	acyl-CoA metabolic process	2	14	0.136	23305	acyl-CoA synthetase long-chain family member 6
GO	acyl-CoA metabolic process	2	14	0.136	57678	glycerol-3-phosphate acyltransferase, mitochondrial
GO	isoprenoid biosynthetic process	2	14	0.136	23590	prenyl (decaprenyl) diphosphate synthase, subunit 1
GO	isoprenoid biosynthetic process	2	14	0.136	3157	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 (soluble)
GO	behavioral fear response	2	14	0.136	2558	gamma-aminobutyric acid (GABA) A receptor, alpha 5
GO	behavioral fear response	2	14	0.136	2898	glutamate receptor, ionotropic, kainate 2
GO	regulation of action potential in neuron	2	14	0.136	2898	glutamate receptor, ionotropic, kainate 2
GO	regulation of action potential in neuron	2	14	0.136	3778	potassium large conductance calcium-activated channel, subfamily M, alph
GO	kinesin complex	2	14	0.136	3797	kinesin family member 3C
GO	kinesin complex	2	14	0.136	3800	kinesin family member 5C
GO	Wnt-protein binding	2	14	0.136	6422	secreted frizzled-related protein 1
GO	Wnt-protein binding	2	14	0.136	8325	frizzled homolog 8 (Drosophila)
GO	dystrophin-associated glycoprotein com	2	14	0.136	6442	sarcoglycan, alpha (50kDa dystrophin-associated glycoprotein)
GO	dystrophin-associated glycoprotein com	2	14	0.136	6444	sarcoglycan, delta (35kDa dystrophin-associated glycoprotein)
GO	DNA damage response, signal transduct	2	14	0.136	64782	apoptosis enhancing nuclease
GO	DNA damage response, signal transduct	2	14	0.136	8626	tumor protein p63
GO	cell fate specification	2	14	0.136	6657	SRY (sex determining region Y)-box 2
GO	cell fate specification	2	14	0.136	6662	SRY (sex determining region Y)-box 9
GO	ubiquitin-protein ligase activity	10	145	0.138	1161	excision repair cross-complementing rodent repair deficiency, complement

GO	ubiquitin-protein ligase activity	10	145	0.138	130507	ubiquitin protein ligase E3 component n-recognin 3 (putative)
GO	ubiquitin-protein ligase activity	10	145	0.138	1643	damage-specific DNA binding protein 2, 48kDa
GO	ubiquitin-protein ligase activity	10	145	0.138	23194	F-box and leucine-rich repeat protein 7
GO	ubiquitin-protein ligase activity	10	145	0.138	25827	F-box and leucine-rich repeat protein 2
GO	ubiquitin-protein ligase activity	10	145	0.138	26223	F-box and leucine-rich repeat protein 21 (gene/pseudogene)
GO	ubiquitin-protein ligase activity	10	145	0.138	26263	F-box protein 22
GO	ubiquitin-protein ligase activity	10	145	0.138	4734	neural precursor cell expressed, developmentally down-regulated 4
GO	ubiquitin-protein ligase activity	10	145	0.138	672	breast cancer 1, early onset
GO	ubiquitin-protein ligase activity	10	145	0.138	7324	ubiquitin-conjugating enzyme E2E 1 (UBC4/5 homolog, yeast)
GO	nuclear mRNA splicing, via spliceosome	4	43	0.138	10212	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39
GO	nuclear mRNA splicing, via spliceosome	4	43	0.138	10465	peptidylprolyl isomerase H (cyclophilin H)
GO	nuclear mRNA splicing, via spliceosome	4	43	0.138	3183	heterogeneous nuclear ribonucleoprotein C (C1/C2)
GO	nuclear mRNA splicing, via spliceosome	4	43	0.138	79833	gem (nuclear organelle) associated protein 6
GO	nucleoside-triphosphatase activity	5	59	0.138	5000	origin recognition complex, subunit 4-like (yeast)
GO	nucleoside-triphosphatase activity	5	59	0.138	55137	fidgetin
GO	nucleoside-triphosphatase activity	5	59	0.138	5702	proteasome (prosome, macropain) 26S subunit, ATPase, 3
GO	nucleoside-triphosphatase activity	5	59	0.138	5889	RAD51 homolog C (S. cerevisiae)
GO	nucleoside-triphosphatase activity	5	59	0.138	6683	spastin
GO	single fertilization	3	28	0.139	1047	calmegin
GO	single fertilization	3	28	0.139	53340	sperm autoantigenic protein 17
GO	single fertilization	3	28	0.139	8747	ADAM metallopeptidase domain 21
GO	regulation of cell migration	3	28	0.139	10672	guanine nucleotide binding protein (G protein), alpha 13
GO	regulation of cell migration	3	28	0.139	182	jagged 1 (Alagille syndrome)
GO	regulation of cell migration	3	28	0.139	91624	nexilin (F actin binding protein)
GO	RNA polymerase II transcription mediat	3	28	0.139	116931	mediator complex subunit 12-like
GO	RNA polymerase II transcription mediat	3	28	0.139	51003	mediator complex subunit 31
GO	RNA polymerase II transcription mediat	3	28	0.139	5469	mediator complex subunit 1
GO	camera-type eye development	3	28	0.139	1543	cytochrome P450, family 1, subfamily A, polypeptide 1
GO	camera-type eye development	3	28	0.139	5469	mediator complex subunit 1
GO	camera-type eye development	3	28	0.139	7490	Wilms tumor 1
GO	integrin complex	3	28	0.139	22801	integrin, alpha 11
GO	integrin complex	3	28	0.139	3685	integrin, alpha V (vitronectin receptor, alpha polypeptide, antigen CD51)
GO	integrin complex	3	28	0.139	3694	integrin, beta 6
GO	lactation	3	28	0.139	4830	non-metastatic cells 1, protein (NM23A) expressed in
GO	lactation	3	28	0.139	5021	oxytocin receptor
GO	lactation	3	28	0.139	5469	mediator complex subunit 1

GO	protein oligomerization	3	28	0.139	6241	ribonucleotide reductase M2
GO	protein oligomerization	3	28	0.139	641	Bloom syndrome, RecQ helicase-like
GO	protein oligomerization	3	28	0.139	7010	TEK tyrosine kinase, endothelial
GO	nucleus	234	4735	0.14	1E+08	forkhead box O6
GO	nucleus	234	4735	0.14	10051	structural maintenance of chromosomes 4
GO	nucleus	234	4735	0.14	10055	SUMO1 activating enzyme subunit 1
GO	nucleus	234	4735	0.14	10123	ADP-ribosylation factor-like 4C
GO	nucleus	234	4735	0.14	10189	THO complex 4
GO	nucleus	234	4735	0.14	10199	M-phase phosphoprotein 10 (U3 small nucleolar ribonucleoprotein)
GO	nucleus	234	4735	0.14	10202	dehydrogenase/reductase (SDR family) member 2
GO	nucleus	234	4735	0.14	10212	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39
GO	nucleus	234	4735	0.14	1026	cyclin-dependent kinase inhibitor 1A (p21, Cip1)
GO	nucleus	234	4735	0.14	10395	deleted in liver cancer 1
GO	nucleus	234	4735	0.14	1045	caudal type homeobox 2
GO	nucleus	234	4735	0.14	10465	peptidylprolyl isomerase H (cyclophilin H)
GO	nucleus	234	4735	0.14	10474	transcriptional adaptor 3
GO	nucleus	234	4735	0.14	10492	synaptotagmin binding, cytoplasmic RNA interacting protein
GO	nucleus	234	4735	0.14	10528	NOP56 ribonucleoprotein homolog (yeast)
GO	nucleus	234	4735	0.14	10622	polymerase (RNA) III (DNA directed) polypeptide G (32kD)
GO	nucleus	234	4735	0.14	10656	KH domain containing, RNA binding, signal transduction associated 3
GO	nucleus	234	4735	0.14	10785	WD repeat domain 4
GO	nucleus	234	4735	0.14	10799	ribonuclease P/MRP 40kDa subunit
GO	nucleus	234	4735	0.14	11056	DEAD (Asp-Glu-Ala-Asp) box polypeptide 52
GO	nucleus	234	4735	0.14	11169	WD repeat and HMG-box DNA binding protein 1
GO	nucleus	234	4735	0.14	11259	filamin A interacting protein 1-like
GO	nucleus	234	4735	0.14	11278	Kruppel-like factor 12
GO	nucleus	234	4735	0.14	113130	cell division cycle associated 5
GO	nucleus	234	4735	0.14	1161	excision repair cross-complementing rodent repair deficiency, complement
GO	nucleus	234	4735	0.14	116931	mediator complex subunit 12-like
GO	nucleus	234	4735	0.14	118924	chromosome 10 open reading frame 4
GO	nucleus	234	4735	0.14	12	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), me
GO	nucleus	234	4735	0.14	126374	Wilms tumor 1 interacting protein
GO	nucleus	234	4735	0.14	132625	zinc finger protein 42 homolog (mouse)
GO	nucleus	234	4735	0.14	135114	histidine triad nucleotide binding protein 3
GO	nucleus	234	4735	0.14	135295	splicing factor, arginine/serine-rich 13B
GO	nucleus	234	4735	0.14	139324	highly divergent homeobox

GO	nucleus	234	4735	0.14	148213	zinc finger protein 681
GO	nucleus	234	4735	0.14	150684	copper metabolism (Murr1) domain containing 1
GO	nucleus	234	4735	0.14	157570	establishment of cohesion 1 homolog 2 (S. cerevisiae)
GO	nucleus	234	4735	0.14	1643	damage-specific DNA binding protein 2, 48kDa
GO	nucleus	234	4735	0.14	166336	prickle homolog 2 (Drosophila)
GO	nucleus	234	4735	0.14	170082	transcription elongation factor A (SII) N-terminal and central domain contai
GO	nucleus	234	4735	0.14	1746	distal-less homeobox 2
GO	nucleus	234	4735	0.14	1787	tRNA aspartic acid methyltransferase 1
GO	nucleus	234	4735	0.14	1788	DNA (cytosine-5-)-methyltransferase 3 alpha
GO	nucleus	234	4735	0.14	195828	zinc finger protein 367
GO	nucleus	234	4735	0.14	1984	eukaryotic translation initiation factor 5A
GO	nucleus	234	4735	0.14	201299	RAD52 motif 1
GO	nucleus	234	4735	0.14	203	adenylate kinase 1
GO	nucleus	234	4735	0.14	2139	eyes absent homolog 2 (Drosophila)
GO	nucleus	234	4735	0.14	219736	storkhead box 1
GO	nucleus	234	4735	0.14	220042	chromosome 11 open reading frame 82
GO	nucleus	234	4735	0.14	2237	flap structure-specific endonuclease 1
GO	nucleus	234	4735	0.14	2273	four and a half LIM domains 1
GO	nucleus	234	4735	0.14	2305	forkhead box M1
GO	nucleus	234	4735	0.14	23305	acyl-CoA synthetase long-chain family member 6
GO	nucleus	234	4735	0.14	23594	origin recognition complex, subunit 6 like (yeast)
GO	nucleus	234	4735	0.14	23658	LSM5 homolog, U6 small nuclear RNA associated (S. cerevisiae)
GO	nucleus	234	4735	0.14	241	arachidonate 5-lipoxygenase-activating protein
GO	nucleus	234	4735	0.14	2533	FYN binding protein (FYB-120/130)
GO	nucleus	234	4735	0.14	25758	chromosome 11 open reading frame 41
GO	nucleus	234	4735	0.14	25885	polymerase (RNA) I polypeptide A, 194kDa
GO	nucleus	234	4735	0.14	25926	nucleolar protein 11
GO	nucleus	234	4735	0.14	25953	paroxysmal nonkinesigenic dyskinesia
GO	nucleus	234	4735	0.14	26019	UPF2 regulator of nonsense transcripts homolog (yeast)
GO	nucleus	234	4735	0.14	27065	DNA segment on chromosome 4 (unique) 234 expressed sequence
GO	nucleus	234	4735	0.14	27244	sestrin 1
GO	nucleus	234	4735	0.14	27258	LSM3 homolog, U6 small nuclear RNA associated (S. cerevisiae)
GO	nucleus	234	4735	0.14	2736	GLI family zinc finger 2
GO	nucleus	234	4735	0.14	27429	HtrA serine peptidase 2
GO	nucleus	234	4735	0.14	2842	G protein-coupled receptor 19
GO	nucleus	234	4735	0.14	284443	zinc finger protein 493

GO	nucleus	234	4735	0.14	28984	chromosome 13 open reading frame 15
GO	nucleus	234	4735	0.14	29128	ubiquitin-like with PHD and ring finger domains 1
GO	nucleus	234	4735	0.14	2965	general transcription factor IIH, polypeptide 1, 62kDa
GO	nucleus	234	4735	0.14	29842	transcription factor CP2-like 1
GO	nucleus	234	4735	0.14	29893	PSMC3 interacting protein
GO	nucleus	234	4735	0.14	29995	LIM and cysteine-rich domains 1
GO	nucleus	234	4735	0.14	30011	SH3-domain kinase binding protein 1
GO	nucleus	234	4735	0.14	3149	high-mobility group box 3
GO	nucleus	234	4735	0.14	3183	heterogeneous nuclear ribonucleoprotein C (C1/C2)
GO	nucleus	234	4735	0.14	3224	homeobox C8
GO	nucleus	234	4735	0.14	3236	homeobox D10
GO	nucleus	234	4735	0.14	3237	homeobox D11
GO	nucleus	234	4735	0.14	3248	hydroxyprostaglandin dehydrogenase 15-(NAD)
GO	nucleus	234	4735	0.14	3276	protein arginine methyltransferase 1
GO	nucleus	234	4735	0.14	332	baculoviral IAP repeat-containing 5
GO	nucleus	234	4735	0.14	344191	even-skipped homeobox 2
GO	nucleus	234	4735	0.14	345630	fibrillarin-like 1
GO	nucleus	234	4735	0.14	347902	adhesion molecule with Ig-like domain 2
GO	nucleus	234	4735	0.14	3516	recombination signal binding protein for immunoglobulin kappa J region
GO	nucleus	234	4735	0.14	3836	karyopherin alpha 1 (importin alpha 5)
GO	nucleus	234	4735	0.14	3838	karyopherin alpha 2 (RAG cohort 1, importin alpha 1)
GO	nucleus	234	4735	0.14	387103	centromere protein W
GO	nucleus	234	4735	0.14	389421	lin-28 homolog B (C. elegans)
GO	nucleus	234	4735	0.14	3975	LIM homeobox 1
GO	nucleus	234	4735	0.14	406	aryl hydrocarbon receptor nuclear translocator-like
GO	nucleus	234	4735	0.14	409	arrestin, beta 2
GO	nucleus	234	4735	0.14	4094	v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian)
GO	nucleus	234	4735	0.14	4171	minichromosome maintenance complex component 2
GO	nucleus	234	4735	0.14	4287	ataxin 3
GO	nucleus	234	4735	0.14	4291	myeloid leukemia factor 1
GO	nucleus	234	4735	0.14	4292	mutL homolog 1, colon cancer, nonpolyposis type 2 (E. coli)
GO	nucleus	234	4735	0.14	431707	LIM homeobox 8
GO	nucleus	234	4735	0.14	4436	mutS homolog 2, colon cancer, nonpolyposis type 1 (E. coli)
GO	nucleus	234	4735	0.14	4603	v-myb myeloblastosis viral oncogene homolog (avian)-like 1
GO	nucleus	234	4735	0.14	4763	neurofibromin 1
GO	nucleus	234	4735	0.14	4830	non-metastatic cells 1, protein (NM23A) expressed in

GO	nucleus	234	4735	0.14	4928	nucleoporin 98kDa
GO	nucleus	234	4735	0.14	4968	8-oxoguanine DNA glycosylase
GO	nucleus	234	4735	0.14	5000	origin recognition complex, subunit 4-like (yeast)
GO	nucleus	234	4735	0.14	5015	orthodenticle homeobox 2
GO	nucleus	234	4735	0.14	50485	SWI/SNF related, matrix associated, actin dependent regulator of chromati
GO	nucleus	234	4735	0.14	5081	paired box 7
GO	nucleus	234	4735	0.14	51003	mediator complex subunit 31
GO	nucleus	234	4735	0.14	51177	pleckstrin homology domain containing, family O member 1
GO	nucleus	234	4735	0.14	51213	leucine zipper protein 4
GO	nucleus	234	4735	0.14	51339	dapper, antagonist of beta-catenin, homolog 1 (Xenopus laevis)
GO	nucleus	234	4735	0.14	51460	Scm-like with four mbt domains 1
GO	nucleus	234	4735	0.14	51491	NOP16 nucleolar protein homolog (yeast)
GO	nucleus	234	4735	0.14	5216	profilin 1
GO	nucleus	234	4735	0.14	5245	prohibitin
GO	nucleus	234	4735	0.14	5303	protein (peptidylprolyl cis/trans isomerase) NIMA-interacting, 4 (parvulin)
GO	nucleus	234	4735	0.14	5378	PMS1 postmeiotic segregation increased 1 (S. cerevisiae)
GO	nucleus	234	4735	0.14	53981	cleavage and polyadenylation specific factor 2, 100kDa
GO	nucleus	234	4735	0.14	5440	polymerase (RNA) II (DNA directed) polypeptide K, 7.0kDa
GO	nucleus	234	4735	0.14	5469	mediator complex subunit 1
GO	nucleus	234	4735	0.14	54796	basonuclin 2
GO	nucleus	234	4735	0.14	54828	breast carcinoma amplified sequence 3
GO	nucleus	234	4735	0.14	54984	PIN2-interacting protein 1
GO	nucleus	234	4735	0.14	54993	zinc finger and SCAN domain containing 2
GO	nucleus	234	4735	0.14	55003	PAK1 interacting protein 1
GO	nucleus	234	4735	0.14	55012	protein phosphatase 2 (formerly 2A), regulatory subunit B'', gamma
GO	nucleus	234	4735	0.14	55135	WD repeat containing, antisense to TP53
GO	nucleus	234	4735	0.14	55137	fidgetin
GO	nucleus	234	4735	0.14	55215	Fanconi anemia, complementation group I
GO	nucleus	234	4735	0.14	55323	La ribonucleoprotein domain family, member 6
GO	nucleus	234	4735	0.14	55506	H2A histone family, member Y2
GO	nucleus	234	4735	0.14	5569	protein kinase (cAMP-dependent, catalytic) inhibitor alpha
GO	nucleus	234	4735	0.14	55759	WD repeat domain 12
GO	nucleus	234	4735	0.14	55854	zinc finger CCCH-type containing 15
GO	nucleus	234	4735	0.14	5588	protein kinase C, theta
GO	nucleus	234	4735	0.14	55916	nuclear transport factor 2-like export factor 2
GO	nucleus	234	4735	0.14	56339	methyltransferase like 3

GO	nucleus	234	4735	0.14	56655	polymerase (DNA-directed), epsilon 4 (p12 subunit)
GO	nucleus	234	4735	0.14	56852	RAD18 homolog (S. cerevisiae)
GO	nucleus	234	4735	0.14	56902	partner of NOB1 homolog (S. cerevisiae)
GO	nucleus	234	4735	0.14	5702	proteasome (prosome, macropain) 26S subunit, ATPase, 3
GO	nucleus	234	4735	0.14	5744	parathyroid hormone-like hormone
GO	nucleus	234	4735	0.14	57590	WD repeat and FYVE domain containing 1
GO	nucleus	234	4735	0.14	57599	WD repeat domain 48
GO	nucleus	234	4735	0.14	5795	protein tyrosine phosphatase, receptor type, J
GO	nucleus	234	4735	0.14	58155	polypyrimidine tract binding protein 2
GO	nucleus	234	4735	0.14	58499	zinc finger protein 462
GO	nucleus	234	4735	0.14	5889	RAD51 homolog C (S. cerevisiae)
GO	nucleus	234	4735	0.14	59336	PR domain containing 13
GO	nucleus	234	4735	0.14	5965	RecQ protein-like (DNA helicase Q1-like)
GO	nucleus	234	4735	0.14	6000	regulator of G-protein signaling 7
GO	nucleus	234	4735	0.14	6299	sal-like 1 (Drosophila)
GO	nucleus	234	4735	0.14	641	Bloom syndrome, RecQ helicase-like
GO	nucleus	234	4735	0.14	64151	non-SMC condensin I complex, subunit G
GO	nucleus	234	4735	0.14	64318	nucleolar complex associated 3 homolog (S. cerevisiae)
GO	nucleus	234	4735	0.14	64393	zinc finger, matrin type 3
GO	nucleus	234	4735	0.14	644890	meiosis expressed gene 1 homolog (mouse)
GO	nucleus	234	4735	0.14	6474	short stature homeobox 2
GO	nucleus	234	4735	0.14	64782	apoptosis enhancing nuclease
GO	nucleus	234	4735	0.14	64785	GINS complex subunit 3 (Psf3 homolog)
GO	nucleus	234	4735	0.14	6591	snail homolog 2 (Drosophila)
GO	nucleus	234	4735	0.14	6615	snail homolog 1 (Drosophila)
GO	nucleus	234	4735	0.14	6637	small nuclear ribonucleoprotein polypeptide G
GO	nucleus	234	4735	0.14	6657	SRY (sex determining region Y)-box 2
GO	nucleus	234	4735	0.14	6659	SRY (sex determining region Y)-box 4
GO	nucleus	234	4735	0.14	6662	SRY (sex determining region Y)-box 9
GO	nucleus	234	4735	0.14	6672	SP100 nuclear antigen
GO	nucleus	234	4735	0.14	6683	spastin
GO	nucleus	234	4735	0.14	6711	spectrin, beta, non-erythrocytic 1
GO	nucleus	234	4735	0.14	672	breast cancer 1, early onset
GO	nucleus	234	4735	0.14	6741	Sjogren syndrome antigen B (autoantigen La)
GO	nucleus	234	4735	0.14	6899	T-box 1
GO	nucleus	234	4735	0.14	7021	transcription factor AP-2 beta (activating enhancer binding protein 2 beta)

GO	nucleus	234	4735	0.14	7029	transcription factor Dp-2 (E2F dimerization partner 2)
GO	nucleus	234	4735	0.14	7341	SMT3 suppressor of mif two 3 homolog 1 (S. cerevisiae)
GO	nucleus	234	4735	0.14	7353	ubiquitin fusion degradation 1 like (yeast)
GO	nucleus	234	4735	0.14	7490	Wilms tumor 1
GO	nucleus	234	4735	0.14	7552	zinc finger protein 711
GO	nucleus	234	4735	0.14	7711	zinc finger protein 155
GO	nucleus	234	4735	0.14	773	calcium channel, voltage-dependent, P/Q type, alpha 1A subunit
GO	nucleus	234	4735	0.14	79075	defective in sister chromatid cohesion 1 homolog (S. cerevisiae)
GO	nucleus	234	4735	0.14	79172	centromere protein O
GO	nucleus	234	4735	0.14	79187	fibronectin type III and SPRY domain containing 1
GO	nucleus	234	4735	0.14	79677	structural maintenance of chromosomes 6
GO	nucleus	234	4735	0.14	79682	MLF1 interacting protein
GO	nucleus	234	4735	0.14	79698	zinc finger, matrin type 4
GO	nucleus	234	4735	0.14	79833	gem (nuclear organelle) associated protein 6
GO	nucleus	234	4735	0.14	80712	ESX homeobox 1
GO	nucleus	234	4735	0.14	8091	high mobility group AT-hook 2
GO	nucleus	234	4735	0.14	81606	limb bud and heart development homolog (mouse)
GO	nucleus	234	4735	0.14	81786	tripartite motif-containing 7
GO	nucleus	234	4735	0.14	81892	chromosome 14 open reading frame 156
GO	nucleus	234	4735	0.14	8193	D4, zinc and double PHD fingers family 1
GO	nucleus	234	4735	0.14	8348	histone cluster 1, H2bo
GO	nucleus	234	4735	0.14	8349	histone cluster 2, H2be
GO	nucleus	234	4735	0.14	83879	cell division cycle associated 7
GO	nucleus	234	4735	0.14	8409	ubiquitously-expressed transcript
GO	nucleus	234	4735	0.14	84101	ubiquitin specific peptidase 44
GO	nucleus	234	4735	0.14	84172	polymerase (RNA) I polypeptide B, 128kDa
GO	nucleus	234	4735	0.14	84206	mex-3 homolog B (C. elegans)
GO	nucleus	234	4735	0.14	84296	GINS complex subunit 4 (Sld5 homolog)
GO	nucleus	234	4735	0.14	84365	MKI67 (FHA domain) interacting nucleolar phosphoprotein
GO	nucleus	234	4735	0.14	8458	transcription termination factor, RNA polymerase II
GO	nucleus	234	4735	0.14	84622	zinc finger protein 594
GO	nucleus	234	4735	0.14	84665	myopalladin
GO	nucleus	234	4735	0.14	84878	zinc finger and BTB domain containing 45
GO	nucleus	234	4735	0.14	84959	ubiquitin associated and SH3 domain containing, B
GO	nucleus	234	4735	0.14	8520	histone acetyltransferase 1
GO	nucleus	234	4735	0.14	8533	COP9 constitutive photomorphogenic homolog subunit 3 (Arabidopsis)

GO	nucleus	234	4735	0.14	8536	calcium/calmodulin-dependent protein kinase I
GO	nucleus	234	4735	0.14	8563	THO complex 5
GO	nucleus	234	4735	0.14	8626	tumor protein p63
GO	nucleus	234	4735	0.14	890	cyclin A2
GO	nucleus	234	4735	0.14	8970	histone cluster 1, H2bj
GO	nucleus	234	4735	0.14	89797	neuron navigator 2
GO	nucleus	234	4735	0.14	898	cyclin E1
GO	nucleus	234	4735	0.14	91442	chromosome 19 open reading frame 40
GO	nucleus	234	4735	0.14	91801	alkB, alkylation repair homolog 8 (E. coli)
GO	nucleus	234	4735	0.14	91975	zinc finger protein 300
GO	nucleus	234	4735	0.14	92312	mex-3 homolog A (C. elegans)
GO	nucleus	234	4735	0.14	9242	musculin (activated B-cell factor-1)
GO	nucleus	234	4735	0.14	9262	serine/threonine kinase 17b
GO	nucleus	234	4735	0.14	93474	zinc finger protein 670
GO	nucleus	234	4735	0.14	9355	LIM homeobox 2
GO	nucleus	234	4735	0.14	93649	myocardin
GO	nucleus	234	4735	0.14	94241	tumor protein p53 inducible nuclear protein 1
GO	nucleus	234	4735	0.14	9688	nucleoporin 93kDa
GO	nucleus	234	4735	0.14	9805	secernin 1
GO	nucleus	234	4735	0.14	9839	zinc finger E-box binding homeobox 2
GO	nucleus	234	4735	0.14	9910	RAB GTPase activating protein 1-like
GO	cellular calcium ion homeostasis	5	60	0.145	2898	glutamate receptor, ionotropic, kainate 2
GO	cellular calcium ion homeostasis	5	60	0.145	348	apolipoprotein E
GO	cellular calcium ion homeostasis	5	60	0.145	6347	chemokine (C-C motif) ligand 2
GO	cellular calcium ion homeostasis	5	60	0.145	6546	solute carrier family 8 (sodium/calcium exchanger), member 1
GO	cellular calcium ion homeostasis	5	60	0.145	7137	troponin I type 3 (cardiac)
GO	pattern specification process	4	44	0.146	1045	caudal type homeobox 2
GO	pattern specification process	4	44	0.146	2736	GLI family zinc finger 2
GO	pattern specification process	4	44	0.146	3237	homeobox D11
GO	pattern specification process	4	44	0.146	8626	tumor protein p63
GO	ubiquitin protein ligase binding	4	44	0.146	2898	glutamate receptor, ionotropic, kainate 2
GO	ubiquitin protein ligase binding	4	44	0.146	409	arrestin, beta 2
GO	ubiquitin protein ligase binding	4	44	0.146	56852	RAD18 homolog (S. cerevisiae)
GO	ubiquitin protein ligase binding	4	44	0.146	7046	transforming growth factor, beta receptor 1
GO	scavenger receptor activity	4	44	0.146	56241	sushi domain containing 2
GO	scavenger receptor activity	4	44	0.146	7113	transmembrane protease, serine 2

GO	scavenger receptor activity	4	44	0.146	81035	collectin sub-family member 12
GO	scavenger receptor activity	4	44	0.146	8685	macrophage receptor with collagenous structure
GO	protein homotetramerization	3	29	0.15	2878	glutathione peroxidase 3 (plasma)
GO	protein homotetramerization	3	29	0.15	3028	hydroxysteroid (17-beta) dehydrogenase 10
GO	protein homotetramerization	3	29	0.15	8626	tumor protein p63
GO	androgen receptor binding	3	29	0.15	29893	PSMC3 interacting protein
GO	androgen receptor binding	3	29	0.15	672	breast cancer 1, early onset
GO	androgen receptor binding	3	29	0.15	898	cyclin E1
GO	metanephros development	3	29	0.15	3237	homeobox D11
GO	metanephros development	3	29	0.15	4763	neurofibromin 1
GO	metanephros development	3	29	0.15	7490	Wilms tumor 1
GO	chaperone binding	3	29	0.15	332	baculoviral IAP repeat-containing 5
GO	chaperone binding	3	29	0.15	3336	heat shock 10kDa protein 1 (chaperonin 10)
GO	chaperone binding	3	29	0.15	5203	prefoldin subunit 4
GO	ruffle membrane	3	29	0.15	3936	lymphocyte cytosolic protein 1 (L-plastin)
GO	ruffle membrane	3	29	0.15	5341	pleckstrin
GO	ruffle membrane	3	29	0.15	7168	tropomyosin 1 (alpha)
GO	neuronal cell body	10	148	0.151	1136	cholinergic receptor, nicotinic, alpha 3
GO	neuronal cell body	10	148	0.151	1138	cholinergic receptor, nicotinic, alpha 5
GO	neuronal cell body	10	148	0.151	114757	cytoglobin
GO	neuronal cell body	10	148	0.151	1984	eukaryotic translation initiation factor 5A
GO	neuronal cell body	10	148	0.151	2045	EPH receptor A7
GO	neuronal cell body	10	148	0.151	348	apolipoprotein E
GO	neuronal cell body	10	148	0.151	3751	potassium voltage-gated channel, Shal-related subfamily, member 2
GO	neuronal cell body	10	148	0.151	6347	chemokine (C-C motif) ligand 2
GO	neuronal cell body	10	148	0.151	8997	kalirin, RhoGEF kinase
GO	neuronal cell body	10	148	0.151	92737	delta/notch-like EGF repeat containing
GO	cellular response to extracellular stimulu	2	15	0.152	1026	cyclin-dependent kinase inhibitor 1A (p21, Cip1)
GO	cellular response to extracellular stimulu	2	15	0.152	558	AXL receptor tyrosine kinase
GO	neural tube development	2	15	0.152	10512	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (
GO	neural tube development	2	15	0.152	2736	GLI family zinc finger 2
GO	protein disulfide oxidoreductase activity	2	15	0.152	10539	glutaredoxin 3
GO	protein disulfide oxidoreductase activity	2	15	0.152	51218	glutaredoxin 5
GO	acyl-CoA binding	2	15	0.152	1622	diazepam binding inhibitor (GABA receptor modulator, acyl-Coenzyme A bi
GO	acyl-CoA binding	2	15	0.152	414149	acyl-Coenzyme A binding domain containing 7
GO	cellular component organization	2	15	0.152	1730	diaphanous homolog 2 (Drosophila)

GO	cellular component organization	2	15	0.152	81624	diaphanous homolog 3 (Drosophila)
GO	estrogen receptor binding	2	15	0.152	29893	PSMC3 interacting protein
GO	estrogen receptor binding	2	15	0.152	5469	mediator complex subunit 1
GO	protein amino acid methylation	2	15	0.152	3276	protein arginine methyltransferase 1
GO	protein amino acid methylation	2	15	0.152	5110	protein-L-isoaspartate (D-aspartate) O-methyltransferase
GO	male germ cell nucleus	2	15	0.152	4292	mutL homolog 1, colon cancer, nonpolyposis type 2 (E. coli)
GO	male germ cell nucleus	2	15	0.152	641	Bloom syndrome, RecQ helicase-like
GO	phosphatidylinositol-4,5-bisphosphate b	2	15	0.152	54843	synaptotagmin-like 2
GO	phosphatidylinositol-4,5-bisphosphate b	2	15	0.152	55803	ArfGAP with dual PH domains 2
GO	double-strand break repair via homolog	2	15	0.152	641	Bloom syndrome, RecQ helicase-like
GO	double-strand break repair via homolog	2	15	0.152	672	breast cancer 1, early onset
GO	actin filament-based movement	2	15	0.152	70	actin, alpha, cardiac muscle 1
GO	actin filament-based movement	2	15	0.152	7456	WAS/WASL interacting protein family, member 1
GO	ATP-dependent helicase activity	5	61	0.153	10212	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39
GO	ATP-dependent helicase activity	5	61	0.153	11056	DEAD (Asp-Glu-Ala-Asp) box polypeptide 52
GO	ATP-dependent helicase activity	5	61	0.153	641	Bloom syndrome, RecQ helicase-like
GO	ATP-dependent helicase activity	5	61	0.153	84319	chromosome 3 open reading frame 26
GO	ATP-dependent helicase activity	5	61	0.153	8458	transcription termination factor, RNA polymerase II
GO	axonogenesis	5	61	0.153	1496	catenin (cadherin-associated protein), alpha 2
GO	axonogenesis	5	61	0.153	4897	neuronal cell adhesion molecule
GO	axonogenesis	5	61	0.153	51062	atlastin GTPase 1
GO	axonogenesis	5	61	0.153	84189	SLIT and NTRK-like family, member 6
GO	axonogenesis	5	61	0.153	8997	kalirin, RhoGEF kinase
GO	protein tyrosine kinase activity	6	78	0.154	2045	EPH receptor A7
GO	protein tyrosine kinase activity	6	78	0.154	2242	feline sarcoma oncogene
GO	protein tyrosine kinase activity	6	78	0.154	2264	fibroblast growth factor receptor 4
GO	protein tyrosine kinase activity	6	78	0.154	2534	FYN oncogene related to SRC, FGR, YES
GO	protein tyrosine kinase activity	6	78	0.154	3932	lymphocyte-specific protein tyrosine kinase
GO	protein tyrosine kinase activity	6	78	0.154	7010	TEK tyrosine kinase, endothelial
GO	proteinaceous extracellular matrix	14	223	0.157	10893	matrix metallopeptidase 24 (membrane-inserted)
GO	proteinaceous extracellular matrix	14	223	0.157	115908	collagen triple helix repeat containing 1
GO	proteinaceous extracellular matrix	14	223	0.157	145864	hyaluronan and proteoglycan link protein 3
GO	proteinaceous extracellular matrix	14	223	0.157	1690	coagulation factor C homolog, cochlin (Limulus polyphemus)
GO	proteinaceous extracellular matrix	14	223	0.157	221044	upper zone of growth plate and cartilage matrix associated
GO	proteinaceous extracellular matrix	14	223	0.157	23768	fibronectin leucine rich transmembrane protein 2
GO	proteinaceous extracellular matrix	14	223	0.157	4052	latent transforming growth factor beta binding protein 1

GO	proteinaceous extracellular matrix	14	223	0.157	4060	lumican
GO	proteinaceous extracellular matrix	14	223	0.157	4312	matrix metallopeptidase 1 (interstitial collagenase)
GO	proteinaceous extracellular matrix	14	223	0.157	4318	matrix metallopeptidase 9 (gelatinase B, 92kDa gelatinase, 92kDa type IV c
GO	proteinaceous extracellular matrix	14	223	0.157	4319	matrix metallopeptidase 10 (stromelysin 2)
GO	proteinaceous extracellular matrix	14	223	0.157	6695	sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 1
GO	proteinaceous extracellular matrix	14	223	0.157	7481	wingless-type MMTV integration site family, member 11
GO	proteinaceous extracellular matrix	14	223	0.157	81029	wingless-type MMTV integration site family, member 5B
GO	multicellular organismal development	48	890	0.157	10683	delta-like 3 (Drosophila)
GO	multicellular organismal development	48	890	0.157	10761	placenta-specific 1
GO	multicellular organismal development	48	890	0.157	11149	blood vessel epicardial substance
GO	multicellular organismal development	48	890	0.157	120114	FAT tumor suppressor homolog 3 (Drosophila)
GO	multicellular organismal development	48	890	0.157	132671	spermatogenesis associated 18 homolog (rat)
GO	multicellular organismal development	48	890	0.157	1496	catenin (cadherin-associated protein), alpha 2
GO	multicellular organismal development	48	890	0.157	1730	diaphanous homolog 2 (Drosophila)
GO	multicellular organismal development	48	890	0.157	1746	distal-less homeobox 2
GO	multicellular organismal development	48	890	0.157	182	jagged 1 (Alagille syndrome)
GO	multicellular organismal development	48	890	0.157	2139	eyes absent homolog 2 (Drosophila)
GO	multicellular organismal development	48	890	0.157	2242	feline sarcoma oncogene
GO	multicellular organismal development	48	890	0.157	2273	four and a half LIM domains 1
GO	multicellular organismal development	48	890	0.157	2321	fms-related tyrosine kinase 1 (vascular endothelial growth factor/vascular
GO	multicellular organismal development	48	890	0.157	23432	G protein-coupled receptor 161
GO	multicellular organismal development	48	890	0.157	23705	cell adhesion molecule 1
GO	multicellular organismal development	48	890	0.157	2534	FYN oncogene related to SRC, FGR, YES
GO	multicellular organismal development	48	890	0.157	25884	chordin-like 2
GO	multicellular organismal development	48	890	0.157	266727	MAM domain containing glycosylphosphatidylinositol anchor 1
GO	multicellular organismal development	48	890	0.157	3149	high-mobility group box 3
GO	multicellular organismal development	48	890	0.157	3224	homeobox C8
GO	multicellular organismal development	48	890	0.157	3236	homeobox D10
GO	multicellular organismal development	48	890	0.157	344191	even-skipped homeobox 2
GO	multicellular organismal development	48	890	0.157	4291	myeloid leukemia factor 1
GO	multicellular organismal development	48	890	0.157	5015	orthodenticle homeobox 2
GO	multicellular organismal development	48	890	0.157	5081	paired box 7
GO	multicellular organismal development	48	890	0.157	51339	dapper, antagonist of beta-catenin, homolog 1 (Xenopus laevis)
GO	multicellular organismal development	48	890	0.157	5228	placental growth factor
GO	multicellular organismal development	48	890	0.157	5469	mediator complex subunit 1
GO	multicellular organismal development	48	890	0.157	54993	zinc finger and SCAN domain containing 2

GO	multicellular organismal development	48	890	0.157	6422	secreted frizzled-related protein 1
GO	multicellular organismal development	48	890	0.157	6474	short stature homeobox 2
GO	multicellular organismal development	48	890	0.157	65009	NDRG family member 4
GO	multicellular organismal development	48	890	0.157	6586	slit homolog 3 (Drosophila)
GO	multicellular organismal development	48	890	0.157	6591	snail homolog 2 (Drosophila)
GO	multicellular organismal development	48	890	0.157	6615	snail homolog 1 (Drosophila)
GO	multicellular organismal development	48	890	0.157	6683	spastin
GO	multicellular organismal development	48	890	0.157	6695	sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 1
GO	multicellular organismal development	48	890	0.157	7481	wingless-type MMTV integration site family, member 11
GO	multicellular organismal development	48	890	0.157	8091	high mobility group AT-hook 2
GO	multicellular organismal development	48	890	0.157	81029	wingless-type MMTV integration site family, member 5B
GO	multicellular organismal development	48	890	0.157	81606	limb bud and heart development homolog (mouse)
GO	multicellular organismal development	48	890	0.157	8325	frizzled homolog 8 (Drosophila)
GO	multicellular organismal development	48	890	0.157	84620	ST6 beta-galactosamide alpha-2,6-sialyltranferase 2
GO	multicellular organismal development	48	890	0.157	8482	semaphorin 7A, GPI membrane anchor (John Milton Hagen blood group)
GO	multicellular organismal development	48	890	0.157	8536	calcium/calmodulin-dependent protein kinase I
GO	multicellular organismal development	48	890	0.157	8788	delta-like 1 homolog (Drosophila)
GO	multicellular organismal development	48	890	0.157	91584	plexin A4
GO	multicellular organismal development	48	890	0.157	9260	PDZ and LIM domain 7 (enigma)
GO	cell differentiation	27	474	0.16	10672	guanine nucleotide binding protein (G protein), alpha 13
GO	cell differentiation	27	474	0.16	10683	delta-like 3 (Drosophila)
GO	cell differentiation	27	474	0.16	132671	spermatogenesis associated 18 homolog (rat)
GO	cell differentiation	27	474	0.16	1496	catenin (cadherin-associated protein), alpha 2
GO	cell differentiation	27	474	0.16	1730	diaphanous homolog 2 (Drosophila)
GO	cell differentiation	27	474	0.16	1746	distal-less homeobox 2
GO	cell differentiation	27	474	0.16	2273	four and a half LIM domains 1
GO	cell differentiation	27	474	0.16	2321	fms-related tyrosine kinase 1 (vascular endothelial growth factor/vascular
GO	cell differentiation	27	474	0.16	23705	cell adhesion molecule 1
GO	cell differentiation	27	474	0.16	25884	chordin-like 2
GO	cell differentiation	27	474	0.16	266727	MAM domain containing glycosylphosphatidylinositol anchor 1
GO	cell differentiation	27	474	0.16	2736	GLI family zinc finger 2
GO	cell differentiation	27	474	0.16	3624	inhibin, beta A
GO	cell differentiation	27	474	0.16	3975	LIM homeobox 1
GO	cell differentiation	27	474	0.16	4291	myeloid leukemia factor 1
GO	cell differentiation	27	474	0.16	4830	non-metastatic cells 1, protein (NM23A) expressed in
GO	cell differentiation	27	474	0.16	5228	placental growth factor

GO	cell differentiation	27	474	0.16	54993	zinc finger and SCAN domain containing 2
GO	cell differentiation	27	474	0.16	6422	secreted frizzled-related protein 1
GO	cell differentiation	27	474	0.16	65009	NDRG family member 4
GO	cell differentiation	27	474	0.16	6586	slit homolog 3 (Drosophila)
GO	cell differentiation	27	474	0.16	6683	spastin
GO	cell differentiation	27	474	0.16	8482	semaphorin 7A, GPI membrane anchor (John Milton Hagen blood group)
GO	cell differentiation	27	474	0.16	8536	calcium/calmodulin-dependent protein kinase I
GO	cell differentiation	27	474	0.16	8563	THO complex 5
GO	cell differentiation	27	474	0.16	8788	delta-like 1 homolog (Drosophila)
GO	cell differentiation	27	474	0.16	9260	PDZ and LIM domain 7 (enigma)
GO	nuclear matrix	5	62	0.16	1161	excision repair cross-complementing rodent repair deficiency, complement
GO	nuclear matrix	5	62	0.16	1788	DNA (cytosine-5-)-methyltransferase 3 alpha
GO	nuclear matrix	5	62	0.16	4287	ataxin 3
GO	nuclear matrix	5	62	0.16	55137	fidgetin
GO	nuclear matrix	5	62	0.16	641	Bloom syndrome, RecQ helicase-like
GO	extracellular matrix organization	5	62	0.16	1284	collagen, type IV, alpha 2
GO	extracellular matrix organization	5	62	0.16	1288	collagen, type IV, alpha 6
GO	extracellular matrix organization	5	62	0.16	1301	collagen, type XI, alpha 1
GO	extracellular matrix organization	5	62	0.16	4318	matrix metallopeptidase 9 (gelatinase B, 92kDa gelatinase, 92kDa type IV c
GO	extracellular matrix organization	5	62	0.16	4763	neurofibromin 1
GO	response to organic nitrogen	3	30	0.161	1026	cyclin-dependent kinase inhibitor 1A (p21, Cip1)
GO	response to organic nitrogen	3	30	0.161	3157	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 (soluble)
GO	response to organic nitrogen	3	30	0.161	898	cyclin E1
GO	cellular response to insulin stimulus	4	46	0.164	10395	deleted in liver cancer 1
GO	cellular response to insulin stimulus	4	46	0.164	23305	acyl-CoA synthetase long-chain family member 6
GO	cellular response to insulin stimulus	4	46	0.164	5140	phosphodiesterase 3B, cGMP-inhibited
GO	cellular response to insulin stimulus	4	46	0.164	57678	glycerol-3-phosphate acyltransferase, mitochondrial
GO	regulation of small GTPase mediated sig	4	46	0.164	10788	IQ motif containing GTPase activating protein 2
GO	regulation of small GTPase mediated sig	4	46	0.164	25780	RAS guanyl releasing protein 3 (calcium and DAG-regulated)
GO	regulation of small GTPase mediated sig	4	46	0.164	4763	neurofibromin 1
GO	regulation of small GTPase mediated sig	4	46	0.164	5924	Ras protein-specific guanine nucleotide-releasing factor 2
GO	extracellular ligand-gated ion channel a	4	46	0.164	1136	cholinergic receptor, nicotinic, alpha 3
GO	extracellular ligand-gated ion channel a	4	46	0.164	1138	cholinergic receptor, nicotinic, alpha 5
GO	extracellular ligand-gated ion channel a	4	46	0.164	200959	gamma-aminobutyric acid (GABA) receptor, rho 3
GO	extracellular ligand-gated ion channel a	4	46	0.164	2558	gamma-aminobutyric acid (GABA) A receptor, alpha 5
GO	response to calcium ion	4	46	0.164	3778	potassium large conductance calcium-activated channel, subfamily M, alph

GO	response to calcium ion	4	46	0.164	4734	neural precursor cell expressed, developmentally down-regulated 4
GO	response to calcium ion	4	46	0.164	7220	transient receptor potential cation channel, subfamily C, member 1
GO	response to calcium ion	4	46	0.164	8604	solute carrier family 25 (mitochondrial carrier, Aralar), member 12
GO	organ morphogenesis	8	115	0.166	1045	caudal type homeobox 2
GO	organ morphogenesis	8	115	0.166	182	jagged 1 (Alagille syndrome)
GO	organ morphogenesis	8	115	0.166	2273	four and a half LIM domains 1
GO	organ morphogenesis	8	115	0.166	3975	LIM homeobox 1
GO	organ morphogenesis	8	115	0.166	5469	mediator complex subunit 1
GO	organ morphogenesis	8	115	0.166	6347	chemokine (C-C motif) ligand 2
GO	organ morphogenesis	8	115	0.166	6586	slit homolog 3 (Drosophila)
GO	organ morphogenesis	8	115	0.166	8626	tumor protein p63
GO	regulation of transcription from RNA po	13	207	0.167	10474	transcriptional adaptor 3
GO	regulation of transcription from RNA po	13	207	0.167	11278	Kruppel-like factor 12
GO	regulation of transcription from RNA po	13	207	0.167	116931	mediator complex subunit 12-like
GO	regulation of transcription from RNA po	13	207	0.167	170082	transcription elongation factor A (SII) N-terminal and central domain contai
GO	regulation of transcription from RNA po	13	207	0.167	195828	zinc finger protein 367
GO	regulation of transcription from RNA po	13	207	0.167	29128	ubiquitin-like with PHD and ring finger domains 1
GO	regulation of transcription from RNA po	13	207	0.167	29842	transcription factor CP2-like 1
GO	regulation of transcription from RNA po	13	207	0.167	50485	SWI/SNF related, matrix associated, actin dependent regulator of chromati
GO	regulation of transcription from RNA po	13	207	0.167	5216	profilin 1
GO	regulation of transcription from RNA po	13	207	0.167	6662	SRY (sex determining region Y)-box 9
GO	regulation of transcription from RNA po	13	207	0.167	672	breast cancer 1, early onset
GO	regulation of transcription from RNA po	13	207	0.167	6899	T-box 1
GO	regulation of transcription from RNA po	13	207	0.167	7021	transcription factor AP-2 beta (activating enhancer binding protein 2 beta)
GO	gap junction	2	16	0.169	10052	gap junction protein, gamma 1, 45kDa
GO	gap junction	2	16	0.169	127534	gap junction protein, beta 4, 30.3kDa
GO	regulation of the force of heart contract	2	16	0.169	10539	glutaredoxin 3
GO	regulation of the force of heart contract	2	16	0.169	6546	solute carrier family 8 (sodium/calcium exchanger), member 1
GO	regulation of GTPase activity	2	16	0.169	1121	choroideremia (Rab escort protein 1)
GO	regulation of GTPase activity	2	16	0.169	25780	RAS guanyl releasing protein 3 (calcium and DAG-regulated)
GO	nicotinic acetylcholine-activated cation-	2	16	0.169	1136	cholinergic receptor, nicotinic, alpha 3
GO	nicotinic acetylcholine-activated cation-	2	16	0.169	1138	cholinergic receptor, nicotinic, alpha 5
GO	nicotinic acetylcholine-gated receptor-c	2	16	0.169	1136	cholinergic receptor, nicotinic, alpha 3
GO	nicotinic acetylcholine-gated receptor-c	2	16	0.169	1138	cholinergic receptor, nicotinic, alpha 5
GO	purine nucleotide biosynthetic process	2	16	0.169	158	adenylosuccinate lyase
GO	purine nucleotide biosynthetic process	2	16	0.169	2618	phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide

GO	mitochondrial envelope	2	16	0.169	2534	FYN oncogene related to SRC, FGR, YES
GO	mitochondrial envelope	2	16	0.169	55803	ArfGAP with dual PH domains 2
GO	neuron apoptosis	2	16	0.169	2898	glutamate receptor, ionotropic, kainate 2
GO	neuron apoptosis	2	16	0.169	8626	tumor protein p63
GO	negative regulation of MAP kinase activ	2	16	0.169	348	apolipoprotein E
GO	negative regulation of MAP kinase activ	2	16	0.169	4763	neurofibromin 1
GO	carbonate dehydratase activity	2	16	0.169	377677	carbonic anhydrase XIII
GO	carbonate dehydratase activity	2	16	0.169	767	carbonic anhydrase VIII
GO	DNA-dependent DNA replication initiati	2	16	0.169	4171	minichromosome maintenance complex component 2
GO	DNA-dependent DNA replication initiati	2	16	0.169	5000	origin recognition complex, subunit 4-like (yeast)
GO	cerebral cortex development	2	16	0.169	4763	neurofibromin 1
GO	cerebral cortex development	2	16	0.169	6657	SRY (sex determining region Y)-box 2
GO	hair follicle morphogenesis	2	16	0.169	6615	snail homolog 1 (Drosophila)
GO	hair follicle morphogenesis	2	16	0.169	8626	tumor protein p63
GO	spliceosome assembly	2	16	0.169	6637	small nuclear ribonucleoprotein polypeptide G
GO	spliceosome assembly	2	16	0.169	79833	gem (nuclear organelle) associated protein 6
GO	stereocilium	2	16	0.169	9497	solute carrier family 4, sodium bicarbonate cotransporter, member 7
GO	stereocilium	2	16	0.169	9732	dedicator of cytokinesis 4
GO	cellular component movement	7	98	0.171	10096	ARP3 actin-related protein 3 homolog (yeast)
GO	cellular component movement	7	98	0.171	10097	ARP2 actin-related protein 2 homolog (yeast)
GO	cellular component movement	7	98	0.171	10672	guanine nucleotide binding protein (G protein), alpha 13
GO	cellular component movement	7	98	0.171	6695	sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 1
GO	cellular component movement	7	98	0.171	7168	tropomyosin 1 (alpha)
GO	cellular component movement	7	98	0.171	7171	tropomyosin 4
GO	cellular component movement	7	98	0.171	7857	secretogranin II (chromogranin C)
GO	mediator complex	3	31	0.173	116931	mediator complex subunit 12-like
GO	mediator complex	3	31	0.173	51003	mediator complex subunit 31
GO	mediator complex	3	31	0.173	5469	mediator complex subunit 1
GO	SMAD binding	3	31	0.173	1290	collagen, type V, alpha 2
GO	SMAD binding	3	31	0.173	7046	transforming growth factor, beta receptor 1
GO	SMAD binding	3	31	0.173	9839	zinc finger E-box binding homeobox 2
GO	MAPKKK cascade	3	31	0.173	25780	RAS guanyl releasing protein 3 (calcium and DAG-regulated)
GO	MAPKKK cascade	3	31	0.173	4763	neurofibromin 1
GO	MAPKKK cascade	3	31	0.173	7857	secretogranin II (chromogranin C)
GO	embryonic digit morphogenesis	3	31	0.173	2736	GLI family zinc finger 2
GO	embryonic digit morphogenesis	3	31	0.173	3237	homeobox D11

GO	embryonic digit morphogenesis	3	31	0.173	6299	sal-like 1 (Drosophila)
GO	ATPase activity, coupled to transmembr	3	31	0.173	340273	ATP-binding cassette, sub-family B (MDR/TAP), member 5
GO	ATPase activity, coupled to transmembr	3	31	0.173	51382	ATPase, H+ transporting, lysosomal 34kDa, V1 subunit D
GO	ATPase activity, coupled to transmembr	3	31	0.173	6833	ATP-binding cassette, sub-family C (CFTR/MRP), member 8
GO	keratinization	3	31	0.173	353133	late cornified envelope 1C
GO	keratinization	3	31	0.173	84518	cornifelin
GO	keratinization	3	31	0.173	84648	late cornified envelope 3D
GO	chromosome, centromeric region	4	47	0.173	1788	DNA (cytosine-5-)-methyltransferase 3 alpha
GO	chromosome, centromeric region	4	47	0.173	332	baculoviral IAP repeat-containing 5
GO	chromosome, centromeric region	4	47	0.173	387103	centromere protein W
GO	chromosome, centromeric region	4	47	0.173	79075	defective in sister chromatid cohesion 1 homolog (S. cerevisiae)
GO	RPTP-like protein binding	1	4	0.173	1000	cadherin 2, type 1, N-cadherin (neuronal)
GO	ATP-dependent protein binding	1	4	0.173	10055	SUMO1 activating enzyme subunit 1
GO	phenylalanyl-tRNA aminoacylation	1	4	0.173	10056	phenylalanyl-tRNA synthetase, beta subunit
GO	excitatory synapse	1	4	0.173	10096	ARP3 actin-related protein 3 homolog (yeast)
GO	positive regulation of programmed cell	1	4	0.173	1026	cyclin-dependent kinase inhibitor 1A (p21, Cip1)
GO	hindbrain morphogenesis	1	4	0.173	10395	deleted in liver cancer 1
GO	positive regulation of protein amino aci	1	4	0.173	10395	deleted in liver cancer 1
GO	U4/U6 x U5 tri-snRNP complex	1	4	0.173	10465	peptidylprolyl isomerase H (cyclophilin H)
GO	box C/D snoRNP complex	1	4	0.173	10528	NOP56 ribonucleoprotein homolog (yeast)
GO	compartment pattern formation	1	4	0.173	10683	delta-like 3 (Drosophila)
GO	protein amino acid geranylgeranylation	1	4	0.173	1121	choroideremia (Rab escort protein 1)
GO	Rab geranylgeranyltransferase activity	1	4	0.173	1121	choroideremia (Rab escort protein 1)
GO	regulation of dendrite morphogenesis	1	4	0.173	1136	cholinergic receptor, nicotinic, alpha 3
GO	transmembrane receptor protein tyrosi	1	4	0.173	118788	phosphoinositide-3-kinase adaptor protein 1
GO	TOR signaling pathway	1	4	0.173	121268	Ras homolog enriched in brain like 1
GO	9-cis-retinoic acid biosynthetic process	1	4	0.173	1543	cytochrome P450, family 1, subfamily A, polypeptide 1
GO	embryonic development ending in birth	1	4	0.173	1543	cytochrome P450, family 1, subfamily A, polypeptide 1
GO	hepatocyte differentiation	1	4	0.173	1543	cytochrome P450, family 1, subfamily A, polypeptide 1
GO	pyrimidine dimer repair	1	4	0.173	1643	damage-specific DNA binding protein 2, 48kDa
GO	inner ear receptor cell differentiation	1	4	0.173	1687	deafness, autosomal dominant 5
GO	methylation-dependent chromatin silen	1	4	0.173	1788	DNA (cytosine-5-)-methyltransferase 3 alpha
GO	unmethylated CpG binding	1	4	0.173	1788	DNA (cytosine-5-)-methyltransferase 3 alpha
GO	U6 snRNA binding	1	4	0.173	1984	eukaryotic translation initiation factor 5A
GO	phosphopyruvate hydratase activity	1	4	0.173	2027	enolase 3 (beta, muscle)
GO	phosphopyruvate hydratase complex	1	4	0.173	2027	enolase 3 (beta, muscle)

GO	regulation of microtubule polymerizatic	1	4	0.173	220134	spindle and kinetochore associated complex subunit 1
GO	paranode region of axon	1	4	0.173	23136	erythrocyte membrane protein band 4.1-like 3
GO	arachidonic acid binding	1	4	0.173	241	arachidonate 5-lipoxygenase-activating protein
GO	detection of mechanical stimulus involv	1	4	0.173	2534	FYN oncogene related to SRC, FGR, YES
GO	fatty acid alpha-oxidation	1	4	0.173	26061	2-hydroxyacyl-CoA lyase 1
GO	hindgut morphogenesis	1	4	0.173	2736	GLI family zinc finger 2
GO	mammary gland duct morphogenesis	1	4	0.173	2736	GLI family zinc finger 2
GO	smoothened signaling pathway involvec	1	4	0.173	2736	GLI family zinc finger 2
GO	procollagen-proline 4-dioxygenase activ	1	4	0.173	283208	prolyl 4-hydroxylase, alpha polypeptide III
GO	ubiquitin conjugating enzyme binding	1	4	0.173	2898	glutamate receptor, ionotropic, kainate 2
GO	epithelial cell maturation	1	4	0.173	29842	transcription factor CP2-like 1
GO	positive regulation of exit from mitosis	1	4	0.173	332	baculoviral IAP repeat-containing 5
GO	protein complex localization	1	4	0.173	332	baculoviral IAP repeat-containing 5
GO	regulation of cholesterol transport	1	4	0.173	341	apolipoprotein C-I
GO	axon regeneration in the peripheral ner	1	4	0.173	348	apolipoprotein E
GO	Cdc42 protein signal transduction	1	4	0.173	348	apolipoprotein E
GO	cGMP-mediated signaling	1	4	0.173	348	apolipoprotein E
GO	death-inducing signaling complex	1	4	0.173	355	Fas (TNF receptor superfamily, member 6)
GO	megakaryocyte differentiation	1	4	0.173	3589	interleukin 11
GO	hemoglobin biosynthetic process	1	4	0.173	3624	inhibin, beta A
GO	negative regulation of follicle-stimulatin	1	4	0.173	3624	inhibin, beta A
GO	negative regulation of macrophage diffe	1	4	0.173	3624	inhibin, beta A
GO	apoptotic cell clearance	1	4	0.173	3685	integrin, alpha V (vitronectin receptor, alpha polypeptide, antigen CD51)
GO	negative regulation of lipid storage	1	4	0.173	3685	integrin, alpha V (vitronectin receptor, alpha polypeptide, antigen CD51)
GO	negative regulation of lipid transport	1	4	0.173	3685	integrin, alpha V (vitronectin receptor, alpha polypeptide, antigen CD51)
GO	G-protein activated inward rectifier pot	1	4	0.173	3763	potassium inwardly-rectifying channel, subfamily J, member 6
GO	RNA 3'-end processing	1	4	0.173	389421	lin-28 homolog B (C. elegans)
GO	negative regulation of appetite	1	4	0.173	3952	leptin
GO	regulation of intestinal cholesterol abso	1	4	0.173	3952	leptin
GO	pachytene	1	4	0.173	4292	mutL homolog 1, colon cancer, nonpolyposis type 2 (E. coli)
GO	forebrain neuron development	1	4	0.173	431707	LIM homeobox 8
GO	positive regulation of keratinocyte migr	1	4	0.173	4318	matrix metallopeptidase 9 (gelatinase B, 92kDa gelatinase, 92kDa type IV c
GO	somatic recombination of immunoglobu	1	4	0.173	4436	mutS homolog 2, colon cancer, nonpolyposis type 1 (E. coli)
GO	progesterone receptor signaling pathwa	1	4	0.173	4734	neural precursor cell expressed, developmentally down-regulated 4
GO	receptor catabolic process	1	4	0.173	4734	neural precursor cell expressed, developmentally down-regulated 4
GO	positive regulation of adenylate cyclase	1	4	0.173	4763	neurofibromin 1

GO	positive regulation of Rac protein signal	1	4	0.173	4893	neuroblastoma RAS viral (v-ras) oncogene homolog
GO	ERK1 and ERK2 cascade	1	4	0.173	5021	oxytocin receptor
GO	positive regulation of ion transport	1	4	0.173	5028	purinergic receptor P2Y, G-protein coupled, 1
GO	cellular response to chemical stimulus	1	4	0.173	5054	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor t
GO	Golgi cis cisterna	1	4	0.173	51062	atlastin GTPase 1
GO	protein repair	1	4	0.173	5110	protein-L-isoaspartate (D-aspartate) O-methyltransferase
GO	cytokine biosynthetic process	1	4	0.173	5125	proprotein convertase subtilisin/kexin type 5
GO	nerve growth factor processing	1	4	0.173	5125	proprotein convertase subtilisin/kexin type 5
GO	platelet aggregation	1	4	0.173	5341	pleckstrin
GO	positive regulation of platelet activation	1	4	0.173	5341	pleckstrin
GO	regulation of transcription from RNA po	1	4	0.173	5440	polymerase (RNA) II (DNA directed) polypeptide K, 7.0kDa
GO	peroxisome proliferator activated recep	1	4	0.173	5469	mediator complex subunit 1
GO	retinoic acid receptor binding	1	4	0.173	5469	mediator complex subunit 1
GO	positive regulation of telomerase activit	1	4	0.173	55135	WD repeat containing, antisense to TP53
GO	DNA primase activity	1	4	0.173	5558	primase, DNA, polypeptide 2 (58kDa)
GO	DNA replication, synthesis of RNA prime	1	4	0.173	5558	primase, DNA, polypeptide 2 (58kDa)
GO	peptide-aspartate beta-dioxygenase act	1	4	0.173	57168	aspartate beta-hydroxylase domain containing 2
GO	glycerol-3-phosphate O-acyltransferase	1	4	0.173	57678	glycerol-3-phosphate acyltransferase, mitochondrial
GO	mitochondrial fusion	1	4	0.173	581	BCL2-associated X protein
GO	regulation of protein heterodimerization	1	4	0.173	581	BCL2-associated X protein
GO	choline metabolic process	1	4	0.173	590	butyrylcholinesterase
GO	outer ear morphogenesis	1	4	0.173	6299	sal-like 1 (Drosophila)
GO	ventricular septum development	1	4	0.173	6299	sal-like 1 (Drosophila)
GO	monocyte chemotaxis	1	4	0.173	6347	chemokine (C-C motif) ligand 2
GO	positive regulation of macrophage chem	1	4	0.173	6347	chemokine (C-C motif) ligand 2
GO	bubble DNA binding	1	4	0.173	641	Bloom syndrome, RecQ helicase-like
GO	lateral element	1	4	0.173	641	Bloom syndrome, RecQ helicase-like
GO	calcium ion transmembrane transporter	1	4	0.173	6546	solute carrier family 8 (sodium/calcium exchanger), member 1
GO	calcium:sodium antiporter activity	1	4	0.173	6546	solute carrier family 8 (sodium/calcium exchanger), member 1
GO	sodium ion transmembrane transporter	1	4	0.173	6546	solute carrier family 8 (sodium/calcium exchanger), member 1
GO	Roundabout binding	1	4	0.173	6586	slit homolog 3 (Drosophila)
GO	lens induction in camera-type eye	1	4	0.173	6657	SRY (sex determining region Y)-box 2
GO	Sertoli cell development	1	4	0.173	6662	SRY (sex determining region Y)-box 9
GO	intermediate filament cytoskeleton orga	1	4	0.173	667	dystonin
GO	soft palate development	1	4	0.173	6899	T-box 1
GO	cardiac myofibril assembly	1	4	0.173	70	actin, alpha, cardiac muscle 1

GO	negative regulation of membrane prote	1	4	0.173	7078	TIMP metallopeptidase inhibitor 3
GO	calcium channel inhibitor activity	1	4	0.173	7137	troponin I type 3 (cardiac)
GO	negative regulation of ATPase activity	1	4	0.173	7137	troponin I type 3 (cardiac)
GO	troponin C binding	1	4	0.173	7137	troponin I type 3 (cardiac)
GO	troponin T binding	1	4	0.173	7137	troponin I type 3 (cardiac)
GO	ISG15-protein conjugation	1	4	0.173	7324	ubiquitin-conjugating enzyme E2E 1 (UBC4/5 homolog, yeast)
GO	protein sumoylation	1	4	0.173	7341	SMT3 suppressor of mif two 3 homolog 1 (S. cerevisiae)
GO	high voltage-gated calcium channel acti	1	4	0.173	773	calcium channel, voltage-dependent, P/Q type, alpha 1A subunit
GO	pantothenate kinase activity	1	4	0.173	79646	pantothenate kinase 3
GO	AT DNA binding	1	4	0.173	8091	high mobility group AT-hook 2
GO	galactose binding	1	4	0.173	81035	collectin sub-family member 12
GO	aspartate transport	1	4	0.173	8604	solute carrier family 25 (mitochondrial carrier, Aralar), member 12
GO	L-aspartate transmembrane transporter	1	4	0.173	8604	solute carrier family 25 (mitochondrial carrier, Aralar), member 12
GO	urinary bladder development	1	4	0.173	8626	tumor protein p63
GO	growth hormone receptor binding	1	4	0.173	8835	suppressor of cytokine signaling 2
GO	tRNA methylation	1	4	0.173	91801	alkB, alkylation repair homolog 8 (E. coli)
GO	cardiac cell differentiation	1	4	0.173	93649	myocardin
GO	metabotropic glutamate receptor signal	1	4	0.173	9455	homer homolog 2 (Drosophila)
GO	NADP metabolic process	1	4	0.173	9540	tumor protein p53 inducible protein 3
GO	NADPH:quinone reductase activity	1	4	0.173	9540	tumor protein p53 inducible protein 3
GO	heparan sulfate proteoglycan biosynthe	1	4	0.173	9653	heparan sulfate 2-O-sulfotransferase 1
GO	cell proliferation in forebrain	1	4	0.173	9839	zinc finger E-box binding homeobox 2
GO	embryonic morphogenesis	1	4	0.173	9839	zinc finger E-box binding homeobox 2
GO	chromatin	6	81	0.174	4094	v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian)
GO	chromatin	6	81	0.174	4171	minichromosome maintenance complex component 2
GO	chromatin	6	81	0.174	4734	neural precursor cell expressed, developmentally down-regulated 4
GO	chromatin	6	81	0.174	56852	RAD18 homolog (S. cerevisiae)
GO	chromatin	6	81	0.174	79075	defective in sister chromatid cohesion 1 homolog (S. cerevisiae)
GO	chromatin	6	81	0.174	8091	high mobility group AT-hook 2
GO	Ras protein signal transduction	5	64	0.176	1026	cyclin-dependent kinase inhibitor 1A (p21, Cip1)
GO	Ras protein signal transduction	5	64	0.176	25780	RAS guanyl releasing protein 3 (calcium and DAG-regulated)
GO	Ras protein signal transduction	5	64	0.176	4763	neurofibromin 1
GO	Ras protein signal transduction	5	64	0.176	4893	neuroblastoma RAS viral (v-ras) oncogene homolog
GO	Ras protein signal transduction	5	64	0.176	890	cyclin A2
GO	kinase activity	8	117	0.177	1716	deoxyguanosine kinase
GO	kinase activity	8	117	0.177	1841	deoxythymidylate kinase (thymidylate kinase)

GO	kinase activity	8	117	0.177	27330	ribosomal protein S6 kinase, 90kDa, polypeptide 6
GO	kinase activity	8	117	0.177	29922	non-metastatic cells 7, protein expressed in (nucleoside-diphosphate kinas
GO	kinase activity	8	117	0.177	4830	non-metastatic cells 1, protein (NM23A) expressed in
GO	kinase activity	8	117	0.177	54822	transient receptor potential cation channel, subfamily M, member 7
GO	kinase activity	8	117	0.177	55577	N-acetylglucosamine kinase
GO	kinase activity	8	117	0.177	64080	ribokinase
GO	nucleosome assembly	5	65	0.184	4171	minichromosome maintenance complex component 2
GO	nucleosome assembly	5	65	0.184	55506	H2A histone family, member Y2
GO	nucleosome assembly	5	65	0.184	8348	histone cluster 1, H2bo
GO	nucleosome assembly	5	65	0.184	8349	histone cluster 2, H2be
GO	nucleosome assembly	5	65	0.184	8970	histone cluster 1, H2bj
GO	neural tube closure	3	32	0.184	10395	deleted in liver cancer 1
GO	neural tube closure	3	32	0.184	5216	profilin 1
GO	neural tube closure	3	32	0.184	9839	zinc finger E-box binding homeobox 2
GO	peptidyl-tyrosine phosphorylation	3	32	0.184	2242	feline sarcoma oncogene
GO	peptidyl-tyrosine phosphorylation	3	32	0.184	2321	fms-related tyrosine kinase 1 (vascular endothelial growth factor/vascular
GO	peptidyl-tyrosine phosphorylation	3	32	0.184	2534	FYN oncogene related to SRC, FGR, YES
GO	regulation of G-protein coupled recept	3	32	0.184	2786	guanine nucleotide binding protein (G protein), gamma 4
GO	regulation of G-protein coupled recept	3	32	0.184	6000	regulator of G-protein signaling 7
GO	regulation of G-protein coupled recept	3	32	0.184	8490	regulator of G-protein signaling 5
GO	regulation of gene expression	3	32	0.184	348	apolipoprotein E
GO	regulation of gene expression	3	32	0.184	5744	parathyroid hormone-like hormone
GO	regulation of gene expression	3	32	0.184	6657	SRY (sex determining region Y)-box 2
GO	positive regulation of cell differentiatio	2	17	0.186	1045	caudal type homeobox 2
GO	positive regulation of cell differentiatio	2	17	0.186	898	cyclin E1
GO	guanyl nucleotide binding	2	17	0.186	10672	guanine nucleotide binding protein (G protein), alpha 13
GO	guanyl nucleotide binding	2	17	0.186	2774	guanine nucleotide binding protein (G protein), alpha activating activity pol
GO	regulation of excitatory postsynaptic m	2	17	0.186	1136	cholinergic receptor, nicotinic, alpha 3
GO	regulation of excitatory postsynaptic m	2	17	0.186	2898	glutamate receptor, ionotropic, kainate 2
GO	positive regulation of DNA repair	2	17	0.186	1161	excision repair cross-complementing rodent repair deficiency, complement
GO	positive regulation of DNA repair	2	17	0.186	672	breast cancer 1, early onset
GO	anchored to plasma membrane	2	17	0.186	146760	reticulon 4 receptor-like 1
GO	anchored to plasma membrane	2	17	0.186	266727	MAM domain containing glycosylphosphatidylinositol anchor 1
GO	purine ribonucleoside monophosphate	2	17	0.186	158	adenylosuccinate lyase
GO	purine ribonucleoside monophosphate	2	17	0.186	2618	phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide
GO	negative regulation of osteoblast differe	2	17	0.186	221044	upper zone of growth plate and cartilage matrix associated

GO	negative regulation of osteoblast differe	2	17	0.186	6657	SRY (sex determining region Y)-box 2
GO	regulation of long-term neuronal synapt	2	17	0.186	2898	glutamate receptor, ionotropic, kainate 2
GO	regulation of long-term neuronal synapt	2	17	0.186	4893	neuroblastoma RAS viral (v-ras) oncogene homolog
GO	cytoplasmic microtubule	2	17	0.186	332	baculoviral IAP repeat-containing 5
GO	cytoplasmic microtubule	2	17	0.186	7846	tubulin, alpha 1a
GO	DNA damage response, signal transduct	2	17	0.186	4292	mutL homolog 1, colon cancer, nonpolyposis type 2 (E. coli)
GO	DNA damage response, signal transduct	2	17	0.186	672	breast cancer 1, early onset
GO	cAMP binding	2	17	0.186	50940	phosphodiesterase 11A
GO	cAMP binding	2	17	0.186	5140	phosphodiesterase 3B, cGMP-inhibited
GO	positive regulation of pathway-restricte	2	17	0.186	659	bone morphogenetic protein receptor, type II (serine/threonine kinase)
GO	positive regulation of pathway-restricte	2	17	0.186	7046	transforming growth factor, beta receptor 1
GO	male genitalia development	2	17	0.186	6657	SRY (sex determining region Y)-box 2
GO	male genitalia development	2	17	0.186	7490	Wilms tumor 1
GO	nucleobase, nucleoside, nucleotide and	5	66	0.192	1503	CTP synthase
GO	nucleobase, nucleoside, nucleotide and	5	66	0.192	1716	deoxyguanosine kinase
GO	nucleobase, nucleoside, nucleotide and	5	66	0.192	203	adenylate kinase 1
GO	nucleobase, nucleoside, nucleotide and	5	66	0.192	56339	methyltransferase like 3
GO	nucleobase, nucleoside, nucleotide and	5	66	0.192	7298	thymidylate synthetase
GO	biosynthetic process	4	49	0.192	23057	nicotinamide nucleotide adenylyltransferase 2
GO	biosynthetic process	4	49	0.192	2618	phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide
GO	biosynthetic process	4	49	0.192	5833	phosphate cytidylyltransferase 2, ethanolamine
GO	biosynthetic process	4	49	0.192	79712	glycosyltransferase-like domain containing 1
GO	PDZ domain binding	4	49	0.192	23705	cell adhesion molecule 1
GO	PDZ domain binding	4	49	0.192	2898	glutamate receptor, ionotropic, kainate 2
GO	PDZ domain binding	4	49	0.192	9076	claudin 1
GO	PDZ domain binding	4	49	0.192	9732	dedicator of cytokinesis 4
GO	microtubule-based movement	6	84	0.195	1781	dynein, cytoplasmic 1, intermediate chain 2
GO	microtubule-based movement	6	84	0.195	347733	tubulin, beta 2B
GO	microtubule-based movement	6	84	0.195	3797	kinesin family member 3C
GO	microtubule-based movement	6	84	0.195	3800	kinesin family member 5C
GO	microtubule-based movement	6	84	0.195	7846	tubulin, alpha 1a
GO	microtubule-based movement	6	84	0.195	79861	tubulin, alpha-like 3
GO	actin filament binding	4	50	0.202	3936	lymphocyte cytosolic protein 1 (L-plastin)
GO	actin filament binding	4	50	0.202	8409	ubiquitously-expressed transcript
GO	actin filament binding	4	50	0.202	84168	anthrax toxin receptor 1
GO	actin filament binding	4	50	0.202	91624	nexilin (F actin binding protein)

GO	response to estrogen stimulus	4	50	0.202	411	arylsulfatase B
GO	response to estrogen stimulus	4	50	0.202	672	breast cancer 1, early onset
GO	response to estrogen stimulus	4	50	0.202	7046	transforming growth factor, beta receptor 1
GO	response to estrogen stimulus	4	50	0.202	7078	TIMP metallopeptidase inhibitor 3
GO	response to cytokine stimulus	4	50	0.202	5021	oxytocin receptor
GO	response to cytokine stimulus	4	50	0.202	5054	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor t
GO	response to cytokine stimulus	4	50	0.202	6672	SP100 nuclear antigen
GO	response to cytokine stimulus	4	50	0.202	898	cyclin E1
GO	rRNA processing	6	85	0.202	10199	M-phase phosphoprotein 10 (U3 small nucleolar ribonucleoprotein)
GO	rRNA processing	6	85	0.202	10528	NOP56 ribonucleoprotein homolog (yeast)
GO	rRNA processing	6	85	0.202	345630	fibrillarin-like 1
GO	rRNA processing	6	85	0.202	5303	protein (peptidylprolyl cis/trans isomerase) NIMA-interacting, 4 (parvulin)
GO	rRNA processing	6	85	0.202	55759	WD repeat domain 12
GO	rRNA processing	6	85	0.202	6154	ribosomal protein L26
GO	inward rectifier potassium channel activ	2	18	0.203	3763	potassium inwardly-rectifying channel, subfamily J, member 6
GO	inward rectifier potassium channel activ	2	18	0.203	56479	potassium voltage-gated channel, KQT-like subfamily, member 5
GO	ADP binding	2	18	0.203	4436	mutS homolog 2, colon cancer, nonpolyposis type 1 (E. coli)
GO	ADP binding	2	18	0.203	5028	purinergic receptor P2Y, G-protein coupled, 1
GO	proton-transporting ATPase activity, rot	2	18	0.203	51382	ATPase, H+ transporting, lysosomal 34kDa, V1 subunit D
GO	proton-transporting ATPase activity, rot	2	18	0.203	528	ATPase, H+ transporting, lysosomal 42kDa, V1 subunit C1
GO	hydrolase activity, acting on ester bond	2	18	0.203	55301	oleoyl-ACP hydrolase
GO	hydrolase activity, acting on ester bond	2	18	0.203	92675	D-tyrosyl-tRNA deacylase 1 homolog (S. cerevisiae)
GO	response to activity	2	18	0.203	57678	glycerol-3-phosphate acyltransferase, mitochondrial
GO	response to activity	2	18	0.203	6347	chemokine (C-C motif) ligand 2
GO	negative regulation of apoptosis	9	140	0.204	10202	dehydrogenase/reductase (SDR family) member 2
GO	negative regulation of apoptosis	9	140	0.204	1026	cyclin-dependent kinase inhibitor 1A (p21, Cip1)
GO	negative regulation of apoptosis	9	140	0.204	1984	eukaryotic translation initiation factor 5A
GO	negative regulation of apoptosis	9	140	0.204	5054	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor t
GO	negative regulation of apoptosis	9	140	0.204	5624	protein C (inactivator of coagulation factors Va and VIIIa)
GO	negative regulation of apoptosis	9	140	0.204	6659	SRY (sex determining region Y)-box 4
GO	negative regulation of apoptosis	9	140	0.204	7046	transforming growth factor, beta receptor 1
GO	negative regulation of apoptosis	9	140	0.204	7490	Wilms tumor 1
GO	negative regulation of apoptosis	9	140	0.204	7857	secretogranin II (chromogranin C)
GO	calmodulin binding	9	140	0.204	10788	IQ motif containing GTPase activating protein 2
GO	calmodulin binding	9	140	0.204	1264	calponin 1, basic, smooth muscle
GO	calmodulin binding	9	140	0.204	3756	potassium voltage-gated channel, subfamily H (eag-related), member 1

GO	calmodulin binding	9	140	0.204	4430	myosin IB
GO	calmodulin binding	9	140	0.204	6546	solute carrier family 8 (sodium/calcium exchanger), member 1
GO	calmodulin binding	9	140	0.204	6711	spectrin, beta, non-erythrocytic 1
GO	calmodulin binding	9	140	0.204	773	calcium channel, voltage-dependent, P/Q type, alpha 1A subunit
GO	calmodulin binding	9	140	0.204	79929	MAP6 domain containing 1
GO	calmodulin binding	9	140	0.204	8536	calcium/calmodulin-dependent protein kinase I
GO	protein homooligomerization	5	68	0.208	3778	potassium large conductance calcium-activated channel, subfamily M, alph
GO	protein homooligomerization	5	68	0.208	51062	atlastin GTPase 1
GO	protein homooligomerization	5	68	0.208	581	BCL2-associated X protein
GO	protein homooligomerization	5	68	0.208	6683	spastin
GO	protein homooligomerization	5	68	0.208	81035	collectin sub-family member 12
GO	receptor signaling protein activity	3	34	0.208	10293	TRAF interacting protein
GO	receptor signaling protein activity	3	34	0.208	23768	fibronectin leucine rich transmembrane protein 2
GO	receptor signaling protein activity	3	34	0.208	26230	T-cell lymphoma invasion and metastasis 2
GO	cytokinesis	3	34	0.208	1730	diaphanous homolog 2 (Drosophila)
GO	cytokinesis	3	34	0.208	23157	septin 6
GO	cytokinesis	3	34	0.208	332	baculoviral IAP repeat-containing 5
GO	perikaryon	3	34	0.208	2898	glutamate receptor, ionotropic, kainate 2
GO	perikaryon	3	34	0.208	50940	phosphodiesterase 11A
GO	perikaryon	3	34	0.208	773	calcium channel, voltage-dependent, P/Q type, alpha 1A subunit
GO	PML body	3	34	0.208	641	Bloom syndrome, RecQ helicase-like
GO	PML body	3	34	0.208	6672	SP100 nuclear antigen
GO	PML body	3	34	0.208	7341	SMT3 suppressor of mif two 3 homolog 1 (S. cerevisiae)
GO	transmembrane transport	27	492	0.211	1836	solute carrier family 26 (sulfate transporter), member 2
GO	transmembrane transport	27	492	0.211	1984	eukaryotic translation initiation factor 5A
GO	transmembrane transport	27	492	0.211	26519	translocase of inner mitochondrial membrane 10 homolog (yeast)
GO	transmembrane transport	27	492	0.211	26521	translocase of inner mitochondrial membrane 8 homolog B (yeast)
GO	transmembrane transport	27	492	0.211	340273	ATP-binding cassette, sub-family B (MDR/TAP), member 5
GO	transmembrane transport	27	492	0.211	3751	potassium voltage-gated channel, Shal-related subfamily, member 2
GO	transmembrane transport	27	492	0.211	3754	potassium voltage-gated channel, subfamily F, member 1
GO	transmembrane transport	27	492	0.211	3756	potassium voltage-gated channel, subfamily H (eag-related), member 1
GO	transmembrane transport	27	492	0.211	3778	potassium large conductance calcium-activated channel, subfamily M, alph
GO	transmembrane transport	27	492	0.211	387700	solute carrier family 16, member 12 (monocarboxylic acid transporter 12)
GO	transmembrane transport	27	492	0.211	4928	nucleoporin 98kDa
GO	transmembrane transport	27	492	0.211	54822	transient receptor potential cation channel, subfamily M, member 7
GO	transmembrane transport	27	492	0.211	56479	potassium voltage-gated channel, KQT-like subfamily, member 5

GO	transmembrane transport	27	492	0.211	60386	solute carrier family 25 (mitochondrial thiamine pyrophosphate carrier), m
GO	transmembrane transport	27	492	0.211	6335	sodium channel, voltage-gated, type IX, alpha subunit
GO	transmembrane transport	27	492	0.211	64393	zinc finger, matrin type 3
GO	transmembrane transport	27	492	0.211	64747	major facilitator superfamily domain containing 1
GO	transmembrane transport	27	492	0.211	6518	solute carrier family 2 (facilitated glucose/fructose transporter), member 5
GO	transmembrane transport	27	492	0.211	6527	solute carrier family 5 (low affinity glucose cotransporter), member 4
GO	transmembrane transport	27	492	0.211	6546	solute carrier family 8 (sodium/calcium exchanger), member 1
GO	transmembrane transport	27	492	0.211	6549	solute carrier family 9 (sodium/hydrogen exchanger), member 2
GO	transmembrane transport	27	492	0.211	6580	solute carrier family 22 (organic cation transporter), member 1
GO	transmembrane transport	27	492	0.211	6833	ATP-binding cassette, sub-family C (CFTR/MRP), member 8
GO	transmembrane transport	27	492	0.211	7220	transient receptor potential cation channel, subfamily C, member 1
GO	transmembrane transport	27	492	0.211	773	calcium channel, voltage-dependent, P/Q type, alpha 1A subunit
GO	transmembrane transport	27	492	0.211	8604	solute carrier family 25 (mitochondrial carrier, Aralar), member 12
GO	transmembrane transport	27	492	0.211	9688	nucleoporin 93kDa
GO	plasma membrane	137	2763	0.211	1000	cadherin 2, type 1, N-cadherin (neuronal)
GO	plasma membrane	137	2763	0.211	1002	cadherin 4, type 1, R-cadherin (retinal)
GO	plasma membrane	137	2763	0.211	10052	gap junction protein, gamma 1, 45kDa
GO	plasma membrane	137	2763	0.211	1008	cadherin 10, type 2 (T2-cadherin)
GO	plasma membrane	137	2763	0.211	10672	guanine nucleotide binding protein (G protein), alpha 13
GO	plasma membrane	137	2763	0.211	10890	RAB10, member RAS oncogene family
GO	plasma membrane	137	2763	0.211	10893	matrix metallopeptidase 24 (membrane-inserted)
GO	plasma membrane	137	2763	0.211	11149	blood vessel epicardial substance
GO	plasma membrane	137	2763	0.211	1136	cholinergic receptor, nicotinic, alpha 3
GO	plasma membrane	137	2763	0.211	1138	cholinergic receptor, nicotinic, alpha 5
GO	plasma membrane	137	2763	0.211	116372	LY6/PLAUR domain containing 1
GO	plasma membrane	137	2763	0.211	118788	phosphoinositide-3-kinase adaptor protein 1
GO	plasma membrane	137	2763	0.211	119749	olfactory receptor, family 4, subfamily C, member 46
GO	plasma membrane	137	2763	0.211	120114	FAT tumor suppressor homolog 3 (Drosophila)
GO	plasma membrane	137	2763	0.211	121268	Ras homolog enriched in brain like 1
GO	plasma membrane	137	2763	0.211	122786	FERM domain containing 6
GO	plasma membrane	137	2763	0.211	125962	olfactory receptor, family 7, subfamily G, member 1
GO	plasma membrane	137	2763	0.211	127534	gap junction protein, beta 4, 30.3kDa
GO	plasma membrane	137	2763	0.211	128414	Na+/K+ transporting ATPase interacting 4
GO	plasma membrane	137	2763	0.211	128853	dual specificity phosphatase 15
GO	plasma membrane	137	2763	0.211	131450	CD200 receptor 1
GO	plasma membrane	137	2763	0.211	146760	reticulon 4 receptor-like 1

GO	plasma membrane	137	2763	0.211	1496	catenin (cadherin-associated protein), alpha 2
GO	plasma membrane	137	2763	0.211	154215	Na+/K+ transporting ATPase interacting 2
GO	plasma membrane	137	2763	0.211	1733	deiodinase, iodothyronine, type I
GO	plasma membrane	137	2763	0.211	182	jagged 1 (Alagille syndrome)
GO	plasma membrane	137	2763	0.211	1830	desmoglein 3 (pemphigus vulgaris antigen)
GO	plasma membrane	137	2763	0.211	200959	gamma-aminobutyric acid (GABA) receptor, rho 3
GO	plasma membrane	137	2763	0.211	2037	erythrocyte membrane protein band 4.1-like 2
GO	plasma membrane	137	2763	0.211	2149	coagulation factor II (thrombin) receptor
GO	plasma membrane	137	2763	0.211	2150	coagulation factor II (thrombin) receptor-like 1
GO	plasma membrane	137	2763	0.211	2151	coagulation factor II (thrombin) receptor-like 2
GO	plasma membrane	137	2763	0.211	222611	G protein-coupled receptor 111
GO	plasma membrane	137	2763	0.211	2264	fibroblast growth factor receptor 4
GO	plasma membrane	137	2763	0.211	23136	erythrocyte membrane protein band 4.1-like 3
GO	plasma membrane	137	2763	0.211	2321	fms-related tyrosine kinase 1 (vascular endothelial growth factor/vascular
GO	plasma membrane	137	2763	0.211	23305	acyl-CoA synthetase long-chain family member 6
GO	plasma membrane	137	2763	0.211	23432	G protein-coupled receptor 161
GO	plasma membrane	137	2763	0.211	23562	claudin 14
GO	plasma membrane	137	2763	0.211	23705	cell adhesion molecule 1
GO	plasma membrane	137	2763	0.211	2534	FYN oncogene related to SRC, FGR, YES
GO	plasma membrane	137	2763	0.211	2558	gamma-aminobutyric acid (GABA) A receptor, alpha 5
GO	plasma membrane	137	2763	0.211	26499	pleckstrin 2
GO	plasma membrane	137	2763	0.211	266727	MAM domain containing glycosylphosphatidylinositol anchor 1
GO	plasma membrane	137	2763	0.211	27241	Bardet-Biedl syndrome 9
GO	plasma membrane	137	2763	0.211	27289	Rho family GTPase 1
GO	plasma membrane	137	2763	0.211	2774	guanine nucleotide binding protein (G protein), alpha activating activity pol
GO	plasma membrane	137	2763	0.211	2786	guanine nucleotide binding protein (G protein), gamma 4
GO	plasma membrane	137	2763	0.211	282770	olfactory receptor, family 10, subfamily AG, member 1
GO	plasma membrane	137	2763	0.211	283111	olfactory receptor, family 51, subfamily V, member 1
GO	plasma membrane	137	2763	0.211	2842	G protein-coupled receptor 19
GO	plasma membrane	137	2763	0.211	2845	G protein-coupled receptor 22
GO	plasma membrane	137	2763	0.211	2850	G protein-coupled receptor 27
GO	plasma membrane	137	2763	0.211	285659	olfactory receptor, family 2, subfamily V, member 2
GO	plasma membrane	137	2763	0.211	2863	G protein-coupled receptor 39
GO	plasma membrane	137	2763	0.211	287	ankyrin 2, neuronal
GO	plasma membrane	137	2763	0.211	2898	glutamate receptor, ionotropic, kainate 2
GO	plasma membrane	137	2763	0.211	2906	glutamate receptor, ionotropic, N-methyl D-aspartate 2D

GO	plasma membrane	137	2763	0.211	30011	SH3-domain kinase binding protein 1
GO	plasma membrane	137	2763	0.211	3028	hydroxysteroid (17-beta) dehydrogenase 10
GO	plasma membrane	137	2763	0.211	340273	ATP-binding cassette, sub-family B (MDR/TAP), member 5
GO	plasma membrane	137	2763	0.211	344805	transmembrane protease, serine 7
GO	plasma membrane	137	2763	0.211	347902	adhesion molecule with Ig-like domain 2
GO	plasma membrane	137	2763	0.211	348	apolipoprotein E
GO	plasma membrane	137	2763	0.211	353091	retinoic acid early transcript 1G
GO	plasma membrane	137	2763	0.211	355	Fas (TNF receptor superfamily, member 6)
GO	plasma membrane	137	2763	0.211	3685	integrin, alpha V (vitronectin receptor, alpha polypeptide, antigen CD51)
GO	plasma membrane	137	2763	0.211	3751	potassium voltage-gated channel, Shal-related subfamily, member 2
GO	plasma membrane	137	2763	0.211	3763	potassium inwardly-rectifying channel, subfamily J, member 6
GO	plasma membrane	137	2763	0.211	3778	potassium large conductance calcium-activated channel, subfamily M, alph
GO	plasma membrane	137	2763	0.211	387700	solute carrier family 16, member 12 (monocarboxylic acid transporter 12)
GO	plasma membrane	137	2763	0.211	390061	olfactory receptor, family 51, subfamily Q, member 1
GO	plasma membrane	137	2763	0.211	391114	olfactory receptor, family 6, subfamily K, member 3
GO	plasma membrane	137	2763	0.211	3932	lymphocyte-specific protein tyrosine kinase
GO	plasma membrane	137	2763	0.211	3936	lymphocyte cytosolic protein 1 (L-plastin)
GO	plasma membrane	137	2763	0.211	409	arrestin, beta 2
GO	plasma membrane	137	2763	0.211	4158	melanocortin 2 receptor (adrenocorticotropic hormone)
GO	plasma membrane	137	2763	0.211	4734	neural precursor cell expressed, developmentally down-regulated 4
GO	plasma membrane	137	2763	0.211	4893	neuroblastoma RAS viral (v-ras) oncogene homolog
GO	plasma membrane	137	2763	0.211	4897	neuronal cell adhesion molecule
GO	plasma membrane	137	2763	0.211	5021	oxytocin receptor
GO	plasma membrane	137	2763	0.211	5028	purinergic receptor P2Y, G-protein coupled, 1
GO	plasma membrane	137	2763	0.211	5031	pyrimidinergic receptor P2Y, G-protein coupled, 6
GO	plasma membrane	137	2763	0.211	5054	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor t
GO	plasma membrane	137	2763	0.211	5101	protocadherin 9
GO	plasma membrane	137	2763	0.211	51177	pleckstrin homology domain containing, family O member 1
GO	plasma membrane	137	2763	0.211	5145	phosphodiesterase 6A, cGMP-specific, rod, alpha
GO	plasma membrane	137	2763	0.211	51768	transmembrane 7 superfamily member 3
GO	plasma membrane	137	2763	0.211	528	ATPase, H+ transporting, lysosomal 42kDa, V1 subunit C1
GO	plasma membrane	137	2763	0.211	53637	sphingosine-1-phosphate receptor 5
GO	plasma membrane	137	2763	0.211	5420	podocalyxin-like
GO	plasma membrane	137	2763	0.211	54210	triggering receptor expressed on myeloid cells 1
GO	plasma membrane	137	2763	0.211	54331	guanine nucleotide binding protein (G protein), gamma 2
GO	plasma membrane	137	2763	0.211	54756	interleukin 17 receptor D

GO	plasma membrane	137	2763	0.211	54822	transient receptor potential cation channel, subfamily M, member 7
GO	plasma membrane	137	2763	0.211	54843	synaptotagmin-like 2
GO	plasma membrane	137	2763	0.211	55117	solute carrier family 6 (neutral amino acid transporter), member 15
GO	plasma membrane	137	2763	0.211	55244	solute carrier family 47, member 1
GO	plasma membrane	137	2763	0.211	55283	mucolipin 3
GO	plasma membrane	137	2763	0.211	55803	ArfGAP with dual PH domains 2
GO	plasma membrane	137	2763	0.211	56104	protocadherin gamma subfamily B, 1
GO	plasma membrane	137	2763	0.211	56126	protocadherin beta 10
GO	plasma membrane	137	2763	0.211	56133	protocadherin beta 2
GO	plasma membrane	137	2763	0.211	5624	protein C (inactivator of coagulation factors Va and VIIIa)
GO	plasma membrane	137	2763	0.211	56937	prostate transmembrane protein, androgen induced 1
GO	plasma membrane	137	2763	0.211	57575	protocadherin 10
GO	plasma membrane	137	2763	0.211	5795	protein tyrosine phosphatase, receptor type, J
GO	plasma membrane	137	2763	0.211	5924	Ras protein-specific guanine nucleotide-releasing factor 2
GO	plasma membrane	137	2763	0.211	6000	regulator of G-protein signaling 7
GO	plasma membrane	137	2763	0.211	6444	sarcoglycan, delta (35kDa dystrophin-associated glycoprotein)
GO	plasma membrane	137	2763	0.211	6518	solute carrier family 2 (facilitated glucose/fructose transporter), member 5
GO	plasma membrane	137	2763	0.211	6546	solute carrier family 8 (sodium/calcium exchanger), member 1
GO	plasma membrane	137	2763	0.211	6580	solute carrier family 22 (organic cation transporter), member 1
GO	plasma membrane	137	2763	0.211	659	bone morphogenetic protein receptor, type II (serine/threonine kinase)
GO	plasma membrane	137	2763	0.211	6711	spectrin, beta, non-erythrocytic 1
GO	plasma membrane	137	2763	0.211	7010	TEK tyrosine kinase, endothelial
GO	plasma membrane	137	2763	0.211	7037	transferrin receptor (p90, CD71)
GO	plasma membrane	137	2763	0.211	7046	transforming growth factor, beta receptor 1
GO	plasma membrane	137	2763	0.211	7113	transmembrane protease, serine 2
GO	plasma membrane	137	2763	0.211	7220	transient receptor potential cation channel, subfamily C, member 1
GO	plasma membrane	137	2763	0.211	729230	chemokine (C-C motif) receptor 2
GO	plasma membrane	137	2763	0.211	773	calcium channel, voltage-dependent, P/Q type, alpha 1A subunit
GO	plasma membrane	137	2763	0.211	83700	junctional adhesion molecule 3
GO	plasma membrane	137	2763	0.211	84168	anthrax toxin receptor 1
GO	plasma membrane	137	2763	0.211	84552	par-6 partitioning defective 6 homolog gamma (C. elegans)
GO	plasma membrane	137	2763	0.211	8482	semaphorin 7A, GPI membrane anchor (John Milton Hagen blood group)
GO	plasma membrane	137	2763	0.211	8777	multiple PDZ domain protein
GO	plasma membrane	137	2763	0.211	9053	microtubule-associated protein 7
GO	plasma membrane	137	2763	0.211	9076	claudin 1
GO	plasma membrane	137	2763	0.211	91584	plexin A4

GO	plasma membrane	137	2763	0.211	92737	delta/notch-like EGF repeat containing
GO	plasma membrane	137	2763	0.211	9455	homer homolog 2 (Drosophila)
GO	plasma membrane	137	2763	0.211	9497	solute carrier family 4, sodium bicarbonate cotransporter, member 7
GO	plasma membrane	137	2763	0.211	953	ectonucleoside triphosphate diphosphohydrolase 1
GO	plasma membrane	137	2763	0.211	9542	neuregulin 2
GO	plasma membrane	137	2763	0.211	9568	gamma-aminobutyric acid (GABA) B receptor, 2
GO	plasma membrane	137	2763	0.211	9635	chloride channel accessory 2
GO	GTPase activity	12	198	0.211	10123	ADP-ribosylation factor-like 4C
GO	GTPase activity	12	198	0.211	10672	guanine nucleotide binding protein (G protein), alpha 13
GO	GTPase activity	12	198	0.211	121268	Ras homolog enriched in brain like 1
GO	GTPase activity	12	198	0.211	1983	eukaryotic translation initiation factor 5
GO	GTPase activity	12	198	0.211	27289	Rho family GTPase 1
GO	GTPase activity	12	198	0.211	2774	guanine nucleotide binding protein (G protein), alpha activating activity pol
GO	GTPase activity	12	198	0.211	347733	tubulin, beta 2B
GO	GTPase activity	12	198	0.211	4893	neuroblastoma RAS viral (v-ras) oncogene homolog
GO	GTPase activity	12	198	0.211	51062	atlastin GTPase 1
GO	GTPase activity	12	198	0.211	55207	ADP-ribosylation factor-like 8B
GO	GTPase activity	12	198	0.211	7846	tubulin, alpha 1a
GO	GTPase activity	12	198	0.211	79861	tubulin, alpha-like 3
GO	phenylalanine-tRNA ligase activity	1	5	0.212	10056	phenylalanyl-tRNA synthetase, beta subunit
GO	negative regulation of Rho protein signa	1	5	0.212	10395	deleted in liver cancer 1
GO	CRD-mediated mRNA stability complex	1	5	0.212	10492	synaptotagmin binding, cytoplasmic RNA interacting protein
GO	CRD-mediated mRNA stabilization	1	5	0.212	10492	synaptotagmin binding, cytoplasmic RNA interacting protein
GO	histone pre-mRNA 3'end processing cor	1	5	0.212	10492	synaptotagmin binding, cytoplasmic RNA interacting protein
GO	dichotomous subdivision of terminal un	1	5	0.212	10512	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (
GO	outflow tract morphogenesis	1	5	0.212	10512	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (
GO	negative regulation of cardiac muscle hy	1	5	0.212	10539	glutaredoxin 3
GO	type 1 angiotensin receptor binding	1	5	0.212	10672	guanine nucleotide binding protein (G protein), alpha 13
GO	negative regulation of astrocyte differer	1	5	0.212	10683	delta-like 3 (Drosophila)
GO	negative regulation of Notch signaling p	1	5	0.212	10683	delta-like 3 (Drosophila)
GO	epithelial cell-cell adhesion	1	5	0.212	11149	blood vessel epicardial substance
GO	positive regulation of receptor recycling	1	5	0.212	11149	blood vessel epicardial substance
GO	transcription-coupled nucleotide-excisio	1	5	0.212	1161	excision repair cross-complementing rodent repair deficiency, complement
GO	collagen biosynthetic process	1	5	0.212	1289	collagen, type V, alpha 1
GO	positive regulation of triglyceride catabo	1	5	0.212	13	arylacetamide deacetylase (esterase)
GO	positive regulation of fibroblast growth	1	5	0.212	143282	fibroblast growth factor binding protein 3

GO	vitamin D metabolic process	1	5	0.212	1543	cytochrome P450, family 1, subfamily A, polypeptide 1
GO	establishment or maintenance of epithe	1	5	0.212	166336	prickle homolog 2 (Drosophila)
GO	DNA catabolic process	1	5	0.212	1775	deoxyribonuclease I-like 2
GO	dynactin complex	1	5	0.212	1781	dynein, cytoplasmic 1, intermediate chain 2
GO	sulfate transmembrane transporter acti	1	5	0.212	1836	solute carrier family 26 (sulfate transporter), member 2
GO	peptidyl-lysine modification to hypusine	1	5	0.212	1984	eukaryotic translation initiation factor 5A
GO	nucleobase, nucleoside, nucleotide kina	1	5	0.212	203	adenylate kinase 1
GO	chemorepellent activity	1	5	0.212	2045	EPH receptor A7
GO	embryonic camera-type eye developme	1	5	0.212	220	aldehyde dehydrogenase 1 family, member A3
GO	embryonic eye morphogenesis	1	5	0.212	220	aldehyde dehydrogenase 1 family, member A3
GO	face development	1	5	0.212	220	aldehyde dehydrogenase 1 family, member A3
GO	ribonuclease H activity	1	5	0.212	2237	flap structure-specific endonuclease 1
GO	fibroblast growth factor receptor activit	1	5	0.212	2264	fibroblast growth factor receptor 4
GO	neuronal action potential propagation	1	5	0.212	2281	FK506 binding protein 1B, 12.6 kDa
GO	protein maturation by protein folding	1	5	0.212	2281	FK506 binding protein 1B, 12.6 kDa
GO	protein refolding	1	5	0.212	2281	FK506 binding protein 1B, 12.6 kDa
GO	ryanodine-sensitive calcium-release cha	1	5	0.212	2281	FK506 binding protein 1B, 12.6 kDa
GO	long-chain fatty acid metabolic process	1	5	0.212	23305	acyl-CoA synthetase long-chain family member 6
GO	response to gravity	1	5	0.212	23305	acyl-CoA synthetase long-chain family member 6
GO	thiamin pyrophosphate binding	1	5	0.212	26061	2-hydroxyacyl-CoA lyase 1
GO	purine base biosynthetic process	1	5	0.212	2618	phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide
GO	phosphatidylinositol transporter activity	1	5	0.212	26207	phosphatidylinositol transfer protein, cytoplasmic 1
GO	dopamine receptor binding	1	5	0.212	27065	DNA segment on chromosome 4 (unique) 234 expressed sequence
GO	neuron remodeling	1	5	0.212	27289	Rho family GTPase 1
GO	motile primary cilium	1	5	0.212	2736	GLI family zinc finger 2
GO	spinal cord dorsal/ventral patterning	1	5	0.212	2736	GLI family zinc finger 2
GO	regulation of short-term neuronal synap	1	5	0.212	2898	glutamate receptor, ionotropic, kainate 2
GO	nerve-nerve synaptic transmission	1	5	0.212	29767	tropomodulin 2 (neuronal)
GO	neuromuscular process	1	5	0.212	3236	homeobox D10
GO	cartilage development involved in endo	1	5	0.212	3237	homeobox D11
GO	prostaglandin E receptor activity	1	5	0.212	3248	hydroxyprostaglandin dehydrogenase 15-(NAD)
GO	negative regulation of lipoprotein lipase	1	5	0.212	341	apolipoprotein C-I
GO	negative regulation of receptor-mediate	1	5	0.212	341	apolipoprotein C-I
GO	high-density lipoprotein particle assemb	1	5	0.212	348	apolipoprotein E
GO	high-density lipoprotein particle clearan	1	5	0.212	348	apolipoprotein E
GO	lipoprotein biosynthetic process	1	5	0.212	348	apolipoprotein E

GO	lipoprotein catabolic process	1	5	0.212	348	apolipoprotein E
GO	positive regulation of cGMP biosyntheti	1	5	0.212	348	apolipoprotein E
GO	tau protein binding	1	5	0.212	348	apolipoprotein E
GO	magnesium ion transport	1	5	0.212	348938	NIPA-like domain containing 4
GO	regulation of activin receptor signaling p	1	5	0.212	3624	inhibin, beta A
GO	peptide hormone receptor binding	1	5	0.212	3952	leptin
GO	endoderm formation	1	5	0.212	3975	LIM homeobox 1
GO	G-protein coupled receptor internalizati	1	5	0.212	409	arrestin, beta 2
GO	melanocortin receptor activity	1	5	0.212	4158	melanocortin 2 receptor (adrenocorticotropic hormone)
GO	MutSalpha complex binding	1	5	0.212	4292	mutL homolog 1, colon cancer, nonpolyposis type 2 (E. coli)
GO	intra-S DNA damage checkpoint	1	5	0.212	4436	mutS homolog 2, colon cancer, nonpolyposis type 1 (E. coli)
GO	positive regulation of helicase activity	1	5	0.212	4436	mutS homolog 2, colon cancer, nonpolyposis type 1 (E. coli)
GO	RNA polymerase binding	1	5	0.212	4734	neural precursor cell expressed, developmentally down-regulated 4
GO	forebrain morphogenesis	1	5	0.212	4763	neurofibromin 1
GO	myelination in the peripheral nervous sy	1	5	0.212	4763	neurofibromin 1
GO	negative regulation of neuroblast prolife	1	5	0.212	4763	neurofibromin 1
GO	structural constituent of nuclear pore	1	5	0.212	4928	nucleoporin 98kDa
GO	eukaryotic initiation factor 4E binding	1	5	0.212	5015	orthodenticle homeobox 2
GO	gastric acid secretion	1	5	0.212	5021	oxytocin receptor
GO	positive regulation of uterine smooth m	1	5	0.212	5021	oxytocin receptor
GO	sperm ejaculation	1	5	0.212	5021	oxytocin receptor
GO	vasopressin receptor activity	1	5	0.212	5021	oxytocin receptor
GO	transepithelial chloride transport	1	5	0.212	5031	pyrimidinergic receptor P2Y, G-protein coupled, 6
GO	regulation of receptor activity	1	5	0.212	5054	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor t
GO	protein kinase B binding	1	5	0.212	5140	phosphodiesterase 3B, cGMP-inhibited
GO	proton-transporting two-sector ATPase	1	5	0.212	528	ATPase, H+ transporting, lysosomal 42kDa, V1 subunit C1
GO	mammary gland branching involved in t	1	5	0.212	5469	mediator complex subunit 1
GO	neurotransmitter transporter activity	1	5	0.212	55117	solute carrier family 6 (neutral amino acid transporter), member 15
GO	telomerase holoenzyme complex	1	5	0.212	55135	WD repeat containing, antisense to TP53
GO	spindle midzone	1	5	0.212	55207	ADP-ribosylation factor-like 8B
GO	Barr body	1	5	0.212	55506	H2A histone family, member Y2
GO	negative regulation of synaptic transmis	1	5	0.212	590	butyrylcholinesterase
GO	mesenchymal to epithelial transition inv	1	5	0.212	6299	sal-like 1 (Drosophila)
GO	regulation of binding	1	5	0.212	641	Bloom syndrome, RecQ helicase-like
GO	luteolysis	1	5	0.212	6586	slit homolog 3 (Drosophila)
GO	regulation of caspase activity	1	5	0.212	6657	SRY (sex determining region Y)-box 2

GO	retina morphogenesis in camera-type e	1	5	0.212	6657	SRY (sex determining region Y)-box 2
GO	pro-B cell differentiation	1	5	0.212	6659	SRY (sex determining region Y)-box 4
GO	negative regulation of cellular compone	1	5	0.212	6672	SP100 nuclear antigen
GO	microtubule-severing ATPase activity	1	5	0.212	6683	spastin
GO	cellular response to indole-3-methanol	1	5	0.212	672	breast cancer 1, early onset
GO	skeletal muscle thin filament assembly	1	5	0.212	70	actin, alpha, cardiac muscle 1
GO	response to cholesterol	1	5	0.212	7046	transforming growth factor, beta receptor 1
GO	response to prostaglandin E stimulus	1	5	0.212	7046	transforming growth factor, beta receptor 1
GO	oligopeptide transport	1	5	0.212	729025	solute carrier family 15, member 5
GO	positive regulation of protein complex a	1	5	0.212	7341	SMT3 suppressor of mif two 3 homolog 1 (S. cerevisiae)
GO	glomerular basement membrane devel	1	5	0.212	7490	Wilms tumor 1
GO	glomerulus development	1	5	0.212	7490	Wilms tumor 1
GO	behavioral response to pain	1	5	0.212	773	calcium channel, voltage-dependent, P/Q type, alpha 1A subunit
GO	protein serine/threonine phosphatase i	1	5	0.212	81706	protein phosphatase 1, regulatory (inhibitor) subunit 14C
GO	gamma-tubulin complex	1	5	0.212	8409	ubiquitously-expressed transcript
GO	mitochondrion transport along microtul	1	5	0.212	8409	ubiquitously-expressed transcript
GO	transcription termination	1	5	0.212	8458	transcription termination factor, RNA polymerase II
GO	THO complex part of transcription expo	1	5	0.212	8563	THO complex 5
GO	THO complex	1	5	0.212	8563	THO complex 5
GO	establishment of planar polarity	1	5	0.212	8626	tumor protein p63
GO	multicellular organismal aging	1	5	0.212	8626	tumor protein p63
GO	skin morphogenesis	1	5	0.212	8626	tumor protein p63
GO	mitotic cell cycle G2/M transition DNA	1	5	0.212	890	cyclin A2
GO	AP-type membrane coat adaptor compl	1	5	0.212	8905	adaptor-related protein complex 1, sigma 2 subunit
GO	regulation of cytoskeleton organization	1	5	0.212	91624	nexilin (F actin binding protein)
GO	regulation of smooth muscle cell differe	1	5	0.212	93649	myocardin
GO	NADPH binding	1	5	0.212	9540	tumor protein p53 inducible protein 3
GO	ligand-gated ion channel activity	1	5	0.212	9635	chloride channel accessory 2
GO	G2/M transition of mitotic cell cycle	2	19	0.22	1026	cyclin-dependent kinase inhibitor 1A (p21, Cip1)
GO	G2/M transition of mitotic cell cycle	2	19	0.22	332	baculoviral IAP repeat-containing 5
GO	hyaluronic acid binding	2	19	0.22	145864	hyaluronan and proteoglycan link protein 3
GO	hyaluronic acid binding	2	19	0.22	26032	sushi domain containing 5
GO	nucleotide-excision repair, DNA damag	2	19	0.22	1643	damage-specific DNA binding protein 2, 48kDa
GO	nucleotide-excision repair, DNA damag	2	19	0.22	2965	general transcription factor IIH, polypeptide 1, 62kDa
GO	base-excision repair	2	19	0.22	1763	DNA replication helicase 2 homolog (yeast)
GO	base-excision repair	2	19	0.22	4968	8-oxoguanine DNA glycosylase

GO	GABA-A receptor activity	2	19	0.22	200959	gamma-aminobutyric acid (GABA) receptor, rho 3
GO	GABA-A receptor activity	2	19	0.22	2558	gamma-aminobutyric acid (GABA) A receptor, alpha 5
GO	extracellular-glutamate-gated ion chanr	2	19	0.22	2898	glutamate receptor, ionotropic, kainate 2
GO	extracellular-glutamate-gated ion chanr	2	19	0.22	2906	glutamate receptor, ionotropic, N-methyl D-aspartate 2D
GO	cofactor binding	2	19	0.22	332	baculoviral IAP repeat-containing 5
GO	cofactor binding	2	19	0.22	7298	thymidylate synthetase
GO	cholesterol efflux	2	19	0.22	341	apolipoprotein C-I
GO	cholesterol efflux	2	19	0.22	348	apolipoprotein E
GO	T cell differentiation	2	19	0.22	3932	lymphocyte-specific protein tyrosine kinase
GO	T cell differentiation	2	19	0.22	6659	SRY (sex determining region Y)-box 4
GO	hydrolase activity, acting on acid anhydı	2	19	0.22	50485	SWI/SNF related, matrix associated, actin dependent regulator of chromati
GO	hydrolase activity, acting on acid anhydı	2	19	0.22	641	Bloom syndrome, RecQ helicase-like
GO	actin cytoskeleton reorganization	2	19	0.22	5341	pleckstrin
GO	actin cytoskeleton reorganization	2	19	0.22	84168	anthrax toxin receptor 1
GO	vesicle docking involved in exocytosis	2	19	0.22	5341	pleckstrin
GO	vesicle docking involved in exocytosis	2	19	0.22	54843	synaptotagmin-like 2
GO	chromatin organization	2	19	0.22	6657	SRY (sex determining region Y)-box 2
GO	chromatin organization	2	19	0.22	8091	high mobility group AT-hook 2
GO	negative regulation of adenylate cyclase	2	19	0.22	729230	chemokine (C-C motif) receptor 2
GO	negative regulation of adenylate cyclase	2	19	0.22	9568	gamma-aminobutyric acid (GABA) B receptor, 2
GO	extracellular matrix	3	35	0.221	1289	collagen, type V, alpha 1
GO	extracellular matrix	3	35	0.221	1290	collagen, type V, alpha 2
GO	extracellular matrix	3	35	0.221	5054	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor t
GO	nucleosome	4	52	0.221	55506	H2A histone family, member Y2
GO	nucleosome	4	52	0.221	8348	histone cluster 1, H2bo
GO	nucleosome	4	52	0.221	8349	histone cluster 2, H2be
GO	nucleosome	4	52	0.221	8970	histone cluster 1, H2bj
GO	cell-cell adhesion	5	70	0.225	1008	cadherin 10, type 2 (T2-cadherin)
GO	cell-cell adhesion	5	70	0.225	1496	catenin (cadherin-associated protein), alpha 2
GO	cell-cell adhesion	5	70	0.225	26999	cytoplasmic FMR1 interacting protein 2
GO	cell-cell adhesion	5	70	0.225	4867	nephronophthisis 1 (juvenile)
GO	cell-cell adhesion	5	70	0.225	4897	neuronal cell adhesion molecule
GO	response to ethanol	5	70	0.225	2534	FYN oncogene related to SRC, FGR, YES
GO	response to ethanol	5	70	0.225	348	apolipoprotein E
GO	response to ethanol	5	70	0.225	6347	chemokine (C-C motif) ligand 2
GO	response to ethanol	5	70	0.225	70	actin, alpha, cardiac muscle 1

GO	response to ethanol	5	70	0.225	898	cyclin E1
GO	intracellular signaling pathway	11	182	0.226	25780	RAS guanyl releasing protein 3 (calcium and DAG-regulated)
GO	intracellular signaling pathway	11	182	0.226	26499	pleckstrin 2
GO	intracellular signaling pathway	11	182	0.226	51676	ankyrin repeat and SOCS box-containing 2
GO	intracellular signaling pathway	11	182	0.226	5341	pleckstrin
GO	intracellular signaling pathway	11	182	0.226	54210	triggering receptor expressed on myeloid cells 1
GO	intracellular signaling pathway	11	182	0.226	55789	DEP domain containing 1B
GO	intracellular signaling pathway	11	182	0.226	5588	protein kinase C, theta
GO	intracellular signaling pathway	11	182	0.226	7857	secretogranin II (chromogranin C)
GO	intracellular signaling pathway	11	182	0.226	8835	suppressor of cytokine signaling 2
GO	intracellular signaling pathway	11	182	0.226	8997	kalirin, RhoGEF kinase
GO	intracellular signaling pathway	11	182	0.226	9744	ArfGAP with coiled-coil, ankyrin repeat and PH domains 1
GO	serine-type endopeptidase activity	9	144	0.227	132724	transmembrane protease, serine 11B
GO	serine-type endopeptidase activity	9	144	0.227	162494	rhomboid, veinlet-like 3 (Drosophila)
GO	serine-type endopeptidase activity	9	144	0.227	27429	HtrA serine peptidase 2
GO	serine-type endopeptidase activity	9	144	0.227	344805	transmembrane protease, serine 7
GO	serine-type endopeptidase activity	9	144	0.227	5054	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor t
GO	serine-type endopeptidase activity	9	144	0.227	5125	proprotein convertase subtilisin/kexin type 5
GO	serine-type endopeptidase activity	9	144	0.227	5624	protein C (inactivator of coagulation factors Va and VIIIa)
GO	serine-type endopeptidase activity	9	144	0.227	5654	HtrA serine peptidase 1
GO	serine-type endopeptidase activity	9	144	0.227	7113	transmembrane protease, serine 2
GO	helicase activity	7	107	0.229	10212	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39
GO	helicase activity	7	107	0.229	11056	DEAD (Asp-Glu-Ala-Asp) box polypeptide 52
GO	helicase activity	7	107	0.229	1763	DNA replication helicase 2 homolog (yeast)
GO	helicase activity	7	107	0.229	641	Bloom syndrome, RecQ helicase-like
GO	helicase activity	7	107	0.229	84083	zinc finger, RAN-binding domain containing 3
GO	helicase activity	7	107	0.229	8458	transcription termination factor, RNA polymerase II
GO	helicase activity	7	107	0.229	89797	neuron navigator 2
GO	double-strand break repair	3	36	0.233	2237	flap structure-specific endonuclease 1
GO	double-strand break repair	3	36	0.233	4436	mutS homolog 2, colon cancer, nonpolyposis type 1 (E. coli)
GO	double-strand break repair	3	36	0.233	672	breast cancer 1, early onset
GO	response to organic substance	3	36	0.233	2618	phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide
GO	response to organic substance	3	36	0.233	2628	glycine amidinotransferase (L-arginine:glycine amidinotransferase)
GO	response to organic substance	3	36	0.233	7037	transferrin receptor (p90, CD71)
GO	skeletal muscle tissue development	3	36	0.233	3236	homeobox D10
GO	skeletal muscle tissue development	3	36	0.233	4637	myosin, light chain 6, alkali, smooth muscle and non-muscle

GO	skeletal muscle tissue development	3	36	0.233	5081	paired box 7
GO	lamellipodium	5	71	0.234	1000	cadherin 2, type 1, N-cadherin (neuronal)
GO	lamellipodium	5	71	0.234	10096	ARP3 actin-related protein 3 homolog (yeast)
GO	lamellipodium	5	71	0.234	1496	catenin (cadherin-associated protein), alpha 2
GO	lamellipodium	5	71	0.234	26230	T-cell lymphoma invasion and metastasis 2
GO	lamellipodium	5	71	0.234	5420	podocalyxin-like
GO	regulation of Rho protein signal transdu	5	71	0.234	1000	cadherin 2, type 1, N-cadherin (neuronal)
GO	regulation of Rho protein signal transdu	5	71	0.234	153478	pleckstrin homology domain containing, family G (with RhoGef domain) me
GO	regulation of Rho protein signal transdu	5	71	0.234	26230	T-cell lymphoma invasion and metastasis 2
GO	regulation of Rho protein signal transdu	5	71	0.234	5924	Ras protein-specific guanine nucleotide-releasing factor 2
GO	regulation of Rho protein signal transdu	5	71	0.234	8997	kalirin, RhoGEF kinase
GO	transmembrane receptor protein tyrosi	5	71	0.234	2045	EPH receptor A7
GO	transmembrane receptor protein tyrosi	5	71	0.234	2321	fms-related tyrosine kinase 1 (vascular endothelial growth factor/vascular
GO	transmembrane receptor protein tyrosi	5	71	0.234	558	AXL receptor tyrosine kinase
GO	transmembrane receptor protein tyrosi	5	71	0.234	5795	protein tyrosine phosphatase, receptor type, J
GO	transmembrane receptor protein tyrosi	5	71	0.234	7010	TEK tyrosine kinase, endothelial
GO	spermatogenesis	15	261	0.234	10656	KH domain containing, RNA binding, signal transduction associated 3
GO	spermatogenesis	15	261	0.234	11077	heat shock transcription factor 2 binding protein
GO	spermatogenesis	15	261	0.234	132671	spermatogenesis associated 18 homolog (rat)
GO	spermatogenesis	15	261	0.234	132851	spermatogenesis associated 4
GO	spermatogenesis	15	261	0.234	1788	DNA (cytosine-5-)-methyltransferase 3 alpha
GO	spermatogenesis	15	261	0.234	23705	cell adhesion molecule 1
GO	spermatogenesis	15	261	0.234	4292	mutL homolog 1, colon cancer, nonpolyposis type 2 (E. coli)
GO	spermatogenesis	15	261	0.234	4436	mutS homolog 2, colon cancer, nonpolyposis type 1 (E. coli)
GO	spermatogenesis	15	261	0.234	53340	sperm autoantigenic protein 17
GO	spermatogenesis	15	261	0.234	54993	zinc finger and SCAN domain containing 2
GO	spermatogenesis	15	261	0.234	56852	RAD18 homolog (S. cerevisiae)
GO	spermatogenesis	15	261	0.234	5889	RAD51 homolog C (S. cerevisiae)
GO	spermatogenesis	15	261	0.234	60675	prokineticin 2
GO	spermatogenesis	15	261	0.234	6662	SRY (sex determining region Y)-box 9
GO	spermatogenesis	15	261	0.234	8626	tumor protein p63
GO	connexon complex	2	20	0.237	10052	gap junction protein, gamma 1, 45kDa
GO	connexon complex	2	20	0.237	127534	gap junction protein, beta 4, 30.3kDa
GO	neural crest cell migration	2	20	0.237	10512	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (
GO	neural crest cell migration	2	20	0.237	9839	zinc finger E-box binding homeobox 2
GO	hippocampus development	2	20	0.237	1746	distal-less homeobox 2

GO	hippocampus development	2	20	0.237	9839	zinc finger E-box binding homeobox 2
GO	response to amphetamine	2	20	0.237	1787	tRNA aspartic acid methyltransferase 1
GO	response to amphetamine	2	20	0.237	5021	oxytocin receptor
GO	L-ascorbic acid binding	2	20	0.237	283208	prolyl 4-hydroxylase, alpha polypeptide III
GO	L-ascorbic acid binding	2	20	0.237	5264	phytanoyl-CoA 2-hydroxylase
GO	positive regulation of protein kinase B s	2	20	0.237	7010	TEK tyrosine kinase, endothelial
GO	positive regulation of protein kinase B s	2	20	0.237	7046	transforming growth factor, beta receptor 1
GO	protein C-terminus binding	9	146	0.238	10055	SUMO1 activating enzyme subunit 1
GO	protein C-terminus binding	9	146	0.238	10612	tripartite motif-containing 3
GO	protein C-terminus binding	9	146	0.238	23705	cell adhesion molecule 1
GO	protein C-terminus binding	9	146	0.238	3932	lymphocyte-specific protein tyrosine kinase
GO	protein C-terminus binding	9	146	0.238	4436	mutS homolog 2, colon cancer, nonpolyposis type 1 (E. coli)
GO	protein C-terminus binding	9	146	0.238	5494	protein phosphatase, Mg2+/Mn2+ dependent, 1A
GO	protein C-terminus binding	9	146	0.238	55137	fidgetin
GO	protein C-terminus binding	9	146	0.238	667	dystonin
GO	protein C-terminus binding	9	146	0.238	8777	multiple PDZ domain protein
GO	proton transport	4	54	0.241	479	ATPase, H+/K+ transporting, nongastric, alpha polypeptide
GO	proton transport	4	54	0.241	51382	ATPase, H+ transporting, lysosomal 34kDa, V1 subunit D
GO	proton transport	4	54	0.241	516	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit C1 (subu
GO	proton transport	4	54	0.241	528	ATPase, H+ transporting, lysosomal 42kDa, V1 subunit C1
GO	tight junction	5	72	0.242	11149	blood vessel epicardial substance
GO	tight junction	5	72	0.242	23562	claudin 14
GO	tight junction	5	72	0.242	84552	par-6 partitioning defective 6 homolog gamma (C. elegans)
GO	tight junction	5	72	0.242	8777	multiple PDZ domain protein
GO	tight junction	5	72	0.242	9076	claudin 1
GO	cartilage development	3	37	0.246	1746	distal-less homeobox 2
GO	cartilage development	3	37	0.246	25884	chordin-like 2
GO	cartilage development	3	37	0.246	5081	paired box 7
GO	NAD or NADH binding	3	37	0.246	23171	glycerol-3-phosphate dehydrogenase 1-like
GO	NAD or NADH binding	3	37	0.246	3028	hydroxysteroid (17-beta) dehydrogenase 10
GO	NAD or NADH binding	3	37	0.246	3248	hydroxyprostaglandin dehydrogenase 15-(NAD)
GO	podosome	1	6	0.248	10096	ARP3 actin-related protein 3 homolog (yeast)
GO	pre-snoRNP complex	1	6	0.248	10528	NOP56 ribonucleoprotein homolog (yeast)
GO	paraxial mesoderm development	1	6	0.248	10683	delta-like 3 (Drosophila)
GO	activation of transmembrane receptor p	1	6	0.248	1136	cholinergic receptor, nicotinic, alpha 3
GO	maintenance of gastrointestinal epitheli	1	6	0.248	12	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), me

GO	poly(U) RNA binding	1	6	0.248	124540	musashi homolog 2 (Drosophila)
GO	assembly of spliceosomal tri-snRNP	1	6	0.248	135295	splicing factor, arginine/serine-rich 13B
GO	RS domain binding	1	6	0.248	135295	splicing factor, arginine/serine-rich 13B
GO	protein neddylation	1	6	0.248	140739	ubiquitin-conjugating enzyme E2F (putative)
GO	fucose metabolic process	1	6	0.248	145173	beta 1,3-galactosyltransferase-like
GO	amine metabolic process	1	6	0.248	1543	cytochrome P450, family 1, subfamily A, polypeptide 1
GO	mitochondrial DNA replication	1	6	0.248	1763	DNA replication helicase 2 homolog (yeast)
GO	S-adenosylhomocysteine metabolic pro	1	6	0.248	1788	DNA (cytosine-5-)-methyltransferase 3 alpha
GO	endothelial cell differentiation	1	6	0.248	182	jagged 1 (Alagille syndrome)
GO	aldehyde dehydrogenase [NAD(P)+] acti	1	6	0.248	220	aldehyde dehydrogenase 1 family, member A3
GO	retinoic acid metabolic process	1	6	0.248	220	aldehyde dehydrogenase 1 family, member A3
GO	5'-3' exonuclease activity	1	6	0.248	2237	flap structure-specific endonuclease 1
GO	regulation of ryanodine-sensitive calciu	1	6	0.248	2281	FK506 binding protein 1B, 12.6 kDa
GO	response to redox state	1	6	0.248	2281	FK506 binding protein 1B, 12.6 kDa
GO	regulation of Ras protein signal transdu	1	6	0.248	2305	forkhead box M1
GO	juxtaparanode region of axon	1	6	0.248	23136	erythrocyte membrane protein band 4.1-like 3
GO	aminomethyltransferase activity	1	6	0.248	2653	glycine cleavage system protein H (aminomethyl carrier)
GO	lipoic acid binding	1	6	0.248	2653	glycine cleavage system protein H (aminomethyl carrier)
GO	glutathione binding	1	6	0.248	2878	glutathione peroxidase 3 (plasma)
GO	negative regulation of synaptic transmis	1	6	0.248	2898	glutamate receptor, ionotropic, kainate 2
GO	regulation of inhibitory postsynaptic me	1	6	0.248	2898	glutamate receptor, ionotropic, kainate 2
GO	N-methyl-D-aspartate selective glutama	1	6	0.248	2906	glutamate receptor, ionotropic, N-methyl D-aspartate 2D
GO	startle response	1	6	0.248	2906	glutamate receptor, ionotropic, N-methyl D-aspartate 2D
GO	glucocorticoid receptor binding	1	6	0.248	29893	PSMC3 interacting protein
GO	Leydig cell differentiation	1	6	0.248	3028	hydroxysteroid (17-beta) dehydrogenase 10
GO	forelimb morphogenesis	1	6	0.248	3236	homeobox D10
GO	hindlimb morphogenesis	1	6	0.248	3236	homeobox D10
GO	parturition	1	6	0.248	3248	hydroxyprostaglandin dehydrogenase 15-(NAD)
GO	very-low-density lipoprotein particle as	1	6	0.248	341	apolipoprotein C-I
GO	extrinsic to external side of plasma men	1	6	0.248	348	apolipoprotein E
GO	negative regulation of platelet activatio	1	6	0.248	348	apolipoprotein E
GO	very-low-density lipoprotein particle rer	1	6	0.248	348	apolipoprotein E
GO	interleukin-1 receptor antagonist activit	1	6	0.248	3557	interleukin 1 receptor antagonist
GO	pre-microRNA processing	1	6	0.248	389421	lin-28 homolog B (C. elegans)
GO	regulation of steroid biosynthetic proce	1	6	0.248	3952	leptin
GO	centromeric DNA binding	1	6	0.248	4436	mutS homolog 2, colon cancer, nonpolyposis type 1 (E. coli)

GO	MutLalpha complex binding	1	6	0.248	4436	mutS homolog 2, colon cancer, nonpolyposis type 1 (E. coli)
GO	cellular response to UV	1	6	0.248	4734	neural precursor cell expressed, developmentally down-regulated 4
GO	glucocorticoid receptor signaling pathw	1	6	0.248	4734	neural precursor cell expressed, developmentally down-regulated 4
GO	regulation of synaptic transmission, GA	1	6	0.248	4893	neuroblastoma RAS viral (v-ras) oncogene homolog
GO	striated muscle cell differentiation	1	6	0.248	4893	neuroblastoma RAS viral (v-ras) oncogene homolog
GO	positive regulation of synaptic transmis	1	6	0.248	5021	oxytocin receptor
GO	positive regulation of synaptogenesis	1	6	0.248	5021	oxytocin receptor
GO	DNA damage response, signal transduct	1	6	0.248	51499	TP53 regulated inhibitor of apoptosis 1
GO	proton-transporting ATP synthase com	1	6	0.248	516	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit C1 (sub
GO	negative regulation of G-protein couple	1	6	0.248	5341	pleckstrin
GO	histone mRNA 3'-end processing	1	6	0.248	53981	cleavage and polyadenylation specific factor 2, 100kDa
GO	exocytic vesicle	1	6	0.248	54843	synaptotagmin-like 2
GO	neurexin binding	1	6	0.248	54843	synaptotagmin-like 2
GO	drug transmembrane transporter activit	1	6	0.248	55244	solute carrier family 47, member 1
GO	alpha DNA polymerase:primase comple	1	6	0.248	5558	primase, DNA, polypeptide 2 (58kDa)
GO	phospholipid homeostasis	1	6	0.248	57678	glycerol-3-phosphate acyltransferase, mitochondrial
GO	response to fructose stimulus	1	6	0.248	57678	glycerol-3-phosphate acyltransferase, mitochondrial
GO	apical cortex	1	6	0.248	57817	hepcidin antimicrobial peptide
GO	negative regulation of survival gene pro	1	6	0.248	581	BCL2-associated X protein
GO	nuclear envelope lumen	1	6	0.248	590	butyrylcholinesterase
GO	vitamin A metabolic process	1	6	0.248	5947	retinol binding protein 1, cellular
GO	transition metal ion binding	1	6	0.248	6241	ribonucleotide reductase M2
GO	lymphocyte chemotaxis	1	6	0.248	6347	chemokine (C-C motif) ligand 2
GO	prostate epithelial cord arborization inv	1	6	0.248	6422	secreted frizzled-related protein 1
GO	regulation of branching involved in pros	1	6	0.248	6422	secreted frizzled-related protein 1
GO	protein insertion into membrane	1	6	0.248	65055	receptor accessory protein 1
GO	positive regulation of BMP signaling pat	1	6	0.248	659	bone morphogenetic protein receptor, type II (serine/threonine kinase)
GO	tongue development	1	6	0.248	6657	SRY (sex determining region Y)-box 2
GO	exocrine pancreas development	1	6	0.248	6659	SRY (sex determining region Y)-box 4
GO	chromo shadow domain binding	1	6	0.248	6672	SP100 nuclear antigen
GO	erythrocyte development	1	6	0.248	669	2,3-bisphosphoglycerate mutase
GO	SMAD protein nuclear translocation	1	6	0.248	6711	spectrin, beta, non-erythrocytic 1
GO	gamma-tubulin ring complex	1	6	0.248	672	breast cancer 1, early onset
GO	G-protein coupled photoreceptor activit	1	6	0.248	6785	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like
GO	cardiac muscle tissue morphogenesis	1	6	0.248	70	actin, alpha, cardiac muscle 1
GO	response to manganese ion	1	6	0.248	7037	transferrin receptor (p90, CD71)

GO	cell motility	1	6	0.248	7046	transforming growth factor, beta receptor 1
GO	germ cell migration	1	6	0.248	7046	transforming growth factor, beta receptor 1
GO	store-operated calcium channel activity	1	6	0.248	7220	transient receptor potential cation channel, subfamily C, member 1
GO	sex determination	1	6	0.248	7490	Wilms tumor 1
GO	spinal cord motor neuron differentiatio	1	6	0.248	773	calcium channel, voltage-dependent, P/Q type, alpha 1A subunit
GO	DNA packaging	1	6	0.248	8520	histone acetyltransferase 1
GO	epithelial cell development	1	6	0.248	8626	tumor protein p63
GO	prostate gland development	1	6	0.248	8626	tumor protein p63
GO	proline biosynthetic process	1	6	0.248	8659	aldehyde dehydrogenase 4 family, member A1
GO	response to glucagon stimulus	1	6	0.248	890	cyclin A2
GO	glycoprotein biosynthetic process	1	6	0.248	9215	like-glycosyltransferase
GO	Notch receptor processing	1	6	0.248	92737	delta/notch-like EGF repeat containing
GO	bicarbonate transport	1	6	0.248	9497	solute carrier family 4, sodium bicarbonate cotransporter, member 7
GO	response to toxin	4	55	0.252	10202	dehydrogenase/reductase (SDR family) member 2
GO	response to toxin	4	55	0.252	1026	cyclin-dependent kinase inhibitor 1A (p21, Cip1)
GO	response to toxin	4	55	0.252	581	BCL2-associated X protein
GO	response to toxin	4	55	0.252	7046	transforming growth factor, beta receptor 1
GO	post-embryonic development	4	55	0.252	10512	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (
GO	post-embryonic development	4	55	0.252	3975	LIM homeobox 1
GO	post-embryonic development	4	55	0.252	7046	transforming growth factor, beta receptor 1
GO	post-embryonic development	4	55	0.252	8788	delta-like 1 homolog (Drosophila)
GO	ossification	4	55	0.252	1290	collagen, type V, alpha 2
GO	ossification	4	55	0.252	1836	solute carrier family 26 (sulfate transporter), member 2
GO	ossification	4	55	0.252	25884	chordin-like 2
GO	ossification	4	55	0.252	9260	PDZ and LIM domain 7 (enigma)
GO	transforming growth factor beta recept	4	55	0.252	3248	hydroxyprostaglandin dehydrogenase 15-(NAD)
GO	transforming growth factor beta recept	4	55	0.252	409	arrestin, beta 2
GO	transforming growth factor beta recept	4	55	0.252	6347	chemokine (C-C motif) ligand 2
GO	transforming growth factor beta recept	4	55	0.252	7046	transforming growth factor, beta receptor 1
GO	signal transducer activity	16	285	0.252	10672	guanine nucleotide binding protein (G protein), alpha 13
GO	signal transducer activity	16	285	0.252	25780	RAS guanyl releasing protein 3 (calcium and DAG-regulated)
GO	signal transducer activity	16	285	0.252	2774	guanine nucleotide binding protein (G protein), alpha activating activity pol
GO	signal transducer activity	16	285	0.252	2786	guanine nucleotide binding protein (G protein), gamma 4
GO	signal transducer activity	16	285	0.252	355	Fas (TNF receptor superfamily, member 6)
GO	signal transducer activity	16	285	0.252	3624	inhibin, beta A
GO	signal transducer activity	16	285	0.252	406	aryl hydrocarbon receptor nuclear translocator-like

GO	signal transducer activity	16	285	0.252	54331	guanine nucleotide binding protein (G protein), gamma 2
GO	signal transducer activity	16	285	0.252	5494	protein phosphatase, Mg2+/Mn2+ dependent, 1A
GO	signal transducer activity	16	285	0.252	59345	guanine nucleotide binding protein (G protein), beta polypeptide 4
GO	signal transducer activity	16	285	0.252	6000	regulator of G-protein signaling 7
GO	signal transducer activity	16	285	0.252	6347	chemokine (C-C motif) ligand 2
GO	signal transducer activity	16	285	0.252	7481	wingless-type MMTV integration site family, member 11
GO	signal transducer activity	16	285	0.252	81029	wingless-type MMTV integration site family, member 5B
GO	signal transducer activity	16	285	0.252	84668	family with sequence similarity 126, member A
GO	signal transducer activity	16	285	0.252	8490	regulator of G-protein signaling 5
GO	calcium-dependent phospholipid bindin	2	21	0.255	27445	piccolo (presynaptic cytomatrix protein)
GO	calcium-dependent phospholipid bindin	2	21	0.255	309	annexin A6
GO	ventricular cardiac muscle tissue morph	2	21	0.255	7137	troponin I type 3 (cardiac)
GO	ventricular cardiac muscle tissue morph	2	21	0.255	7168	tropomyosin 1 (alpha)
GO	Wnt receptor signaling pathway, calciur	2	21	0.255	7481	wingless-type MMTV integration site family, member 11
GO	Wnt receptor signaling pathway, calciur	2	21	0.255	81029	wingless-type MMTV integration site family, member 5B
GO	transferase activity, transferring glycosy	9	149	0.257	11226	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltr
GO	transferase activity, transferring glycosy	9	149	0.257	11227	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltr
GO	transferase activity, transferring glycosy	9	149	0.257	114805	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltr
GO	transferase activity, transferring glycosy	9	149	0.257	145173	beta 1,3-galactosyltransferase-like
GO	transferase activity, transferring glycosy	9	149	0.257	64131	xylosyltransferase I
GO	transferase activity, transferring glycosy	9	149	0.257	79623	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltr
GO	transferase activity, transferring glycosy	9	149	0.257	79712	glycosyltransferase-like domain containing 1
GO	transferase activity, transferring glycosy	9	149	0.257	84752	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 9
GO	transferase activity, transferring glycosy	9	149	0.257	9215	like-glycosyltransferase
GO	response to mechanical stimulus	3	38	0.258	5028	purinergic receptor P2Y, G-protein coupled, 1
GO	response to mechanical stimulus	3	38	0.258	6347	chemokine (C-C motif) ligand 2
GO	response to mechanical stimulus	3	38	0.258	7078	TIMP metallopeptidase inhibitor 3
GO	antiporter activity	3	38	0.258	55244	solute carrier family 47, member 1
GO	antiporter activity	3	38	0.258	6546	solute carrier family 8 (sodium/calcium exchanger), member 1
GO	antiporter activity	3	38	0.258	6549	solute carrier family 9 (sodium/hydrogen exchanger), member 2
GO	protein amino acid phosphorylation	26	488	0.262	10000	v-akt murine thymoma viral oncogene homolog 3 (protein kinase B, gamma
GO	protein amino acid phosphorylation	26	488	0.262	132158	glycerate kinase
GO	protein amino acid phosphorylation	26	488	0.262	1716	deoxyguanosine kinase
GO	protein amino acid phosphorylation	26	488	0.262	2045	EPH receptor A7
GO	protein amino acid phosphorylation	26	488	0.262	2242	feline sarcoma oncogene
GO	protein amino acid phosphorylation	26	488	0.262	2264	fibroblast growth factor receptor 4

GO	protein amino acid phosphorylation	26	488	0.262	2533	FYN binding protein (FYB-120/130)
GO	protein amino acid phosphorylation	26	488	0.262	2534	FYN oncogene related to SRC, FGR, YES
GO	protein amino acid phosphorylation	26	488	0.262	27330	ribosomal protein S6 kinase, 90kDa, polypeptide 6
GO	protein amino acid phosphorylation	26	488	0.262	283455	kinase suppressor of ras 2
GO	protein amino acid phosphorylation	26	488	0.262	3932	lymphocyte-specific protein tyrosine kinase
GO	protein amino acid phosphorylation	26	488	0.262	558	AXL receptor tyrosine kinase
GO	protein amino acid phosphorylation	26	488	0.262	5588	protein kinase C, theta
GO	protein amino acid phosphorylation	26	488	0.262	57144	p21 protein (Cdc42/Rac)-activated kinase 7
GO	protein amino acid phosphorylation	26	488	0.262	5754	PTK7 protein tyrosine kinase 7
GO	protein amino acid phosphorylation	26	488	0.262	6347	chemokine (C-C motif) ligand 2
GO	protein amino acid phosphorylation	26	488	0.262	659	bone morphogenetic protein receptor, type II (serine/threonine kinase)
GO	protein amino acid phosphorylation	26	488	0.262	7010	TEK tyrosine kinase, endothelial
GO	protein amino acid phosphorylation	26	488	0.262	7046	transforming growth factor, beta receptor 1
GO	protein amino acid phosphorylation	26	488	0.262	84206	mex-3 homolog B (C. elegans)
GO	protein amino acid phosphorylation	26	488	0.262	8536	calcium/calmodulin-dependent protein kinase I
GO	protein amino acid phosphorylation	26	488	0.262	8997	kalirin, RhoGEF kinase
GO	protein amino acid phosphorylation	26	488	0.262	9262	serine/threonine kinase 17b
GO	protein amino acid phosphorylation	26	488	0.262	9448	mitogen-activated protein kinase kinase kinase kinase 4
GO	protein amino acid phosphorylation	26	488	0.262	9535	glia maturation factor, gamma
GO	protein amino acid phosphorylation	26	488	0.262	9833	maternal embryonic leucine zipper kinase
GO	GTP binding	19	347	0.262	10123	ADP-ribosylation factor-like 4C
GO	GTP binding	19	347	0.262	10672	guanine nucleotide binding protein (G protein), alpha 13
GO	GTP binding	19	347	0.262	10890	RAB10, member RAS oncogene family
GO	GTP binding	19	347	0.262	121268	Ras homolog enriched in brain like 1
GO	GTP binding	19	347	0.262	1983	eukaryotic translation initiation factor 5
GO	GTP binding	19	347	0.262	23157	septin 6
GO	GTP binding	19	347	0.262	27289	Rho family GTPase 1
GO	GTP binding	19	347	0.262	2774	guanine nucleotide binding protein (G protein), alpha activating activity pol
GO	GTP binding	19	347	0.262	347733	tubulin, beta 2B
GO	GTP binding	19	347	0.262	4830	non-metastatic cells 1, protein (NM23A) expressed in
GO	GTP binding	19	347	0.262	4893	neuroblastoma RAS viral (v-ras) oncogene homolog
GO	GTP binding	19	347	0.262	51062	atlastin GTPase 1
GO	GTP binding	19	347	0.262	55207	ADP-ribosylation factor-like 8B
GO	GTP binding	19	347	0.262	55752	septin 11
GO	GTP binding	19	347	0.262	6242	rhotekin
GO	GTP binding	19	347	0.262	7846	tubulin, alpha 1a

GO	GTP binding	19	347	0.262	79861	tubulin, alpha-like 3
GO	GTP binding	19	347	0.262	83871	RAB34, member RAS oncogene family
GO	GTP binding	19	347	0.262	9732	dedicator of cytokinesis 4
GO	transferase activity	57	1127	0.268	10000	v-akt murine thymoma viral oncogene homolog 3 (protein kinase B, gamma
GO	transferase activity	57	1127	0.268	131965	methyltransferase like 6
GO	transferase activity	57	1127	0.268	132158	glycerate kinase
GO	transferase activity	57	1127	0.268	149281	methyltransferase like 11B
GO	transferase activity	57	1127	0.268	157570	establishment of cohesion 1 homolog 2 (S. cerevisiae)
GO	transferase activity	57	1127	0.268	1716	deoxyguanosine kinase
GO	transferase activity	57	1127	0.268	1787	tRNA aspartic acid methyltransferase 1
GO	transferase activity	57	1127	0.268	1788	DNA (cytosine-5-)-methyltransferase 3 alpha
GO	transferase activity	57	1127	0.268	1841	deoxythymidylate kinase (thymidylate kinase)
GO	transferase activity	57	1127	0.268	203	adenylate kinase 1
GO	transferase activity	57	1127	0.268	2045	EPH receptor A7
GO	transferase activity	57	1127	0.268	221357	glutathione S-transferase alpha 5
GO	transferase activity	57	1127	0.268	2242	feline sarcoma oncogene
GO	transferase activity	57	1127	0.268	2264	fibroblast growth factor receptor 4
GO	transferase activity	57	1127	0.268	23057	nicotinamide nucleotide adenylyltransferase 2
GO	transferase activity	57	1127	0.268	2321	fms-related tyrosine kinase 1 (vascular endothelial growth factor/vascular p
GO	transferase activity	57	1127	0.268	23590	prenyl (decaprenyl) diphosphate synthase, subunit 1
GO	transferase activity	57	1127	0.268	2534	FYN oncogene related to SRC, FGR, YES
GO	transferase activity	57	1127	0.268	25885	polymerase (RNA) I polypeptide A, 194kDa
GO	transferase activity	57	1127	0.268	2618	phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide
GO	transferase activity	57	1127	0.268	2628	glycine amidinotransferase (L-arginine:glycine amidinotransferase)
GO	transferase activity	57	1127	0.268	27330	ribosomal protein S6 kinase, 90kDa, polypeptide 6
GO	transferase activity	57	1127	0.268	283209	phosphoglucomutase 2-like 1
GO	transferase activity	57	1127	0.268	29922	non-metastatic cells 7, protein expressed in (nucleoside-diphosphate kinase
GO	transferase activity	57	1127	0.268	3157	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 (soluble)
GO	transferase activity	57	1127	0.268	3276	protein arginine methyltransferase 1
GO	transferase activity	57	1127	0.268	345630	fibrillarin-like 1
GO	transferase activity	57	1127	0.268	3932	lymphocyte-specific protein tyrosine kinase
GO	transferase activity	57	1127	0.268	4830	non-metastatic cells 1, protein (NM23A) expressed in
GO	transferase activity	57	1127	0.268	5110	protein-L-isoaspartate (D-aspartate) O-methyltransferase
GO	transferase activity	57	1127	0.268	54822	transient receptor potential cation channel, subfamily M, member 7
GO	transferase activity	57	1127	0.268	55577	N-acetylglucosamine kinase
GO	transferase activity	57	1127	0.268	5558	primase, DNA, polypeptide 2 (58kDa)

GO	transferase activity	57	1127	0.268	558	AXL receptor tyrosine kinase
GO	transferase activity	57	1127	0.268	5588	protein kinase C, theta
GO	transferase activity	57	1127	0.268	56339	methyltransferase like 3
GO	transferase activity	57	1127	0.268	56655	polymerase (DNA-directed), epsilon 4 (p12 subunit)
GO	transferase activity	57	1127	0.268	57144	p21 protein (Cdc42/Rac)-activated kinase 7
GO	transferase activity	57	1127	0.268	57678	glycerol-3-phosphate acyltransferase, mitochondrial
GO	transferase activity	57	1127	0.268	5833	phosphate cytidylyltransferase 2, ethanolamine
GO	transferase activity	57	1127	0.268	586	branched chain aminotransferase 1, cytosolic
GO	transferase activity	57	1127	0.268	64080	ribokinase
GO	transferase activity	57	1127	0.268	659	bone morphogenetic protein receptor, type II (serine/threonine kinase)
GO	transferase activity	57	1127	0.268	6820	sulfotransferase family, cytosolic, 2B, member 1
GO	transferase activity	57	1127	0.268	7010	TEK tyrosine kinase, endothelial
GO	transferase activity	57	1127	0.268	7046	transforming growth factor, beta receptor 1
GO	transferase activity	57	1127	0.268	7298	thymidylate synthetase
GO	transferase activity	57	1127	0.268	79646	pantothenate kinase 3
GO	transferase activity	57	1127	0.268	84172	polymerase (RNA) I polypeptide B, 128kDa
GO	transferase activity	57	1127	0.268	8520	histone acetyltransferase 1
GO	transferase activity	57	1127	0.268	8536	calcium/calmodulin-dependent protein kinase I
GO	transferase activity	57	1127	0.268	8997	kalirin, RhoGEF kinase
GO	transferase activity	57	1127	0.268	91801	alkB, alkylation repair homolog 8 (E. coli)
GO	transferase activity	57	1127	0.268	9262	serine/threonine kinase 17b
GO	transferase activity	57	1127	0.268	9448	mitogen-activated protein kinase kinase kinase kinase 4
GO	transferase activity	57	1127	0.268	9653	heparan sulfate 2-O-sulfotransferase 1
GO	transferase activity	57	1127	0.268	9833	maternal embryonic leucine zipper kinase
GO	ion channel activity	9	151	0.269	1136	cholinergic receptor, nicotinic, alpha 3
GO	ion channel activity	9	151	0.269	1138	cholinergic receptor, nicotinic, alpha 5
GO	ion channel activity	9	151	0.269	200959	gamma-aminobutyric acid (GABA) receptor, rho 3
GO	ion channel activity	9	151	0.269	2558	gamma-aminobutyric acid (GABA) A receptor, alpha 5
GO	ion channel activity	9	151	0.269	2898	glutamate receptor, ionotropic, kainate 2
GO	ion channel activity	9	151	0.269	5026	purinergic receptor P2X, ligand-gated ion channel, 5
GO	ion channel activity	9	151	0.269	54822	transient receptor potential cation channel, subfamily M, member 7
GO	ion channel activity	9	151	0.269	55283	mucolipin 3
GO	ion channel activity	9	151	0.269	7220	transient receptor potential cation channel, subfamily C, member 1
GO	potassium ion transport	9	151	0.269	283518	potassium channel regulator
GO	potassium ion transport	9	151	0.269	3751	potassium voltage-gated channel, Shal-related subfamily, member 2
GO	potassium ion transport	9	151	0.269	3754	potassium voltage-gated channel, subfamily F, member 1

GO	potassium ion transport	9	151	0.269	3756	potassium voltage-gated channel, subfamily H (eag-related), member 1
GO	potassium ion transport	9	151	0.269	3763	potassium inwardly-rectifying channel, subfamily J, member 6
GO	potassium ion transport	9	151	0.269	3778	potassium large conductance calcium-activated channel, subfamily M, alph
GO	potassium ion transport	9	151	0.269	479	ATPase, H+/K+ transporting, nongastric, alpha polypeptide
GO	potassium ion transport	9	151	0.269	56479	potassium voltage-gated channel, KQT-like subfamily, member 5
GO	potassium ion transport	9	151	0.269	6833	ATP-binding cassette, sub-family C (CFTR/MRP), member 8
GO	epithelial cell differentiation	3	39	0.271	1282	collagen, type IV, alpha 1
GO	epithelial cell differentiation	3	39	0.271	7348	uroplakin 1B
GO	epithelial cell differentiation	3	39	0.271	7490	Wilms tumor 1
GO	intracellular protein kinase cascade	6	94	0.271	10672	guanine nucleotide binding protein (G protein), alpha 13
GO	intracellular protein kinase cascade	6	94	0.271	2533	FYN binding protein (FYB-120/130)
GO	intracellular protein kinase cascade	6	94	0.271	2534	FYN oncogene related to SRC, FGR, YES
GO	intracellular protein kinase cascade	6	94	0.271	27330	ribosomal protein S6 kinase, 90kDa, polypeptide 6
GO	intracellular protein kinase cascade	6	94	0.271	9262	serine/threonine kinase 17b
GO	intracellular protein kinase cascade	6	94	0.271	9448	mitogen-activated protein kinase kinase kinase kinase 4
GO	muscle organ development	6	94	0.271	11149	blood vessel epicardial substance
GO	muscle organ development	6	94	0.271	2273	four and a half LIM domains 1
GO	muscle organ development	6	94	0.271	22801	integrin, alpha 11
GO	muscle organ development	6	94	0.271	6442	sarcoglycan, alpha (50kDa dystrophin-associated glycoprotein)
GO	muscle organ development	6	94	0.271	6444	sarcoglycan, delta (35kDa dystrophin-associated glycoprotein)
GO	muscle organ development	6	94	0.271	6525	smoothelin
GO	endonuclease activity	4	57	0.272	1775	deoxyribonuclease I-like 2
GO	endonuclease activity	4	57	0.272	2237	flap structure-specific endonuclease 1
GO	endonuclease activity	4	57	0.272	4968	8-oxoguanine DNA glycosylase
GO	endonuclease activity	4	57	0.272	84083	zinc finger, RAN-binding domain containing 3
GO	response to glucose stimulus	4	57	0.272	2281	FK506 binding protein 1B, 12.6 kDa
GO	response to glucose stimulus	4	57	0.272	5588	protein kinase C, theta
GO	response to glucose stimulus	4	57	0.272	57678	glycerol-3-phosphate acyltransferase, mitochondrial
GO	response to glucose stimulus	4	57	0.272	6546	solute carrier family 8 (sodium/calcium exchanger), member 1
GO	regulation of cell growth	4	57	0.272	2305	forkhead box M1
GO	regulation of cell growth	4	57	0.272	5588	protein kinase C, theta
GO	regulation of cell growth	4	57	0.272	5654	HtrA serine peptidase 1
GO	regulation of cell growth	4	57	0.272	8835	suppressor of cytokine signaling 2
GO	liver development	4	57	0.272	23705	cell adhesion molecule 1
GO	liver development	4	57	0.272	4763	neurofibromin 1
GO	liver development	4	57	0.272	5469	mediator complex subunit 1

GO	liver development	4	57	0.272	898	cyclin E1
GO	placenta development	2	22	0.272	1045	caudal type homeobox 2
GO	placenta development	2	22	0.272	10761	placenta-specific 1
GO	germ cell development	2	22	0.272	4436	mutS homolog 2, colon cancer, nonpolyposis type 1 (E. coli)
GO	germ cell development	2	22	0.272	7490	Wilms tumor 1
GO	microvillus	2	22	0.272	5021	oxytocin receptor
GO	microvillus	2	22	0.272	7010	TEK tyrosine kinase, endothelial
GO	purinergic nucleotide receptor activity,	2	22	0.272	5028	purinergic receptor P2Y, G-protein coupled, 1
GO	purinergic nucleotide receptor activity,	2	22	0.272	5031	pyrimidinergic receptor P2Y, G-protein coupled, 6
GO	voltage-gated calcium channel complex	2	22	0.272	5494	protein phosphatase, Mg2+/Mn2+ dependent, 1A
GO	voltage-gated calcium channel complex	2	22	0.272	773	calcium channel, voltage-dependent, P/Q type, alpha 1A subunit
GO	basal plasma membrane	2	22	0.272	667	dystonin
GO	basal plasma membrane	2	22	0.272	9635	chloride channel accessory 2
GO	cysteine-type peptidase activity	5	76	0.278	373856	ubiquitin specific peptidase 41
GO	cysteine-type peptidase activity	5	76	0.278	4287	ataxin 3
GO	cysteine-type peptidase activity	5	76	0.278	57478	ubiquitin specific peptidase 31
GO	cysteine-type peptidase activity	5	76	0.278	7347	ubiquitin carboxyl-terminal esterase L3 (ubiquitin thiolesterase)
GO	cysteine-type peptidase activity	5	76	0.278	84101	ubiquitin specific peptidase 44
GO	ribosome	10	172	0.278	11222	mitochondrial ribosomal protein L3
GO	ribosome	10	172	0.278	28998	mitochondrial ribosomal protein L13
GO	ribosome	10	172	0.278	51023	mitochondrial ribosomal protein S18C
GO	ribosome	10	172	0.278	51121	ribosomal protein L26-like 1
GO	ribosome	10	172	0.278	54534	mitochondrial ribosomal protein L50
GO	ribosome	10	172	0.278	6133	ribosomal protein L9
GO	ribosome	10	172	0.278	6154	ribosomal protein L26
GO	ribosome	10	172	0.278	6204	ribosomal protein S10
GO	ribosome	10	172	0.278	65003	mitochondrial ribosomal protein L11
GO	ribosome	10	172	0.278	65008	mitochondrial ribosomal protein L1
GO	regulation of apoptosis	7	114	0.279	355	Fas (TNF receptor superfamily, member 6)
GO	regulation of apoptosis	7	114	0.279	4830	non-metastatic cells 1, protein (NM23A) expressed in
GO	regulation of apoptosis	7	114	0.279	5245	prohibitin
GO	regulation of apoptosis	7	114	0.279	581	BCL2-associated X protein
GO	regulation of apoptosis	7	114	0.279	597	BCL2-related protein A1
GO	regulation of apoptosis	7	114	0.279	6662	SRY (sex determining region Y)-box 9
GO	regulation of apoptosis	7	114	0.279	672	breast cancer 1, early onset
GO	ribonucleoprotein complex	6	95	0.279	10492	synaptotagmin binding, cytoplasmic RNA interacting protein

GO	ribonucleoprotein complex	6	95	0.279	23658	LSM5 homolog, U6 small nuclear RNA associated (S. cerevisiae)
GO	ribonucleoprotein complex	6	95	0.279	345630	fibrillarin-like 1
GO	ribonucleoprotein complex	6	95	0.279	55323	La ribonucleoprotein domain family, member 6
GO	ribonucleoprotein complex	6	95	0.279	672	breast cancer 1, early onset
GO	ribonucleoprotein complex	6	95	0.279	6741	Sjogren syndrome antigen B (autoantigen La)
GO	regulation of cell shape	4	58	0.283	10395	deleted in liver cancer 1
GO	regulation of cell shape	4	58	0.283	10672	guanine nucleotide binding protein (G protein), alpha 13
GO	regulation of cell shape	4	58	0.283	11149	blood vessel epicardial substance
GO	regulation of cell shape	4	58	0.283	2534	FYN oncogene related to SRC, FGR, YES
GO	meiosis	4	58	0.283	132625	zinc finger protein 42 homolog (mouse)
GO	meiosis	4	58	0.283	254528	chromosome 16 open reading frame 73
GO	meiosis	4	58	0.283	286151	F-box protein 43
GO	meiosis	4	58	0.283	29893	PSMC3 interacting protein
GO	growth cone	4	58	0.283	26059	ELKS/RAB6-interacting/CAST family member 2
GO	growth cone	4	58	0.283	26230	T-cell lymphoma invasion and metastasis 2
GO	growth cone	4	58	0.283	29767	tropomodulin 2 (neuronal)
GO	growth cone	4	58	0.283	5015	orthodenticle homeobox 2
GO	alpha-catenin binding	1	7	0.283	1000	cadherin 2, type 1, N-cadherin (neuronal)
GO	proteasome binding	1	7	0.283	10213	proteasome (prosome, macropain) 26S subunit, non-ATPase, 14
GO	labyrinthine layer development	1	7	0.283	1045	caudal type homeobox 2
GO	cyclosporin A binding	1	7	0.283	10465	peptidylprolyl isomerase H (cyclophilin H)
GO	snoRNA binding	1	7	0.283	10528	NOP56 ribonucleoprotein homolog (yeast)
GO	DNA-directed RNA polymerase III compl	1	7	0.283	10622	polymerase (RNA) III (DNA directed) polypeptide G (32kD)
GO	nucleolar ribonuclease P complex	1	7	0.283	10799	ribonuclease P/MRP 40kDa subunit
GO	regulation of Cdc42 GTPase activity	1	7	0.283	11149	blood vessel epicardial substance
GO	cyclin-dependent protein kinase regulat	1	7	0.283	1164	CDC28 protein kinase regulatory subunit 2
GO	fibril organization	1	7	0.283	1289	collagen, type V, alpha 1
GO	wound healing, spreading of epidermal	1	7	0.283	1289	collagen, type V, alpha 1
GO	axon regeneration	1	7	0.283	146760	reticulon 4 receptor-like 1
GO	brain morphogenesis	1	7	0.283	1496	catenin (cadherin-associated protein), alpha 2
GO	pyrimidine nucleotide biosynthetic proc	1	7	0.283	1503	CTP synthase
GO	steroid hydroxylase activity	1	7	0.283	1543	cytochrome P450, family 1, subfamily A, polypeptide 1
GO	morphogenesis of an epithelial sheet	1	7	0.283	182	jagged 1 (Alagille syndrome)
GO	bile acid:sodium symporter activity	1	7	0.283	201780	solute carrier family 10 (sodium/bile acid cotransporter family), member 4
GO	spectrin binding	1	7	0.283	2037	erythrocyte membrane protein band 4.1-like 2
GO	death	1	7	0.283	2149	coagulation factor II (thrombin) receptor

GO	mitotic anaphase	1	7	0.283	220134	spindle and kinetochore associated complex subunit 1
GO	NAD biosynthetic process	1	7	0.283	23057	nicotinamide nucleotide adenylyltransferase 2
GO	Ras guanyl-nucleotide exchange factor a	1	7	0.283	25780	RAS guanyl releasing protein 3 (calcium and DAG-regulated)
GO	cellular homeostasis	1	7	0.283	26154	ATP-binding cassette, sub-family A (ABC1), member 12
GO	response to mercury ion	1	7	0.283	2628	glycine amidinotransferase (L-arginine:glycine amidinotransferase)
GO	BBSome	1	7	0.283	27241	Bardet-Biedl syndrome 9
GO	synaptic vesicle exocytosis	1	7	0.283	27445	piccolo (presynaptic cytomatrix protein)
GO	response to selenium ion	1	7	0.283	2878	glutathione peroxidase 3 (plasma)
GO	kainate selective glutamate receptor ac	1	7	0.283	2898	glutamate receptor, ionotropic, kainate 2
GO	regulation of JNK cascade	1	7	0.283	2898	glutamate receptor, ionotropic, kainate 2
GO	glutamate binding	1	7	0.283	2906	glutamate receptor, ionotropic, N-methyl D-aspartate 2D
GO	neurotransmitter binding	1	7	0.283	2906	glutamate receptor, ionotropic, N-methyl D-aspartate 2D
GO	3-hydroxyacyl-CoA dehydrogenase activ	1	7	0.283	3028	hydroxysteroid (17-beta) dehydrogenase 10
GO	cellular zinc ion homeostasis	1	7	0.283	3932	lymphocyte-specific protein tyrosine kinase
GO	central nervous system neuron develop	1	7	0.283	3952	leptin
GO	fatty acid catabolic process	1	7	0.283	3952	leptin
GO	urogenital system development	1	7	0.283	3975	LIM homeobox 1
GO	cell chemotaxis	1	7	0.283	409	arrestin, beta 2
GO	oxidative phosphorylation	1	7	0.283	4436	mutS homolog 2, colon cancer, nonpolyposis type 1 (E. coli)
GO	unconventional myosin complex	1	7	0.283	4637	myosin, light chain 6, alkali, smooth muscle and non-muscle
GO	protein targeting to lysosome	1	7	0.283	4734	neural precursor cell expressed, developmentally down-regulated 4
GO	regulation of cell-matrix adhesion	1	7	0.283	4763	neurofibromin 1
GO	monovalent inorganic cation transmem	1	7	0.283	479	ATPase, H+/K+ transporting, nongastric, alpha polypeptide
GO	ankyrin binding	1	7	0.283	4897	neuronal cell adhesion molecule
GO	maternal behavior	1	7	0.283	5021	oxytocin receptor
GO	positive regulation of synaptic transmiss	1	7	0.283	5021	oxytocin receptor
GO	extracellular ATP-gated cation channel a	1	7	0.283	5026	purinergic receptor P2X, ligand-gated ion channel, 5
GO	purinergic nucleotide receptor activity	1	7	0.283	5026	purinergic receptor P2X, ligand-gated ion channel, 5
GO	regulation of vasodilation	1	7	0.283	5028	purinergic receptor P2Y, G-protein coupled, 1
GO	cellular response to lipopolysaccharide	1	7	0.283	5054	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor t
GO	peptide biosynthetic process	1	7	0.283	5125	proprotein convertase subtilisin/kexin type 5
GO	extrinsic to plasma membrane	1	7	0.283	54843	synaptotagmin-like 2
GO	negative regulation of catalytic activity	1	7	0.283	5569	protein kinase (cAMP-dependent, catalytic) inhibitor alpha
GO	fructose-2,6-bisphosphate 2-phosphata	1	7	0.283	57103	chromosome 12 open reading frame 5
GO	regulation of protein homodimerization	1	7	0.283	581	BCL2-associated X protein
GO	GTP-Rho binding	1	7	0.283	6242	rhotekin

GO	positive regulation of alpha-beta T cell p	1	7	0.283	641	Bloom syndrome, RecQ helicase-like
GO	pronucleus	1	7	0.283	641	Bloom syndrome, RecQ helicase-like
GO	organic cation transmembrane transpor	1	7	0.283	6580	solute carrier family 22 (organic cation transporter), member 1
GO	U7 snRNP	1	7	0.283	6637	small nuclear ribonucleoprotein polypeptide G
GO	adenohypophysis development	1	7	0.283	6657	SRY (sex determining region Y)-box 2
GO	negative regulation of bone mineralizati	1	7	0.283	6662	SRY (sex determining region Y)-box 9
GO	negative regulation of myoblast differer	1	7	0.283	6662	SRY (sex determining region Y)-box 9
GO	BRCA1-A complex	1	7	0.283	672	breast cancer 1, early onset
GO	transmembrane receptor protein serine	1	7	0.283	7046	transforming growth factor, beta receptor 1
GO	type II transforming growth factor beta	1	7	0.283	7046	transforming growth factor, beta receptor 1
GO	contractile fiber	1	7	0.283	7137	troponin I type 3 (cardiac)
GO	coenzyme A biosynthetic process	1	7	0.283	79646	pantothenate kinase 3
GO	filopodium membrane	1	7	0.283	84168	anthrax toxin receptor 1
GO	semaphorin receptor activity	1	7	0.283	91584	plexin A4
GO	male gonad development	3	40	0.284	132625	zinc finger protein 42 homolog (mouse)
GO	male gonad development	3	40	0.284	4436	mutS homolog 2, colon cancer, nonpolyposis type 1 (E. coli)
GO	male gonad development	3	40	0.284	7490	Wilms tumor 1
GO	non-membrane spanning protein tyrosi	3	40	0.284	2242	feline sarcoma oncogene
GO	non-membrane spanning protein tyrosi	3	40	0.284	2534	FYN oncogene related to SRC, FGR, YES
GO	non-membrane spanning protein tyrosi	3	40	0.284	3932	lymphocyte-specific protein tyrosine kinase
GO	dendritic spine	3	40	0.284	3751	potassium voltage-gated channel, Shal-related subfamily, member 2
GO	dendritic spine	3	40	0.284	55752	septin 11
GO	dendritic spine	3	40	0.284	9419	cysteine-rich PDZ-binding protein
GO	brain development	7	115	0.286	1746	distal-less homeobox 2
GO	brain development	7	115	0.286	2558	gamma-aminobutyric acid (GABA) A receptor, alpha 5
GO	brain development	7	115	0.286	266727	MAM domain containing glycosylphosphatidylinositol anchor 1
GO	brain development	7	115	0.286	4763	neurofibromin 1
GO	brain development	7	115	0.286	5028	purinergic receptor P2Y, G-protein coupled, 1
GO	brain development	7	115	0.286	5469	mediator complex subunit 1
GO	brain development	7	115	0.286	6586	slit homolog 3 (Drosophila)
GO	condensed nuclear chromosome	2	23	0.29	1045	caudal type homeobox 2
GO	condensed nuclear chromosome	2	23	0.29	84365	MKI67 (FHA domain) interacting nucleolar phosphoprotein
GO	neuromuscular process controlling bala	2	23	0.29	3778	potassium large conductance calcium-activated channel, subfamily M, alph
GO	neuromuscular process controlling bala	2	23	0.29	773	calcium channel, voltage-dependent, P/Q type, alpha 1A subunit
GO	positive regulation of cAMP biosyntheti	2	23	0.29	4158	melanocortin 2 receptor (adrenocorticotropic hormone)
GO	positive regulation of cAMP biosyntheti	2	23	0.29	5744	parathyroid hormone-like hormone

GO	chromosome, telomeric region	2	23	0.29	54984	PIN2-interacting protein 1
GO	chromosome, telomeric region	2	23	0.29	641	Bloom syndrome, RecQ helicase-like
GO	regulation of ARF GTPase activity	2	23	0.29	55803	ArfGAP with dual PH domains 2
GO	regulation of ARF GTPase activity	2	23	0.29	9744	ArfGAP with coiled-coil, ankyrin repeat and PH domains 1
GO	positive regulation of osteoblast differe	2	23	0.29	659	bone morphogenetic protein receptor, type II (serine/threonine kinase)
GO	positive regulation of osteoblast differe	2	23	0.29	9260	PDZ and LIM domain 7 (enigma)
GO	Wnt receptor signaling pathway througl	2	23	0.29	6659	SRY (sex determining region Y)-box 4
GO	Wnt receptor signaling pathway througl	2	23	0.29	8325	frizzled homolog 8 (Drosophila)
GO	thymus development	2	23	0.29	6899	T-box 1
GO	thymus development	2	23	0.29	7046	transforming growth factor, beta receptor 1
GO	cytoplasmic mRNA processing body	2	23	0.29	84206	mex-3 homolog B (C. elegans)
GO	cytoplasmic mRNA processing body	2	23	0.29	92312	mex-3 homolog A (C. elegans)
GO	negative regulation of protein kinase ac	3	41	0.297	11142	protein kinase (cAMP-dependent, catalytic) inhibitor gamma
GO	negative regulation of protein kinase ac	3	41	0.297	4763	neurofibromin 1
GO	negative regulation of protein kinase ac	3	41	0.297	5569	protein kinase (cAMP-dependent, catalytic) inhibitor alpha
GO	positive regulation of transcription from	16	295	0.297	11278	Kruppel-like factor 12
GO	positive regulation of transcription from	16	295	0.297	1746	distal-less homeobox 2
GO	positive regulation of transcription from	16	295	0.297	2736	GLI family zinc finger 2
GO	positive regulation of transcription from	16	295	0.297	2965	general transcription factor IIH, polypeptide 1, 62kDa
GO	positive regulation of transcription from	16	295	0.297	29893	PSMC3 interacting protein
GO	positive regulation of transcription from	16	295	0.297	3236	homeobox D10
GO	positive regulation of transcription from	16	295	0.297	3589	interleukin 11
GO	positive regulation of transcription from	16	295	0.297	3624	inhibin, beta A
GO	positive regulation of transcription from	16	295	0.297	406	aryl hydrocarbon receptor nuclear translocator-like
GO	positive regulation of transcription from	16	295	0.297	5469	mediator complex subunit 1
GO	positive regulation of transcription from	16	295	0.297	58499	zinc finger protein 462
GO	positive regulation of transcription from	16	295	0.297	6299	sal-like 1 (Drosophila)
GO	positive regulation of transcription from	16	295	0.297	6657	SRY (sex determining region Y)-box 2
GO	positive regulation of transcription from	16	295	0.297	6662	SRY (sex determining region Y)-box 9
GO	positive regulation of transcription from	16	295	0.297	7490	Wilms tumor 1
GO	positive regulation of transcription from	16	295	0.297	8626	tumor protein p63
GO	GTPase activator activity	9	156	0.3	10395	deleted in liver cancer 1
GO	GTPase activator activity	9	156	0.3	1121	choroideremia (Rab escort protein 1)
GO	GTPase activator activity	9	156	0.3	1123	chimerin (chimaerin) 1
GO	GTPase activator activity	9	156	0.3	51256	TBC1 domain family, member 7
GO	GTPase activator activity	9	156	0.3	55789	DEP domain containing 1B

GO	GTPase activator activity	9	156	0.3	55803	ArfGAP with dual PH domains 2
GO	GTPase activator activity	9	156	0.3	8490	regulator of G-protein signaling 5
GO	GTPase activator activity	9	156	0.3	9882	TBC1 domain family, member 4
GO	GTPase activator activity	9	156	0.3	9910	RAB GTPase activating protein 1-like
GO	chromatin binding	9	156	0.3	113130	cell division cycle associated 5
GO	chromatin binding	9	156	0.3	1746	distal-less homeobox 2
GO	chromatin binding	9	156	0.3	1788	DNA (cytosine-5-)-methyltransferase 3 alpha
GO	chromatin binding	9	156	0.3	2736	GLI family zinc finger 2
GO	chromatin binding	9	156	0.3	3236	homeobox D10
GO	chromatin binding	9	156	0.3	5469	mediator complex subunit 1
GO	chromatin binding	9	156	0.3	6657	SRY (sex determining region Y)-box 2
GO	chromatin binding	9	156	0.3	8626	tumor protein p63
GO	chromatin binding	9	156	0.3	91442	chromosome 19 open reading frame 40
GO	hormone activity	5	79	0.305	3624	inhibin, beta A
GO	hormone activity	5	79	0.305	3952	leptin
GO	hormone activity	5	79	0.305	5744	parathyroid hormone-like hormone
GO	hormone activity	5	79	0.305	57817	hepcidin antimicrobial peptide
GO	hormone activity	5	79	0.305	6019	relaxin 2
GO	extracellular region	85	1730	0.305	10512	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (
GO	extracellular region	85	1730	0.305	10761	placenta-specific 1
GO	extracellular region	85	1730	0.305	10893	matrix metallopeptidase 24 (membrane-inserted)
GO	extracellular region	85	1730	0.305	11010	GLI pathogenesis-related 1
GO	extracellular region	85	1730	0.305	11249	neurexophilin 2
GO	extracellular region	85	1730	0.305	115908	collagen triple helix repeat containing 1
GO	extracellular region	85	1730	0.305	12	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), me
GO	extracellular region	85	1730	0.305	1282	collagen, type IV, alpha 1
GO	extracellular region	85	1730	0.305	1284	collagen, type IV, alpha 2
GO	extracellular region	85	1730	0.305	1288	collagen, type IV, alpha 6
GO	extracellular region	85	1730	0.305	1289	collagen, type V, alpha 1
GO	extracellular region	85	1730	0.305	1290	collagen, type V, alpha 2
GO	extracellular region	85	1730	0.305	1301	collagen, type XI, alpha 1
GO	extracellular region	85	1730	0.305	131450	CD200 receptor 1
GO	extracellular region	85	1730	0.305	132724	transmembrane protease, serine 11B
GO	extracellular region	85	1730	0.305	1379	complement component (3b/4b) receptor 1-like
GO	extracellular region	85	1730	0.305	140902	R3H domain containing-like
GO	extracellular region	85	1730	0.305	143282	fibroblast growth factor binding protein 3

GO	extracellular region	85	1730	0.305	145864	hyaluronan and proteoglycan link protein 3
GO	extracellular region	85	1730	0.305	146556	chromosome 16 open reading frame 89
GO	extracellular region	85	1730	0.305	147920	IGF-like family member 2
GO	extracellular region	85	1730	0.305	152007	GLI pathogenesis-related 2
GO	extracellular region	85	1730	0.305	152816	chromosome 4 open reading frame 26
GO	extracellular region	85	1730	0.305	162681	chromosome 18 open reading frame 54
GO	extracellular region	85	1730	0.305	1690	coagulation factor C homolog, cochlin (Limulus polyphemus)
GO	extracellular region	85	1730	0.305	1775	deoxyribonuclease I-like 2
GO	extracellular region	85	1730	0.305	182	jagged 1 (Alagille syndrome)
GO	extracellular region	85	1730	0.305	2135	exostoses (multiple)-like 2
GO	extracellular region	85	1730	0.305	219990	placenta-specific 1-like
GO	extracellular region	85	1730	0.305	221044	upper zone of growth plate and cartilage matrix associated
GO	extracellular region	85	1730	0.305	2321	fms-related tyrosine kinase 1 (vascular endothelial growth factor/vascular
GO	extracellular region	85	1730	0.305	24147	four jointed box 1 (Drosophila)
GO	extracellular region	85	1730	0.305	245929	defensin, beta 115
GO	extracellular region	85	1730	0.305	25817	family with sequence similarity 19 (chemokine (C-C motif)-like), member A
GO	extracellular region	85	1730	0.305	25884	chordin-like 2
GO	extracellular region	85	1730	0.305	26577	procollagen C-endopeptidase enhancer 2
GO	extracellular region	85	1730	0.305	284207	meteorin, glial cell differentiation regulator-like
GO	extracellular region	85	1730	0.305	2878	glutathione peroxidase 3 (plasma)
GO	extracellular region	85	1730	0.305	341	apolipoprotein C-I
GO	extracellular region	85	1730	0.305	348	apolipoprotein E
GO	extracellular region	85	1730	0.305	355	Fas (TNF receptor superfamily, member 6)
GO	extracellular region	85	1730	0.305	3557	interleukin 1 receptor antagonist
GO	extracellular region	85	1730	0.305	3589	interleukin 11
GO	extracellular region	85	1730	0.305	3624	inhibin, beta A
GO	extracellular region	85	1730	0.305	374897	suprabasin
GO	extracellular region	85	1730	0.305	374918	IGF-like family member 1
GO	extracellular region	85	1730	0.305	388555	IGF-like family member 3
GO	extracellular region	85	1730	0.305	3918	laminin, gamma 2
GO	extracellular region	85	1730	0.305	3952	leptin
GO	extracellular region	85	1730	0.305	4052	latent transforming growth factor beta binding protein 1
GO	extracellular region	85	1730	0.305	4060	lumican
GO	extracellular region	85	1730	0.305	4312	matrix metallopeptidase 1 (interstitial collagenase)
GO	extracellular region	85	1730	0.305	4318	matrix metallopeptidase 9 (gelatinase B, 92kDa gelatinase, 92kDa type IV c
GO	extracellular region	85	1730	0.305	4319	matrix metallopeptidase 10 (stromelysin 2)

GO	extracellular region	85	1730	0.305	5054	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor t
GO	extracellular region	85	1730	0.305	51050	peptidase inhibitor 15
GO	extracellular region	85	1730	0.305	5125	proprotein convertase subtilisin/kexin type 5
GO	extracellular region	85	1730	0.305	5228	placental growth factor
GO	extracellular region	85	1730	0.305	5341	pleckstrin
GO	extracellular region	85	1730	0.305	5360	phospholipid transfer protein
GO	extracellular region	85	1730	0.305	54210	triggering receptor expressed on myeloid cells 1
GO	extracellular region	85	1730	0.305	5624	protein C (inactivator of coagulation factors Va and VIIIa)
GO	extracellular region	85	1730	0.305	5654	HtrA serine peptidase 1
GO	extracellular region	85	1730	0.305	5744	parathyroid hormone-like hormone
GO	extracellular region	85	1730	0.305	57642	collagen, type XX, alpha 1
GO	extracellular region	85	1730	0.305	57817	hepcidin antimicrobial peptide
GO	extracellular region	85	1730	0.305	590	butyrylcholinesterase
GO	extracellular region	85	1730	0.305	6019	relaxin 2
GO	extracellular region	85	1730	0.305	60675	prokineticin 2
GO	extracellular region	85	1730	0.305	6347	chemokine (C-C motif) ligand 2
GO	extracellular region	85	1730	0.305	64131	xylosyltransferase I
GO	extracellular region	85	1730	0.305	6422	secreted frizzled-related protein 1
GO	extracellular region	85	1730	0.305	6586	slit homolog 3 (Drosophila)
GO	extracellular region	85	1730	0.305	6695	sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 1
GO	extracellular region	85	1730	0.305	7037	transferrin receptor (p90, CD71)
GO	extracellular region	85	1730	0.305	7058	thrombospondin 2
GO	extracellular region	85	1730	0.305	7078	TIMP metallopeptidase inhibitor 3
GO	extracellular region	85	1730	0.305	7113	transmembrane protease, serine 2
GO	extracellular region	85	1730	0.305	7481	wingless-type MMTV integration site family, member 11
GO	extracellular region	85	1730	0.305	7857	secretogranin II (chromogranin C)
GO	extracellular region	85	1730	0.305	79135	apolipoprotein O
GO	extracellular region	85	1730	0.305	81029	wingless-type MMTV integration site family, member 5B
GO	extracellular region	85	1730	0.305	9244	cytokine receptor-like factor 1
GO	extracellular region	85	1730	0.305	9542	neuregulin 2
GO	extracellular region	85	1730	0.305	9635	chloride channel accessory 2
GO	learning	2	24	0.307	2534	FYN oncogene related to SRC, FGR, YES
GO	learning	2	24	0.307	590	butyrylcholinesterase
GO	visual learning	2	24	0.307	4763	neurofibromin 1
GO	visual learning	2	24	0.307	4893	neuroblastoma RAS viral (v-ras) oncogene homolog
GO	ARF GTPase activator activity	2	24	0.307	55803	ArfGAP with dual PH domains 2

GO	ARF GTPase activator activity	2	24	0.307	9744	ArfGAP with coiled-coil, ankyrin repeat and PH domains 1
GO	cellular iron ion homeostasis	2	24	0.307	57817	hepcidin antimicrobial peptide
GO	cellular iron ion homeostasis	2	24	0.307	7037	transferrin receptor (p90, CD71)
GO	lung alveolus development	2	24	0.307	659	bone morphogenetic protein receptor, type II (serine/threonine kinase)
GO	lung alveolus development	2	24	0.307	6657	SRY (sex determining region Y)-box 2
GO	regulation of protein metabolic process	3	42	0.31	140739	ubiquitin-conjugating enzyme E2F (putative)
GO	regulation of protein metabolic process	3	42	0.31	389898	ubiquitin-conjugating enzyme E2N-like
GO	regulation of protein metabolic process	3	42	0.31	7324	ubiquitin-conjugating enzyme E2E 1 (UBC4/5 homolog, yeast)
GO	cell growth	3	42	0.31	2273	four and a half LIM domains 1
GO	cell growth	3	42	0.31	65009	NDRG family member 4
GO	cell growth	3	42	0.31	773	calcium channel, voltage-dependent, P/Q type, alpha 1A subunit
GO	RNA processing	5	80	0.314	10199	M-phase phosphoprotein 10 (U3 small nucleolar ribonucleoprotein)
GO	RNA processing	5	80	0.314	10492	synaptotagmin binding, cytoplasmic RNA interacting protein
GO	RNA processing	5	80	0.314	55323	La ribonucleoprotein domain family, member 6
GO	RNA processing	5	80	0.314	65008	mitochondrial ribosomal protein L1
GO	RNA processing	5	80	0.314	6741	Sjogren syndrome antigen B (autoantigen La)
GO	basement membrane	4	61	0.314	1289	collagen, type V, alpha 1
GO	basement membrane	4	61	0.314	3918	laminin, gamma 2
GO	basement membrane	4	61	0.314	667	dystonin
GO	basement membrane	4	61	0.314	7078	TIMP metallopeptidase inhibitor 3
GO	cytoplasmic vesicle membrane	4	61	0.314	23138	Nedd4 binding protein 3
GO	cytoplasmic vesicle membrane	4	61	0.314	30011	SH3-domain kinase binding protein 1
GO	cytoplasmic vesicle membrane	4	61	0.314	55016	membrane-associated ring finger (C3HC4) 1
GO	cytoplasmic vesicle membrane	4	61	0.314	8905	adaptor-related protein complex 1, sigma 2 subunit
GO	cytoskeleton organization	4	61	0.314	27445	piccolo (presynaptic cytomatrix protein)
GO	cytoskeleton organization	4	61	0.314	348	apolipoprotein E
GO	cytoskeleton organization	4	61	0.314	6444	sarcoglycan, delta (35kDa dystrophin-associated glycoprotein)
GO	cytoskeleton organization	4	61	0.314	7168	tropomyosin 1 (alpha)
GO	response to estradiol stimulus	4	61	0.314	5021	oxytocin receptor
GO	response to estradiol stimulus	4	61	0.314	8835	suppressor of cytokine signaling 2
GO	response to estradiol stimulus	4	61	0.314	890	cyclin A2
GO	response to estradiol stimulus	4	61	0.314	898	cyclin E1
GO	catenin complex	1	8	0.316	1000	cadherin 2, type 1, N-cadherin (neuronal)
GO	positive regulation of dendrite morphog	1	8	0.316	10096	ARP3 actin-related protein 3 homolog (yeast)
GO	response to carbohydrate stimulus	1	8	0.316	10096	ARP3 actin-related protein 3 homolog (yeast)
GO	protein K63-linked deubiquitination	1	8	0.316	10213	proteasome (prosome, macropain) 26S subunit, non-ATPase, 14

GO	cyclin binding	1	8	0.316	1026	cyclin-dependent kinase inhibitor 1A (p21, Cip1)
GO	cyclin-dependent protein kinase holoen	1	8	0.316	1026	cyclin-dependent kinase inhibitor 1A (p21, Cip1)
GO	poly(A) RNA binding	1	8	0.316	10492	synaptotagmin binding, cytoplasmic RNA interacting protein
GO	negative regulation of neurogenesis	1	8	0.316	10683	delta-like 3 (Drosophila)
GO	prepulse inhibition	1	8	0.316	1496	catenin (cadherin-associated protein), alpha 2
GO	hydrogen peroxide biosynthetic process	1	8	0.316	1543	cytochrome P450, family 1, subfamily A, polypeptide 1
GO	olfactory bulb development	1	8	0.316	1746	distal-less homeobox 2
GO	secondary active sulfate transmembran	1	8	0.316	1836	solute carrier family 26 (sulfate transporter), member 2
GO	adenylate kinase activity	1	8	0.316	203	adenylate kinase 1
GO	ephrin receptor binding	1	8	0.316	2045	EPH receptor A7
GO	positive regulation of JAK-STAT cascade	1	8	0.316	2149	coagulation factor II (thrombin) receptor
GO	positive regulation of leukocyte chemot	1	8	0.316	2150	coagulation factor II (thrombin) receptor-like 1
GO	retinal metabolic process	1	8	0.316	220	aldehyde dehydrogenase 1 family, member A3
GO	calcium channel complex	1	8	0.316	2281	FK506 binding protein 1B, 12.6 kDa
GO	FK506 binding	1	8	0.316	2281	FK506 binding protein 1B, 12.6 kDa
GO	vascular endothelial growth factor rece	1	8	0.316	2321	fms-related tyrosine kinase 1 (vascular endothelial growth factor/vascular
GO	protein homotrimerization	1	8	0.316	241	arachidonate 5-lipoxygenase-activating protein
GO	diacylglycerol binding	1	8	0.316	25780	RAS guanyl releasing protein 3 (calcium and DAG-regulated)
GO	creatine metabolic process	1	8	0.316	2628	glycine amidinotransferase (L-arginine:glycine amidinotransferase)
GO	glycine catabolic process	1	8	0.316	2653	glycine cleavage system protein H (aminomethyl carrier)
GO	dopamine receptor signaling pathway	1	8	0.316	27065	DNA segment on chromosome 4 (unique) 234 expressed sequence
GO	N-methyl-D-aspartate selective glutama	1	8	0.316	2906	glutamate receptor, ionotropic, N-methyl D-aspartate 2D
GO	positive regulation of G-protein couple	1	8	0.316	29767	tropomodulin 2 (neuronal)
GO	positive regulation of chondrocyte diffe	1	8	0.316	3237	homeobox D11
GO	phosphatidylcholine binding	1	8	0.316	341	apolipoprotein C-I
GO	phospholipase inhibitor activity	1	8	0.316	341	apolipoprotein C-I
GO	negative regulation of programmed cell	1	8	0.316	347902	adhesion molecule with Ig-like domain 2
GO	antioxidant activity	1	8	0.316	348	apolipoprotein E
GO	positive regulation of cholesterol efflux	1	8	0.316	348	apolipoprotein E
GO	protein-DNA complex	1	8	0.316	3516	recombination signal binding protein for immunoglobulin kappa J region
GO	ciliary rootlet	1	8	0.316	3800	kinesin family member 5C
GO	energy reserve metabolic process	1	8	0.316	3952	leptin
GO	response to UV-B	1	8	0.316	4436	mutS homolog 2, colon cancer, nonpolyposis type 1 (E. coli)
GO	actin-dependent ATPase activity	1	8	0.316	4637	myosin, light chain 6, alkali, smooth muscle and non-muscle
GO	phosphoinositide 3-kinase cascade	1	8	0.316	4763	neurofibromin 1
GO	hydrogen-exporting ATPase activity, ph	1	8	0.316	528	ATPase, H+ transporting, lysosomal 42kDa, V1 subunit C1

GO	proton-transporting V-type ATPase, V1	1	8	0.316	528	ATPase, H+ transporting, lysosomal 42kDa, V1 subunit C1
GO	embryonic hemopoiesis	1	8	0.316	5469	mediator complex subunit 1
GO	positive regulation of NF-kappaB impor	1	8	0.316	5588	protein kinase C, theta
GO	activation of caspase activity by cytochr	1	8	0.316	581	BCL2-associated X protein
GO	retinoid binding	1	8	0.316	5947	retinol binding protein 1, cellular
GO	heterochromatin	1	8	0.316	6299	sal-like 1 (Drosophila)
GO	regulation of ossification	1	8	0.316	6422	secreted frizzled-related protein 1
GO	regulation of sodium ion transport	1	8	0.316	6546	solute carrier family 8 (sodium/calcium exchanger), member 1
GO	organic cation transport	1	8	0.316	6580	solute carrier family 22 (organic cation transporter), member 1
GO	negative chemotaxis	1	8	0.316	6586	slit homolog 3 (Drosophila)
GO	transmembrane receptor protein serine	1	8	0.316	659	bone morphogenetic protein receptor, type II (serine/threonine kinase)
GO	positive regulation of neuroblast prolife	1	8	0.316	6657	SRY (sex determining region Y)-box 2
GO	embryonic viscerocranium morphogene	1	8	0.316	6899	T-box 1
GO	positive regulation of SMAD protein nuc	1	8	0.316	7046	transforming growth factor, beta receptor 1
GO	troponin complex	1	8	0.316	7137	troponin I type 3 (cardiac)
GO	sarcomere organization	1	8	0.316	7168	tropomyosin 1 (alpha)
GO	cytosolic calcium ion homeostasis	1	8	0.316	7220	transient receptor potential cation channel, subfamily C, member 1
GO	histone H2B ubiquitination	1	8	0.316	7324	ubiquitin-conjugating enzyme E2E 1 (UBC4/5 homolog, yeast)
GO	C2H2 zinc finger domain binding	1	8	0.316	7490	Wilms tumor 1
GO	mesonephros development	1	8	0.316	7490	Wilms tumor 1
GO	regulation of calcium ion-dependent ex	1	8	0.316	773	calcium channel, voltage-dependent, P/Q type, alpha 1A subunit
GO	epithelial cell proliferation	1	8	0.316	7840	Alstrom syndrome 1
GO	positive regulation of fat cell differentia	1	8	0.316	81029	wingless-type MMTV integration site family, member 5B
GO	L-glutamate transport	1	8	0.316	8604	solute carrier family 25 (mitochondrial carrier, Aralar), member 12
GO	tail morphogenesis	1	8	0.316	8626	tumor protein p63
GO	glycosphingolipid biosynthetic process	1	8	0.316	9215	like-glycosyltransferase
GO	clathrin binding	1	8	0.316	92737	delta/notch-like EGF repeat containing
GO	HAUS complex	1	8	0.316	93323	HAUS augmin-like complex, subunit 8
GO	bile acid biosynthetic process	1	8	0.316	9420	cytochrome P450, family 7, subfamily B, polypeptide 1
GO	induction of apoptosis by oxidative stre	1	8	0.316	9540	tumor protein p53 inducible protein 3
GO	protein folding	8	139	0.318	10465	peptidylprolyl isomerase H (cyclophilin H)
GO	protein folding	8	139	0.318	1047	calmegin
GO	protein folding	8	139	0.318	3336	heat shock 10kDa protein 1 (chaperonin 10)
GO	protein folding	8	139	0.318	51645	peptidylprolyl isomerase (cyclophilin)-like 1
GO	protein folding	8	139	0.318	5203	prefoldin subunit 4
GO	protein folding	8	139	0.318	5303	protein (peptidylprolyl cis/trans isomerase) NIMA-interacting, 4 (parvulin)

GO	protein folding	8	139	0.318	81562	lectin, mannose-binding 2-like
GO	protein folding	8	139	0.318	8409	ubiquitously-expressed transcript
GO	ion transport	26	505	0.322	1136	cholinergic receptor, nicotinic, alpha 3
GO	ion transport	26	505	0.322	1138	cholinergic receptor, nicotinic, alpha 5
GO	ion transport	26	505	0.322	200959	gamma-aminobutyric acid (GABA) receptor, rho 3
GO	ion transport	26	505	0.322	201780	solute carrier family 10 (sodium/bile acid cotransporter family), member 4
GO	ion transport	26	505	0.322	2558	gamma-aminobutyric acid (GABA) A receptor, alpha 5
GO	ion transport	26	505	0.322	2898	glutamate receptor, ionotropic, kainate 2
GO	ion transport	26	505	0.322	2906	glutamate receptor, ionotropic, N-methyl D-aspartate 2D
GO	ion transport	26	505	0.322	348938	NIPA-like domain containing 4
GO	ion transport	26	505	0.322	3751	potassium voltage-gated channel, Shal-related subfamily, member 2
GO	ion transport	26	505	0.322	3754	potassium voltage-gated channel, subfamily F, member 1
GO	ion transport	26	505	0.322	3756	potassium voltage-gated channel, subfamily H (eag-related), member 1
GO	ion transport	26	505	0.322	3763	potassium inwardly-rectifying channel, subfamily J, member 6
GO	ion transport	26	505	0.322	3778	potassium large conductance calcium-activated channel, subfamily M, alph
GO	ion transport	26	505	0.322	5026	purinergic receptor P2X, ligand-gated ion channel, 5
GO	ion transport	26	505	0.322	51382	ATPase, H+ transporting, lysosomal 34kDa, V1 subunit D
GO	ion transport	26	505	0.322	516	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit C1 (subu
GO	ion transport	26	505	0.322	528	ATPase, H+ transporting, lysosomal 42kDa, V1 subunit C1
GO	ion transport	26	505	0.322	54822	transient receptor potential cation channel, subfamily M, member 7
GO	ion transport	26	505	0.322	55283	mucolipin 3
GO	ion transport	26	505	0.322	56479	potassium voltage-gated channel, KQT-like subfamily, member 5
GO	ion transport	26	505	0.322	6335	sodium channel, voltage-gated, type IX, alpha subunit
GO	ion transport	26	505	0.322	6527	solute carrier family 5 (low affinity glucose cotransporter), member 4
GO	ion transport	26	505	0.322	6546	solute carrier family 8 (sodium/calcium exchanger), member 1
GO	ion transport	26	505	0.322	7220	transient receptor potential cation channel, subfamily C, member 1
GO	ion transport	26	505	0.322	773	calcium channel, voltage-dependent, P/Q type, alpha 1A subunit
GO	ion transport	26	505	0.322	9635	chloride channel accessory 2
GO	Notch signaling pathway	3	43	0.322	182	jagged 1 (Alagille syndrome)
GO	Notch signaling pathway	3	43	0.322	3516	recombination signal binding protein for immunoglobulin kappa J region
GO	Notch signaling pathway	3	43	0.322	55759	WD repeat domain 12
GO	glucose metabolic process	3	43	0.322	283209	phosphoglucomutase 2-like 1
GO	glucose metabolic process	3	43	0.322	3952	leptin
GO	glucose metabolic process	3	43	0.322	773	calcium channel, voltage-dependent, P/Q type, alpha 1A subunit
GO	protein polyubiquitination	2	25	0.325	1161	excision repair cross-complementing rodent repair deficiency, complement
GO	protein polyubiquitination	2	25	0.325	1643	damage-specific DNA binding protein 2, 48kDa

GO	spindle microtubule	2	25	0.325	220134	spindle and kinetochore associated complex subunit 1
GO	spindle microtubule	2	25	0.325	332	baculoviral IAP repeat-containing 5
GO	glycoprotein binding	2	25	0.325	2534	FYN oncogene related to SRC, FGR, YES
GO	glycoprotein binding	2	25	0.325	3932	lymphocyte-specific protein tyrosine kinase
GO	filopodium	2	25	0.325	26230	T-cell lymphoma invasion and metastasis 2
GO	filopodium	2	25	0.325	5420	podocalyxin-like
GO	mitochondrial intermembrane space	2	25	0.325	2628	glycine amidinotransferase (L-arginine:glycine amidinotransferase)
GO	mitochondrial intermembrane space	2	25	0.325	27429	HtrA serine peptidase 2
GO	protein targeting to mitochondrion	2	25	0.325	26519	translocase of inner mitochondrial membrane 10 homolog (yeast)
GO	protein targeting to mitochondrion	2	25	0.325	26521	translocase of inner mitochondrial membrane 8 homolog B (yeast)
GO	thyroid hormone receptor binding	2	25	0.325	29893	PSMC3 interacting protein
GO	thyroid hormone receptor binding	2	25	0.325	5469	mediator complex subunit 1
GO	skeletal system morphogenesis	2	25	0.325	3224	homeobox C8
GO	skeletal system morphogenesis	2	25	0.325	7046	transforming growth factor, beta receptor 1
GO	spliceosomal snRNP assembly	2	25	0.325	6637	small nuclear ribonucleoprotein polypeptide G
GO	spliceosomal snRNP assembly	2	25	0.325	79833	gem (nuclear organelle) associated protein 6
GO	negative regulation of ubiquitin-protein	4	62	0.325	10213	proteasome (prosome, macropain) 26S subunit, non-ATPase, 14
GO	negative regulation of ubiquitin-protein	4	62	0.325	5702	proteasome (prosome, macropain) 26S subunit, ATPase, 3
GO	negative regulation of ubiquitin-protein	4	62	0.325	5717	proteasome (prosome, macropain) 26S subunit, non-ATPase, 11
GO	negative regulation of ubiquitin-protein	4	62	0.325	7324	ubiquitin-conjugating enzyme E2E 1 (UBC4/5 homolog, yeast)
GO	integrin binding	4	62	0.325	10457	glycoprotein (transmembrane) nmb
GO	integrin binding	4	62	0.325	1289	collagen, type V, alpha 1
GO	integrin binding	4	62	0.325	3694	integrin, beta 6
GO	integrin binding	4	62	0.325	667	dystonin
GO	positive regulation of cell migration	4	62	0.325	2149	coagulation factor II (thrombin) receptor
GO	positive regulation of cell migration	4	62	0.325	2321	fms-related tyrosine kinase 1 (vascular endothelial growth factor/vascular
GO	positive regulation of cell migration	4	62	0.325	5420	podocalyxin-like
GO	positive regulation of cell migration	4	62	0.325	81029	wingless-type MMTV integration site family, member 5B
GO	protein complex assembly	6	101	0.328	10465	peptidylprolyl isomerase H (cyclophilin H)
GO	protein complex assembly	6	101	0.328	23562	claudin 14
GO	protein complex assembly	6	101	0.328	355	Fas (TNF receptor superfamily, member 6)
GO	protein complex assembly	6	101	0.328	56479	potassium voltage-gated channel, KQT-like subfamily, member 5
GO	protein complex assembly	6	101	0.328	7456	WAS/WASL interacting protein family, member 1
GO	protein complex assembly	6	101	0.328	84365	MKI67 (FHA domain) interacting nucleolar phosphoprotein
GO	cellular_component	27	528	0.33	10190	thioredoxin domain containing 9
GO	cellular_component	27	528	0.33	10761	placenta-specific 1

GO	cellular_component	27	528	0.33	10777	cyclic AMP-regulated phosphoprotein, 21 kD
GO	cellular_component	27	528	0.33	10962	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophi
GO	cellular_component	27	528	0.33	11227	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltr
GO	cellular_component	27	528	0.33	132851	spermatogenesis associated 4
GO	cellular_component	27	528	0.33	1503	CTP synthase
GO	cellular_component	27	528	0.33	200959	gamma-aminobutyric acid (GABA) receptor, rho 3
GO	cellular_component	27	528	0.33	2273	four and a half LIM domains 1
GO	cellular_component	27	528	0.33	23157	septin 6
GO	cellular_component	27	528	0.33	29893	PSMC3 interacting protein
GO	cellular_component	27	528	0.33	29995	LIM and cysteine-rich domains 1
GO	cellular_component	27	528	0.33	50940	phosphodiesterase 11A
GO	cellular_component	27	528	0.33	51050	peptidase inhibitor 15
GO	cellular_component	27	528	0.33	54726	OTU domain containing 4
GO	cellular_component	27	528	0.33	54733	solute carrier family 35, member F2
GO	cellular_component	27	528	0.33	5494	protein phosphatase, Mg2+/Mn2+ dependent, 1A
GO	cellular_component	27	528	0.33	56651	chromosome 18 open reading frame 2
GO	cellular_component	27	528	0.33	5833	phosphate cytidylyltransferase 2, ethanolamine
GO	cellular_component	27	528	0.33	6000	regulator of G-protein signaling 7
GO	cellular_component	27	528	0.33	6242	rhotekin
GO	cellular_component	27	528	0.33	66000	transmembrane protein 108
GO	cellular_component	27	528	0.33	666	BCL2-related ovarian killer
GO	cellular_component	27	528	0.33	6785	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like
GO	cellular_component	27	528	0.33	84668	family with sequence similarity 126, member A
GO	cellular_component	27	528	0.33	9448	mitogen-activated protein kinase kinase kinase kinase 4
GO	cellular_component	27	528	0.33	9540	tumor protein p53 inducible protein 3
GO	ligase activity	16	303	0.335	10055	SUMO1 activating enzyme subunit 1
GO	ligase activity	16	303	0.335	10056	phenylalanyl-tRNA synthetase, beta subunit
GO	ligase activity	16	303	0.335	130507	ubiquitin protein ligase E3 component n-recognin 3 (putative)
GO	ligase activity	16	303	0.335	140739	ubiquitin-conjugating enzyme E2F (putative)
GO	ligase activity	16	303	0.335	1503	CTP synthase
GO	ligase activity	16	303	0.335	23305	acyl-CoA synthetase long-chain family member 6
GO	ligase activity	16	303	0.335	2618	phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide
GO	ligase activity	16	303	0.335	29128	ubiquitin-like with PHD and ring finger domains 1
GO	ligase activity	16	303	0.335	4734	neural precursor cell expressed, developmentally down-regulated 4
GO	ligase activity	16	303	0.335	51191	hect domain and RLD 5
GO	ligase activity	16	303	0.335	55016	membrane-associated ring finger (C3HC4) 1

GO	ligase activity	16	303	0.335	55521	tripartite motif-containing 36
GO	ligase activity	16	303	0.335	56852	RAD18 homolog (S. cerevisiae)
GO	ligase activity	16	303	0.335	57574	membrane-associated ring finger (C3HC4) 4
GO	ligase activity	16	303	0.335	672	breast cancer 1, early onset
GO	ligase activity	16	303	0.335	7324	ubiquitin-conjugating enzyme E2E 1 (UBC4/5 homolog, yeast)
GO	protein binding, bridging	3	44	0.335	1301	collagen, type XI, alpha 1
GO	protein binding, bridging	3	44	0.335	23768	fibronectin leucine rich transmembrane protein 2
GO	protein binding, bridging	3	44	0.335	55803	ArfGAP with dual PH domains 2
GO	Rab GTPase activator activity	3	44	0.335	51256	TBC1 domain family, member 7
GO	Rab GTPase activator activity	3	44	0.335	9882	TBC1 domain family, member 4
GO	Rab GTPase activator activity	3	44	0.335	9910	RAB GTPase activating protein 1-like
GO	regulation of Rab GTPase activity	3	44	0.335	51256	TBC1 domain family, member 7
GO	regulation of Rab GTPase activity	3	44	0.335	9882	TBC1 domain family, member 4
GO	regulation of Rab GTPase activity	3	44	0.335	9910	RAB GTPase activating protein 1-like
GO	anaphase-promoting complex-depende	4	63	0.336	10213	proteasome (prosome, macropain) 26S subunit, non-ATPase, 14
GO	anaphase-promoting complex-depende	4	63	0.336	5702	proteasome (prosome, macropain) 26S subunit, ATPase, 3
GO	anaphase-promoting complex-depende	4	63	0.336	5717	proteasome (prosome, macropain) 26S subunit, non-ATPase, 11
GO	anaphase-promoting complex-depende	4	63	0.336	7324	ubiquitin-conjugating enzyme E2E 1 (UBC4/5 homolog, yeast)
GO	voltage-gated potassium channel activit	4	63	0.336	283518	potassium channel regulator
GO	voltage-gated potassium channel activit	4	63	0.336	3751	potassium voltage-gated channel, Shal-related subfamily, member 2
GO	voltage-gated potassium channel activit	4	63	0.336	3754	potassium voltage-gated channel, subfamily F, member 1
GO	voltage-gated potassium channel activit	4	63	0.336	3778	potassium large conductance calcium-activated channel, subfamily M, alph
GO	metalloendopeptidase activity	6	102	0.337	10893	matrix metallopeptidase 24 (membrane-inserted)
GO	metalloendopeptidase activity	6	102	0.337	4312	matrix metallopeptidase 1 (interstitial collagenase)
GO	metalloendopeptidase activity	6	102	0.337	4318	matrix metallopeptidase 9 (gelatinase B, 92kDa gelatinase, 92kDa type IV c
GO	metalloendopeptidase activity	6	102	0.337	4319	matrix metallopeptidase 10 (stromelysin 2)
GO	metalloendopeptidase activity	6	102	0.337	8728	ADAM metallopeptidase domain 19 (meltrin beta)
GO	metalloendopeptidase activity	6	102	0.337	8747	ADAM metallopeptidase domain 21
GO	positive regulation of transcription, DN/	7	122	0.339	2149	coagulation factor II (thrombin) receptor
GO	positive regulation of transcription, DN/	7	122	0.339	5494	protein phosphatase, Mg2+/Mn2+ dependent, 1A
GO	positive regulation of transcription, DN/	7	122	0.339	6659	SRY (sex determining region Y)-box 4
GO	positive regulation of transcription, DN/	7	122	0.339	6672	SP100 nuclear antigen
GO	positive regulation of transcription, DN/	7	122	0.339	672	breast cancer 1, early onset
GO	positive regulation of transcription, DN/	7	122	0.339	8626	tumor protein p63
GO	positive regulation of transcription, DN/	7	122	0.339	898	cyclin E1
GO	integral to plasma membrane	48	969	0.341	1002	cadherin 4, type 1, R-cadherin (retinal)

GO	integral to plasma membrane	48	969	0.341	10457	glycoprotein (transmembrane) nmb
GO	integral to plasma membrane	48	969	0.341	10893	matrix metallopeptidase 24 (membrane-inserted)
GO	integral to plasma membrane	48	969	0.341	132724	transmembrane protease, serine 11B
GO	integral to plasma membrane	48	969	0.341	182	jagged 1 (Alagille syndrome)
GO	integral to plasma membrane	48	969	0.341	1836	solute carrier family 26 (sulfate transporter), member 2
GO	integral to plasma membrane	48	969	0.341	2045	EPH receptor A7
GO	integral to plasma membrane	48	969	0.341	2149	coagulation factor II (thrombin) receptor
GO	integral to plasma membrane	48	969	0.341	2150	coagulation factor II (thrombin) receptor-like 1
GO	integral to plasma membrane	48	969	0.341	2151	coagulation factor II (thrombin) receptor-like 2
GO	integral to plasma membrane	48	969	0.341	2264	fibroblast growth factor receptor 4
GO	integral to plasma membrane	48	969	0.341	2321	fms-related tyrosine kinase 1 (vascular endothelial growth factor/vascular
GO	integral to plasma membrane	48	969	0.341	23768	fibronectin leucine rich transmembrane protein 2
GO	integral to plasma membrane	48	969	0.341	2558	gamma-aminobutyric acid (GABA) A receptor, alpha 5
GO	integral to plasma membrane	48	969	0.341	25780	RAS guanyl releasing protein 3 (calcium and DAG-regulated)
GO	integral to plasma membrane	48	969	0.341	2842	G protein-coupled receptor 19
GO	integral to plasma membrane	48	969	0.341	2845	G protein-coupled receptor 22
GO	integral to plasma membrane	48	969	0.341	2863	G protein-coupled receptor 39
GO	integral to plasma membrane	48	969	0.341	2898	glutamate receptor, ionotropic, kainate 2
GO	integral to plasma membrane	48	969	0.341	3037	hyaluronan synthase 2
GO	integral to plasma membrane	48	969	0.341	3685	integrin, alpha V (vitronectin receptor, alpha polypeptide, antigen CD51)
GO	integral to plasma membrane	48	969	0.341	4158	melanocortin 2 receptor (adrenocorticotropic hormone)
GO	integral to plasma membrane	48	969	0.341	4897	neuronal cell adhesion molecule
GO	integral to plasma membrane	48	969	0.341	5021	oxytocin receptor
GO	integral to plasma membrane	48	969	0.341	5026	purinergic receptor P2X, ligand-gated ion channel, 5
GO	integral to plasma membrane	48	969	0.341	5028	purinergic receptor P2Y, G-protein coupled, 1
GO	integral to plasma membrane	48	969	0.341	5031	pyrimidinergic receptor P2Y, G-protein coupled, 6
GO	integral to plasma membrane	48	969	0.341	5245	prohibitin
GO	integral to plasma membrane	48	969	0.341	5420	podocalyxin-like
GO	integral to plasma membrane	48	969	0.341	55117	solute carrier family 6 (neutral amino acid transporter), member 15
GO	integral to plasma membrane	48	969	0.341	558	AXL receptor tyrosine kinase
GO	integral to plasma membrane	48	969	0.341	56133	protocadherin beta 2
GO	integral to plasma membrane	48	969	0.341	5754	PTK7 protein tyrosine kinase 7
GO	integral to plasma membrane	48	969	0.341	5795	protein tyrosine phosphatase, receptor type, J
GO	integral to plasma membrane	48	969	0.341	6546	solute carrier family 8 (sodium/calcium exchanger), member 1
GO	integral to plasma membrane	48	969	0.341	6580	solute carrier family 22 (organic cation transporter), member 1
GO	integral to plasma membrane	48	969	0.341	659	bone morphogenetic protein receptor, type II (serine/threonine kinase)

GO	integral to plasma membrane	48	969	0.341	7010	TEK tyrosine kinase, endothelial
GO	integral to plasma membrane	48	969	0.341	7037	transferrin receptor (p90, CD71)
GO	integral to plasma membrane	48	969	0.341	7113	transmembrane protease, serine 2
GO	integral to plasma membrane	48	969	0.341	7220	transient receptor potential cation channel, subfamily C, member 1
GO	integral to plasma membrane	48	969	0.341	729230	chemokine (C-C motif) receptor 2
GO	integral to plasma membrane	48	969	0.341	8685	macrophage receptor with collagenous structure
GO	integral to plasma membrane	48	969	0.341	9076	claudin 1
GO	integral to plasma membrane	48	969	0.341	9482	syntaxin 8
GO	integral to plasma membrane	48	969	0.341	953	ectonucleoside triphosphate diphosphohydrolase 1
GO	integral to plasma membrane	48	969	0.341	9568	gamma-aminobutyric acid (GABA) B receptor, 2
GO	integral to plasma membrane	48	969	0.341	9635	chloride channel accessory 2
GO	skin development	2	26	0.342	1289	collagen, type V, alpha 1
GO	skin development	2	26	0.342	1290	collagen, type V, alpha 2
GO	terminal button	2	26	0.342	2898	glutamate receptor, ionotropic, kainate 2
GO	terminal button	2	26	0.342	3778	potassium large conductance calcium-activated channel, subfamily M, alph
GO	unfolded protein binding	6	103	0.345	1047	calmegin
GO	unfolded protein binding	6	103	0.345	135295	splicing factor, arginine/serine-rich 13B
GO	unfolded protein binding	6	103	0.345	27429	HtrA serine peptidase 2
GO	unfolded protein binding	6	103	0.345	3336	heat shock 10kDa protein 1 (chaperonin 10)
GO	unfolded protein binding	6	103	0.345	5203	prefoldin subunit 4
GO	unfolded protein binding	6	103	0.345	8409	ubiquitously-expressed transcript
GO	membrane raft	6	103	0.345	146760	reticulon 4 receptor-like 1
GO	membrane raft	6	103	0.345	3932	lymphocyte-specific protein tyrosine kinase
GO	membrane raft	6	103	0.345	5420	podocalyxin-like
GO	membrane raft	6	103	0.345	6442	sarcoglycan, alpha (50kDa dystrophin-associated glycoprotein)
GO	membrane raft	6	103	0.345	7010	TEK tyrosine kinase, endothelial
GO	membrane raft	6	103	0.345	7220	transient receptor potential cation channel, subfamily C, member 1
GO	endocytosis	6	103	0.345	30011	SH3-domain kinase binding protein 1
GO	endocytosis	6	103	0.345	4830	non-metastatic cells 1, protein (NM23A) expressed in
GO	endocytosis	6	103	0.345	4893	neuroblastoma RAS viral (v-ras) oncogene homolog
GO	endocytosis	6	103	0.345	7037	transferrin receptor (p90, CD71)
GO	endocytosis	6	103	0.345	8905	adaptor-related protein complex 1, sigma 2 subunit
GO	endocytosis	6	103	0.345	92737	delta/notch-like EGF repeat containing
GO	cell death	7	123	0.346	27429	HtrA serine peptidase 2
GO	cell death	7	123	0.346	4287	ataxin 3
GO	cell death	7	123	0.346	51062	atlastin GTPase 1

GO	cell death	7	123	0.346	65055	receptor accessory protein 1
GO	cell death	7	123	0.346	6683	spastin
GO	cell death	7	123	0.346	773	calcium channel, voltage-dependent, P/Q type, alpha 1A subunit
GO	cell death	7	123	0.346	9420	cytochrome P450, family 7, subfamily B, polypeptide 1
GO	motor activity	4	64	0.346	3797	kinesin family member 3C
GO	motor activity	4	64	0.346	4430	myosin IB
GO	motor activity	4	64	0.346	4637	myosin, light chain 6, alkali, smooth muscle and non-muscle
GO	motor activity	4	64	0.346	4651	myosin X
GO	glucose homeostasis	3	45	0.348	5054	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor t
GO	glucose homeostasis	3	45	0.348	5140	phosphodiesterase 3B, cGMP-inhibited
GO	glucose homeostasis	3	45	0.348	7840	Alstrom syndrome 1
GO	blood vessel morphogenesis	1	9	0.348	1000	cadherin 2, type 1, N-cadherin (neuronal)
GO	fascia adherens	1	9	0.348	1000	cadherin 2, type 1, N-cadherin (neuronal)
GO	myeloid dendritic cell differentiation	1	9	0.348	10202	dehydrogenase/reductase (SDR family) member 2
GO	phospholipase binding	1	9	0.348	10395	deleted in liver cancer 1
GO	vinculin binding	1	9	0.348	10395	deleted in liver cancer 1
GO	ribonuclease P activity	1	9	0.348	10799	ribonuclease P/MRP 40kDa subunit
GO	regulation of alternative nuclear mRNA	1	9	0.348	135295	splicing factor, arginine/serine-rich 13B
GO	response to food	1	9	0.348	1543	cytochrome P450, family 1, subfamily A, polypeptide 1
GO	outer kinetochore of condensed chrom	1	9	0.348	220134	spindle and kinetochore associated complex subunit 1
GO	UV protection	1	9	0.348	2237	flap structure-specific endonuclease 1
GO	ubiquinone biosynthetic process	1	9	0.348	23590	prenyl (decaprenyl) diphosphate synthase, subunit 1
GO	associative learning	1	9	0.348	2558	gamma-aminobutyric acid (GABA) A receptor, alpha 5
GO	dendrite cytoplasm	1	9	0.348	2898	glutamate receptor, ionotropic, kainate 2
GO	holo TFIIH complex	1	9	0.348	2965	general transcription factor IIH, polypeptide 1, 62kDa
GO	prostaglandin metabolic process	1	9	0.348	3248	hydroxyprostaglandin dehydrogenase 15-(NAD)
GO	negative regulation of blood vessel end	1	9	0.348	348	apolipoprotein E
GO	positive regulation of membrane protei	1	9	0.348	348	apolipoprotein E
GO	positive regulation of nitric-oxide synth	1	9	0.348	348	apolipoprotein E
GO	regulation of gene-specific transcription	1	9	0.348	3624	inhibin, beta A
GO	two-component signal transduction sys	1	9	0.348	3756	potassium voltage-gated channel, subfamily H (eag-related), member 1
GO	organelle organization	1	9	0.348	3800	kinesin family member 5C
GO	adult feeding behavior	1	9	0.348	3952	leptin
GO	ovulation from ovarian follicle	1	9	0.348	3952	leptin
GO	anterior/posterior axis specification	1	9	0.348	3975	LIM homeobox 1
GO	Hsp90 protein binding	1	9	0.348	406	aryl hydrocarbon receptor nuclear translocator-like

GO	regulation of protein catabolic process	1	9	0.348	406	aryl hydrocarbon receptor nuclear translocator-like
GO	synaptonemal complex	1	9	0.348	4292	mutL homolog 1, colon cancer, nonpolyposis type 2 (E. coli)
GO	macrophage differentiation	1	9	0.348	4318	matrix metallopeptidase 9 (gelatinase B, 92kDa gelatinase, 92kDa type IV c
GO	axonal fasciculation	1	9	0.348	4897	neuronal cell adhesion molecule
GO	Nup107-160 complex	1	9	0.348	4928	nucleoporin 98kDa
GO	sleep	1	9	0.348	5021	oxytocin receptor
GO	telencephalon development	1	9	0.348	5021	oxytocin receptor
GO	positive regulation of receptor-mediate	1	9	0.348	5054	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor t
GO	vacuolar proton-transporting V-type AT	1	9	0.348	51382	ATPase, H+ transporting, lysosomal 34kDa, V1 subunit D
GO	phosphoinositide metabolic process	1	9	0.348	5341	pleckstrin
GO	respiratory burst	1	9	0.348	5588	protein kinase C, theta
GO	triglyceride biosynthetic process	1	9	0.348	57678	glycerol-3-phosphate acyltransferase, mitochondrial
GO	male meiosis I	1	9	0.348	5889	RAD51 homolog C (S. cerevisiae)
GO	gonad development	1	9	0.348	6299	sal-like 1 (Drosophila)
GO	proteoglycan biosynthetic process	1	9	0.348	64131	xylosyltransferase I
GO	sodium:hydrogen antiporter activity	1	9	0.348	6549	solute carrier family 9 (sodium/hydrogen exchanger), member 2
GO	embryonic organ development	1	9	0.348	6657	SRY (sex determining region Y)-box 2
GO	epithelial tube branching involved in lu	1	9	0.348	6657	SRY (sex determining region Y)-box 2
GO	cellular response to reactive oxygen spe	1	9	0.348	7168	tropomyosin 1 (alpha)
GO	positive regulation of ATPase activity	1	9	0.348	7168	tropomyosin 1 (alpha)
GO	positive regulation of release of seques	1	9	0.348	7220	transient receptor potential cation channel, subfamily C, member 1
GO	histone monoubiquitination	1	9	0.348	7324	ubiquitin-conjugating enzyme E2E 1 (UBC4/5 homolog, yeast)
GO	actin polymerization or depolymerizatio	1	9	0.348	7456	WAS/WASL interacting protein family, member 1
GO	oligosaccharide metabolic process	1	9	0.348	84620	ST6 beta-galactosamide alpha-2,6-sialyltranferase 2
GO	clathrin coat of trans-Golgi network ves	1	9	0.348	8905	adaptor-related protein complex 1, sigma 2 subunit
GO	skeletal muscle fiber development	1	9	0.348	92737	delta/notch-like EGF repeat containing
GO	quinone binding	1	9	0.348	9540	tumor protein p53 inducible protein 3
GO	positive regulation of JUN kinase activit	1	9	0.348	9839	zinc finger E-box binding homeobox 2
GO	melanosome	5	84	0.351	10457	glycoprotein (transmembrane) nmb
GO	melanosome	5	84	0.351	10672	guanine nucleotide binding protein (G protein), alpha 13
GO	melanosome	5	84	0.351	309	annexin A6
GO	melanosome	5	84	0.351	54843	synaptotagmin-like 2
GO	melanosome	5	84	0.351	7037	transferrin receptor (p90, CD71)
GO	positive regulation of ubiquitin-protein	4	65	0.357	10213	proteasome (prosome, macropain) 26S subunit, non-ATPase, 14
GO	positive regulation of ubiquitin-protein	4	65	0.357	5702	proteasome (prosome, macropain) 26S subunit, ATPase, 3
GO	positive regulation of ubiquitin-protein	4	65	0.357	5717	proteasome (prosome, macropain) 26S subunit, non-ATPase, 11

GO	positive regulation of ubiquitin-protein	4	65	0.357	7324	ubiquitin-conjugating enzyme E2E 1 (UBC4/5 homolog, yeast)
GO	positive regulation of fibroblast prolifera	2	27	0.359	1026	cyclin-dependent kinase inhibitor 1A (p21, Cip1)
GO	positive regulation of fibroblast prolifera	2	27	0.359	890	cyclin A2
GO	SH2 domain binding	2	27	0.359	10395	deleted in liver cancer 1
GO	SH2 domain binding	2	27	0.359	3932	lymphocyte-specific protein tyrosine kinase
GO	cell-cell adherens junction	2	27	0.359	1496	catenin (cadherin-associated protein), alpha 2
GO	cell-cell adherens junction	2	27	0.359	5021	oxytocin receptor
GO	cell aging	2	27	0.359	3028	hydroxysteroid (17-beta) dehydrogenase 10
GO	cell aging	2	27	0.359	4893	neuroblastoma RAS viral (v-ras) oncogene homolog
GO	protein ubiquitination	5	85	0.361	10055	SUMO1 activating enzyme subunit 1
GO	protein ubiquitination	5	85	0.361	26223	F-box and leucine-rich repeat protein 21 (gene/pseudogene)
GO	protein ubiquitination	5	85	0.361	409	arrestin, beta 2
GO	protein ubiquitination	5	85	0.361	672	breast cancer 1, early onset
GO	protein ubiquitination	5	85	0.361	7324	ubiquitin-conjugating enzyme E2E 1 (UBC4/5 homolog, yeast)
GO	cytoplasmic membrane-bounded vesicle	5	85	0.361	10457	glycoprotein (transmembrane) nmb
GO	cytoplasmic membrane-bounded vesicle	5	85	0.361	409	arrestin, beta 2
GO	cytoplasmic membrane-bounded vesicle	5	85	0.361	667	dystonin
GO	cytoplasmic membrane-bounded vesicle	5	85	0.361	7037	transferrin receptor (p90, CD71)
GO	cytoplasmic membrane-bounded vesicle	5	85	0.361	7456	WAS/WASL interacting protein family, member 1
GO	early endosome	5	85	0.361	10612	tripartite motif-containing 3
GO	early endosome	5	85	0.361	1730	diaphanous homolog 2 (Drosophila)
GO	early endosome	5	85	0.361	57590	WD repeat and FYVE domain containing 1
GO	early endosome	5	85	0.361	92737	delta/notch-like EGF repeat containing
GO	early endosome	5	85	0.361	9910	RAB GTPase activating protein 1-like
GO	peptidase inhibitor activity	5	85	0.361	12	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), me
GO	peptidase inhibitor activity	5	85	0.361	140902	R3H domain containing-like
GO	peptidase inhibitor activity	5	85	0.361	332	baculoviral IAP repeat-containing 5
GO	peptidase inhibitor activity	5	85	0.361	5054	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor ty
GO	peptidase inhibitor activity	5	85	0.361	51050	peptidase inhibitor 15
GO	cytosol	60	1230	0.364	10056	phenylalanyl-tRNA synthetase, beta subunit
GO	cytosol	60	1230	0.364	10254	signal transducing adaptor molecule (SH3 domain and ITAM motif) 2
GO	cytosol	60	1230	0.364	1026	cyclin-dependent kinase inhibitor 1A (p21, Cip1)
GO	cytosol	60	1230	0.364	10395	deleted in liver cancer 1
GO	cytosol	60	1230	0.364	11077	heat shock transcription factor 2 binding protein
GO	cytosol	60	1230	0.364	158	adenylosuccinate lyase
GO	cytosol	60	1230	0.364	1716	deoxyguanosine kinase

GO	cytosol	60	1230	0.364	1730	diaphanous homolog 2 (Drosophila)
GO	cytosol	60	1230	0.364	1781	dynein, cytoplasmic 1, intermediate chain 2
GO	cytosol	60	1230	0.364	1830	desmoglein 3 (pemphigus vulgaris antigen)
GO	cytosol	60	1230	0.364	1841	deoxythymidylate kinase (thymidylate kinase)
GO	cytosol	60	1230	0.364	1983	eukaryotic translation initiation factor 5
GO	cytosol	60	1230	0.364	1984	eukaryotic translation initiation factor 5A
GO	cytosol	60	1230	0.364	2172	fatty acid binding protein 6, ileal
GO	cytosol	60	1230	0.364	2242	feline sarcoma oncogene
GO	cytosol	60	1230	0.364	2273	four and a half LIM domains 1
GO	cytosol	60	1230	0.364	2281	FK506 binding protein 1B, 12.6 kDa
GO	cytosol	60	1230	0.364	22934	ribose 5-phosphate isomerase A
GO	cytosol	60	1230	0.364	2534	FYN oncogene related to SRC, FGR, YES
GO	cytosol	60	1230	0.364	26230	T-cell lymphoma invasion and metastasis 2
GO	cytosol	60	1230	0.364	27289	Rho family GTPase 1
GO	cytosol	60	1230	0.364	27330	ribosomal protein S6 kinase, 90kDa, polypeptide 6
GO	cytosol	60	1230	0.364	27429	HtrA serine peptidase 2
GO	cytosol	60	1230	0.364	30011	SH3-domain kinase binding protein 1
GO	cytosol	60	1230	0.364	3157	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 (soluble)
GO	cytosol	60	1230	0.364	3248	hydroxyprostaglandin dehydrogenase 15-(NAD)
GO	cytosol	60	1230	0.364	332	baculoviral IAP repeat-containing 5
GO	cytosol	60	1230	0.364	355	Fas (TNF receptor superfamily, member 6)
GO	cytosol	60	1230	0.364	3836	karyopherin alpha 1 (importin alpha 5)
GO	cytosol	60	1230	0.364	3932	lymphocyte-specific protein tyrosine kinase
GO	cytosol	60	1230	0.364	3936	lymphocyte cytosolic protein 1 (L-plastin)
GO	cytosol	60	1230	0.364	4734	neural precursor cell expressed, developmentally down-regulated 4
GO	cytosol	60	1230	0.364	4830	non-metastatic cells 1, protein (NM23A) expressed in
GO	cytosol	60	1230	0.364	50940	phosphodiesterase 11A
GO	cytosol	60	1230	0.364	51121	ribosomal protein L26-like 1
GO	cytosol	60	1230	0.364	5203	prefoldin subunit 4
GO	cytosol	60	1230	0.364	5341	pleckstrin
GO	cytosol	60	1230	0.364	57590	WD repeat and FYVE domain containing 1
GO	cytosol	60	1230	0.364	57678	glycerol-3-phosphate acyltransferase, mitochondrial
GO	cytosol	60	1230	0.364	581	BCL2-associated X protein
GO	cytosol	60	1230	0.364	586	branched chain aminotransferase 1, cytosolic
GO	cytosol	60	1230	0.364	5924	Ras protein-specific guanine nucleotide-releasing factor 2
GO	cytosol	60	1230	0.364	6133	ribosomal protein L9

GO	cytosol	60	1230	0.364	6154	ribosomal protein L26
GO	cytosol	60	1230	0.364	6204	ribosomal protein S10
GO	cytosol	60	1230	0.364	6251	Ras suppressor protein 1
GO	cytosol	60	1230	0.364	6637	small nuclear ribonucleoprotein polypeptide G
GO	cytosol	60	1230	0.364	6657	SRY (sex determining region Y)-box 2
GO	cytosol	60	1230	0.364	6711	spectrin, beta, non-erythrocytic 1
GO	cytosol	60	1230	0.364	6820	sulfotransferase family, cytosolic, 2B, member 1
GO	cytosol	60	1230	0.364	7324	ubiquitin-conjugating enzyme E2E 1 (UBC4/5 homolog, yeast)
GO	cytosol	60	1230	0.364	7353	ubiquitin fusion degradation 1 like (yeast)
GO	cytosol	60	1230	0.364	7389	uroporphyrinogen decarboxylase
GO	cytosol	60	1230	0.364	7840	Alstrom syndrome 1
GO	cytosol	60	1230	0.364	7846	tubulin, alpha 1a
GO	cytosol	60	1230	0.364	79833	gem (nuclear organelle) associated protein 6
GO	cytosol	60	1230	0.364	8905	adaptor-related protein complex 1, sigma 2 subunit
GO	cytosol	60	1230	0.364	898	cyclin E1
GO	cytosol	60	1230	0.364	8997	kalirin, RhoGEF kinase
GO	cytosol	60	1230	0.364	91801	alkB, alkylation repair homolog 8 (E. coli)
GO	positive regulation of transcription	8	146	0.368	10474	transcriptional adaptor 3
GO	positive regulation of transcription	8	146	0.368	2736	GLI family zinc finger 2
GO	positive regulation of transcription	8	146	0.368	3516	recombination signal binding protein for immunoglobulin kappa J region
GO	positive regulation of transcription	8	146	0.368	641	Bloom syndrome, RecQ helicase-like
GO	positive regulation of transcription	8	146	0.368	6657	SRY (sex determining region Y)-box 2
GO	positive regulation of transcription	8	146	0.368	7046	transforming growth factor, beta receptor 1
GO	positive regulation of transcription	8	146	0.368	7490	Wilms tumor 1
GO	positive regulation of transcription	8	146	0.368	890	cyclin A2
GO	structural constituent of ribosome	8	146	0.368	11222	mitochondrial ribosomal protein L3
GO	structural constituent of ribosome	8	146	0.368	28998	mitochondrial ribosomal protein L13
GO	structural constituent of ribosome	8	146	0.368	51023	mitochondrial ribosomal protein S18C
GO	structural constituent of ribosome	8	146	0.368	51121	ribosomal protein L26-like 1
GO	structural constituent of ribosome	8	146	0.368	6133	ribosomal protein L9
GO	structural constituent of ribosome	8	146	0.368	6154	ribosomal protein L26
GO	structural constituent of ribosome	8	146	0.368	65003	mitochondrial ribosomal protein L11
GO	structural constituent of ribosome	8	146	0.368	65008	mitochondrial ribosomal protein L1
GO	RNA polymerase II transcription factor a	7	126	0.369	2305	forkhead box M1
GO	RNA polymerase II transcription factor a	7	126	0.369	29128	ubiquitin-like with PHD and ring finger domains 1
GO	RNA polymerase II transcription factor a	7	126	0.369	3236	homeobox D10

GO	RNA polymerase II transcription factor a	7	126	0.369	3975	LIM homeobox 1
GO	RNA polymerase II transcription factor a	7	126	0.369	4094	v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian)
GO	RNA polymerase II transcription factor a	7	126	0.369	6662	SRY (sex determining region Y)-box 9
GO	RNA polymerase II transcription factor a	7	126	0.369	6899	T-box 1
GO	protein heterooligomerization	3	47	0.374	1000	cadherin 2, type 1, N-cadherin (neuronal)
GO	protein heterooligomerization	3	47	0.374	3751	potassium voltage-gated channel, Shal-related subfamily, member 2
GO	protein heterooligomerization	3	47	0.374	55752	septin 11
GO	neuron differentiation	3	47	0.374	3224	homeobox C8
GO	neuron differentiation	3	47	0.374	347733	tubulin, beta 2B
GO	neuron differentiation	3	47	0.374	5588	protein kinase C, theta
GO	voltage-gated ion channel activity	8	147	0.375	3751	potassium voltage-gated channel, Shal-related subfamily, member 2
GO	voltage-gated ion channel activity	8	147	0.375	3754	potassium voltage-gated channel, subfamily F, member 1
GO	voltage-gated ion channel activity	8	147	0.375	3756	potassium voltage-gated channel, subfamily H (eag-related), member 1
GO	voltage-gated ion channel activity	8	147	0.375	3763	potassium inwardly-rectifying channel, subfamily J, member 6
GO	voltage-gated ion channel activity	8	147	0.375	3778	potassium large conductance calcium-activated channel, subfamily M, alph
GO	voltage-gated ion channel activity	8	147	0.375	56479	potassium voltage-gated channel, KQT-like subfamily, member 5
GO	voltage-gated ion channel activity	8	147	0.375	6335	sodium channel, voltage-gated, type IX, alpha subunit
GO	voltage-gated ion channel activity	8	147	0.375	773	calcium channel, voltage-dependent, P/Q type, alpha 1A subunit
GO	negative regulation of angiogenesis	2	28	0.376	1284	collagen, type IV, alpha 2
GO	negative regulation of angiogenesis	2	28	0.376	6347	chemokine (C-C motif) ligand 2
GO	positive regulation of DNA replication	2	28	0.376	1763	DNA replication helicase 2 homolog (yeast)
GO	positive regulation of DNA replication	2	28	0.376	2736	GLI family zinc finger 2
GO	memory	2	28	0.376	5021	oxytocin receptor
GO	memory	2	28	0.376	9420	cytochrome P450, family 7, subfamily B, polypeptide 1
GO	activation of phospholipase C activity by	2	28	0.376	5028	purinergic receptor P2Y, G-protein coupled, 1
GO	activation of phospholipase C activity by	2	28	0.376	5031	pyrimidinergic receptor P2Y, G-protein coupled, 6
GO	sensory perception of pain	2	28	0.376	5028	purinergic receptor P2Y, G-protein coupled, 1
GO	sensory perception of pain	2	28	0.376	60675	prokineticin 2
GO	axon	7	127	0.377	1496	catenin (cadherin-associated protein), alpha 2
GO	axon	7	127	0.377	23705	cell adhesion molecule 1
GO	axon	7	127	0.377	2898	glutamate receptor, ionotropic, kainate 2
GO	axon	7	127	0.377	3763	potassium inwardly-rectifying channel, subfamily J, member 6
GO	axon	7	127	0.377	4763	neurofibromin 1
GO	axon	7	127	0.377	51062	atlastin GTPase 1
GO	axon	7	127	0.377	55752	septin 11
GO	cardiac muscle tissue development	1	10	0.379	10052	gap junction protein, gamma 1, 45kDa

GO	regulation of actin cytoskeleton organiz	1	10	0.379	10395	deleted in liver cancer 1
GO	ribonucleoprotein binding	1	10	0.379	10465	peptidylprolyl isomerase H (cyclophilin H)
GO	acetylcholine binding	1	10	0.379	1136	cholinergic receptor, nicotinic, alpha 3
GO	oxygen transporter activity	1	10	0.379	114757	cytoglobin
GO	oxygen transport	1	10	0.379	114757	cytoglobin
GO	transcription elongation regulator activi	1	10	0.379	170082	transcription elongation factor A (SII) N-terminal and central domain contai
GO	hormone biosynthetic process	1	10	0.379	1733	deiodinase, iodothyronine, type I
GO	cytoplasmic dynein complex	1	10	0.379	1781	dynein, cytoplasmic 1, intermediate chain 2
GO	regulation of gene expression by geneti	1	10	0.379	1788	DNA (cytosine-5-)-methyltransferase 3 alpha
GO	ATP metabolic process	1	10	0.379	203	adenylate kinase 1
GO	elevation of cytosolic calcium ion conce	1	10	0.379	2149	coagulation factor II (thrombin) receptor
GO	positive regulation of collagen biosynth	1	10	0.379	2149	coagulation factor II (thrombin) receptor
GO	positive regulation of positive chemota	1	10	0.379	2150	coagulation factor II (thrombin) receptor-like 1
GO	NAD metabolic process	1	10	0.379	23057	nicotinamide nucleotide adenylyltransferase 2
GO	fatty acid transport	1	10	0.379	23305	acyl-CoA synthetase long-chain family member 6
GO	cilium membrane	1	10	0.379	27241	Bardet-Biedl syndrome 9
GO	osteoblast development	1	10	0.379	2736	GLI family zinc finger 2
GO	glutathione peroxidase activity	1	10	0.379	2878	glutathione peroxidase 3 (plasma)
GO	outer membrane-bounded periplasmic	1	10	0.379	2906	glutamate receptor, ionotropic, N-methyl D-aspartate 2D
GO	Ran GTPase binding	1	10	0.379	332	baculoviral IAP repeat-containing 5
GO	cholesterol catabolic process	1	10	0.379	348	apolipoprotein E
GO	lipoprotein binding	1	10	0.379	348	apolipoprotein E
GO	negative regulation of hormone secretio	1	10	0.379	3589	interleukin 11
GO	small conjugating protein ligase activity	1	10	0.379	389898	ubiquitin-conjugating enzyme E2N-like
GO	phosphoinositide 3-kinase binding	1	10	0.379	3932	lymphocyte-specific protein tyrosine kinase
GO	positive regulation of T cell activation	1	10	0.379	3932	lymphocyte-specific protein tyrosine kinase
GO	double-strand break repair via nonhom	1	10	0.379	4292	mutL homolog 1, colon cancer, nonpolyposis type 2 (E. coli)
GO	cognition	1	10	0.379	4763	neurofibromin 1
GO	positive regulation of smooth muscle ce	1	10	0.379	5031	pyrimidinergic receptor P2Y, G-protein coupled, 6
GO	defense response to Gram-negative bac	1	10	0.379	5054	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor t
GO	negative regulation of fibrinolysis	1	10	0.379	5054	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor t
GO	positive regulation of interleukin-8 prod	1	10	0.379	5054	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor t
GO	Golgi lumen	1	10	0.379	5125	proprotein convertase subtilisin/kexin type 5
GO	3',5'-cyclic-AMP phosphodiesterase acti	1	10	0.379	5140	phosphodiesterase 3B, cGMP-inhibited
GO	XY body	1	10	0.379	56852	RAD18 homolog (S. cerevisiae)
GO	positive regulation of activated T cell pr	1	10	0.379	57678	glycerol-3-phosphate acyltransferase, mitochondrial

GO	defense response to fungus	1	10	0.379	57817	hepcidin antimicrobial peptide
GO	killing of cells of another organism	1	10	0.379	57817	hepcidin antimicrobial peptide
GO	apoptotic mitochondrial changes	1	10	0.379	581	BCL2-associated X protein
GO	regulation of mitochondrial membrane	1	10	0.379	581	BCL2-associated X protein
GO	limb development	1	10	0.379	6299	sal-like 1 (Drosophila)
GO	macrophage chemotaxis	1	10	0.379	6347	chemokine (C-C motif) ligand 2
GO	positive regulation of epithelial cell mig	1	10	0.379	659	bone morphogenetic protein receptor, type II (serine/threonine kinase)
GO	microtubule plus-end binding	1	10	0.379	667	dystonin
GO	microtubule bundle formation	1	10	0.379	6683	spastin
GO	I band	1	10	0.379	70	actin, alpha, cardiac muscle 1
GO	response to iron ion	1	10	0.379	7037	transferrin receptor (p90, CD71)
GO	I-SMAD binding	1	10	0.379	7046	transforming growth factor, beta receptor 1
GO	transforming growth factor beta bindin	1	10	0.379	7046	transforming growth factor, beta receptor 1
GO	metalloendopeptidase inhibitor activity	1	10	0.379	7078	TIMP metallopeptidase inhibitor 3
GO	Wnt receptor activity	1	10	0.379	8325	frizzled homolog 8 (Drosophila)
GO	signalosome	1	10	0.379	8533	COP9 constitutive photomorphogenic homolog subunit 3 (Arabidopsis)
GO	L-glutamate transmembrane transporte	1	10	0.379	8604	solute carrier family 25 (mitochondrial carrier, Aralar), member 12
GO	G1 phase of mitotic cell cycle	1	10	0.379	8872	cell division cycle 123 homolog (S. cerevisiae)
GO	cytokine binding	1	10	0.379	9244	cytokine receptor-like factor 1
GO	prostate gland epithelium morphogene	1	10	0.379	9420	cytochrome P450, family 7, subfamily B, polypeptide 1
GO	nuclear membrane	5	87	0.379	166336	prickle homolog 2 (Drosophila)
GO	nuclear membrane	5	87	0.379	241	arachidonate 5-lipoxygenase-activating protein
GO	nuclear membrane	5	87	0.379	4928	nucleoporin 98kDa
GO	nuclear membrane	5	87	0.379	7341	SMT3 suppressor of mif two 3 homolog 1 (S. cerevisiae)
GO	nuclear membrane	5	87	0.379	9805	secernin 1
GO	visual perception	10	189	0.382	10052	gap junction protein, gamma 1, 45kDa
GO	visual perception	10	189	0.382	1121	choroideremia (Rab escort protein 1)
GO	visual perception	10	189	0.382	1301	collagen, type XI, alpha 1
GO	visual perception	10	189	0.382	27241	Bardet-Biedl syndrome 9
GO	visual perception	10	189	0.382	4060	lumican
GO	visual perception	10	189	0.382	5145	phosphodiesterase 6A, cGMP-specific, rod, alpha
GO	visual perception	10	189	0.382	5264	phytanoyl-CoA 2-hydroxylase
GO	visual perception	10	189	0.382	6785	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like
GO	visual perception	10	189	0.382	7078	TIMP metallopeptidase inhibitor 3
GO	visual perception	10	189	0.382	7840	Alstrom syndrome 1
GO	ATPase activity	7	128	0.385	1763	DNA replication helicase 2 homolog (yeast)

GO	ATPase activity	7	128	0.385	26154	ATP-binding cassette, sub-family A (ABC1), member 12
GO	ATPase activity	7	128	0.385	340273	ATP-binding cassette, sub-family B (MDR/TAP), member 5
GO	ATPase activity	7	128	0.385	4436	mutS homolog 2, colon cancer, nonpolyposis type 1 (E. coli)
GO	ATPase activity	7	128	0.385	641	Bloom syndrome, RecQ helicase-like
GO	ATPase activity	7	128	0.385	6833	ATP-binding cassette, sub-family C (CFTR/MRP), member 8
GO	ATPase activity	7	128	0.385	70	actin, alpha, cardiac muscle 1
GO	serine-type peptidase activity	3	48	0.387	344805	transmembrane protease, serine 7
GO	serine-type peptidase activity	3	48	0.387	7113	transmembrane protease, serine 2
GO	serine-type peptidase activity	3	48	0.387	90701	SEC11 homolog C (S. cerevisiae)
GO	fatty acid biosynthetic process	3	48	0.387	55301	oleoyl-ACP hydrolase
GO	fatty acid biosynthetic process	3	48	0.387	6785	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like
GO	fatty acid biosynthetic process	3	48	0.387	79993	ELOVL family member 7, elongation of long chain fatty acids (yeast)
GO	cytokine-mediated signaling pathway	3	48	0.387	55854	zinc finger CCCH-type containing 15
GO	cytokine-mediated signaling pathway	3	48	0.387	6347	chemokine (C-C motif) ligand 2
GO	cytokine-mediated signaling pathway	3	48	0.387	729230	chemokine (C-C motif) receptor 2
GO	positive regulation of apoptosis	6	108	0.387	220	aldehyde dehydrogenase 1 family, member A3
GO	positive regulation of apoptosis	6	108	0.387	27429	HtrA serine peptidase 2
GO	positive regulation of apoptosis	6	108	0.387	3778	potassium large conductance calcium-activated channel, subfamily M, alph
GO	positive regulation of apoptosis	6	108	0.387	4318	matrix metallopeptidase 9 (gelatinase B, 92kDa gelatinase, 92kDa type IV c
GO	positive regulation of apoptosis	6	108	0.387	4763	neurofibromin 1
GO	positive regulation of apoptosis	6	108	0.387	6659	SRY (sex determining region Y)-box 4
GO	mRNA processing	12	231	0.387	10189	THO complex 4
GO	mRNA processing	12	231	0.387	10492	synaptotagmin binding, cytoplasmic RNA interacting protein
GO	mRNA processing	12	231	0.387	10656	KH domain containing, RNA binding, signal transduction associated 3
GO	mRNA processing	12	231	0.387	135295	splicing factor, arginine/serine-rich 13B
GO	mRNA processing	12	231	0.387	23658	LSM5 homolog, U6 small nuclear RNA associated (S. cerevisiae)
GO	mRNA processing	12	231	0.387	27258	LSM3 homolog, U6 small nuclear RNA associated (S. cerevisiae)
GO	mRNA processing	12	231	0.387	51645	peptidylprolyl isomerase (cyclophilin)-like 1
GO	mRNA processing	12	231	0.387	53981	cleavage and polyadenylation specific factor 2, 100kDa
GO	mRNA processing	12	231	0.387	58155	polypyrimidine tract binding protein 2
GO	mRNA processing	12	231	0.387	6637	small nuclear ribonucleoprotein polypeptide G
GO	mRNA processing	12	231	0.387	8458	transcription termination factor, RNA polymerase II
GO	mRNA processing	12	231	0.387	8563	THO complex 5
GO	electron carrier activity	8	149	0.389	10539	glutaredoxin 3
GO	electron carrier activity	8	149	0.389	1543	cytochrome P450, family 1, subfamily A, polypeptide 1
GO	electron carrier activity	8	149	0.389	339761	cytochrome P450, family 27, subfamily C, polypeptide 1

GO	electron carrier activity	8	149	0.389	51218	glutaredoxin 5
GO	electron carrier activity	8	149	0.389	5264	phytanoyl-CoA 2-hydroxylase
GO	electron carrier activity	8	149	0.389	8659	aldehyde dehydrogenase 4 family, member A1
GO	electron carrier activity	8	149	0.389	91942	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, assembly factor 2
GO	electron carrier activity	8	149	0.389	9420	cytochrome P450, family 7, subfamily B, polypeptide 1
GO	steroid metabolic process	4	68	0.389	114880	oxysterol binding protein-like 6
GO	steroid metabolic process	4	68	0.389	2172	fatty acid binding protein 6, ileal
GO	steroid metabolic process	4	68	0.389	6820	sulfotransferase family, cytosolic, 2B, member 1
GO	steroid metabolic process	4	68	0.389	9420	cytochrome P450, family 7, subfamily B, polypeptide 1
GO	Rho guanyl-nucleotide exchange factor	4	68	0.389	153478	pleckstrin homology domain containing, family G (with RhoGef domain) me
GO	Rho guanyl-nucleotide exchange factor	4	68	0.389	26230	T-cell lymphoma invasion and metastasis 2
GO	Rho guanyl-nucleotide exchange factor	4	68	0.389	5924	Ras protein-specific guanine nucleotide-releasing factor 2
GO	Rho guanyl-nucleotide exchange factor	4	68	0.389	8997	kalirin, RhoGEF kinase
GO	protein kinase C binding	2	29	0.393	10539	glutaredoxin 3
GO	protein kinase C binding	2	29	0.393	5341	pleckstrin
GO	positive regulation of smooth muscle ce	2	29	0.393	2321	fms-related tyrosine kinase 1 (vascular endothelial growth factor/vascular p
GO	positive regulation of smooth muscle ce	2	29	0.393	3516	recombination signal binding protein for immunoglobulin kappa J region
GO	growth	2	29	0.393	3624	inhibin, beta A
GO	growth	2	29	0.393	84620	ST6 beta-galactosamide alpha-2,6-sialyltranferase 2
GO	positive regulation of ERK1 and ERK2 ca	2	29	0.393	409	arrestin, beta 2
GO	positive regulation of ERK1 and ERK2 ca	2	29	0.393	7010	TEK tyrosine kinase, endothelial
GO	soluble fraction	16	315	0.393	10056	phenylalanyl-tRNA synthetase, beta subunit
GO	soluble fraction	16	315	0.393	11142	protein kinase (cAMP-dependent, catalytic) inhibitor gamma
GO	soluble fraction	16	315	0.393	1161	excision repair cross-complementing rodent repair deficiency, complement
GO	soluble fraction	16	315	0.393	2878	glutathione peroxidase 3 (plasma)
GO	soluble fraction	16	315	0.393	3157	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 (soluble)
GO	soluble fraction	16	315	0.393	355	Fas (TNF receptor superfamily, member 6)
GO	soluble fraction	16	315	0.393	4830	non-metastatic cells 1, protein (NM23A) expressed in
GO	soluble fraction	16	315	0.393	5054	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor ty
GO	soluble fraction	16	315	0.393	50940	phosphodiesterase 11A
GO	soluble fraction	16	315	0.393	5341	pleckstrin
GO	soluble fraction	16	315	0.393	55577	N-acetylglucosamine kinase
GO	soluble fraction	16	315	0.393	5569	protein kinase (cAMP-dependent, catalytic) inhibitor alpha
GO	soluble fraction	16	315	0.393	5588	protein kinase C, theta
GO	soluble fraction	16	315	0.393	70	actin, alpha, cardiac muscle 1
GO	soluble fraction	16	315	0.393	729230	chemokine (C-C motif) receptor 2

GO	soluble fraction	16	315	0.393	8788	delta-like 1 homolog (Drosophila)
GO	microtubule	12	233	0.399	1781	dynein, cytoplasmic 1, intermediate chain 2
GO	microtubule	12	233	0.399	26586	cytoskeleton associated protein 2
GO	microtubule	12	233	0.399	347733	tubulin, beta 2B
GO	microtubule	12	233	0.399	3797	kinesin family member 3C
GO	microtubule	12	233	0.399	3800	kinesin family member 5C
GO	microtubule	12	233	0.399	400954	echinoderm microtubule associated protein like 6
GO	microtubule	12	233	0.399	54839	leucine rich repeat containing 49
GO	microtubule	12	233	0.399	6683	spastin
GO	microtubule	12	233	0.399	79187	fibronectin type III and SPRY domain containing 1
GO	microtubule	12	233	0.399	79861	tubulin, alpha-like 3
GO	microtubule	12	233	0.399	9053	microtubule-associated protein 7
GO	microtubule	12	233	0.399	93323	HAUS augmin-like complex, subunit 8
GO	phospholipid biosynthetic process	3	49	0.399	23305	acyl-CoA synthetase long-chain family member 6
GO	phospholipid biosynthetic process	3	49	0.399	57678	glycerol-3-phosphate acyltransferase, mitochondrial
GO	phospholipid biosynthetic process	3	49	0.399	5833	phosphate cytidylyltransferase 2, ethanolamine
GO	single-stranded DNA binding	3	49	0.399	4292	mutL homolog 1, colon cancer, nonpolyposis type 2 (E. coli)
GO	single-stranded DNA binding	3	49	0.399	4436	mutS homolog 2, colon cancer, nonpolyposis type 1 (E. coli)
GO	single-stranded DNA binding	3	49	0.399	641	Bloom syndrome, RecQ helicase-like
GO	mRNA transport	3	49	0.399	4928	nucleoporin 98kDa
GO	mRNA transport	3	49	0.399	55916	nuclear transport factor 2-like export factor 2
GO	mRNA transport	3	49	0.399	9688	nucleoporin 93kDa
GO	protein transporter activity	4	69	0.4	11154	adaptor-related protein complex 4, sigma 1 subunit
GO	protein transporter activity	4	69	0.4	3836	karyopherin alpha 1 (importin alpha 5)
GO	protein transporter activity	4	69	0.4	3838	karyopherin alpha 2 (RAG cohort 1, importin alpha 1)
GO	protein transporter activity	4	69	0.4	8905	adaptor-related protein complex 1, sigma 2 subunit
GO	cell communication	5	90	0.407	127534	gap junction protein, beta 4, 30.3kDa
GO	cell communication	5	90	0.407	182	jagged 1 (Alagille syndrome)
GO	cell communication	5	90	0.407	29887	sorting nexin 10
GO	cell communication	5	90	0.407	4763	neurofibromin 1
GO	cell communication	5	90	0.407	6546	solute carrier family 8 (sodium/calcium exchanger), member 1
GO	spindle	5	90	0.407	23157	septin 6
GO	spindle	5	90	0.407	332	baculoviral IAP repeat-containing 5
GO	spindle	5	90	0.407	5303	protein (peptidylprolyl cis/trans isomerase) NIMA-interacting, 4 (parvulin)
GO	spindle	5	90	0.407	54984	PIN2-interacting protein 1
GO	spindle	5	90	0.407	6683	spastin

GO	gamma-catenin binding	1	11	0.407	1000	cadherin 2, type 1, N-cadherin (neuronal)
GO	positive regulation of axon extension	1	11	0.407	1002	cadherin 4, type 1, R-cadherin (retinal)
GO	mitotic sister chromatid segregation	1	11	0.407	10051	structural maintenance of chromosomes 4
GO	cell-cell junction assembly	1	11	0.407	10052	gap junction protein, gamma 1, 45kDa
GO	cellular response to oxidative stress	1	11	0.407	10202	dehydrogenase/reductase (SDR family) member 2
GO	cyclin-dependent protein kinase inhibit	1	11	0.407	1026	cyclin-dependent kinase inhibitor 1A (p21, Cip1)
GO	trophectodermal cell differentiation	1	11	0.407	1045	caudal type homeobox 2
GO	estrogen receptor signaling pathway	1	11	0.407	10474	transcriptional adaptor 3
GO	positive regulation of neurogenesis	1	11	0.407	10683	delta-like 3 (Drosophila)
GO	gap junction channel activity	1	11	0.407	127534	gap junction protein, beta 4, 30.3kDa
GO	response to vitamin A	1	11	0.407	1543	cytochrome P450, family 1, subfamily A, polypeptide 1
GO	protein tetramerization	1	11	0.407	158	adenylosuccinate lyase
GO	DNA methylation involved in gamete ge	1	11	0.407	1788	DNA (cytosine-5-)-methyltransferase 3 alpha
GO	cell fate determination	1	11	0.407	182	jagged 1 (Alagille syndrome)
GO	pyridine nucleotide biosynthetic proces	1	11	0.407	23057	nicotinamide nucleotide adenylyltransferase 2
GO	positive regulation of vascular endothel	1	11	0.407	2321	fms-related tyrosine kinase 1 (vascular endothelial growth factor/vascular
GO	long-chain fatty acid-CoA ligase activity	1	11	0.407	23305	acyl-CoA synthetase long-chain family member 6
GO	positive regulation of neuron projection	1	11	0.407	23305	acyl-CoA synthetase long-chain family member 6
GO	cell recognition	1	11	0.407	23705	cell adhesion molecule 1
GO	Ras GTPase binding	1	11	0.407	25780	RAS guanyl releasing protein 3 (calcium and DAG-regulated)
GO	morphogenesis of an epithelium	1	11	0.407	2736	GLI family zinc finger 2
GO	adenylate cyclase activity	1	11	0.407	2774	guanine nucleotide binding protein (G protein), alpha activating activity po
GO	regulation of synaptic transmission	1	11	0.407	2898	glutamate receptor, ionotropic, kainate 2
GO	RNA polymerase II carboxy-terminal do	1	11	0.407	2965	general transcription factor IIH, polypeptide 1, 62kDa
GO	DNA bending activity	1	11	0.407	3149	high-mobility group box 3
GO	low-density lipoprotein receptor bindin	1	11	0.407	348	apolipoprotein E
GO	positive regulation of erythrocyte differ	1	11	0.407	3624	inhibin, beta A
GO	delayed rectifier potassium channel acti	1	11	0.407	3756	potassium voltage-gated channel, subfamily H (eag-related), member 1
GO	myoblast fusion	1	11	0.407	3756	potassium voltage-gated channel, subfamily H (eag-related), member 1
GO	motor axon guidance	1	11	0.407	3800	kinesin family member 5C
GO	hemidesmosome assembly	1	11	0.407	3918	laminin, gamma 2
GO	pericentriolar material	1	11	0.407	3932	lymphocyte-specific protein tyrosine kinase
GO	bile acid metabolic process	1	11	0.407	3952	leptin
GO	cerebellum development	1	11	0.407	3975	LIM homeobox 1
GO	negative regulation of protein ubiquitin	1	11	0.407	409	arrestin, beta 2
GO	negative regulation of MAPKKK cascade	1	11	0.407	4763	neurofibromin 1

GO	gamma-tubulin binding	1	11	0.407	4830	non-metastatic cells 1, protein (NM23A) expressed in
GO	positive regulation of DNA binding	1	11	0.407	4830	non-metastatic cells 1, protein (NM23A) expressed in
GO	positive regulation of calcium ion transp	1	11	0.407	5026	purinergic receptor P2X, ligand-gated ion channel, 5
GO	endoplasmic reticulum organization	1	11	0.407	51062	atlastin GTPase 1
GO	peptide hormone processing	1	11	0.407	5125	proprotein convertase subtilisin/kexin type 5
GO	protein maturation by peptide bond cle	1	11	0.407	5125	proprotein convertase subtilisin/kexin type 5
GO	phosphatidylserine binding	1	11	0.407	54843	synaptotagmin-like 2
GO	polysaccharide binding	1	11	0.407	56241	sushi domain containing 2
GO	glucose transmembrane transporter act	1	11	0.407	6518	solute carrier family 2 (facilitated glucose/fructose transporter), member 5
GO	regulation of calcium ion transport	1	11	0.407	6546	solute carrier family 8 (sodium/calcium exchanger), member 1
GO	neural crest cell development	1	11	0.407	6662	SRY (sex determining region Y)-box 9
GO	oligodendrocyte differentiation	1	11	0.407	6662	SRY (sex determining region Y)-box 9
GO	non-G-protein coupled 7TM receptor ac	1	11	0.407	8325	frizzled homolog 8 (Drosophila)
GO	phospholipase C activity	1	11	0.407	9744	ArfGAP with coiled-coil, ankyrin repeat and PH domains 1
GO	peptidase activity	23	465	0.408	10213	proteasome (prosome, macropain) 26S subunit, non-ATPase, 14
GO	peptidase activity	23	465	0.408	10893	matrix metallopeptidase 24 (membrane-inserted)
GO	peptidase activity	23	465	0.408	132724	transmembrane protease, serine 11B
GO	peptidase activity	23	465	0.408	162494	rhomboid, veinlet-like 3 (Drosophila)
GO	peptidase activity	23	465	0.408	27429	HtrA serine peptidase 2
GO	peptidase activity	23	465	0.408	344805	transmembrane protease, serine 7
GO	peptidase activity	23	465	0.408	373856	ubiquitin specific peptidase 41
GO	peptidase activity	23	465	0.408	4287	ataxin 3
GO	peptidase activity	23	465	0.408	4312	matrix metallopeptidase 1 (interstitial collagenase)
GO	peptidase activity	23	465	0.408	4318	matrix metallopeptidase 9 (gelatinase B, 92kDa gelatinase, 92kDa type IV c
GO	peptidase activity	23	465	0.408	4319	matrix metallopeptidase 10 (stromelysin 2)
GO	peptidase activity	23	465	0.408	5125	proprotein convertase subtilisin/kexin type 5
GO	peptidase activity	23	465	0.408	5184	peptidase D
GO	peptidase activity	23	465	0.408	5624	protein C (inactivator of coagulation factors Va and VIIIa)
GO	peptidase activity	23	465	0.408	5654	HtrA serine peptidase 1
GO	peptidase activity	23	465	0.408	57478	ubiquitin specific peptidase 31
GO	peptidase activity	23	465	0.408	7037	transferrin receptor (p90, CD71)
GO	peptidase activity	23	465	0.408	7113	transmembrane protease, serine 2
GO	peptidase activity	23	465	0.408	7347	ubiquitin carboxyl-terminal esterase L3 (ubiquitin thiolesterase)
GO	peptidase activity	23	465	0.408	84101	ubiquitin specific peptidase 44
GO	peptidase activity	23	465	0.408	8728	ADAM metallopeptidase domain 19 (meltrin beta)
GO	peptidase activity	23	465	0.408	8747	ADAM metallopeptidase domain 21

GO	peptidase activity	23	465	0.408	90701	SEC11 homolog C (S. cerevisiae)
GO	DNA-directed DNA polymerase activity	2	30	0.409	157570	establishment of cohesion 1 homolog 2 (S. cerevisiae)
GO	DNA-directed DNA polymerase activity	2	30	0.409	56655	polymerase (DNA-directed), epsilon 4 (p12 subunit)
GO	steroid biosynthetic process	2	30	0.409	2232	ferredoxin reductase
GO	steroid biosynthetic process	2	30	0.409	29842	transcription factor CP2-like 1
GO	adult locomotory behavior	2	30	0.409	2906	glutamate receptor, ionotropic, N-methyl D-aspartate 2D
GO	adult locomotory behavior	2	30	0.409	3236	homeobox D10
GO	dorsal/ventral pattern formation	2	30	0.409	3237	homeobox D11
GO	dorsal/ventral pattern formation	2	30	0.409	3975	LIM homeobox 1
GO	one-carbon metabolic process	2	30	0.409	377677	carbonic anhydrase XIII
GO	one-carbon metabolic process	2	30	0.409	767	carbonic anhydrase VIII
GO	response to ionizing radiation	2	30	0.409	64782	apoptosis enhancing nuclease
GO	response to ionizing radiation	2	30	0.409	672	breast cancer 1, early onset
GO	negative regulation of transcription fact	2	30	0.409	6672	SP100 nuclear antigen
GO	negative regulation of transcription fact	2	30	0.409	7341	SMT3 suppressor of mif two 3 homolog 1 (S. cerevisiae)
GO	nuclear speck	6	111	0.412	10189	THO complex 4
GO	nuclear speck	6	111	0.412	10465	peptidylprolyl isomerase H (cyclophilin H)
GO	nuclear speck	6	111	0.412	56339	methyltransferase like 3
GO	nuclear speck	6	111	0.412	64318	nucleolar complex associated 3 homolog (S. cerevisiae)
GO	nuclear speck	6	111	0.412	7341	SMT3 suppressor of mif two 3 homolog 1 (S. cerevisiae)
GO	nuclear speck	6	111	0.412	7490	Wilms tumor 1
GO	spindle pole	3	50	0.412	26586	cytoskeleton associated protein 2
GO	spindle pole	3	50	0.412	7840	Alstrom syndrome 1
GO	spindle pole	3	50	0.412	93323	HAUS augmin-like complex, subunit 8
GO	hormone-mediated signaling pathway	3	50	0.412	2786	guanine nucleotide binding protein (G protein), gamma 4
GO	hormone-mediated signaling pathway	3	50	0.412	54331	guanine nucleotide binding protein (G protein), gamma 2
GO	hormone-mediated signaling pathway	3	50	0.412	59345	guanine nucleotide binding protein (G protein), beta polypeptide 4
GO	sequence-specific DNA binding	24	487	0.412	1E+08	forkhead box O6
GO	sequence-specific DNA binding	24	487	0.412	1045	caudal type homeobox 2
GO	sequence-specific DNA binding	24	487	0.412	139324	highly divergent homeobox
GO	sequence-specific DNA binding	24	487	0.412	1746	distal-less homeobox 2
GO	sequence-specific DNA binding	24	487	0.412	2305	forkhead box M1
GO	sequence-specific DNA binding	24	487	0.412	2736	GLI family zinc finger 2
GO	sequence-specific DNA binding	24	487	0.412	3224	homeobox C8
GO	sequence-specific DNA binding	24	487	0.412	3236	homeobox D10
GO	sequence-specific DNA binding	24	487	0.412	3237	homeobox D11

GO	sequence-specific DNA binding	24	487	0.412	344191	even-skipped homeobox 2
GO	sequence-specific DNA binding	24	487	0.412	3975	LIM homeobox 1
GO	sequence-specific DNA binding	24	487	0.412	4094	v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian)
GO	sequence-specific DNA binding	24	487	0.412	431707	LIM homeobox 8
GO	sequence-specific DNA binding	24	487	0.412	5015	orthodenticle homeobox 2
GO	sequence-specific DNA binding	24	487	0.412	5081	paired box 7
GO	sequence-specific DNA binding	24	487	0.412	56655	polymerase (DNA-directed), epsilon 4 (p12 subunit)
GO	sequence-specific DNA binding	24	487	0.412	6474	short stature homeobox 2
GO	sequence-specific DNA binding	24	487	0.412	6899	T-box 1
GO	sequence-specific DNA binding	24	487	0.412	7021	transcription factor AP-2 beta (activating enhancer binding protein 2 beta)
GO	sequence-specific DNA binding	24	487	0.412	7490	Wilms tumor 1
GO	sequence-specific DNA binding	24	487	0.412	80712	ESX homeobox 1
GO	sequence-specific DNA binding	24	487	0.412	8626	tumor protein p63
GO	sequence-specific DNA binding	24	487	0.412	9355	LIM homeobox 2
GO	sequence-specific DNA binding	24	487	0.412	9839	zinc finger E-box binding homeobox 2
GO	induction of apoptosis by extracellular s	5	91	0.416	26230	T-cell lymphoma invasion and metastasis 2
GO	induction of apoptosis by extracellular s	5	91	0.416	355	Fas (TNF receptor superfamily, member 6)
GO	induction of apoptosis by extracellular s	5	91	0.416	581	BCL2-associated X protein
GO	induction of apoptosis by extracellular s	5	91	0.416	5924	Ras protein-specific guanine nucleotide-releasing factor 2
GO	induction of apoptosis by extracellular s	5	91	0.416	8997	kalirin, RhoGEF kinase
GO	protein complex	8	153	0.417	1161	excision repair cross-complementing rodent repair deficiency, complement
GO	protein complex	8	153	0.417	1643	damage-specific DNA binding protein 2, 48kDa
GO	protein complex	8	153	0.417	309	annexin A6
GO	protein complex	8	153	0.417	3516	recombination signal binding protein for immunoglobulin kappa J region
GO	protein complex	8	153	0.417	6711	spectrin, beta, non-erythrocytic 1
GO	protein complex	8	153	0.417	672	breast cancer 1, early onset
GO	protein complex	8	153	0.417	7220	transient receptor potential cation channel, subfamily C, member 1
GO	protein complex	8	153	0.417	8626	tumor protein p63
GO	axon guidance	4	71	0.421	1002	cadherin 4, type 1, R-cadherin (retinal)
GO	axon guidance	4	71	0.421	2736	GLI family zinc finger 2
GO	axon guidance	4	71	0.421	5015	orthodenticle homeobox 2
GO	axon guidance	4	71	0.421	6586	slit homolog 3 (Drosophila)
GO	response to glucocorticoid stimulus	4	71	0.421	3557	interleukin 1 receptor antagonist
GO	response to glucocorticoid stimulus	4	71	0.421	5054	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor t
GO	response to glucocorticoid stimulus	4	71	0.421	590	butyrylcholinesterase
GO	response to glucocorticoid stimulus	4	71	0.421	6347	chemokine (C-C motif) ligand 2

GO	hemopoiesis	3	51	0.424	182	jagged 1 (Alagille syndrome)
GO	hemopoiesis	3	51	0.424	3932	lymphocyte-specific protein tyrosine kinase
GO	hemopoiesis	3	51	0.424	51218	glutaredoxin 5
GO	heart morphogenesis	2	31	0.425	10395	deleted in liver cancer 1
GO	heart morphogenesis	2	31	0.425	1289	collagen, type V, alpha 1
GO	ligand-dependent nuclear receptor tran	2	31	0.425	10474	transcriptional adaptor 3
GO	ligand-dependent nuclear receptor tran	2	31	0.425	5469	mediator complex subunit 1
GO	exonuclease activity	2	31	0.425	2237	flap structure-specific endonuclease 1
GO	exonuclease activity	2	31	0.425	64782	apoptosis enhancing nuclease
GO	symporter activity	6	113	0.429	201780	solute carrier family 10 (sodium/bile acid cotransporter family), member 4
GO	symporter activity	6	113	0.429	387700	solute carrier family 16, member 12 (monocarboxylic acid transporter 12)
GO	symporter activity	6	113	0.429	55117	solute carrier family 6 (neutral amino acid transporter), member 15
GO	symporter activity	6	113	0.429	6527	solute carrier family 5 (low affinity glucose cotransporter), member 4
GO	symporter activity	6	113	0.429	729025	solute carrier family 15, member 5
GO	symporter activity	6	113	0.429	9497	solute carrier family 4, sodium bicarbonate cotransporter, member 7
GO	protein homodimerization activity	18	365	0.431	114088	tripartite motif-containing 9
GO	protein homodimerization activity	18	365	0.431	2027	enolase 3 (beta, muscle)
GO	protein homodimerization activity	18	365	0.431	220	aldehyde dehydrogenase 1 family, member A3
GO	protein homodimerization activity	18	365	0.431	23171	glycerol-3-phosphate dehydrogenase 1-like
GO	protein homodimerization activity	18	365	0.431	23705	cell adhesion molecule 1
GO	protein homodimerization activity	18	365	0.431	241	arachidonate 5-lipoxygenase-activating protein
GO	protein homodimerization activity	18	365	0.431	2898	glutamate receptor, ionotropic, kainate 2
GO	protein homodimerization activity	18	365	0.431	3248	hydroxyprostaglandin dehydrogenase 15-(NAD)
GO	protein homodimerization activity	18	365	0.431	332	baculoviral IAP repeat-containing 5
GO	protein homodimerization activity	18	365	0.431	348	apolipoprotein E
GO	protein homodimerization activity	18	365	0.431	4436	mutS homolog 2, colon cancer, nonpolyposis type 1 (E. coli)
GO	protein homodimerization activity	18	365	0.431	5228	placental growth factor
GO	protein homodimerization activity	18	365	0.431	5341	pleckstrin
GO	protein homodimerization activity	18	365	0.431	581	BCL2-associated X protein
GO	protein homodimerization activity	18	365	0.431	6672	SP100 nuclear antigen
GO	protein homodimerization activity	18	365	0.431	6899	T-box 1
GO	protein homodimerization activity	18	365	0.431	83851	synaptotagmin XVI
GO	protein homodimerization activity	18	365	0.431	9540	tumor protein p53 inducible protein 3
GO	translation	10	197	0.433	10056	phenylalanyl-tRNA synthetase, beta subunit
GO	translation	10	197	0.433	11222	mitochondrial ribosomal protein L3
GO	translation	10	197	0.433	1984	eukaryotic translation initiation factor 5A

GO	translation	10	197	0.433	28998	mitochondrial ribosomal protein L13
GO	translation	10	197	0.433	51023	mitochondrial ribosomal protein S18C
GO	translation	10	197	0.433	6133	ribosomal protein L9
GO	translation	10	197	0.433	6154	ribosomal protein L26
GO	translation	10	197	0.433	6204	ribosomal protein S10
GO	translation	10	197	0.433	65003	mitochondrial ribosomal protein L11
GO	translation	10	197	0.433	65008	mitochondrial ribosomal protein L1
GO	negative regulation of cyclin-dependent	1	12	0.435	1026	cyclin-dependent kinase inhibitor 1A (p21, Cip1)
GO	STAGA complex	1	12	0.435	10474	transcriptional adaptor 3
GO	iron-sulfur cluster binding	1	12	0.435	10539	glutaredoxin 3
GO	positive regulation of innate immune re	1	12	0.435	10622	polymerase (RNA) III (DNA directed) polypeptide G (32kD)
GO	positive regulation of interferon-beta pr	1	12	0.435	10622	polymerase (RNA) III (DNA directed) polypeptide G (32kD)
GO	regulation of lipid metabolic process	1	12	0.435	12	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), me
GO	drug metabolic process	1	12	0.435	1543	cytochrome P450, family 1, subfamily A, polypeptide 1
GO	ephrin receptor activity	1	12	0.435	2045	EPH receptor A7
GO	positive regulation of calcium ion transp	1	12	0.435	2149	coagulation factor II (thrombin) receptor
GO	positive regulation of caspase activity	1	12	0.435	2149	coagulation factor II (thrombin) receptor
GO	glutamate signaling pathway	1	12	0.435	2898	glutamate receptor, ionotropic, kainate 2
GO	estradiol 17-beta-dehydrogenase activit	1	12	0.435	3028	hydroxysteroid (17-beta) dehydrogenase 10
GO	protein methyltransferase activity	1	12	0.435	3276	protein arginine methyltransferase 1
GO	cholesterol transporter activity	1	12	0.435	348	apolipoprotein E
GO	positive regulation of peptidyl-serine ph	1	12	0.435	3589	interleukin 11
GO	negative regulation of macrophage deri	1	12	0.435	3685	integrin, alpha V (vitronectin receptor, alpha polypeptide, antigen CD51)
GO	arylsulfatase activity	1	12	0.435	411	arylsulfatase B
GO	response to pH	1	12	0.435	411	arylsulfatase B
GO	DNA unwinding involved in replication	1	12	0.435	4171	minichromosome maintenance complex component 2
GO	positive regulation of blood pressure	1	12	0.435	5021	oxytocin receptor
GO	dorsal/ventral neural tube patterning	1	12	0.435	5081	paired box 7
GO	cGMP binding	1	12	0.435	50940	phosphodiesterase 11A
GO	lysosphingolipid and lysophosphatidic a	1	12	0.435	53637	sphingosine-1-phosphate receptor 5
GO	microvillus membrane	1	12	0.435	5420	podocalyxin-like
GO	protein serine/threonine phosphatase c	1	12	0.435	5494	protein phosphatase, Mg2+/Mn2+ dependent, 1A
GO	acrosome reaction	1	12	0.435	55521	tripartite motif-containing 36
GO	immunological synapse	1	12	0.435	5588	protein kinase C, theta
GO	voltage-gated sodium channel complex	1	12	0.435	6335	sodium channel, voltage-gated, type IX, alpha subunit
GO	viral genome replication	1	12	0.435	6347	chemokine (C-C motif) ligand 2

GO	retinoic acid receptor signaling pathway	1	12	0.435	6672	SP100 nuclear antigen
GO	response to copper ion	1	12	0.435	7037	transferrin receptor (p90, CD71)
GO	positive regulation of cellular componer	1	12	0.435	7046	transforming growth factor, beta receptor 1
GO	positive regulation of survival gene proc	1	12	0.435	7046	transforming growth factor, beta receptor 1
GO	costamere	1	12	0.435	7220	transient receptor potential cation channel, subfamily C, member 1
GO	neuromuscular synaptic transmission	1	12	0.435	773	calcium channel, voltage-dependent, P/Q type, alpha 1A subunit
GO	endothelial cell migration	1	12	0.435	7857	secretogranin II (chromogranin C)
GO	induction of positive chemotaxis	1	12	0.435	7857	secretogranin II (chromogranin C)
GO	Golgi-associated vesicle	1	12	0.435	79929	MAP6 domain containing 1
GO	regulation of phosphorylation	1	12	0.435	81706	protein phosphatase 1, regulatory (inhibitor) subunit 14C
GO	nBAF complex	1	12	0.435	8193	D4, zinc and double PHD fingers family 1
GO	histone acetylation	1	12	0.435	8520	histone acetyltransferase 1
GO	keratinocyte proliferation	1	12	0.435	8626	tumor protein p63
GO	anion transmembrane transporter activ	1	12	0.435	9497	solute carrier family 4, sodium bicarbonate cotransporter, member 7
GO	Rac GTPase binding	1	12	0.435	9732	dedicator of cytokinesis 4
GO	calcium ion transport	6	114	0.437	2534	FYN oncogene related to SRC, FGR, YES
GO	calcium ion transport	6	114	0.437	309	annexin A6
GO	calcium ion transport	6	114	0.437	54822	transient receptor potential cation channel, subfamily M, member 7
GO	calcium ion transport	6	114	0.437	6546	solute carrier family 8 (sodium/calcium exchanger), member 1
GO	calcium ion transport	6	114	0.437	7220	transient receptor potential cation channel, subfamily C, member 1
GO	calcium ion transport	6	114	0.437	773	calcium channel, voltage-dependent, P/Q type, alpha 1A subunit
GO	peptide binding	2	32	0.442	347733	tubulin, beta 2B
GO	peptide binding	2	32	0.442	5125	proprotein convertase subtilisin/kexin type 5
GO	carbohydrate transport	2	32	0.442	6518	solute carrier family 2 (facilitated glucose/fructose transporter), member 5
GO	carbohydrate transport	2	32	0.442	6527	solute carrier family 5 (low affinity glucose cotransporter), member 4
GO	mitosis	10	199	0.445	113130	cell division cycle associated 5
GO	mitosis	10	199	0.445	220134	spindle and kinetochore associated complex subunit 1
GO	mitosis	10	199	0.445	332	baculoviral IAP repeat-containing 5
GO	mitosis	10	199	0.445	347733	tubulin, beta 2B
GO	mitosis	10	199	0.445	55165	centrosomal protein 55kDa
GO	mitosis	10	199	0.445	64151	non-SMC condensin I complex, subunit G
GO	mitosis	10	199	0.445	79187	fibronectin type III and SPRY domain containing 1
GO	mitosis	10	199	0.445	8091	high mobility group AT-hook 2
GO	mitosis	10	199	0.445	890	cyclin A2
GO	mitosis	10	199	0.445	93323	HAUS augmin-like complex, subunit 8
GO	transcription from RNA polymerase II pr	9	178	0.446	1045	caudal type homeobox 2

GO	transcription from RNA polymerase II pr	9	178	0.446	11077	heat shock transcription factor 2 binding protein
GO	transcription from RNA polymerase II pr	9	178	0.446	2305	forkhead box M1
GO	transcription from RNA polymerase II pr	9	178	0.446	2965	general transcription factor IIH, polypeptide 1, 62kDa
GO	transcription from RNA polymerase II pr	9	178	0.446	409	arrestin, beta 2
GO	transcription from RNA polymerase II pr	9	178	0.446	4094	v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian)
GO	transcription from RNA polymerase II pr	9	178	0.446	5440	polymerase (RNA) II (DNA directed) polypeptide K, 7.0kDa
GO	transcription from RNA polymerase II pr	9	178	0.446	659	bone morphogenetic protein receptor, type II (serine/threonine kinase)
GO	transcription from RNA polymerase II pr	9	178	0.446	9242	musculin (activated B-cell factor-1)
GO	ruffle	3	53	0.449	5420	podocalyxin-like
GO	ruffle	3	53	0.449	54822	transient receptor potential cation channel, subfamily M, member 7
GO	ruffle	3	53	0.449	9260	PDZ and LIM domain 7 (enigma)
GO	angiogenesis	6	116	0.453	1282	collagen, type IV, alpha 1
GO	angiogenesis	6	116	0.453	182	jagged 1 (Alagille syndrome)
GO	angiogenesis	6	116	0.453	2321	fms-related tyrosine kinase 1 (vascular endothelial growth factor/vascular
GO	angiogenesis	6	116	0.453	5228	placental growth factor
GO	angiogenesis	6	116	0.453	60675	prokineticin 2
GO	angiogenesis	6	116	0.453	7857	secretogranin II (chromogranin C)
GO	Rab GTPase binding	2	33	0.457	1121	choroideremia (Rab escort protein 1)
GO	Rab GTPase binding	2	33	0.457	54843	synaptotagmin-like 2
GO	learning or memory	2	33	0.457	29767	tropomodulin 2 (neuronal)
GO	learning or memory	2	33	0.457	431707	LIM homeobox 8
GO	positive regulation of actin filament pol	1	13	0.461	10096	ARP3 actin-related protein 3 homolog (yeast)
GO	bone mineralization	1	13	0.461	10457	glycoprotein (transmembrane) nmb
GO	transcription factor TFTC complex	1	13	0.461	10474	transcriptional adaptor 3
GO	spindle organization	1	13	0.461	1164	CDC28 protein kinase regulatory subunit 2
GO	extracellular matrix binding	1	13	0.461	1301	collagen, type XI, alpha 1
GO	autophagic vacuole membrane	1	13	0.461	157753	transmembrane protein 74
GO	myoblast differentiation	1	13	0.461	182	jagged 1 (Alagille syndrome)
GO	T cell proliferation	1	13	0.461	2281	FK506 binding protein 1B, 12.6 kDa
GO	induction of an organ	1	13	0.461	3237	homeobox D11
GO	lipid homeostasis	1	13	0.461	348	apolipoprotein E
GO	two-component sensor activity	1	13	0.461	3756	potassium voltage-gated channel, subfamily H (eag-related), member 1
GO	calcium-activated potassium channel ac	1	13	0.461	3778	potassium large conductance calcium-activated channel, subfamily M, alph
GO	response to osmotic stress	1	13	0.461	3778	potassium large conductance calcium-activated channel, subfamily M, alph
GO	positive regulation of phosphoinositide	1	13	0.461	4734	neural precursor cell expressed, developmentally down-regulated 4
GO	camera-type eye morphogenesis	1	13	0.461	4763	neurofibromin 1

GO	positive regulation of hormone secretio	1	13	0.461	5028	purinergic receptor P2Y, G-protein coupled, 1
GO	transcription from RNA polymerase III p	1	13	0.461	5440	polymerase (RNA) II (DNA directed) polypeptide K, 7.0kDa
GO	steroid hormone receptor signaling patl	1	13	0.461	5469	mediator complex subunit 1
GO	positive regulation of interleukin-2 bios	1	13	0.461	5588	protein kinase C, theta
GO	histone deacetylase activity	1	13	0.461	6299	sal-like 1 (Drosophila)
GO	response to bacterium	1	13	0.461	6347	chemokine (C-C motif) ligand 2
GO	syntaxin binding	1	13	0.461	773	calcium channel, voltage-dependent, P/Q type, alpha 1A subunit
GO	negative regulation of microtubule depo	1	13	0.461	79929	MAP6 domain containing 1
GO	labyrinthine layer blood vessel developr	1	13	0.461	80712	ESX homeobox 1
GO	low-density lipoprotein binding	1	13	0.461	81035	collectin sub-family member 12
GO	transcription elongation factor complex	1	13	0.461	8458	transcription termination factor, RNA polymerase II
GO	insulin-like growth factor receptor bindi	1	13	0.461	8835	suppressor of cytokine signaling 2
GO	muscle cell homeostasis	1	13	0.461	9215	like-glycosyltransferase
GO	glial cell differentiation	1	13	0.461	92737	delta/notch-like EGF repeat containing
GO	inorganic anion exchanger activity	1	13	0.461	9497	solute carrier family 4, sodium bicarbonate cotransporter, member 7
GO	cellular defense response	3	54	0.461	51473	doublecortin domain containing 2
GO	cellular defense response	3	54	0.461	729230	chemokine (C-C motif) receptor 2
GO	cellular defense response	3	54	0.461	8712	P antigen family, member 1 (prostate associated)
GO	microtubule organizing center	5	96	0.462	27241	Bardet-Biedl syndrome 9
GO	microtubule organizing center	5	96	0.462	28984	chromosome 13 open reading frame 15
GO	microtubule organizing center	5	96	0.462	6683	spastin
GO	microtubule organizing center	5	96	0.462	79187	fibronectin type III and SPRY domain containing 1
GO	microtubule organizing center	5	96	0.462	93323	HAUS augmin-like complex, subunit 8
GO	defense response to bacterium	4	75	0.462	245929	defensin, beta 115
GO	defense response to bacterium	4	75	0.462	57817	hepcidin antimicrobial peptide
GO	defense response to bacterium	4	75	0.462	8349	histone cluster 2, H2be
GO	defense response to bacterium	4	75	0.462	8970	histone cluster 1, H2bj
GO	negative regulation of cell proliferation	14	287	0.464	10202	dehydrogenase/reductase (SDR family) member 2
GO	negative regulation of cell proliferation	14	287	0.464	1026	cyclin-dependent kinase inhibitor 1A (p21, Cip1)
GO	negative regulation of cell proliferation	14	287	0.464	10395	deleted in liver cancer 1
GO	negative regulation of cell proliferation	14	287	0.464	10457	glycoprotein (transmembrane) nmb
GO	negative regulation of cell proliferation	14	287	0.464	2149	coagulation factor II (thrombin) receptor
GO	negative regulation of cell proliferation	14	287	0.464	2172	fatty acid binding protein 6, ileal
GO	negative regulation of cell proliferation	14	287	0.464	27244	sestrin 1
GO	negative regulation of cell proliferation	14	287	0.464	3624	inhibin, beta A
GO	negative regulation of cell proliferation	14	287	0.464	4830	non-metastatic cells 1, protein (NM23A) expressed in

GO	negative regulation of cell proliferation	14	287	0.464	5245	prohibitin
GO	negative regulation of cell proliferation	14	287	0.464	54984	PIN2-interacting protein 1
GO	negative regulation of cell proliferation	14	287	0.464	5744	parathyroid hormone-like hormone
GO	negative regulation of cell proliferation	14	287	0.464	6586	slit homolog 3 (Drosophila)
GO	negative regulation of cell proliferation	14	287	0.464	7490	Wilms tumor 1
GO	G-protein coupled receptor activity	17	352	0.47	2149	coagulation factor II (thrombin) receptor
GO	G-protein coupled receptor activity	17	352	0.47	2150	coagulation factor II (thrombin) receptor-like 1
GO	G-protein coupled receptor activity	17	352	0.47	2151	coagulation factor II (thrombin) receptor-like 2
GO	G-protein coupled receptor activity	17	352	0.47	222611	G protein-coupled receptor 111
GO	G-protein coupled receptor activity	17	352	0.47	23432	G protein-coupled receptor 161
GO	G-protein coupled receptor activity	17	352	0.47	2842	G protein-coupled receptor 19
GO	G-protein coupled receptor activity	17	352	0.47	2845	G protein-coupled receptor 22
GO	G-protein coupled receptor activity	17	352	0.47	2850	G protein-coupled receptor 27
GO	G-protein coupled receptor activity	17	352	0.47	2863	G protein-coupled receptor 39
GO	G-protein coupled receptor activity	17	352	0.47	4158	melanocortin 2 receptor (adrenocorticotropic hormone)
GO	G-protein coupled receptor activity	17	352	0.47	5021	oxytocin receptor
GO	G-protein coupled receptor activity	17	352	0.47	5028	purinergic receptor P2Y, G-protein coupled, 1
GO	G-protein coupled receptor activity	17	352	0.47	5031	pyrimidinergic receptor P2Y, G-protein coupled, 6
GO	G-protein coupled receptor activity	17	352	0.47	53637	sphingosine-1-phosphate receptor 5
GO	G-protein coupled receptor activity	17	352	0.47	729230	chemokine (C-C motif) receptor 2
GO	G-protein coupled receptor activity	17	352	0.47	8325	frizzled homolog 8 (Drosophila)
GO	G-protein coupled receptor activity	17	352	0.47	9568	gamma-aminobutyric acid (GABA) B receptor, 2
GO	lyase activity	5	97	0.471	158	adenylosuccinate lyase
GO	lyase activity	5	97	0.471	2027	enolase 3 (beta, muscle)
GO	lyase activity	5	97	0.471	377677	carbonic anhydrase XIII
GO	lyase activity	5	97	0.471	4968	8-oxoguanine DNA glycosylase
GO	lyase activity	5	97	0.471	7389	uroporphyrinogen decarboxylase
GO	extrinsic to membrane	2	34	0.473	2037	erythrocyte membrane protein band 4.1-like 2
GO	extrinsic to membrane	2	34	0.473	23136	erythrocyte membrane protein band 4.1-like 3
GO	presynaptic membrane	2	34	0.473	26059	ELKS/RAB6-interacting/CAST family member 2
GO	presynaptic membrane	2	34	0.473	2898	glutamate receptor, ionotropic, kainate 2
GO	B cell differentiation	2	34	0.473	3589	interleukin 11
GO	B cell differentiation	2	34	0.473	4436	mutS homolog 2, colon cancer, nonpolyposis type 1 (E. coli)
GO	acid-amino acid ligase activity	2	34	0.473	4734	neural precursor cell expressed, developmentally down-regulated 4
GO	acid-amino acid ligase activity	2	34	0.473	51191	hect domain and RLD 5
GO	positive regulation of epithelial cell prol	2	34	0.473	4830	non-metastatic cells 1, protein (NM23A) expressed in

GO	positive regulation of epithelial cell prol	2	34	0.473	9420	cytochrome P450, family 7, subfamily B, polypeptide 1
GO	humoral immune response	2	34	0.473	54210	triggering receptor expressed on myeloid cells 1
GO	humoral immune response	2	34	0.473	6347	chemokine (C-C motif) ligand 2
GO	cell-cell junction	3	56	0.486	1000	cadherin 2, type 1, N-cadherin (neuronal)
GO	cell-cell junction	3	56	0.486	23136	erythrocyte membrane protein band 4.1-like 3
GO	cell-cell junction	3	56	0.486	23705	cell adhesion molecule 1
GO	proteasome complex	3	56	0.486	10213	proteasome (prosome, macropain) 26S subunit, non-ATPase, 14
GO	proteasome complex	3	56	0.486	5702	proteasome (prosome, macropain) 26S subunit, ATPase, 3
GO	proteasome complex	3	56	0.486	5717	proteasome (prosome, macropain) 26S subunit, non-ATPase, 11
GO	condensed chromosome kinetochore	3	56	0.486	54984	PIN2-interacting protein 1
GO	condensed chromosome kinetochore	3	56	0.486	79172	centromere protein O
GO	condensed chromosome kinetochore	3	56	0.486	79682	MLF1 interacting protein
GO	glutamine metabolic process	1	14	0.486	1503	CTP synthase
GO	nuclear heterochromatin	1	14	0.486	1788	DNA (cytosine-5-)-methyltransferase 3 alpha
GO	protein export from nucleus	1	14	0.486	1984	eukaryotic translation initiation factor 5A
GO	neuroblast proliferation	1	14	0.486	23305	acyl-CoA synthetase long-chain family member 6
GO	positive regulation of natural killer cell r	1	14	0.486	23705	cell adhesion molecule 1
GO	hindbrain development	1	14	0.486	2736	GLI family zinc finger 2
GO	tropomyosin binding	1	14	0.486	29767	tropomodulin 2 (neuronal)
GO	nitric oxide mediated signal transductio	1	14	0.486	348	apolipoprotein E
GO	regulation of neuronal synaptic plasticit	1	14	0.486	348	apolipoprotein E
GO	regulation of action potential	1	14	0.486	3751	potassium voltage-gated channel, Shal-related subfamily, member 2
GO	rhythmic process	1	14	0.486	402055	SRR1 domain containing
GO	sensory perception	1	14	0.486	409	arrestin, beta 2
GO	positive regulation of protein catabolic	1	14	0.486	4734	neural precursor cell expressed, developmentally down-regulated 4
GO	embryonic heart tube development	1	14	0.486	5469	mediator complex subunit 1
GO	neurotransmitter:sodium symporter act	1	14	0.486	55117	solute carrier family 6 (neutral amino acid transporter), member 15
GO	membrane protein ectodomain proteol	1	14	0.486	5588	protein kinase C, theta
GO	positive regulation of protein secretion	1	14	0.486	5588	protein kinase C, theta
GO	protein kinase C activity	1	14	0.486	5588	protein kinase C, theta
GO	regulation of vasoconstriction	1	14	0.486	5588	protein kinase C, theta
GO	NuRD complex	1	14	0.486	6299	sal-like 1 (Drosophila)
GO	chromosome organization	1	14	0.486	641	Bloom syndrome, RecQ helicase-like
GO	response to ATP	1	14	0.486	6546	solute carrier family 8 (sodium/calcium exchanger), member 1
GO	solute:hydrogen antiporter activity	1	14	0.486	6549	solute carrier family 9 (sodium/hydrogen exchanger), member 2
GO	cellular response to starvation	1	14	0.486	659	bone morphogenetic protein receptor, type II (serine/threonine kinase)

GO	eye development	1	14	0.486	6657	SRY (sex determining region Y)-box 2
GO	response to interferon-gamma	1	14	0.486	6672	SP100 nuclear antigen
GO	pathway-restricted SMAD protein phos	1	14	0.486	7046	transforming growth factor, beta receptor 1
GO	calmodulin-dependent protein kinase a	1	14	0.486	8536	calcium/calmodulin-dependent protein kinase I
GO	mitochondrion	56	1193	0.487	10202	dehydrogenase/reductase (SDR family) member 2
GO	mitochondrion	56	1193	0.487	11022	tudor and KH domain containing
GO	mitochondrion	56	1193	0.487	11222	mitochondrial ribosomal protein L3
GO	mitochondrion	56	1193	0.487	122786	FERM domain containing 6
GO	mitochondrion	56	1193	0.487	132158	glycerate kinase
GO	mitochondrion	56	1193	0.487	1543	cytochrome P450, family 1, subfamily A, polypeptide 1
GO	mitochondrion	56	1193	0.487	154791	chromosome 7 open reading frame 55
GO	mitochondrion	56	1193	0.487	1716	deoxyguanosine kinase
GO	mitochondrion	56	1193	0.487	1763	DNA replication helicase 2 homolog (yeast)
GO	mitochondrion	56	1193	0.487	2232	ferredoxin reductase
GO	mitochondrion	56	1193	0.487	2237	flap structure-specific endonuclease 1
GO	mitochondrion	56	1193	0.487	22868	FAST kinase domains 2
GO	mitochondrion	56	1193	0.487	23305	acyl-CoA synthetase long-chain family member 6
GO	mitochondrion	56	1193	0.487	23590	prenyl (decaprenyl) diphosphate synthase, subunit 1
GO	mitochondrion	56	1193	0.487	255027	MPV17 mitochondrial membrane protein-like
GO	mitochondrion	56	1193	0.487	25884	chordin-like 2
GO	mitochondrion	56	1193	0.487	25953	paroxysmal nonkinesigenic dyskinesia
GO	mitochondrion	56	1193	0.487	26275	3-hydroxyisobutyryl-Coenzyme A hydrolase
GO	mitochondrion	56	1193	0.487	2628	glycine amidinotransferase (L-arginine:glycine amidinotransferase)
GO	mitochondrion	56	1193	0.487	26519	translocase of inner mitochondrial membrane 10 homolog (yeast)
GO	mitochondrion	56	1193	0.487	26521	translocase of inner mitochondrial membrane 8 homolog B (yeast)
GO	mitochondrion	56	1193	0.487	2653	glycine cleavage system protein H (aminomethyl carrier)
GO	mitochondrion	56	1193	0.487	27429	HtrA serine peptidase 2
GO	mitochondrion	56	1193	0.487	284184	chromosome 17 open reading frame 89
GO	mitochondrion	56	1193	0.487	28998	mitochondrial ribosomal protein L13
GO	mitochondrion	56	1193	0.487	3028	hydroxysteroid (17-beta) dehydrogenase 10
GO	mitochondrion	56	1193	0.487	3336	heat shock 10kDa protein 1 (chaperonin 10)
GO	mitochondrion	56	1193	0.487	411	arylsulfatase B
GO	mitochondrion	56	1193	0.487	4709	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 3, 12kDa
GO	mitochondrion	56	1193	0.487	4830	non-metastatic cells 1, protein (NM23A) expressed in
GO	mitochondrion	56	1193	0.487	4968	8-oxoguanine DNA glycosylase
GO	mitochondrion	56	1193	0.487	5028	purinergic receptor P2Y, G-protein coupled, 1

GO	mitochondrion	56	1193	0.487	51023	mitochondrial ribosomal protein S18C
GO	mitochondrion	56	1193	0.487	51218	glutaredoxin 5
GO	mitochondrion	56	1193	0.487	51499	TP53 regulated inhibitor of apoptosis 1
GO	mitochondrion	56	1193	0.487	516	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit C1 (subu
GO	mitochondrion	56	1193	0.487	5245	prohibitin
GO	mitochondrion	56	1193	0.487	5303	protein (peptidylprolyl cis/trans isomerase) NIMA-interacting, 4 (parvulin)
GO	mitochondrion	56	1193	0.487	54534	mitochondrial ribosomal protein L50
GO	mitochondrion	56	1193	0.487	57144	p21 protein (Cdc42/Rac)-activated kinase 7
GO	mitochondrion	56	1193	0.487	57678	glycerol-3-phosphate acyltransferase, mitochondrial
GO	mitochondrion	56	1193	0.487	581	BCL2-associated X protein
GO	mitochondrion	56	1193	0.487	586	branched chain aminotransferase 1, cytosolic
GO	mitochondrion	56	1193	0.487	60386	solute carrier family 25 (mitochondrial thiamine pyrophosphate carrier), m
GO	mitochondrion	56	1193	0.487	60492	coiled-coil domain containing 90B
GO	mitochondrion	56	1193	0.487	65003	mitochondrial ribosomal protein L11
GO	mitochondrion	56	1193	0.487	65008	mitochondrial ribosomal protein L1
GO	mitochondrion	56	1193	0.487	65055	receptor accessory protein 1
GO	mitochondrion	56	1193	0.487	6586	slit homolog 3 (Drosophila)
GO	mitochondrion	56	1193	0.487	7037	transferrin receptor (p90, CD71)
GO	mitochondrion	56	1193	0.487	79071	ELOVL family member 6, elongation of long chain fatty acids (FEN1/Elo2, SU
GO	mitochondrion	56	1193	0.487	79814	agmatine ureohydrolase (agmatinase)
GO	mitochondrion	56	1193	0.487	81892	chromosome 14 open reading frame 156
GO	mitochondrion	56	1193	0.487	8604	solute carrier family 25 (mitochondrial carrier, Aralar), member 12
GO	mitochondrion	56	1193	0.487	8659	aldehyde dehydrogenase 4 family, member A1
GO	mitochondrion	56	1193	0.487	91942	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, assembly factor 2
GO	acute-phase response	2	35	0.488	12	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), me
GO	acute-phase response	2	35	0.488	7037	transferrin receptor (p90, CD71)
GO	embryonic limb morphogenesis	2	35	0.488	3236	homeobox D10
GO	embryonic limb morphogenesis	2	35	0.488	8626	tumor protein p63
GO	centriole	2	35	0.488	332	baculoviral IAP repeat-containing 5
GO	centriole	2	35	0.488	55165	centrosomal protein 55kDa
GO	transcription corepressor activity	7	142	0.491	1045	caudal type homeobox 2
GO	transcription corepressor activity	7	142	0.491	11278	Kruppel-like factor 12
GO	transcription corepressor activity	7	142	0.491	29842	transcription factor CP2-like 1
GO	transcription corepressor activity	7	142	0.491	29995	LIM and cysteine-rich domains 1
GO	transcription corepressor activity	7	142	0.491	5702	proteasome (prosome, macropain) 26S subunit, ATPase, 3
GO	transcription corepressor activity	7	142	0.491	6672	SP100 nuclear antigen

GO	transcription corepressor activity	7	142	0.491	9242	musculin (activated B-cell factor-1)
GO	locomotory behavior	3	57	0.497	1136	cholinergic receptor, nicotinic, alpha 3
GO	locomotory behavior	3	57	0.497	55084	sine oculis binding protein homolog (Drosophila)
GO	locomotory behavior	3	57	0.497	55283	mucolipin 3
GO	DNA binding	65	1392	0.501	11169	WD repeat and HMG-box DNA binding protein 1
GO	DNA binding	65	1392	0.501	11278	Kruppel-like factor 12
GO	DNA binding	65	1392	0.501	12	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), me
GO	DNA binding	65	1392	0.501	148213	zinc finger protein 681
GO	DNA binding	65	1392	0.501	1643	damage-specific DNA binding protein 2, 48kDa
GO	DNA binding	65	1392	0.501	170082	transcription elongation factor A (SII) N-terminal and central domain conta
GO	DNA binding	65	1392	0.501	1763	DNA replication helicase 2 homolog (yeast)
GO	DNA binding	65	1392	0.501	1775	deoxyribonuclease I-like 2
GO	DNA binding	65	1392	0.501	1787	tRNA aspartic acid methyltransferase 1
GO	DNA binding	65	1392	0.501	1788	DNA (cytosine-5-)-methyltransferase 3 alpha
GO	DNA binding	65	1392	0.501	201299	RAD52 motif 1
GO	DNA binding	65	1392	0.501	219736	storkhead box 1
GO	DNA binding	65	1392	0.501	2237	flap structure-specific endonuclease 1
GO	DNA binding	65	1392	0.501	2305	forkhead box M1
GO	DNA binding	65	1392	0.501	23594	origin recognition complex, subunit 6 like (yeast)
GO	DNA binding	65	1392	0.501	25885	polymerase (RNA) I polypeptide A, 194kDa
GO	DNA binding	65	1392	0.501	284443	zinc finger protein 493
GO	DNA binding	65	1392	0.501	29893	PSMC3 interacting protein
GO	DNA binding	65	1392	0.501	344191	even-skipped homeobox 2
GO	DNA binding	65	1392	0.501	3516	recombination signal binding protein for immunoglobulin kappa J region
GO	DNA binding	65	1392	0.501	387103	centromere protein W
GO	DNA binding	65	1392	0.501	389421	lin-28 homolog B (C. elegans)
GO	DNA binding	65	1392	0.501	406	aryl hydrocarbon receptor nuclear translocator-like
GO	DNA binding	65	1392	0.501	4171	minichromosome maintenance complex component 2
GO	DNA binding	65	1392	0.501	4291	myeloid leukemia factor 1
GO	DNA binding	65	1392	0.501	4436	mutS homolog 2, colon cancer, nonpolyposis type 1 (E. coli)
GO	DNA binding	65	1392	0.501	4603	v-myb myeloblastosis viral oncogene homolog (avian)-like 1
GO	DNA binding	65	1392	0.501	5000	origin recognition complex, subunit 4-like (yeast)
GO	DNA binding	65	1392	0.501	50485	SWI/SNF related, matrix associated, actin dependent regulator of chromati
GO	DNA binding	65	1392	0.501	5303	protein (peptidylprolyl cis/trans isomerase) NIMA-interacting, 4 (parvulin)
GO	DNA binding	65	1392	0.501	5378	PMS1 postmeiotic segregation increased 1 (S. cerevisiae)
GO	DNA binding	65	1392	0.501	5440	polymerase (RNA) II (DNA directed) polypeptide K, 7.0kDa

GO	DNA binding	65	1392	0.501	5469	mediator complex subunit 1
GO	DNA binding	65	1392	0.501	54796	basonuclin 2
GO	DNA binding	65	1392	0.501	55506	H2A histone family, member Y2
GO	DNA binding	65	1392	0.501	5558	primase, DNA, polypeptide 2 (58kDa)
GO	DNA binding	65	1392	0.501	58499	zinc finger protein 462
GO	DNA binding	65	1392	0.501	5889	RAD51 homolog C (S. cerevisiae)
GO	DNA binding	65	1392	0.501	59336	PR domain containing 13
GO	DNA binding	65	1392	0.501	5965	RecQ protein-like (DNA helicase Q1-like)
GO	DNA binding	65	1392	0.501	6299	sal-like 1 (Drosophila)
GO	DNA binding	65	1392	0.501	641	Bloom syndrome, RecQ helicase-like
GO	DNA binding	65	1392	0.501	6591	snail homolog 2 (Drosophila)
GO	DNA binding	65	1392	0.501	6615	snail homolog 1 (Drosophila)
GO	DNA binding	65	1392	0.501	6657	SRY (sex determining region Y)-box 2
GO	DNA binding	65	1392	0.501	6672	SP100 nuclear antigen
GO	DNA binding	65	1392	0.501	672	breast cancer 1, early onset
GO	DNA binding	65	1392	0.501	7021	transcription factor AP-2 beta (activating enhancer binding protein 2 beta)
GO	DNA binding	65	1392	0.501	7029	transcription factor Dp-2 (E2F dimerization partner 2)
GO	DNA binding	65	1392	0.501	7552	zinc finger protein 711
GO	DNA binding	65	1392	0.501	79075	defective in sister chromatid cohesion 1 homolog (S. cerevisiae)
GO	DNA binding	65	1392	0.501	79698	zinc finger, matrin type 4
GO	DNA binding	65	1392	0.501	8091	high mobility group AT-hook 2
GO	DNA binding	65	1392	0.501	8348	histone cluster 1, H2bo
GO	DNA binding	65	1392	0.501	8349	histone cluster 2, H2be
GO	DNA binding	65	1392	0.501	84083	zinc finger, RAN-binding domain containing 3
GO	DNA binding	65	1392	0.501	84172	polymerase (RNA) I polypeptide B, 128kDa
GO	DNA binding	65	1392	0.501	8458	transcription termination factor, RNA polymerase II
GO	DNA binding	65	1392	0.501	84622	zinc finger protein 594
GO	DNA binding	65	1392	0.501	84878	zinc finger and BTB domain containing 45
GO	DNA binding	65	1392	0.501	8626	tumor protein p63
GO	DNA binding	65	1392	0.501	8970	histone cluster 1, H2bj
GO	DNA binding	65	1392	0.501	91442	chromosome 19 open reading frame 40
GO	DNA binding	65	1392	0.501	91975	zinc finger protein 300
GO	DNA binding	65	1392	0.501	93474	zinc finger protein 670
GO	postsynaptic density	4	79	0.503	1136	cholinergic receptor, nicotinic, alpha 3
GO	postsynaptic density	4	79	0.503	3751	potassium voltage-gated channel, Shal-related subfamily, member 2
GO	postsynaptic density	4	79	0.503	8777	multiple PDZ domain protein

GO	postsynaptic density	4	79	0.503	9455	homer homolog 2 (Drosophila)
GO	protein amino acid autophosphorylatior	4	79	0.503	2534	FYN oncogene related to SRC, FGR, YES
GO	protein amino acid autophosphorylatior	4	79	0.503	54822	transient receptor potential cation channel, subfamily M, member 7
GO	protein amino acid autophosphorylatior	4	79	0.503	7046	transforming growth factor, beta receptor 1
GO	protein amino acid autophosphorylatior	4	79	0.503	84206	mex-3 homolog B (C. elegans)
GO	Rho protein signal transduction	2	36	0.503	10672	guanine nucleotide binding protein (G protein), alpha 13
GO	Rho protein signal transduction	2	36	0.503	6242	rhotekin
GO	autophagy	2	36	0.503	157753	transmembrane protein 74
GO	autophagy	2	36	0.503	411	arylsulfatase B
GO	microtubule basal body	2	36	0.503	57560	intraflagellar transport 80 homolog (Chlamydomonas)
GO	microtubule basal body	2	36	0.503	7840	Alstrom syndrome 1
GO	response to oxidative stress	5	101	0.507	114757	cytoglobin
GO	response to oxidative stress	5	101	0.507	1161	excision repair cross-complementing rodent repair deficiency, complement
GO	response to oxidative stress	5	101	0.507	2628	glycine amidinotransferase (L-arginine:glycine amidinotransferase)
GO	response to oxidative stress	5	101	0.507	2878	glutathione peroxidase 3 (plasma)
GO	response to oxidative stress	5	101	0.507	7171	tropomyosin 4
GO	chloride channel activity	3	58	0.509	200959	gamma-aminobutyric acid (GABA) receptor, rho 3
GO	chloride channel activity	3	58	0.509	2558	gamma-aminobutyric acid (GABA) A receptor, alpha 5
GO	chloride channel activity	3	58	0.509	9635	chloride channel accessory 2
GO	oxidoreductase activity, acting on single	3	58	0.509	283208	prolyl 4-hydroxylase, alpha polypeptide III
GO	oxidoreductase activity, acting on single	3	58	0.509	5264	phytanoyl-CoA 2-hydroxylase
GO	oxidoreductase activity, acting on single	3	58	0.509	57168	aspartate beta-hydroxylase domain containing 2
GO	cell development	1	15	0.51	10052	gap junction protein, gamma 1, 45kDa
GO	focal adhesion assembly	1	15	0.51	10395	deleted in liver cancer 1
GO	polysome	1	15	0.51	124540	musashi homolog 2 (Drosophila)
GO	female gamete generation	1	15	0.51	1730	diaphanous homolog 2 (Drosophila)
GO	sulfate transport	1	15	0.51	1836	solute carrier family 26 (sulfate transporter), member 2
GO	retinal ganglion cell axon guidance	1	15	0.51	2045	EPH receptor A7
GO	homeostasis of number of cells within a	1	15	0.51	2149	coagulation factor II (thrombin) receptor
GO	positive regulation of cytokine secretior	1	15	0.51	23705	cell adhesion molecule 1
GO	oxidoreductase activity, acting on pairec	1	15	0.51	283208	prolyl 4-hydroxylase, alpha polypeptide III
GO	reverse cholesterol transport	1	15	0.51	348	apolipoprotein E
GO	ATPase binding	1	15	0.51	3932	lymphocyte-specific protein tyrosine kinase
GO	actin filament bundle assembly	1	15	0.51	3936	lymphocyte cytosolic protein 1 (L-plastin)
GO	binding of sperm to zona pellucida	1	15	0.51	53340	sperm autoantigenic protein 17
GO	leukocyte migration	1	15	0.51	5420	podocalyxin-like

GO	protein deubiquitination	1	15	0.51	57599	WD repeat domain 48
GO	voltage-gated sodium channel activity	1	15	0.51	6335	sodium channel, voltage-gated, type IX, alpha subunit
GO	cellular metabolic process	1	15	0.51	641	Bloom syndrome, RecQ helicase-like
GO	cellular response to heat	1	15	0.51	64131	xylosyltransferase I
GO	substrate-specific transmembrane trans	1	15	0.51	6518	solute carrier family 2 (facilitated glucose/fructose transporter), member 5
GO	hair follicle development	1	15	0.51	6662	SRY (sex determining region Y)-box 9
GO	chemoattractant activity	1	15	0.51	7857	secretogranin II (chromogranin C)
GO	chondrocyte differentiation	1	15	0.51	81029	wingless-type MMTV integration site family, member 5B
GO	regulation of mitotic cell cycle	1	15	0.51	8872	cell division cycle 123 homolog (S. cerevisiae)
GO	myosin filament	1	15	0.51	9172	myomesin (M-protein) 2, 165kDa
GO	GTPase binding	1	15	0.51	9732	dedicator of cytokinesis 4
GO	oxygen binding	2	37	0.518	114757	cytoglobin
GO	oxygen binding	2	37	0.518	1543	cytochrome P450, family 1, subfamily A, polypeptide 1
GO	protein catabolic process	2	37	0.518	115290	F-box protein 17
GO	protein catabolic process	2	37	0.518	5702	proteasome (prosome, macropain) 26S subunit, ATPase, 3
GO	activation of adenylate cyclase activity	2	37	0.518	2774	guanine nucleotide binding protein (G protein), alpha activating activity pol
GO	activation of adenylate cyclase activity	2	37	0.518	5744	parathyroid hormone-like hormone
GO	protein serine/threonine phosphatase	2	37	0.518	3932	lymphocyte-specific protein tyrosine kinase
GO	protein serine/threonine phosphatase	2	37	0.518	5494	protein phosphatase, Mg2+/Mn2+ dependent, 1A
GO	NADH dehydrogenase (ubiquinone) acti	2	37	0.518	4709	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 3, 12kDa
GO	NADH dehydrogenase (ubiquinone) acti	2	37	0.518	91942	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, assembly factor 2
GO	receptor binding	10	211	0.52	1730	diaphanous homolog 2 (Drosophila)
GO	receptor binding	10	211	0.52	2149	coagulation factor II (thrombin) receptor
GO	receptor binding	10	211	0.52	2150	coagulation factor II (thrombin) receptor-like 1
GO	receptor binding	10	211	0.52	2281	FK506 binding protein 1B, 12.6 kDa
GO	receptor binding	10	211	0.52	23705	cell adhesion molecule 1
GO	receptor binding	10	211	0.52	409	arrestin, beta 2
GO	receptor binding	10	211	0.52	5054	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor t
GO	receptor binding	10	211	0.52	6347	chemokine (C-C motif) ligand 2
GO	receptor binding	10	211	0.52	81029	wingless-type MMTV integration site family, member 5B
GO	receptor binding	10	211	0.52	9542	neuregulin 2
GO	cell migration	3	59	0.521	1000	cadherin 2, type 1, N-cadherin (neuronal)
GO	cell migration	3	59	0.521	115908	collagen triple helix repeat containing 1
GO	cell migration	3	59	0.521	1289	collagen, type V, alpha 1
GO	sarcolemma	3	59	0.521	5588	protein kinase C, theta
GO	sarcolemma	3	59	0.521	6442	sarcoglycan, alpha (50kDa dystrophin-associated glycoprotein)

GO	sarcolemma	3	59	0.521	6444	sarcoglycan, delta (35kDa dystrophin-associated glycoprotein)
GO	Golgi membrane	16	343	0.529	10096	ARP3 actin-related protein 3 homolog (yeast)
GO	Golgi membrane	16	343	0.529	11226	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltr
GO	Golgi membrane	16	343	0.529	11227	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltr
GO	Golgi membrane	16	343	0.529	114805	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltr
GO	Golgi membrane	16	343	0.529	152007	GLI pathogenesis-related 2
GO	Golgi membrane	16	343	0.529	27065	DNA segment on chromosome 4 (unique) 234 expressed sequence
GO	Golgi membrane	16	343	0.529	4893	neuroblastoma RAS viral (v-ras) oncogene homolog
GO	Golgi membrane	16	343	0.529	51062	atlastin GTPase 1
GO	Golgi membrane	16	343	0.529	54756	interleukin 17 receptor D
GO	Golgi membrane	16	343	0.529	57574	membrane-associated ring finger (C3HC4) 4
GO	Golgi membrane	16	343	0.529	64131	xylosyltransferase I
GO	Golgi membrane	16	343	0.529	79623	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltr
GO	Golgi membrane	16	343	0.529	81562	lectin, mannose-binding 2-like
GO	Golgi membrane	16	343	0.529	84752	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 9
GO	Golgi membrane	16	343	0.529	9215	like-glycosyltransferase
GO	Golgi membrane	16	343	0.529	9653	heparan sulfate 2-O-sulfotransferase 1
GO	histone acetyltransferase activity	2	38	0.532	10474	transcriptional adaptor 3
GO	histone acetyltransferase activity	2	38	0.532	8520	histone acetyltransferase 1
GO	positive regulation of gene expression	2	38	0.532	10474	transcriptional adaptor 3
GO	positive regulation of gene expression	2	38	0.532	6662	SRY (sex determining region Y)-box 9
GO	positive regulation of angiogenesis	2	38	0.532	5054	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor t
GO	positive regulation of angiogenesis	2	38	0.532	79805	vasohibin 2
GO	Cajal body	2	38	0.532	55135	WD repeat containing, antisense to TP53
GO	Cajal body	2	38	0.532	79833	gem (nuclear organelle) associated protein 6
GO	specific transcriptional repressor activit	2	38	0.532	7490	Wilms tumor 1
GO	specific transcriptional repressor activit	2	38	0.532	80712	ESX homeobox 1
GO	triglyceride lipase activity	1	16	0.533	13	arylacetamide deacetylase (esterase)
GO	intrinsic to endoplasmic reticulum mem	1	16	0.533	2135	exostoses (multiple)-like 2
GO	positive regulation of vasoconstriction	1	16	0.533	2149	coagulation factor II (thrombin) receptor
GO	smoothened signaling pathway	1	16	0.533	2736	GLI family zinc finger 2
GO	glutathione metabolic process	1	16	0.533	2878	glutathione peroxidase 3 (plasma)
GO	hydrogen peroxide catabolic process	1	16	0.533	2878	glutathione peroxidase 3 (plasma)
GO	positive regulation of mitotic cell cycle	1	16	0.533	332	baculoviral IAP repeat-containing 5
GO	response to cocaine	1	16	0.533	5021	oxytocin receptor
GO	negative regulation of insulin secretion	1	16	0.533	5140	phosphodiesterase 3B, cGMP-inhibited

GO	mitochondrial proton-transporting ATP	1	16	0.533	516	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit C1 (subu
GO	cAMP-dependent protein kinase regulat	1	16	0.533	53340	sperm autoantigenic protein 17
GO	vitamin D receptor binding	1	16	0.533	5469	mediator complex subunit 1
GO	phosphatidylinositol-3,4,5-trisphosphat	1	16	0.533	55803	ArfGAP with dual PH domains 2
GO	response to cadmium ion	1	16	0.533	57678	glycerol-3-phosphate acyltransferase, mitochondrial
GO	response to nutrient levels	1	16	0.533	57678	glycerol-3-phosphate acyltransferase, mitochondrial
GO	translation regulator activity	1	16	0.533	65003	mitochondrial ribosomal protein L11
GO	ion transmembrane transporter activity	1	16	0.533	6580	solute carrier family 22 (organic cation transporter), member 1
GO	positive regulation of endothelial cell m	1	16	0.533	659	bone morphogenetic protein receptor, type II (serine/threonine kinase)
GO	cartilage condensation	1	16	0.533	6662	SRY (sex determining region Y)-box 9
GO	receptor complex	1	16	0.533	7046	transforming growth factor, beta receptor 1
GO	C-C chemokine receptor activity	1	16	0.533	729230	chemokine (C-C motif) receptor 2
GO	membrane depolarization	1	16	0.533	773	calcium channel, voltage-dependent, P/Q type, alpha 1A subunit
GO	protein secretion	1	16	0.533	7857	secretogranin II (chromogranin C)
GO	mannose binding	1	16	0.533	81562	lectin, mannose-binding 2-like
GO	response to light stimulus	1	16	0.533	8533	COP9 constitutive photomorphogenic homolog subunit 3 (Arabidopsis)
GO	beta-catenin binding	2	39	0.546	1000	cadherin 2, type 1, N-cadherin (neuronal)
GO	beta-catenin binding	2	39	0.546	6299	sal-like 1 (Drosophila)
GO	G-protein signaling, coupled to cyclic nu	2	39	0.546	4158	melanocortin 2 receptor (adrenocorticotropic hormone)
GO	G-protein signaling, coupled to cyclic nu	2	39	0.546	6347	chemokine (C-C motif) ligand 2
GO	transcription cofactor activity	2	39	0.546	5469	mediator complex subunit 1
GO	transcription cofactor activity	2	39	0.546	7029	transcription factor Dp-2 (E2F dimerization partner 2)
GO	microtubule cytoskeleton organization	2	39	0.546	8409	ubiquitously-expressed transcript
GO	microtubule cytoskeleton organization	2	39	0.546	9053	microtubule-associated protein 7
GO	response to peptide hormone stimulus	3	62	0.554	2628	glycine amidinotransferase (L-arginine:glycine amidinotransferase)
GO	response to peptide hormone stimulus	3	62	0.554	5021	oxytocin receptor
GO	response to peptide hormone stimulus	3	62	0.554	8835	suppressor of cytokine signaling 2
GO	peroxidase activity	1	17	0.555	114757	cytoglobin
GO	glutathione transferase activity	1	17	0.555	221357	glutathione S-transferase alpha 5
GO	sarcoplasmic reticulum membrane	1	17	0.555	2281	FK506 binding protein 1B, 12.6 kDa
GO	intracellular transport	1	17	0.555	348	apolipoprotein E
GO	embryonic pattern specification	1	17	0.555	3975	LIM homeobox 1
GO	rough endoplasmic reticulum	1	17	0.555	411	arylsulfatase B
GO	regulation of angiogenesis	1	17	0.555	4763	neurofibromin 1
GO	midbrain development	1	17	0.555	5015	orthodenticle homeobox 2
GO	social behavior	1	17	0.555	5021	oxytocin receptor

GO	positive regulation of calcium-mediated	1	17	0.555	5026	purinergic receptor P2X, ligand-gated ion channel, 5
GO	mitochondrial small ribosomal subunit	1	17	0.555	51023	mitochondrial ribosomal protein S18C
GO	2 iron, 2 sulfur cluster binding	1	17	0.555	51218	glutaredoxin 5
GO	histone deacetylation	1	17	0.555	5245	prohibitin
GO	embryonic hindlimb morphogenesis	1	17	0.555	5469	mediator complex subunit 1
GO	mitochondrial ribosome	1	17	0.555	65003	mitochondrial ribosomal protein L11
GO	regulation of pH	1	17	0.555	6549	solute carrier family 9 (sodium/hydrogen exchanger), member 2
GO	small nuclear ribonucleoprotein comple	1	17	0.555	6637	small nuclear ribonucleoprotein polypeptide G
GO	epithelial to mesenchymal transition	1	17	0.555	6662	SRY (sex determining region Y)-box 9
GO	actin filament capping	1	17	0.555	6711	spectrin, beta, non-erythrocytic 1
GO	nuclear body	1	17	0.555	79833	gem (nuclear organelle) associated protein 6
GO	cis-Golgi network	1	17	0.555	79929	MAP6 domain containing 1
GO	spindle assembly	1	17	0.555	93323	HAUS augmin-like complex, subunit 8
GO	carbohydrate biosynthetic process	1	17	0.555	9653	heparan sulfate 2-O-sulfotransferase 1
GO	sodium ion transport	6	129	0.557	201780	solute carrier family 10 (sodium/bile acid cotransporter family), member 4
GO	sodium ion transport	6	129	0.557	6335	sodium channel, voltage-gated, type IX, alpha subunit
GO	sodium ion transport	6	129	0.557	6527	solute carrier family 5 (low affinity glucose cotransporter), member 4
GO	sodium ion transport	6	129	0.557	6546	solute carrier family 8 (sodium/calcium exchanger), member 1
GO	sodium ion transport	6	129	0.557	6549	solute carrier family 9 (sodium/hydrogen exchanger), member 2
GO	sodium ion transport	6	129	0.557	9497	solute carrier family 4, sodium bicarbonate cotransporter, member 7
GO	receptor-mediated endocytosis	2	40	0.56	348	apolipoprotein E
GO	receptor-mediated endocytosis	2	40	0.56	9260	PDZ and LIM domain 7 (enigma)
GO	cell redox homeostasis	3	63	0.565	10190	thioredoxin domain containing 9
GO	cell redox homeostasis	3	63	0.565	10539	glutaredoxin 3
GO	cell redox homeostasis	3	63	0.565	51218	glutaredoxin 5
GO	glycolysis	2	41	0.574	2027	enolase 3 (beta, muscle)
GO	glycolysis	2	41	0.574	669	2,3-bisphosphoglycerate mutase
GO	peroxisomal membrane	2	41	0.574	23305	acyl-CoA synthetase long-chain family member 6
GO	peroxisomal membrane	2	41	0.574	255027	MPV17 mitochondrial membrane protein-like
GO	negative regulation of cell cycle	2	41	0.574	3248	hydroxyprostaglandin dehydrogenase 15-(NAD)
GO	negative regulation of cell cycle	2	41	0.574	3624	inhibin, beta A
GO	cholesterol homeostasis	2	41	0.574	348	apolipoprotein E
GO	cholesterol homeostasis	2	41	0.574	7840	Alstrom syndrome 1
GO	neuron projection development	2	41	0.574	3516	recombination signal binding protein for immunoglobulin kappa J region
GO	neuron projection development	2	41	0.574	4734	neural precursor cell expressed, developmentally down-regulated 4
GO	ER to Golgi vesicle-mediated transport	2	41	0.574	6683	spastin

GO	ER to Golgi vesicle-mediated transport	2	41	0.574	81562	lectin, mannose-binding 2-like
GO	ribosome binding	1	18	0.575	1984	eukaryotic translation initiation factor 5A
GO	lipoprotein metabolic process	1	18	0.575	341	apolipoprotein C-I
GO	MHC class I protein complex	1	18	0.575	353091	retinoic acid early transcript 1G
GO	regulation of insulin secretion	1	18	0.575	3952	leptin
GO	protein import into nucleus, translocati	1	18	0.575	406	aryl hydrocarbon receptor nuclear translocator-like
GO	protein ubiquitination involved in ubiqu	1	18	0.575	4734	neural precursor cell expressed, developmentally down-regulated 4
GO	endocrine pancreas development	1	18	0.575	5140	phosphodiesterase 3B, cGMP-inhibited
GO	cellular process	1	18	0.575	5184	peptidase D
GO	embryonic placenta development	1	18	0.575	5469	mediator complex subunit 1
GO	WW domain binding	1	18	0.575	56937	prostate transmembrane protein, androgen induced 1
GO	phosphatidylinositol binding	1	18	0.575	57590	WD repeat and FYVE domain containing 1
GO	transmembrane receptor protein tyrosi	1	18	0.575	5795	protein tyrosine phosphatase, receptor type, J
GO	DNA fragmentation involved in apoptot	1	18	0.575	581	BCL2-associated X protein
GO	inner ear development	1	18	0.575	6657	SRY (sex determining region Y)-box 2
GO	cortical cytoskeleton	1	18	0.575	6711	spectrin, beta, non-erythrocytic 1
GO	peptidyl-threonine phosphorylation	1	18	0.575	7046	transforming growth factor, beta receptor 1
GO	heme biosynthetic process	1	18	0.575	7389	uroporphyrinogen decarboxylase
GO	negative regulation of translation	1	18	0.575	7490	Wilms tumor 1
GO	cornified envelope	1	18	0.575	84518	cornifelin
GO	establishment or maintenance of cell p	1	18	0.575	9053	microtubule-associated protein 7
GO	anion transport	1	18	0.575	9497	solute carrier family 4, sodium bicarbonate cotransporter, member 7
GO	transcription initiation from RNA polym	3	64	0.576	2965	general transcription factor IIH, polypeptide 1, 62kDa
GO	transcription initiation from RNA polym	3	64	0.576	5440	polymerase (RNA) II (DNA directed) polypeptide K, 7.0kDa
GO	transcription initiation from RNA polym	3	64	0.576	5469	mediator complex subunit 1
GO	patterning of blood vessels	1	19	0.595	10672	guanine nucleotide binding protein (G protein), alpha 13
GO	protein amino acid O-linked glycosylati	1	19	0.595	11226	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminylt
GO	cadherin binding	1	19	0.595	1496	catenin (cadherin-associated protein), alpha 2
GO	negative regulation of cell differentiatio	1	19	0.595	182	jagged 1 (Alagille syndrome)
GO	leukotriene biosynthetic process	1	19	0.595	241	arachidonate 5-lipoxygenase-activating protein
GO	RNA metabolic process	1	19	0.595	26019	UPF2 regulator of nonsense transcripts homolog (yeast)
GO	lipid transporter activity	1	19	0.595	348	apolipoprotein E
GO	phosphoprotein binding	1	19	0.595	5140	phosphodiesterase 3B, cGMP-inhibited
GO	regulation of neuron differentiation	1	19	0.595	53637	sphingosine-1-phosphate receptor 5
GO	insulin-like growth factor binding	1	19	0.595	5654	HtrA serine peptidase 1
GO	neutrophil chemotaxis	1	19	0.595	6347	chemokine (C-C motif) ligand 2

GO	telomere maintenance	1	19	0.595	641	Bloom syndrome, RecQ helicase-like
GO	T-tubule	1	19	0.595	6546	solute carrier family 8 (sodium/calcium exchanger), member 1
GO	chemokine receptor activity	1	19	0.595	729230	chemokine (C-C motif) receptor 2
GO	regulation of signal transduction	1	19	0.595	8835	suppressor of cytokine signaling 2
GO	inner ear morphogenesis	2	43	0.6	55084	sine oculis binding protein homolog (Drosophila)
GO	inner ear morphogenesis	2	43	0.6	6657	SRY (sex determining region Y)-box 2
GO	phosphotransferase activity, alcohol grc	1	20	0.614	1716	deoxyguanosine kinase
GO	desmosome	1	20	0.614	1830	desmoglein 3 (pemphigus vulgaris antigen)
GO	translation elongation factor activity	1	20	0.614	1984	eukaryotic translation initiation factor 5A
GO	phosphorylation	1	20	0.614	2045	EPH receptor A7
GO	response to steroid hormone stimulus	1	20	0.614	23305	acyl-CoA synthetase long-chain family member 6
GO	proteasomal ubiquitin-dependent prote	1	20	0.614	409	arrestin, beta 2
GO	ubiquitin binding	1	20	0.614	4734	neural precursor cell expressed, developmentally down-regulated 4
GO	hydrogen ion transmembrane transport	1	20	0.614	516	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit C1 (subu
GO	positive regulation of bone mineralizati	1	20	0.614	659	bone morphogenetic protein receptor, type II (serine/threonine kinase)
GO	response to radiation	1	20	0.614	6591	snail homolog 2 (Drosophila)
GO	positive regulation of cell adhesion	1	20	0.614	7168	tropomyosin 1 (alpha)
GO	clathrin adaptor complex	1	20	0.614	8905	adaptor-related protein complex 1, sigma 2 subunit
GO	phosphate metabolic process	1	20	0.614	97	acylphosphatase 1, erythrocyte (common) type
GO	aromatase activity	1	21	0.632	1543	cytochrome P450, family 1, subfamily A, polypeptide 1
GO	translation factor activity, nucleic acid b	1	21	0.632	1983	eukaryotic translation initiation factor 5
GO	transferase activity, transferring hexosy	1	21	0.632	2135	exostoses (multiple)-like 2
GO	branching morphogenesis of a tube	1	21	0.632	2736	GLI family zinc finger 2
GO	regulation of multicellular organism gro	1	21	0.632	27429	HtrA serine peptidase 2
GO	negative regulation of caspase activity	1	21	0.632	332	baculoviral IAP repeat-containing 5
GO	gastrulation with mouth forming seconc	1	21	0.632	3975	LIM homeobox 1
GO	positive regulation of inflammatory resp	1	21	0.632	5054	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor ty
GO	dephosphorylation	1	21	0.632	5494	protein phosphatase, Mg2+/Mn2+ dependent, 1A
GO	negative regulation of BMP signaling pa	1	21	0.632	5654	HtrA serine peptidase 1
GO	defense response to virus	1	21	0.632	57678	glycerol-3-phosphate acyltransferase, mitochondrial
GO	release of cytochrome c from mitochon	1	21	0.632	581	BCL2-associated X protein
GO	p53 binding	1	21	0.632	641	Bloom syndrome, RecQ helicase-like
GO	negative regulation of gene-specific trar	1	21	0.632	7490	Wilms tumor 1
GO	positive regulation of mesenchymal cell	1	21	0.632	8626	tumor protein p63
GO	integral to membrane	177	3857	0.989	1000	cadherin 2, type 1, N-cadherin (neuronal)
GO	integral to membrane	177	3857	0.989	1E+08	transmembrane protein 194B

GO	integral to membrane	177	3857	0.989	10052	gap junction protein, gamma 1, 45kDa
GO	integral to membrane	177	3857	0.989	1008	cadherin 10, type 2 (T2-cadherin)
GO	integral to membrane	177	3857	0.989	10457	glycoprotein (transmembrane) nmb
GO	integral to membrane	177	3857	0.989	1047	calmegin
GO	integral to membrane	177	3857	0.989	10683	delta-like 3 (Drosophila)
GO	integral to membrane	177	3857	0.989	11010	GLI pathogenesis-related 1
GO	integral to membrane	177	3857	0.989	11149	blood vessel epicardial substance
GO	integral to membrane	177	3857	0.989	11226	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltr
GO	integral to membrane	177	3857	0.989	11227	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltr
GO	integral to membrane	177	3857	0.989	112616	CKLF-like MARVEL transmembrane domain containing 7
GO	integral to membrane	177	3857	0.989	1136	cholinergic receptor, nicotinic, alpha 3
GO	integral to membrane	177	3857	0.989	1138	cholinergic receptor, nicotinic, alpha 5
GO	integral to membrane	177	3857	0.989	114805	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltr
GO	integral to membrane	177	3857	0.989	119749	olfactory receptor, family 4, subfamily C, member 46
GO	integral to membrane	177	3857	0.989	120114	FAT tumor suppressor homolog 3 (Drosophila)
GO	integral to membrane	177	3857	0.989	123920	CKLF-like MARVEL transmembrane domain containing 3
GO	integral to membrane	177	3857	0.989	125962	olfactory receptor, family 7, subfamily G, member 1
GO	integral to membrane	177	3857	0.989	127534	gap junction protein, beta 4, 30.3kDa
GO	integral to membrane	177	3857	0.989	127670	transmembrane epididymal protein 1
GO	integral to membrane	177	3857	0.989	128414	Na+/K+ transporting ATPase interacting 4
GO	integral to membrane	177	3857	0.989	13	arylacetamide deacetylase (esterase)
GO	integral to membrane	177	3857	0.989	130507	ubiquitin protein ligase E3 component n-recognin 3 (putative)
GO	integral to membrane	177	3857	0.989	131450	CD200 receptor 1
GO	integral to membrane	177	3857	0.989	134145	family with sequence similarity 173, member B
GO	integral to membrane	177	3857	0.989	134285	transmembrane protein 171
GO	integral to membrane	177	3857	0.989	138255	chromosome 9 open reading frame 135
GO	integral to membrane	177	3857	0.989	144448	tetraspanin 19
GO	integral to membrane	177	3857	0.989	145173	beta 1,3-galactosyltransferase-like
GO	integral to membrane	177	3857	0.989	147645	V-set and immunoglobulin domain containing 10 like
GO	integral to membrane	177	3857	0.989	151188	ADP-ribosylation-like factor 6 interacting protein 6
GO	integral to membrane	177	3857	0.989	151194	family with sequence similarity 119, member A
GO	integral to membrane	177	3857	0.989	154215	Na+/K+ transporting ATPase interacting 2
GO	integral to membrane	177	3857	0.989	157753	transmembrane protein 74
GO	integral to membrane	177	3857	0.989	162494	rhomboid, veinlet-like 3 (Drosophila)
GO	integral to membrane	177	3857	0.989	1733	deiodinase, iodothyronine, type I
GO	integral to membrane	177	3857	0.989	1830	desmoglein 3 (pemphigus vulgaris antigen)

GO	integral to membrane	177	3857	0.989	200959	gamma-aminobutyric acid (GABA) receptor, rho 3
GO	integral to membrane	177	3857	0.989	201780	solute carrier family 10 (sodium/bile acid cotransporter family), member 4
GO	integral to membrane	177	3857	0.989	205251	non-protein coding RNA 116
GO	integral to membrane	177	3857	0.989	2135	exostoses (multiple)-like 2
GO	integral to membrane	177	3857	0.989	221687	ring finger protein 182
GO	integral to membrane	177	3857	0.989	222611	G protein-coupled receptor 111
GO	integral to membrane	177	3857	0.989	22801	integrin, alpha 11
GO	integral to membrane	177	3857	0.989	23245	astrotactin 2
GO	integral to membrane	177	3857	0.989	23305	acyl-CoA synthetase long-chain family member 6
GO	integral to membrane	177	3857	0.989	23432	G protein-coupled receptor 161
GO	integral to membrane	177	3857	0.989	23562	claudin 14
GO	integral to membrane	177	3857	0.989	23705	cell adhesion molecule 1
GO	integral to membrane	177	3857	0.989	241	arachidonate 5-lipoxygenase-activating protein
GO	integral to membrane	177	3857	0.989	253559	cell adhesion molecule 2
GO	integral to membrane	177	3857	0.989	255027	MPV17 mitochondrial membrane protein-like
GO	integral to membrane	177	3857	0.989	25758	chromosome 11 open reading frame 41
GO	integral to membrane	177	3857	0.989	25789	transmembrane protein 59-like
GO	integral to membrane	177	3857	0.989	25817	family with sequence similarity 19 (chemokine (C-C motif)-like), member A
GO	integral to membrane	177	3857	0.989	26032	sushi domain containing 5
GO	integral to membrane	177	3857	0.989	26154	ATP-binding cassette, sub-family A (ABC1), member 12
GO	integral to membrane	177	3857	0.989	27065	DNA segment on chromosome 4 (unique) 234 expressed sequence
GO	integral to membrane	177	3857	0.989	27429	HtrA serine peptidase 2
GO	integral to membrane	177	3857	0.989	282770	olfactory receptor, family 10, subfamily AG, member 1
GO	integral to membrane	177	3857	0.989	283111	olfactory receptor, family 51, subfamily V, member 1
GO	integral to membrane	177	3857	0.989	284415	V-set and transmembrane domain containing 1
GO	integral to membrane	177	3857	0.989	284417	transmembrane protein 150B
GO	integral to membrane	177	3857	0.989	2850	G protein-coupled receptor 27
GO	integral to membrane	177	3857	0.989	285659	olfactory receptor, family 2, subfamily V, member 2
GO	integral to membrane	177	3857	0.989	285761	discoidin, CUB and LCCL domain containing 1
GO	integral to membrane	177	3857	0.989	286234	chromosome 9 open reading frame 79
GO	integral to membrane	177	3857	0.989	2906	glutamate receptor, ionotropic, N-methyl D-aspartate 2D
GO	integral to membrane	177	3857	0.989	29940	dermatan sulfate epimerase
GO	integral to membrane	177	3857	0.989	3037	hyaluronan synthase 2
GO	integral to membrane	177	3857	0.989	340273	ATP-binding cassette, sub-family B (MDR/TAP), member 5
GO	integral to membrane	177	3857	0.989	344805	transmembrane protease, serine 7
GO	integral to membrane	177	3857	0.989	344838	progestin and adipoQ receptor family member IX

GO	integral to membrane	177	3857	0.989	347902	adhesion molecule with Ig-like domain 2
GO	integral to membrane	177	3857	0.989	348938	NIPA-like domain containing 4
GO	integral to membrane	177	3857	0.989	353091	retinoic acid early transcript 1G
GO	integral to membrane	177	3857	0.989	355	Fas (TNF receptor superfamily, member 6)
GO	integral to membrane	177	3857	0.989	3694	integrin, beta 6
GO	integral to membrane	177	3857	0.989	3754	potassium voltage-gated channel, subfamily F, member 1
GO	integral to membrane	177	3857	0.989	3756	potassium voltage-gated channel, subfamily H (eag-related), member 1
GO	integral to membrane	177	3857	0.989	3763	potassium inwardly-rectifying channel, subfamily J, member 6
GO	integral to membrane	177	3857	0.989	3778	potassium large conductance calcium-activated channel, subfamily M, alph
GO	integral to membrane	177	3857	0.989	387700	solute carrier family 16, member 12 (monocarboxylic acid transporter 12)
GO	integral to membrane	177	3857	0.989	388394	reprimo-like
GO	integral to membrane	177	3857	0.989	390061	olfactory receptor, family 51, subfamily Q, member 1
GO	integral to membrane	177	3857	0.989	391114	olfactory receptor, family 6, subfamily K, member 3
GO	integral to membrane	177	3857	0.989	400451	family with sequence similarity 174, member B
GO	integral to membrane	177	3857	0.989	4709	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 3, 12kDa
GO	integral to membrane	177	3857	0.989	479	ATPase, H+/K+ transporting, nongastric, alpha polypeptide
GO	integral to membrane	177	3857	0.989	5101	protocadherin 9
GO	integral to membrane	177	3857	0.989	51062	atlastin GTPase 1
GO	integral to membrane	177	3857	0.989	51136	ring finger protein, transmembrane 1
GO	integral to membrane	177	3857	0.989	51308	receptor accessory protein 2
GO	integral to membrane	177	3857	0.989	5140	phosphodiesterase 3B, cGMP-inhibited
GO	integral to membrane	177	3857	0.989	516	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit C1 (subu
GO	integral to membrane	177	3857	0.989	51768	transmembrane 7 superfamily member 3
GO	integral to membrane	177	3857	0.989	53637	sphingosine-1-phosphate receptor 5
GO	integral to membrane	177	3857	0.989	54210	triggering receptor expressed on myeloid cells 1
GO	integral to membrane	177	3857	0.989	54733	solute carrier family 35, member F2
GO	integral to membrane	177	3857	0.989	54756	interleukin 17 receptor D
GO	integral to membrane	177	3857	0.989	54822	transient receptor potential cation channel, subfamily M, member 7
GO	integral to membrane	177	3857	0.989	55016	membrane-associated ring finger (C3HC4) 1
GO	integral to membrane	177	3857	0.989	55028	chromosome 17 open reading frame 80
GO	integral to membrane	177	3857	0.989	55117	solute carrier family 6 (neutral amino acid transporter), member 15
GO	integral to membrane	177	3857	0.989	55244	solute carrier family 47, member 1
GO	integral to membrane	177	3857	0.989	55283	mucolipin 3
GO	integral to membrane	177	3857	0.989	554279	chromosome 1 open reading frame 98
GO	integral to membrane	177	3857	0.989	56104	protocadherin gamma subfamily B, 1
GO	integral to membrane	177	3857	0.989	56126	protocadherin beta 10

GO	integral to membrane	177	3857	0.989	56133	protocadherin beta 2
GO	integral to membrane	177	3857	0.989	56241	sushi domain containing 2
GO	integral to membrane	177	3857	0.989	56479	potassium voltage-gated channel, KQT-like subfamily, member 5
GO	integral to membrane	177	3857	0.989	56937	prostate transmembrane protein, androgen induced 1
GO	integral to membrane	177	3857	0.989	57168	aspartate beta-hydroxylase domain containing 2
GO	integral to membrane	177	3857	0.989	57484	ring finger protein 150
GO	integral to membrane	177	3857	0.989	57574	membrane-associated ring finger (C3HC4) 4
GO	integral to membrane	177	3857	0.989	57575	protocadherin 10
GO	integral to membrane	177	3857	0.989	57650	KIAA1524
GO	integral to membrane	177	3857	0.989	57678	glycerol-3-phosphate acyltransferase, mitochondrial
GO	integral to membrane	177	3857	0.989	581	BCL2-associated X protein
GO	integral to membrane	177	3857	0.989	60386	solute carrier family 25 (mitochondrial thiamine pyrophosphate carrier), m
GO	integral to membrane	177	3857	0.989	60492	coiled-coil domain containing 90B
GO	integral to membrane	177	3857	0.989	6335	sodium channel, voltage-gated, type IX, alpha subunit
GO	integral to membrane	177	3857	0.989	64131	xylosyltransferase I
GO	integral to membrane	177	3857	0.989	64208	popeye domain containing 3
GO	integral to membrane	177	3857	0.989	64417	chromosome 5 open reading frame 28
GO	integral to membrane	177	3857	0.989	6442	sarcoglycan, alpha (50kDa dystrophin-associated glycoprotein)
GO	integral to membrane	177	3857	0.989	6444	sarcoglycan, delta (35kDa dystrophin-associated glycoprotein)
GO	integral to membrane	177	3857	0.989	64747	major facilitator superfamily domain containing 1
GO	integral to membrane	177	3857	0.989	65055	receptor accessory protein 1
GO	integral to membrane	177	3857	0.989	65062	amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 4
GO	integral to membrane	177	3857	0.989	6518	solute carrier family 2 (facilitated glucose/fructose transporter), member 5
GO	integral to membrane	177	3857	0.989	6527	solute carrier family 5 (low affinity glucose cotransporter), member 4
GO	integral to membrane	177	3857	0.989	6549	solute carrier family 9 (sodium/hydrogen exchanger), member 2
GO	integral to membrane	177	3857	0.989	66000	transmembrane protein 108
GO	integral to membrane	177	3857	0.989	6683	spastin
GO	integral to membrane	177	3857	0.989	6785	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like
GO	integral to membrane	177	3857	0.989	6833	ATP-binding cassette, sub-family C (CFTR/MRP), member 8
GO	integral to membrane	177	3857	0.989	7046	transforming growth factor, beta receptor 1
GO	integral to membrane	177	3857	0.989	729025	solute carrier family 15, member 5
GO	integral to membrane	177	3857	0.989	729230	chemokine (C-C motif) receptor 2
GO	integral to membrane	177	3857	0.989	7348	uroplakin 1B
GO	integral to membrane	177	3857	0.989	773	calcium channel, voltage-dependent, P/Q type, alpha 1A subunit
GO	integral to membrane	177	3857	0.989	79071	ELOVL family member 6, elongation of long chain fatty acids (FEN1/Elo2, SU
GO	integral to membrane	177	3857	0.989	79135	apolipoprotein O

GO	integral to membrane	177	3857	0.989	79623	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltr
GO	integral to membrane	177	3857	0.989	79669	chromosome 3 open reading frame 52
GO	integral to membrane	177	3857	0.989	79993	ELOVL family member 7, elongation of long chain fatty acids (yeast)
GO	integral to membrane	177	3857	0.989	80342	TRAF3 interacting protein 3
GO	integral to membrane	177	3857	0.989	81035	collectin sub-family member 12
GO	integral to membrane	177	3857	0.989	81562	lectin, mannose-binding 2-like
GO	integral to membrane	177	3857	0.989	8325	frizzled homolog 8 (Drosophila)
GO	integral to membrane	177	3857	0.989	83700	junctional adhesion molecule 3
GO	integral to membrane	177	3857	0.989	83930	STARD3 N-terminal like
GO	integral to membrane	177	3857	0.989	84168	anthrax toxin receptor 1
GO	integral to membrane	177	3857	0.989	84189	SLIT and NTRK-like family, member 6
GO	integral to membrane	177	3857	0.989	84230	leucine rich repeat containing 8 family, member C
GO	integral to membrane	177	3857	0.989	84620	ST6 beta-galactosamide alpha-2,6-sialyltranferase 2
GO	integral to membrane	177	3857	0.989	84752	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 9
GO	integral to membrane	177	3857	0.989	84769	MPV17 mitochondrial membrane protein-like 2
GO	integral to membrane	177	3857	0.989	84910	transmembrane protein 87B
GO	integral to membrane	177	3857	0.989	85027	chromosome 5 open reading frame 62
GO	integral to membrane	177	3857	0.989	85455	dispatched homolog 2 (Drosophila)
GO	integral to membrane	177	3857	0.989	8604	solute carrier family 25 (mitochondrial carrier, Aralar), member 12
GO	integral to membrane	177	3857	0.989	8728	ADAM metallopeptidase domain 19 (meltrin beta)
GO	integral to membrane	177	3857	0.989	8747	ADAM metallopeptidase domain 21
GO	integral to membrane	177	3857	0.989	8788	delta-like 1 homolog (Drosophila)
GO	integral to membrane	177	3857	0.989	90701	SEC11 homolog C (S. cerevisiae)
GO	integral to membrane	177	3857	0.989	9076	claudin 1
GO	integral to membrane	177	3857	0.989	90871	chromosome 9 open reading frame 123
GO	integral to membrane	177	3857	0.989	91584	plexin A4
GO	integral to membrane	177	3857	0.989	9215	like-glycosyltransferase
GO	integral to membrane	177	3857	0.989	92737	delta/notch-like EGF repeat containing
GO	integral to membrane	177	3857	0.989	9497	solute carrier family 4, sodium bicarbonate cotransporter, member 7
GO	integral to membrane	177	3857	0.989	9542	neuregulin 2
GO	integral to membrane	177	3857	0.989	9653	heparan sulfate 2-O-sulfotransferase 1
GO	protein kinase binding	3	113	0.989	1000	cadherin 2, type 1, N-cadherin (neuronal)
GO	protein kinase binding	3	113	0.989	3932	lymphocyte-specific protein tyrosine kinase
GO	protein kinase binding	3	113	0.989	7137	troponin I type 3 (cardiac)
GO	protein phosphatase binding	1	25	0.989	1000	cadherin 2, type 1, N-cadherin (neuronal)
GO	membrane	161	3643	0.989	10000	v-akt murine thymoma viral oncogene homolog 3 (protein kinase B, gamma

GO	membrane	161	3643	0.989	1E+08	transmembrane protein 194B
GO	membrane	161	3643	0.989	10254	signal transducing adaptor molecule (SH3 domain and ITAM motif) 2
GO	membrane	161	3643	0.989	10391	coronin, actin binding protein, 2B
GO	membrane	161	3643	0.989	10457	glycoprotein (transmembrane) nmb
GO	membrane	161	3643	0.989	1047	calmegin
GO	membrane	161	3643	0.989	10512	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (
GO	membrane	161	3643	0.989	10683	delta-like 3 (Drosophila)
GO	membrane	161	3643	0.989	11010	GLI pathogenesis-related 1
GO	membrane	161	3643	0.989	11154	adaptor-related protein complex 4, sigma 1 subunit
GO	membrane	161	3643	0.989	11226	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltr
GO	membrane	161	3643	0.989	11227	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltr
GO	membrane	161	3643	0.989	11259	filamin A interacting protein 1-like
GO	membrane	161	3643	0.989	112616	CKLF-like MARVEL transmembrane domain containing 7
GO	membrane	161	3643	0.989	114805	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltr
GO	membrane	161	3643	0.989	123920	CKLF-like MARVEL transmembrane domain containing 3
GO	membrane	161	3643	0.989	127670	transmembrane epididymal protein 1
GO	membrane	161	3643	0.989	13	arylacetamide deacetylase (esterase)
GO	membrane	161	3643	0.989	130507	ubiquitin protein ligase E3 component n-recognin 3 (putative)
GO	membrane	161	3643	0.989	132724	transmembrane protease, serine 11B
GO	membrane	161	3643	0.989	134145	family with sequence similarity 173, member B
GO	membrane	161	3643	0.989	134285	transmembrane protein 171
GO	membrane	161	3643	0.989	1379	complement component (3b/4b) receptor 1-like
GO	membrane	161	3643	0.989	138255	chromosome 9 open reading frame 135
GO	membrane	161	3643	0.989	144448	tetraspanin 19
GO	membrane	161	3643	0.989	145173	beta 1,3-galactosyltransferase-like
GO	membrane	161	3643	0.989	147645	V-set and immunoglobulin domain containing 10 like
GO	membrane	161	3643	0.989	151188	ADP-ribosylation-like factor 6 interacting protein 6
GO	membrane	161	3643	0.989	151194	family with sequence similarity 119, member A
GO	membrane	161	3643	0.989	152007	GLI pathogenesis-related 2
GO	membrane	161	3643	0.989	1543	cytochrome P450, family 1, subfamily A, polypeptide 1
GO	membrane	161	3643	0.989	157753	transmembrane protein 74
GO	membrane	161	3643	0.989	162494	rhomboid, veinlet-like 3 (Drosophila)
GO	membrane	161	3643	0.989	166336	prickle homolog 2 (Drosophila)
GO	membrane	161	3643	0.989	182	jagged 1 (Alagille syndrome)
GO	membrane	161	3643	0.989	1836	solute carrier family 26 (sulfate transporter), member 2
GO	membrane	161	3643	0.989	1984	eukaryotic translation initiation factor 5A

GO	membrane	161	3643	0.989	201780	solute carrier family 10 (sodium/bile acid cotransporter family), member 4
GO	membrane	161	3643	0.989	205251	non-protein coding RNA 116
GO	membrane	161	3643	0.989	2135	exostoses (multiple)-like 2
GO	membrane	161	3643	0.989	221687	ring finger protein 182
GO	membrane	161	3643	0.989	22801	integrin, alpha 11
GO	membrane	161	3643	0.989	23138	Nedd4 binding protein 3
GO	membrane	161	3643	0.989	23245	astrotactin 2
GO	membrane	161	3643	0.989	23768	fibronectin leucine rich transmembrane protein 2
GO	membrane	161	3643	0.989	241	arachidonate 5-lipoxygenase-activating protein
GO	membrane	161	3643	0.989	253559	cell adhesion molecule 2
GO	membrane	161	3643	0.989	255027	MPV17 mitochondrial membrane protein-like
GO	membrane	161	3643	0.989	25758	chromosome 11 open reading frame 41
GO	membrane	161	3643	0.989	25789	transmembrane protein 59-like
GO	membrane	161	3643	0.989	25817	family with sequence similarity 19 (chemokine (C-C motif)-like), member A
GO	membrane	161	3643	0.989	25953	paroxysmal nonkinesigenic dyskinesia
GO	membrane	161	3643	0.989	26032	sushi domain containing 5
GO	membrane	161	3643	0.989	26154	ATP-binding cassette, sub-family A (ABC1), member 12
GO	membrane	161	3643	0.989	2628	glycine amidinotransferase (L-arginine:glycine amidinotransferase)
GO	membrane	161	3643	0.989	26519	translocase of inner mitochondrial membrane 10 homolog (yeast)
GO	membrane	161	3643	0.989	26521	translocase of inner mitochondrial membrane 8 homolog B (yeast)
GO	membrane	161	3643	0.989	27065	DNA segment on chromosome 4 (unique) 234 expressed sequence
GO	membrane	161	3643	0.989	27429	HtrA serine peptidase 2
GO	membrane	161	3643	0.989	27445	piccolo (presynaptic cytomatrix protein)
GO	membrane	161	3643	0.989	283455	kinase suppressor of ras 2
GO	membrane	161	3643	0.989	283518	potassium channel regulator
GO	membrane	161	3643	0.989	284415	V-set and transmembrane domain containing 1
GO	membrane	161	3643	0.989	284417	transmembrane protein 150B
GO	membrane	161	3643	0.989	285761	discoidin, CUB and LCCL domain containing 1
GO	membrane	161	3643	0.989	286234	chromosome 9 open reading frame 79
GO	membrane	161	3643	0.989	29842	transcription factor CP2-like 1
GO	membrane	161	3643	0.989	29940	dermatan sulfate epimerase
GO	membrane	161	3643	0.989	3037	hyaluronan synthase 2
GO	membrane	161	3643	0.989	339761	cytochrome P450, family 27, subfamily C, polypeptide 1
GO	membrane	161	3643	0.989	344838	progestin and adipoQ receptor family member IX
GO	membrane	161	3643	0.989	348938	NIPA-like domain containing 4
GO	membrane	161	3643	0.989	3694	integrin, beta 6

GO	membrane	161	3643	0.989	3754	potassium voltage-gated channel, subfamily F, member 1
GO	membrane	161	3643	0.989	3756	potassium voltage-gated channel, subfamily H (eag-related), member 1
GO	membrane	161	3643	0.989	388394	reprimo-like
GO	membrane	161	3643	0.989	400451	family with sequence similarity 174, member B
GO	membrane	161	3643	0.989	4709	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 3, 12kDa
GO	membrane	161	3643	0.989	479	ATPase, H+/K+ transporting, nongastric, alpha polypeptide
GO	membrane	161	3643	0.989	4867	nephronophthisis 1 (juvenile)
GO	membrane	161	3643	0.989	4928	nucleoporin 98kDa
GO	membrane	161	3643	0.989	5026	purinergic receptor P2X, ligand-gated ion channel, 5
GO	membrane	161	3643	0.989	51062	atlastin GTPase 1
GO	membrane	161	3643	0.989	51136	ring finger protein, transmembrane 1
GO	membrane	161	3643	0.989	51308	receptor accessory protein 2
GO	membrane	161	3643	0.989	51382	ATPase, H+ transporting, lysosomal 34kDa, V1 subunit D
GO	membrane	161	3643	0.989	5140	phosphodiesterase 3B, cGMP-inhibited
GO	membrane	161	3643	0.989	516	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit C1 (subu
GO	membrane	161	3643	0.989	5228	placental growth factor
GO	membrane	161	3643	0.989	5245	prohibitin
GO	membrane	161	3643	0.989	53340	sperm autoantigenic protein 17
GO	membrane	161	3643	0.989	54733	solute carrier family 35, member F2
GO	membrane	161	3643	0.989	55016	membrane-associated ring finger (C3HC4) 1
GO	membrane	161	3643	0.989	55028	chromosome 17 open reading frame 80
GO	membrane	161	3643	0.989	55207	ADP-ribosylation factor-like 8B
GO	membrane	161	3643	0.989	554279	chromosome 1 open reading frame 98
GO	membrane	161	3643	0.989	558	AXL receptor tyrosine kinase
GO	membrane	161	3643	0.989	56241	sushi domain containing 2
GO	membrane	161	3643	0.989	56479	potassium voltage-gated channel, KQT-like subfamily, member 5
GO	membrane	161	3643	0.989	57099	apoptosis, caspase activation inhibitor
GO	membrane	161	3643	0.989	57168	aspartate beta-hydroxylase domain containing 2
GO	membrane	161	3643	0.989	57484	ring finger protein 150
GO	membrane	161	3643	0.989	5754	PTK7 protein tyrosine kinase 7
GO	membrane	161	3643	0.989	57574	membrane-associated ring finger (C3HC4) 4
GO	membrane	161	3643	0.989	57650	KIAA1524
GO	membrane	161	3643	0.989	57678	glycerol-3-phosphate acyltransferase, mitochondrial
GO	membrane	161	3643	0.989	581	BCL2-associated X protein
GO	membrane	161	3643	0.989	590	butyrylcholinesterase
GO	membrane	161	3643	0.989	60386	solute carrier family 25 (mitochondrial thiamine pyrophosphate carrier), m

GO	membrane	161	3643	0.989	60492	coiled-coil domain containing 90B
GO	membrane	161	3643	0.989	6335	sodium channel, voltage-gated, type IX, alpha subunit
GO	membrane	161	3643	0.989	64131	xylosyltransferase I
GO	membrane	161	3643	0.989	64208	popeye domain containing 3
GO	membrane	161	3643	0.989	64417	chromosome 5 open reading frame 28
GO	membrane	161	3643	0.989	64747	major facilitator superfamily domain containing 1
GO	membrane	161	3643	0.989	65055	receptor accessory protein 1
GO	membrane	161	3643	0.989	65062	amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 4
GO	membrane	161	3643	0.989	6527	solute carrier family 5 (low affinity glucose cotransporter), member 4
GO	membrane	161	3643	0.989	6549	solute carrier family 9 (sodium/hydrogen exchanger), member 2
GO	membrane	161	3643	0.989	66000	transmembrane protein 108
GO	membrane	161	3643	0.989	6683	spastin
GO	membrane	161	3643	0.989	6785	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like
GO	membrane	161	3643	0.989	6833	ATP-binding cassette, sub-family C (CFTR/MRP), member 8
GO	membrane	161	3643	0.989	7037	transferrin receptor (p90, CD71)
GO	membrane	161	3643	0.989	729025	solute carrier family 15, member 5
GO	membrane	161	3643	0.989	7341	SMT3 suppressor of mif two 3 homolog 1 (S. cerevisiae)
GO	membrane	161	3643	0.989	7348	uroplakin 1B
GO	membrane	161	3643	0.989	79071	ELOVL family member 6, elongation of long chain fatty acids (FEN1/Elo2, SU
GO	membrane	161	3643	0.989	79135	apolipoprotein O
GO	membrane	161	3643	0.989	79623	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltr
GO	membrane	161	3643	0.989	79669	chromosome 3 open reading frame 52
GO	membrane	161	3643	0.989	79993	ELOVL family member 7, elongation of long chain fatty acids (yeast)
GO	membrane	161	3643	0.989	80342	TRAF3 interacting protein 3
GO	membrane	161	3643	0.989	81035	collectin sub-family member 12
GO	membrane	161	3643	0.989	81562	lectin, mannose-binding 2-like
GO	membrane	161	3643	0.989	81706	protein phosphatase 1, regulatory (inhibitor) subunit 14C
GO	membrane	161	3643	0.989	8325	frizzled homolog 8 (Drosophila)
GO	membrane	161	3643	0.989	83930	STARD3 N-terminal like
GO	membrane	161	3643	0.989	84189	SLIT and NTRK-like family, member 6
GO	membrane	161	3643	0.989	84230	leucine rich repeat containing 8 family, member C
GO	membrane	161	3643	0.989	84620	ST6 beta-galactosamide alpha-2,6-sialyltranferase 2
GO	membrane	161	3643	0.989	84668	family with sequence similarity 126, member A
GO	membrane	161	3643	0.989	84752	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 9
GO	membrane	161	3643	0.989	84769	MPV17 mitochondrial membrane protein-like 2
GO	membrane	161	3643	0.989	84910	transmembrane protein 87B

GO	membrane	161	3643	0.989	85027	chromosome 5 open reading frame 62
GO	membrane	161	3643	0.989	85455	dispatched homolog 2 (Drosophila)
GO	membrane	161	3643	0.989	8604	solute carrier family 25 (mitochondrial carrier, Aralar), member 12
GO	membrane	161	3643	0.989	8685	macrophage receptor with collagenous structure
GO	membrane	161	3643	0.989	8728	ADAM metallopeptidase domain 19 (meltrin beta)
GO	membrane	161	3643	0.989	8747	ADAM metallopeptidase domain 21
GO	membrane	161	3643	0.989	8788	delta-like 1 homolog (Drosophila)
GO	membrane	161	3643	0.989	8905	adaptor-related protein complex 1, sigma 2 subunit
GO	membrane	161	3643	0.989	90701	SEC11 homolog C (S. cerevisiae)
GO	membrane	161	3643	0.989	90871	chromosome 9 open reading frame 123
GO	membrane	161	3643	0.989	91942	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, assembly factor 2
GO	membrane	161	3643	0.989	9215	like-glycosyltransferase
GO	membrane	161	3643	0.989	9420	cytochrome P450, family 7, subfamily B, polypeptide 1
GO	membrane	161	3643	0.989	9482	syntaxin 8
GO	membrane	161	3643	0.989	9653	heparan sulfate 2-O-sulfotransferase 1
GO	membrane	161	3643	0.989	9732	dedicator of cytokinesis 4
GO	protein kinase activity	6	170	0.989	10000	v-akt murine thymoma viral oncogene homolog 3 (protein kinase B, gamma
GO	protein kinase activity	6	170	0.989	22868	FAST kinase domains 2
GO	protein kinase activity	6	170	0.989	27330	ribosomal protein S6 kinase, 90kDa, polypeptide 6
GO	protein kinase activity	6	170	0.989	2965	general transcription factor IIH, polypeptide 1, 62kDa
GO	protein kinase activity	6	170	0.989	6347	chemokine (C-C motif) ligand 2
GO	protein kinase activity	6	170	0.989	7010	TEK tyrosine kinase, endothelial
GO	protein serine/threonine kinase activity	12	335	0.989	10000	v-akt murine thymoma viral oncogene homolog 3 (protein kinase B, gamma
GO	protein serine/threonine kinase activity	12	335	0.989	27330	ribosomal protein S6 kinase, 90kDa, polypeptide 6
GO	protein serine/threonine kinase activity	12	335	0.989	283455	kinase suppressor of ras 2
GO	protein serine/threonine kinase activity	12	335	0.989	54822	transient receptor potential cation channel, subfamily M, member 7
GO	protein serine/threonine kinase activity	12	335	0.989	5588	protein kinase C, theta
GO	protein serine/threonine kinase activity	12	335	0.989	57144	p21 protein (Cdc42/Rac)-activated kinase 7
GO	protein serine/threonine kinase activity	12	335	0.989	659	bone morphogenetic protein receptor, type II (serine/threonine kinase)
GO	protein serine/threonine kinase activity	12	335	0.989	7046	transforming growth factor, beta receptor 1
GO	protein serine/threonine kinase activity	12	335	0.989	8997	kalirin, RhoGEF kinase
GO	protein serine/threonine kinase activity	12	335	0.989	9262	serine/threonine kinase 17b
GO	protein serine/threonine kinase activity	12	335	0.989	9448	mitogen-activated protein kinase kinase kinase kinase 4
GO	protein serine/threonine kinase activity	12	335	0.989	9833	maternal embryonic leucine zipper kinase
GO	signal transduction	78	1796	0.989	10000	v-akt murine thymoma viral oncogene homolog 3 (protein kinase B, gamma
GO	signal transduction	78	1796	0.989	10293	TRAF interacting protein

GO	signal transduction	78	1796	0.989	10395	deleted in liver cancer 1
GO	signal transduction	78	1796	0.989	10672	guanine nucleotide binding protein (G protein), alpha 13
GO	signal transduction	78	1796	0.989	10788	IQ motif containing GTPase activating protein 2
GO	signal transduction	78	1796	0.989	11142	protein kinase (cAMP-dependent, catalytic) inhibitor gamma
GO	signal transduction	78	1796	0.989	1123	chimerin (chimaerin) 1
GO	signal transduction	78	1796	0.989	1136	cholinergic receptor, nicotinic, alpha 3
GO	signal transduction	78	1796	0.989	1138	cholinergic receptor, nicotinic, alpha 5
GO	signal transduction	78	1796	0.989	119749	olfactory receptor, family 4, subfamily C, member 46
GO	signal transduction	78	1796	0.989	121268	Ras homolog enriched in brain like 1
GO	signal transduction	78	1796	0.989	125962	olfactory receptor, family 7, subfamily G, member 1
GO	signal transduction	78	1796	0.989	162494	rhomboid, veinlet-like 3 (Drosophila)
GO	signal transduction	78	1796	0.989	2149	coagulation factor II (thrombin) receptor
GO	signal transduction	78	1796	0.989	2150	coagulation factor II (thrombin) receptor-like 1
GO	signal transduction	78	1796	0.989	2151	coagulation factor II (thrombin) receptor-like 2
GO	signal transduction	78	1796	0.989	222611	G protein-coupled receptor 111
GO	signal transduction	78	1796	0.989	23432	G protein-coupled receptor 161
GO	signal transduction	78	1796	0.989	2533	FYN binding protein (FYB-120/130)
GO	signal transduction	78	1796	0.989	2558	gamma-aminobutyric acid (GABA) A receptor, alpha 5
GO	signal transduction	78	1796	0.989	26207	phosphatidylinositol transfer protein, cytoplasmic 1
GO	signal transduction	78	1796	0.989	26230	T-cell lymphoma invasion and metastasis 2
GO	signal transduction	78	1796	0.989	27330	ribosomal protein S6 kinase, 90kDa, polypeptide 6
GO	signal transduction	78	1796	0.989	2774	guanine nucleotide binding protein (G protein), alpha activating activity pol
GO	signal transduction	78	1796	0.989	2786	guanine nucleotide binding protein (G protein), gamma 4
GO	signal transduction	78	1796	0.989	282770	olfactory receptor, family 10, subfamily AG, member 1
GO	signal transduction	78	1796	0.989	283111	olfactory receptor, family 51, subfamily V, member 1
GO	signal transduction	78	1796	0.989	2842	G protein-coupled receptor 19
GO	signal transduction	78	1796	0.989	2845	G protein-coupled receptor 22
GO	signal transduction	78	1796	0.989	2850	G protein-coupled receptor 27
GO	signal transduction	78	1796	0.989	285659	olfactory receptor, family 2, subfamily V, member 2
GO	signal transduction	78	1796	0.989	2863	G protein-coupled receptor 39
GO	signal transduction	78	1796	0.989	287	ankyrin 2, neuronal
GO	signal transduction	78	1796	0.989	2906	glutamate receptor, ionotropic, N-methyl D-aspartate 2D
GO	signal transduction	78	1796	0.989	355	Fas (TNF receptor superfamily, member 6)
GO	signal transduction	78	1796	0.989	3756	potassium voltage-gated channel, subfamily H (eag-related), member 1
GO	signal transduction	78	1796	0.989	390061	olfactory receptor, family 51, subfamily Q, member 1
GO	signal transduction	78	1796	0.989	391114	olfactory receptor, family 6, subfamily K, member 3

GO	signal transduction	78	1796	0.989	3952	leptin
GO	signal transduction	78	1796	0.989	406	aryl hydrocarbon receptor nuclear translocator-like
GO	signal transduction	78	1796	0.989	4158	melanocortin 2 receptor (adrenocorticotropic hormone)
GO	signal transduction	78	1796	0.989	4651	myosin X
GO	signal transduction	78	1796	0.989	4763	neurofibromin 1
GO	signal transduction	78	1796	0.989	4867	nephronophthisis 1 (juvenile)
GO	signal transduction	78	1796	0.989	4893	neuroblastoma RAS viral (v-ras) oncogene homolog
GO	signal transduction	78	1796	0.989	5021	oxytocin receptor
GO	signal transduction	78	1796	0.989	5026	purinergic receptor P2X, ligand-gated ion channel, 5
GO	signal transduction	78	1796	0.989	5028	purinergic receptor P2Y, G-protein coupled, 1
GO	signal transduction	78	1796	0.989	5031	pyrimidinergic receptor P2Y, G-protein coupled, 6
GO	signal transduction	78	1796	0.989	50940	phosphodiesterase 11A
GO	signal transduction	78	1796	0.989	5140	phosphodiesterase 3B, cGMP-inhibited
GO	signal transduction	78	1796	0.989	5145	phosphodiesterase 6A, cGMP-specific, rod, alpha
GO	signal transduction	78	1796	0.989	51676	ankyrin repeat and SOCS box-containing 2
GO	signal transduction	78	1796	0.989	5228	placental growth factor
GO	signal transduction	78	1796	0.989	5245	prohibitin
GO	signal transduction	78	1796	0.989	53340	sperm autoantigenic protein 17
GO	signal transduction	78	1796	0.989	53637	sphingosine-1-phosphate receptor 5
GO	signal transduction	78	1796	0.989	54331	guanine nucleotide binding protein (G protein), gamma 2
GO	signal transduction	78	1796	0.989	55789	DEP domain containing 1B
GO	signal transduction	78	1796	0.989	558	AXL receptor tyrosine kinase
GO	signal transduction	78	1796	0.989	5754	PTK7 protein tyrosine kinase 7
GO	signal transduction	78	1796	0.989	59345	guanine nucleotide binding protein (G protein), beta polypeptide 4
GO	signal transduction	78	1796	0.989	6242	rhotekin
GO	signal transduction	78	1796	0.989	6251	Ras suppressor protein 1
GO	signal transduction	78	1796	0.989	6347	chemokine (C-C motif) ligand 2
GO	signal transduction	78	1796	0.989	6422	secreted frizzled-related protein 1
GO	signal transduction	78	1796	0.989	6695	sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 1
GO	signal transduction	78	1796	0.989	7010	TEK tyrosine kinase, endothelial
GO	signal transduction	78	1796	0.989	7046	transforming growth factor, beta receptor 1
GO	signal transduction	78	1796	0.989	729230	chemokine (C-C motif) receptor 2
GO	signal transduction	78	1796	0.989	7481	wingless-type MMTV integration site family, member 11
GO	signal transduction	78	1796	0.989	8325	frizzled homolog 8 (Drosophila)
GO	signal transduction	78	1796	0.989	8533	COP9 constitutive photomorphogenic homolog subunit 3 (Arabidopsis)
GO	signal transduction	78	1796	0.989	8536	calcium/calmodulin-dependent protein kinase I

GO	signal transduction	78	1796	0.989	8997	kalirin, RhoGEF kinase
GO	signal transduction	78	1796	0.989	91584	plexin A4
GO	signal transduction	78	1796	0.989	9542	neuregulin 2
GO	signal transduction	78	1796	0.989	9568	gamma-aminobutyric acid (GABA) B receptor, 2
GO	regulation of transcription, DNA-depenc	32	1013	0.989	1E+08	forkhead box O6
GO	regulation of transcription, DNA-depenc	32	1013	0.989	1045	caudal type homeobox 2
GO	regulation of transcription, DNA-depenc	32	1013	0.989	139324	highly divergent homeobox
GO	regulation of transcription, DNA-depenc	32	1013	0.989	1746	distal-less homeobox 2
GO	regulation of transcription, DNA-depenc	32	1013	0.989	2305	forkhead box M1
GO	regulation of transcription, DNA-depenc	32	1013	0.989	3224	homeobox C8
GO	regulation of transcription, DNA-depenc	32	1013	0.989	3236	homeobox D10
GO	regulation of transcription, DNA-depenc	32	1013	0.989	3237	homeobox D11
GO	regulation of transcription, DNA-depenc	32	1013	0.989	344191	even-skipped homeobox 2
GO	regulation of transcription, DNA-depenc	32	1013	0.989	3756	potassium voltage-gated channel, subfamily H (eag-related), member 1
GO	regulation of transcription, DNA-depenc	32	1013	0.989	389421	lin-28 homolog B (C. elegans)
GO	regulation of transcription, DNA-depenc	32	1013	0.989	3975	LIM homeobox 1
GO	regulation of transcription, DNA-depenc	32	1013	0.989	406	aryl hydrocarbon receptor nuclear translocator-like
GO	regulation of transcription, DNA-depenc	32	1013	0.989	4094	v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian)
GO	regulation of transcription, DNA-depenc	32	1013	0.989	431707	LIM homeobox 8
GO	regulation of transcription, DNA-depenc	32	1013	0.989	4603	v-myb myeloblastosis viral oncogene homolog (avian)-like 1
GO	regulation of transcription, DNA-depenc	32	1013	0.989	5015	orthodenticle homeobox 2
GO	regulation of transcription, DNA-depenc	32	1013	0.989	5081	paired box 7
GO	regulation of transcription, DNA-depenc	32	1013	0.989	54993	zinc finger and SCAN domain containing 2
GO	regulation of transcription, DNA-depenc	32	1013	0.989	6474	short stature homeobox 2
GO	regulation of transcription, DNA-depenc	32	1013	0.989	6657	SRY (sex determining region Y)-box 2
GO	regulation of transcription, DNA-depenc	32	1013	0.989	6659	SRY (sex determining region Y)-box 4
GO	regulation of transcription, DNA-depenc	32	1013	0.989	7021	transcription factor AP-2 beta (activating enhancer binding protein 2 beta)
GO	regulation of transcription, DNA-depenc	32	1013	0.989	7029	transcription factor Dp-2 (E2F dimerization partner 2)
GO	regulation of transcription, DNA-depenc	32	1013	0.989	7490	Wilms tumor 1
GO	regulation of transcription, DNA-depenc	32	1013	0.989	7711	zinc finger protein 155
GO	regulation of transcription, DNA-depenc	32	1013	0.989	80712	ESX homeobox 1
GO	regulation of transcription, DNA-depenc	32	1013	0.989	8091	high mobility group AT-hook 2
GO	regulation of transcription, DNA-depenc	32	1013	0.989	91975	zinc finger protein 300
GO	regulation of transcription, DNA-depenc	32	1013	0.989	93474	zinc finger protein 670
GO	regulation of transcription, DNA-depenc	32	1013	0.989	9355	LIM homeobox 2
GO	regulation of transcription, DNA-depenc	32	1013	0.989	9839	zinc finger E-box binding homeobox 2

GO	transcription factor activity	39	922	0.989	1E+08	forkhead box O6
GO	transcription factor activity	39	922	0.989	1045	caudal type homeobox 2
GO	transcription factor activity	39	922	0.989	10474	transcriptional adaptor 3
GO	transcription factor activity	39	922	0.989	11278	Kruppel-like factor 12
GO	transcription factor activity	39	922	0.989	132625	zinc finger protein 42 homolog (mouse)
GO	transcription factor activity	39	922	0.989	139324	highly divergent homeobox
GO	transcription factor activity	39	922	0.989	1746	distal-less homeobox 2
GO	transcription factor activity	39	922	0.989	195828	zinc finger protein 367
GO	transcription factor activity	39	922	0.989	2305	forkhead box M1
GO	transcription factor activity	39	922	0.989	2736	GLI family zinc finger 2
GO	transcription factor activity	39	922	0.989	29128	ubiquitin-like with PHD and ring finger domains 1
GO	transcription factor activity	39	922	0.989	29842	transcription factor CP2-like 1
GO	transcription factor activity	39	922	0.989	3224	homeobox C8
GO	transcription factor activity	39	922	0.989	3236	homeobox D10
GO	transcription factor activity	39	922	0.989	3237	homeobox D11
GO	transcription factor activity	39	922	0.989	344191	even-skipped homeobox 2
GO	transcription factor activity	39	922	0.989	3516	recombination signal binding protein for immunoglobulin kappa J region
GO	transcription factor activity	39	922	0.989	3975	LIM homeobox 1
GO	transcription factor activity	39	922	0.989	406	aryl hydrocarbon receptor nuclear translocator-like
GO	transcription factor activity	39	922	0.989	4094	v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian)
GO	transcription factor activity	39	922	0.989	431707	LIM homeobox 8
GO	transcription factor activity	39	922	0.989	5015	orthodenticle homeobox 2
GO	transcription factor activity	39	922	0.989	5081	paired box 7
GO	transcription factor activity	39	922	0.989	54993	zinc finger and SCAN domain containing 2
GO	transcription factor activity	39	922	0.989	6299	sal-like 1 (Drosophila)
GO	transcription factor activity	39	922	0.989	6474	short stature homeobox 2
GO	transcription factor activity	39	922	0.989	6657	SRY (sex determining region Y)-box 2
GO	transcription factor activity	39	922	0.989	6659	SRY (sex determining region Y)-box 4
GO	transcription factor activity	39	922	0.989	6662	SRY (sex determining region Y)-box 9
GO	transcription factor activity	39	922	0.989	6899	T-box 1
GO	transcription factor activity	39	922	0.989	7021	transcription factor AP-2 beta (activating enhancer binding protein 2 beta)
GO	transcription factor activity	39	922	0.989	7029	transcription factor Dp-2 (E2F dimerization partner 2)
GO	transcription factor activity	39	922	0.989	7490	Wilms tumor 1
GO	transcription factor activity	39	922	0.989	7711	zinc finger protein 155
GO	transcription factor activity	39	922	0.989	80712	ESX homeobox 1
GO	transcription factor activity	39	922	0.989	8626	tumor protein p63

GO	transcription factor activity	39	922	0.989	9242	musculin (activated B-cell factor-1)
GO	transcription factor activity	39	922	0.989	9355	LIM homeobox 2
GO	transcription factor activity	39	922	0.989	9839	zinc finger E-box binding homeobox 2
GO	transport	21	511	0.989	10052	gap junction protein, gamma 1, 45kDa
GO	transport	21	511	0.989	10189	THO complex 4
GO	transport	21	511	0.989	1138	cholinergic receptor, nicotinic, alpha 5
GO	transport	21	511	0.989	114757	cytoglobin
GO	transport	21	511	0.989	116362	retinol binding protein 7, cellular
GO	transport	21	511	0.989	1622	diazepam binding inhibitor (GABA receptor modulator, acyl-Coenzyme A bi
GO	transport	21	511	0.989	1781	dynein, cytoplasmic 1, intermediate chain 2
GO	transport	21	511	0.989	2171	fatty acid binding protein 5 (psoriasis-associated)
GO	transport	21	511	0.989	2172	fatty acid binding protein 6, ileal
GO	transport	21	511	0.989	2232	ferredoxin reductase
GO	transport	21	511	0.989	2558	gamma-aminobutyric acid (GABA) A receptor, alpha 5
GO	transport	21	511	0.989	27445	piccolo (presynaptic cytomatrix protein)
GO	transport	21	511	0.989	2898	glutamate receptor, ionotropic, kainate 2
GO	transport	21	511	0.989	4709	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 3, 12kDa
GO	transport	21	511	0.989	4884	neuronal pentraxin I
GO	transport	21	511	0.989	5026	purinergic receptor P2X, ligand-gated ion channel, 5
GO	transport	21	511	0.989	54733	solute carrier family 35, member F2
GO	transport	21	511	0.989	5947	retinol binding protein 1, cellular
GO	transport	21	511	0.989	8563	THO complex 5
GO	transport	21	511	0.989	9482	syntaxin 8
GO	transport	21	511	0.989	9635	chloride channel accessory 2
GO	metabolic process	20	455	0.989	10055	SUMO1 activating enzyme subunit 1
GO	metabolic process	20	455	0.989	10893	matrix metallopeptidase 24 (membrane-inserted)
GO	metabolic process	20	455	0.989	13	arylacetamide deacetylase (esterase)
GO	metabolic process	20	455	0.989	2139	eyes absent homolog 2 (Drosophila)
GO	metabolic process	20	455	0.989	221357	glutathione S-transferase alpha 5
GO	metabolic process	20	455	0.989	23305	acyl-CoA synthetase long-chain family member 6
GO	metabolic process	20	455	0.989	26275	3-hydroxyisobutyryl-Coenzyme A hydrolase
GO	metabolic process	20	455	0.989	3157	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 (soluble)
GO	metabolic process	20	455	0.989	3778	potassium large conductance calcium-activated channel, subfamily M, alph
GO	metabolic process	20	455	0.989	411	arylsulfatase B
GO	metabolic process	20	455	0.989	4312	matrix metallopeptidase 1 (interstitial collagenase)
GO	metabolic process	20	455	0.989	4318	matrix metallopeptidase 9 (gelatinase B, 92kDa gelatinase, 92kDa type IV c

GO	metabolic process	20	455	0.989	4319	matrix metallopeptidase 10 (stromelysin 2)
GO	metabolic process	20	455	0.989	479	ATPase, H+/K+ transporting, nongastric, alpha polypeptide
GO	metabolic process	20	455	0.989	4968	8-oxoguanine DNA glycosylase
GO	metabolic process	20	455	0.989	57103	chromosome 12 open reading frame 5
GO	metabolic process	20	455	0.989	57678	glycerol-3-phosphate acyltransferase, mitochondrial
GO	metabolic process	20	455	0.989	586	branched chain aminotransferase 1, cytosolic
GO	metabolic process	20	455	0.989	6120	ribulose-5-phosphate-3-epimerase
GO	metabolic process	20	455	0.989	669	2,3-bisphosphoglycerate mutase
GO	protein modification process	6	145	0.989	10055	SUMO1 activating enzyme subunit 1
GO	protein modification process	6	145	0.989	25827	F-box and leucine-rich repeat protein 2
GO	protein modification process	6	145	0.989	26263	F-box protein 22
GO	protein modification process	6	145	0.989	4734	neural precursor cell expressed, developmentally down-regulated 4
GO	protein modification process	6	145	0.989	5110	protein-L-isoaspartate (D-aspartate) O-methyltransferase
GO	protein modification process	6	145	0.989	51191	hect domain and RLD 5
GO	response to protein stimulus	1	42	0.989	10096	ARP3 actin-related protein 3 homolog (yeast)
GO	intracellular	80	1794	0.989	10123	ADP-ribosylation factor-like 4C
GO	intracellular	80	1794	0.989	10395	deleted in liver cancer 1
GO	intracellular	80	1794	0.989	10474	transcriptional adaptor 3
GO	intracellular	80	1794	0.989	10612	tripartite motif-containing 3
GO	intracellular	80	1794	0.989	10788	IQ motif containing GTPase activating protein 2
GO	intracellular	80	1794	0.989	11164	nudix (nucleoside diphosphate linked moiety X)-type motif 5
GO	intracellular	80	1794	0.989	11222	mitochondrial ribosomal protein L3
GO	intracellular	80	1794	0.989	1123	chimerin (chimaerin) 1
GO	intracellular	80	1794	0.989	11278	Kruppel-like factor 12
GO	intracellular	80	1794	0.989	114088	tripartite motif-containing 9
GO	intracellular	80	1794	0.989	12	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), me
GO	intracellular	80	1794	0.989	121268	Ras homolog enriched in brain like 1
GO	intracellular	80	1794	0.989	132625	zinc finger protein 42 homolog (mouse)
GO	intracellular	80	1794	0.989	148213	zinc finger protein 681
GO	intracellular	80	1794	0.989	153478	pleckstrin homology domain containing, family G (with RhoGef domain) me
GO	intracellular	80	1794	0.989	195828	zinc finger protein 367
GO	intracellular	80	1794	0.989	22891	zinc finger protein 365
GO	intracellular	80	1794	0.989	22934	ribose 5-phosphate isomerase A
GO	intracellular	80	1794	0.989	25780	RAS guanyl releasing protein 3 (calcium and DAG-regulated)
GO	intracellular	80	1794	0.989	26207	phosphatidylinositol transfer protein, cytoplasmic 1
GO	intracellular	80	1794	0.989	26230	T-cell lymphoma invasion and metastasis 2

GO	intracellular	80	1794	0.989	27289	Rho family GTPase 1
GO	intracellular	80	1794	0.989	2736	GLI family zinc finger 2
GO	intracellular	80	1794	0.989	284443	zinc finger protein 493
GO	intracellular	80	1794	0.989	28998	mitochondrial ribosomal protein L13
GO	intracellular	80	1794	0.989	332	baculoviral IAP repeat-containing 5
GO	intracellular	80	1794	0.989	3557	interleukin 1 receptor antagonist
GO	intracellular	80	1794	0.989	3975	LIM homeobox 1
GO	intracellular	80	1794	0.989	4734	neural precursor cell expressed, developmentally down-regulated 4
GO	intracellular	80	1794	0.989	4763	neurofibromin 1
GO	intracellular	80	1794	0.989	4893	neuroblastoma RAS viral (v-ras) oncogene homolog
GO	intracellular	80	1794	0.989	51023	mitochondrial ribosomal protein S18C
GO	intracellular	80	1794	0.989	51121	ribosomal protein L26-like 1
GO	intracellular	80	1794	0.989	51191	hect domain and RLD 5
GO	intracellular	80	1794	0.989	51256	TBC1 domain family, member 7
GO	intracellular	80	1794	0.989	54796	basonuclin 2
GO	intracellular	80	1794	0.989	54984	PIN2-interacting protein 1
GO	intracellular	80	1794	0.989	54993	zinc finger and SCAN domain containing 2
GO	intracellular	80	1794	0.989	55207	ADP-ribosylation factor-like 8B
GO	intracellular	80	1794	0.989	55521	tripartite motif-containing 36
GO	intracellular	80	1794	0.989	55789	DEP domain containing 1B
GO	intracellular	80	1794	0.989	5588	protein kinase C, theta
GO	intracellular	80	1794	0.989	55916	nuclear transport factor 2-like export factor 2
GO	intracellular	80	1794	0.989	56655	polymerase (DNA-directed), epsilon 4 (p12 subunit)
GO	intracellular	80	1794	0.989	57099	apoptosis, caspase activation inhibitor
GO	intracellular	80	1794	0.989	57103	chromosome 12 open reading frame 5
GO	intracellular	80	1794	0.989	58499	zinc finger protein 462
GO	intracellular	80	1794	0.989	5924	Ras protein-specific guanine nucleotide-releasing factor 2
GO	intracellular	80	1794	0.989	59336	PR domain containing 13
GO	intracellular	80	1794	0.989	6133	ribosomal protein L9
GO	intracellular	80	1794	0.989	6154	ribosomal protein L26
GO	intracellular	80	1794	0.989	619279	zinc finger protein 704
GO	intracellular	80	1794	0.989	6242	rhotekin
GO	intracellular	80	1794	0.989	6299	sal-like 1 (Drosophila)
GO	intracellular	80	1794	0.989	641	Bloom syndrome, RecQ helicase-like
GO	intracellular	80	1794	0.989	64393	zinc finger, matrin type 3
GO	intracellular	80	1794	0.989	64782	apoptosis enhancing nuclease

GO	intracellular	80	1794	0.989	65008	mitochondrial ribosomal protein L1
GO	intracellular	80	1794	0.989	6591	snail homolog 2 (Drosophila)
GO	intracellular	80	1794	0.989	6615	snail homolog 1 (Drosophila)
GO	intracellular	80	1794	0.989	672	breast cancer 1, early onset
GO	intracellular	80	1794	0.989	7347	ubiquitin carboxyl-terminal esterase L3 (ubiquitin thiolesterase)
GO	intracellular	80	1794	0.989	7490	Wilms tumor 1
GO	intracellular	80	1794	0.989	7552	zinc finger protein 711
GO	intracellular	80	1794	0.989	7711	zinc finger protein 155
GO	intracellular	80	1794	0.989	79187	fibronectin type III and SPRY domain containing 1
GO	intracellular	80	1794	0.989	79677	structural maintenance of chromosomes 6
GO	intracellular	80	1794	0.989	79698	zinc finger, matrin type 4
GO	intracellular	80	1794	0.989	81786	tripartite motif-containing 7
GO	intracellular	80	1794	0.989	84083	zinc finger, RAN-binding domain containing 3
GO	intracellular	80	1794	0.989	84622	zinc finger protein 594
GO	intracellular	80	1794	0.989	84878	zinc finger and BTB domain containing 45
GO	intracellular	80	1794	0.989	8997	kalirin, RhoGEF kinase
GO	intracellular	80	1794	0.989	91584	plexin A4
GO	intracellular	80	1794	0.989	91975	zinc finger protein 300
GO	intracellular	80	1794	0.989	93474	zinc finger protein 670
GO	intracellular	80	1794	0.989	9535	glia maturation factor, gamma
GO	intracellular	80	1794	0.989	9839	zinc finger E-box binding homeobox 2
GO	intracellular	80	1794	0.989	9882	TBC1 domain family, member 4
GO	intracellular	80	1794	0.989	9910	RAB GTPase activating protein 1-like
GO	small GTPase mediated signal transduct	8	193	0.989	10123	ADP-ribosylation factor-like 4C
GO	small GTPase mediated signal transduct	8	193	0.989	10890	RAB10, member RAS oncogene family
GO	small GTPase mediated signal transduct	8	193	0.989	121268	Ras homolog enriched in brain like 1
GO	small GTPase mediated signal transduct	8	193	0.989	25780	RAS guanyl releasing protein 3 (calcium and DAG-regulated)
GO	small GTPase mediated signal transduct	8	193	0.989	27289	Rho family GTPase 1
GO	small GTPase mediated signal transduct	8	193	0.989	4893	neuroblastoma RAS viral (v-ras) oncogene homolog
GO	small GTPase mediated signal transduct	8	193	0.989	55207	ADP-ribosylation factor-like 8B
GO	small GTPase mediated signal transduct	8	193	0.989	83871	RAB34, member RAS oncogene family
GO	biological_process	17	547	0.989	10190	thioredoxin domain containing 9
GO	biological_process	17	547	0.989	10777	cyclic AMP-regulated phosphoprotein, 21 kD
GO	biological_process	17	547	0.989	11259	filamin A interacting protein 1-like
GO	biological_process	17	547	0.989	23136	erythrocyte membrane protein band 4.1-like 3
GO	biological_process	17	547	0.989	23768	fibronectin leucine rich transmembrane protein 2

GO	biological_process	17	547	0.989	29893	PSMC3 interacting protein
GO	biological_process	17	547	0.989	344191	even-skipped homeobox 2
GO	biological_process	17	547	0.989	4052	latent transforming growth factor beta binding protein 1
GO	biological_process	17	547	0.989	51050	peptidase inhibitor 15
GO	biological_process	17	547	0.989	54726	OTU domain containing 4
GO	biological_process	17	547	0.989	54733	solute carrier family 35, member F2
GO	biological_process	17	547	0.989	56651	chromosome 18 open reading frame 2
GO	biological_process	17	547	0.989	57590	WD repeat and FYVE domain containing 1
GO	biological_process	17	547	0.989	64208	popeye domain containing 3
GO	biological_process	17	547	0.989	66000	transmembrane protein 108
GO	biological_process	17	547	0.989	7840	Alstrom syndrome 1
GO	biological_process	17	547	0.989	84668	family with sequence similarity 126, member A
GO	RNA splicing, via transesterification reac	1	25	0.989	10199	M-phase phosphoprotein 10 (U3 small nucleolar ribonucleoprotein)
GO	binding	16	500	0.989	10202	dehydrogenase/reductase (SDR family) member 2
GO	binding	16	500	0.989	11077	heat shock transcription factor 2 binding protein
GO	binding	16	500	0.989	122786	FERM domain containing 6
GO	binding	16	500	0.989	145864	hyaluronan and proteoglycan link protein 3
GO	binding	16	500	0.989	22979	EFR3 homolog B (S. cerevisiae)
GO	binding	16	500	0.989	23171	glycerol-3-phosphate dehydrogenase 1-like
GO	binding	16	500	0.989	26032	sushi domain containing 5
GO	binding	16	500	0.989	26115	tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 2
GO	binding	16	500	0.989	283208	prolyl 4-hydroxylase, alpha polypeptide III
GO	binding	16	500	0.989	3248	hydroxyprostaglandin dehydrogenase 15-(NAD)
GO	binding	16	500	0.989	3694	integrin, beta 6
GO	binding	16	500	0.989	4052	latent transforming growth factor beta binding protein 1
GO	binding	16	500	0.989	414149	acyl-Coenzyme A binding domain containing 7
GO	binding	16	500	0.989	60386	solute carrier family 25 (mitochondrial thiamine pyrophosphate carrier), m
GO	binding	16	500	0.989	81035	collectin sub-family member 12
GO	binding	16	500	0.989	9540	tumor protein p53 inducible protein 3
GO	nuclear envelope	4	92	0.989	10202	dehydrogenase/reductase (SDR family) member 2
GO	nuclear envelope	4	92	0.989	241	arachidonate 5-lipoxygenase-activating protein
GO	nuclear envelope	4	92	0.989	4928	nucleoporin 98kDa
GO	nuclear envelope	4	92	0.989	9688	nucleoporin 93kDa
GO	oxidation reduction	18	515	0.989	10202	dehydrogenase/reductase (SDR family) member 2
GO	oxidation reduction	18	515	0.989	1543	cytochrome P450, family 1, subfamily A, polypeptide 1
GO	oxidation reduction	18	515	0.989	1733	deiodinase, iodothyronine, type I

GO	oxidation reduction	18	515	0.989	220	aldehyde dehydrogenase 1 family, member A3
GO	oxidation reduction	18	515	0.989	2232	ferredoxin reductase
GO	oxidation reduction	18	515	0.989	23171	glycerol-3-phosphate dehydrogenase 1-like
GO	oxidation reduction	18	515	0.989	283208	prolyl 4-hydroxylase, alpha polypeptide III
GO	oxidation reduction	18	515	0.989	2878	glutathione peroxidase 3 (plasma)
GO	oxidation reduction	18	515	0.989	3028	hydroxysteroid (17-beta) dehydrogenase 10
GO	oxidation reduction	18	515	0.989	3248	hydroxyprostaglandin dehydrogenase 15-(NAD)
GO	oxidation reduction	18	515	0.989	339761	cytochrome P450, family 27, subfamily C, polypeptide 1
GO	oxidation reduction	18	515	0.989	5264	phytanoyl-CoA 2-hydroxylase
GO	oxidation reduction	18	515	0.989	57168	aspartate beta-hydroxylase domain containing 2
GO	oxidation reduction	18	515	0.989	6241	ribonucleotide reductase M2
GO	oxidation reduction	18	515	0.989	8659	aldehyde dehydrogenase 4 family, member A1
GO	oxidation reduction	18	515	0.989	91801	alkB, alkylation repair homolog 8 (E. coli)
GO	oxidation reduction	18	515	0.989	9420	cytochrome P450, family 7, subfamily B, polypeptide 1
GO	oxidation reduction	18	515	0.989	9540	tumor protein p53 inducible protein 3
GO	oxidoreductase activity	12	418	0.989	10202	dehydrogenase/reductase (SDR family) member 2
GO	oxidoreductase activity	12	418	0.989	1543	cytochrome P450, family 1, subfamily A, polypeptide 1
GO	oxidoreductase activity	12	418	0.989	220	aldehyde dehydrogenase 1 family, member A3
GO	oxidoreductase activity	12	418	0.989	2232	ferredoxin reductase
GO	oxidoreductase activity	12	418	0.989	2878	glutathione peroxidase 3 (plasma)
GO	oxidoreductase activity	12	418	0.989	3028	hydroxysteroid (17-beta) dehydrogenase 10
GO	oxidoreductase activity	12	418	0.989	3248	hydroxyprostaglandin dehydrogenase 15-(NAD)
GO	oxidoreductase activity	12	418	0.989	57168	aspartate beta-hydroxylase domain containing 2
GO	oxidoreductase activity	12	418	0.989	6241	ribonucleotide reductase M2
GO	oxidoreductase activity	12	418	0.989	8659	aldehyde dehydrogenase 4 family, member A1
GO	oxidoreductase activity	12	418	0.989	91801	alkB, alkylation repair homolog 8 (E. coli)
GO	oxidoreductase activity	12	418	0.989	9540	tumor protein p53 inducible protein 3
GO	hydrolase activity	39	917	0.989	10212	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39
GO	hydrolase activity	39	917	0.989	10799	ribonuclease P/MRP 40kDa subunit
GO	hydrolase activity	39	917	0.989	11056	DEAD (Asp-Glu-Ala-Asp) box polypeptide 52
GO	hydrolase activity	39	917	0.989	11164	nudix (nucleoside diphosphate linked moiety X)-type motif 5
GO	hydrolase activity	39	917	0.989	128853	dual specificity phosphatase 15
GO	hydrolase activity	39	917	0.989	134637	adenosine deaminase, tRNA-specific 2, TAD2 homolog (S. cerevisiae)
GO	hydrolase activity	39	917	0.989	135114	histidine triad nucleotide binding protein 3
GO	hydrolase activity	39	917	0.989	147699	protein phosphatase, Mg2+/Mn2+ dependent, 1N (putative)
GO	hydrolase activity	39	917	0.989	1763	DNA replication helicase 2 homolog (yeast)

GO	hydrolase activity	39	917	0.989	1775	deoxyribonuclease I-like 2
GO	hydrolase activity	39	917	0.989	2139	eyes absent homolog 2 (Drosophila)
GO	hydrolase activity	39	917	0.989	2237	flap structure-specific endonuclease 1
GO	hydrolase activity	39	917	0.989	25953	paroxysmal nonkinesigenic dyskinesia
GO	hydrolase activity	39	917	0.989	26275	3-hydroxyisobutyryl-Coenzyme A hydrolase
GO	hydrolase activity	39	917	0.989	411	arylsulfatase B
GO	hydrolase activity	39	917	0.989	479	ATPase, H+/K+ transporting, nongastric, alpha polypeptide
GO	hydrolase activity	39	917	0.989	50485	SWI/SNF related, matrix associated, actin dependent regulator of chromati
GO	hydrolase activity	39	917	0.989	50940	phosphodiesterase 11A
GO	hydrolase activity	39	917	0.989	51062	atlastin GTPase 1
GO	hydrolase activity	39	917	0.989	5140	phosphodiesterase 3B, cGMP-inhibited
GO	hydrolase activity	39	917	0.989	5145	phosphodiesterase 6A, cGMP-specific, rod, alpha
GO	hydrolase activity	39	917	0.989	53981	cleavage and polyadenylation specific factor 2, 100kDa
GO	hydrolase activity	39	917	0.989	5494	protein phosphatase, Mg2+/Mn2+ dependent, 1A
GO	hydrolase activity	39	917	0.989	5702	proteasome (prosome, macropain) 26S subunit, ATPase, 3
GO	hydrolase activity	39	917	0.989	57103	chromosome 12 open reading frame 5
GO	hydrolase activity	39	917	0.989	5795	protein tyrosine phosphatase, receptor type, J
GO	hydrolase activity	39	917	0.989	590	butyrylcholinesterase
GO	hydrolase activity	39	917	0.989	5965	RecQ protein-like (DNA helicase Q1-like)
GO	hydrolase activity	39	917	0.989	641	Bloom syndrome, RecQ helicase-like
GO	hydrolase activity	39	917	0.989	64782	apoptosis enhancing nuclease
GO	hydrolase activity	39	917	0.989	64943	5'-nucleotidase domain containing 2
GO	hydrolase activity	39	917	0.989	6683	spastin
GO	hydrolase activity	39	917	0.989	669	2,3-bisphosphoglycerate mutase
GO	hydrolase activity	39	917	0.989	79814	agmatine ureohydrolase (agmatinase)
GO	hydrolase activity	39	917	0.989	84083	zinc finger, RAN-binding domain containing 3
GO	hydrolase activity	39	917	0.989	8458	transcription termination factor, RNA polymerase II
GO	hydrolase activity	39	917	0.989	89797	neuron navigator 2
GO	hydrolase activity	39	917	0.989	953	ectonucleoside triphosphate diphosphohydrolase 1
GO	hydrolase activity	39	917	0.989	97	acylphosphatase 1, erythrocyte (common) type
GO	nucleic acid binding	9	254	0.989	10212	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39
GO	nucleic acid binding	9	254	0.989	10777	cyclic AMP-regulated phosphoprotein, 21 kD
GO	nucleic acid binding	9	254	0.989	348093	RNA binding protein with multiple splicing 2
GO	nucleic acid binding	9	254	0.989	54984	PIN2-interacting protein 1
GO	nucleic acid binding	9	254	0.989	55854	zinc finger CCCH-type containing 15
GO	nucleic acid binding	9	254	0.989	64782	apoptosis enhancing nuclease

GO	nucleic acid binding	9	254	0.989	79736	chromosome 17 open reading frame 42
GO	nucleic acid binding	9	254	0.989	84319	chromosome 3 open reading frame 26
GO	nucleic acid binding	9	254	0.989	93649	myocardin
GO	metal ion binding	116	2658	0.989	10213	proteasome (prosome, macropain) 26S subunit, non-ATPase, 14
GO	metal ion binding	116	2658	0.989	1026	cyclin-dependent kinase inhibitor 1A (p21, Cip1)
GO	metal ion binding	116	2658	0.989	10293	TRAF interacting protein
GO	metal ion binding	116	2658	0.989	10539	glutaredoxin 3
GO	metal ion binding	116	2658	0.989	10612	tripartite motif-containing 3
GO	metal ion binding	116	2658	0.989	1123	chimerin (chimaerin) 1
GO	metal ion binding	116	2658	0.989	11278	Kruppel-like factor 12
GO	metal ion binding	116	2658	0.989	114088	tripartite motif-containing 9
GO	metal ion binding	116	2658	0.989	114757	cytoglobin
GO	metal ion binding	116	2658	0.989	114804	ring finger protein 157
GO	metal ion binding	116	2658	0.989	126374	Wilms tumor 1 interacting protein
GO	metal ion binding	116	2658	0.989	130507	ubiquitin protein ligase E3 component n-recognin 3 (putative)
GO	metal ion binding	116	2658	0.989	132625	zinc finger protein 42 homolog (mouse)
GO	metal ion binding	116	2658	0.989	134637	adenosine deaminase, tRNA-specific 2, TAD2 homolog (S. cerevisiae)
GO	metal ion binding	116	2658	0.989	148213	zinc finger protein 681
GO	metal ion binding	116	2658	0.989	1543	cytochrome P450, family 1, subfamily A, polypeptide 1
GO	metal ion binding	116	2658	0.989	157570	establishment of cohesion 1 homolog 2 (S. cerevisiae)
GO	metal ion binding	116	2658	0.989	166336	prickle homolog 2 (Drosophila)
GO	metal ion binding	116	2658	0.989	1788	DNA (cytosine-5-)-methyltransferase 3 alpha
GO	metal ion binding	116	2658	0.989	195828	zinc finger protein 367
GO	metal ion binding	116	2658	0.989	2135	exostoses (multiple)-like 2
GO	metal ion binding	116	2658	0.989	221687	ring finger protein 182
GO	metal ion binding	116	2658	0.989	2273	four and a half LIM domains 1
GO	metal ion binding	116	2658	0.989	23590	prenyl (decaprenyl) diphosphate synthase, subunit 1
GO	metal ion binding	116	2658	0.989	2534	FYN oncogene related to SRC, FGR, YES
GO	metal ion binding	116	2658	0.989	25885	polymerase (RNA) I polypeptide A, 194kDa
GO	metal ion binding	116	2658	0.989	25953	paroxysmal nonkinesigenic dyskinesia
GO	metal ion binding	116	2658	0.989	2618	phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide
GO	metal ion binding	116	2658	0.989	26519	translocase of inner mitochondrial membrane 10 homolog (yeast)
GO	metal ion binding	116	2658	0.989	26521	translocase of inner mitochondrial membrane 8 homolog B (yeast)
GO	metal ion binding	116	2658	0.989	2736	GLI family zinc finger 2
GO	metal ion binding	116	2658	0.989	283208	prolyl 4-hydroxylase, alpha polypeptide III
GO	metal ion binding	116	2658	0.989	283455	kinase suppressor of ras 2

GO	metal ion binding	116	2658	0.989	284443	zinc finger protein 493
GO	metal ion binding	116	2658	0.989	286151	F-box protein 43
GO	metal ion binding	116	2658	0.989	2863	G protein-coupled receptor 39
GO	metal ion binding	116	2658	0.989	29128	ubiquitin-like with PHD and ring finger domains 1
GO	metal ion binding	116	2658	0.989	29922	non-metastatic cells 7, protein expressed in (nucleoside-diphosphate kinas
GO	metal ion binding	116	2658	0.989	29995	LIM and cysteine-rich domains 1
GO	metal ion binding	116	2658	0.989	332	baculoviral IAP repeat-containing 5
GO	metal ion binding	116	2658	0.989	339761	cytochrome P450, family 27, subfamily C, polypeptide 1
GO	metal ion binding	116	2658	0.989	3751	potassium voltage-gated channel, Shal-related subfamily, member 2
GO	metal ion binding	116	2658	0.989	377677	carbonic anhydrase XIII
GO	metal ion binding	116	2658	0.989	3778	potassium large conductance calcium-activated channel, subfamily M, alph
GO	metal ion binding	116	2658	0.989	389421	lin-28 homolog B (C. elegans)
GO	metal ion binding	116	2658	0.989	3975	LIM homeobox 1
GO	metal ion binding	116	2658	0.989	411	arylsulfatase B
GO	metal ion binding	116	2658	0.989	4171	minichromosome maintenance complex component 2
GO	metal ion binding	116	2658	0.989	431707	LIM homeobox 8
GO	metal ion binding	116	2658	0.989	4318	matrix metallopeptidase 9 (gelatinase B, 92kDa gelatinase, 92kDa type IV c
GO	metal ion binding	116	2658	0.989	479	ATPase, H+/K+ transporting, nongastric, alpha polypeptide
GO	metal ion binding	116	2658	0.989	4884	neuronal pentraxin I
GO	metal ion binding	116	2658	0.989	50940	phosphodiesterase 11A
GO	metal ion binding	116	2658	0.989	51136	ring finger protein, transmembrane 1
GO	metal ion binding	116	2658	0.989	51218	glutaredoxin 5
GO	metal ion binding	116	2658	0.989	5140	phosphodiesterase 3B, cGMP-inhibited
GO	metal ion binding	116	2658	0.989	5145	phosphodiesterase 6A, cGMP-specific, rod, alpha
GO	metal ion binding	116	2658	0.989	5184	peptidase D
GO	metal ion binding	116	2658	0.989	5264	phytanoyl-CoA 2-hydroxylase
GO	metal ion binding	116	2658	0.989	5440	polymerase (RNA) II (DNA directed) polypeptide K, 7.0kDa
GO	metal ion binding	116	2658	0.989	54796	basonuclin 2
GO	metal ion binding	116	2658	0.989	54822	transient receptor potential cation channel, subfamily M, member 7
GO	metal ion binding	116	2658	0.989	54849	differentially expressed in FDCP 8 homolog (mouse)
GO	metal ion binding	116	2658	0.989	54993	zinc finger and SCAN domain containing 2
GO	metal ion binding	116	2658	0.989	55016	membrane-associated ring finger (C3HC4) 1
GO	metal ion binding	116	2658	0.989	55084	sine oculis binding protein homolog (Drosophila)
GO	metal ion binding	116	2658	0.989	55521	tripartite motif-containing 36
GO	metal ion binding	116	2658	0.989	5558	primase, DNA, polypeptide 2 (58kDa)
GO	metal ion binding	116	2658	0.989	55803	ArfGAP with dual PH domains 2

GO	metal ion binding	116	2658	0.989	55854	zinc finger CCCH-type containing 15
GO	metal ion binding	116	2658	0.989	5588	protein kinase C, theta
GO	metal ion binding	116	2658	0.989	56852	RAD18 homolog (S. cerevisiae)
GO	metal ion binding	116	2658	0.989	57484	ring finger protein 150
GO	metal ion binding	116	2658	0.989	57574	membrane-associated ring finger (C3HC4) 4
GO	metal ion binding	116	2658	0.989	57590	WD repeat and FYVE domain containing 1
GO	metal ion binding	116	2658	0.989	58499	zinc finger protein 462
GO	metal ion binding	116	2658	0.989	59336	PR domain containing 13
GO	metal ion binding	116	2658	0.989	619279	zinc finger protein 704
GO	metal ion binding	116	2658	0.989	6299	sal-like 1 (Drosophila)
GO	metal ion binding	116	2658	0.989	64393	zinc finger, matrin type 3
GO	metal ion binding	116	2658	0.989	64943	5'-nucleotidase domain containing 2
GO	metal ion binding	116	2658	0.989	659	bone morphogenetic protein receptor, type II (serine/threonine kinase)
GO	metal ion binding	116	2658	0.989	6591	snail homolog 2 (Drosophila)
GO	metal ion binding	116	2658	0.989	6615	snail homolog 1 (Drosophila)
GO	metal ion binding	116	2658	0.989	672	breast cancer 1, early onset
GO	metal ion binding	116	2658	0.989	7046	transforming growth factor, beta receptor 1
GO	metal ion binding	116	2658	0.989	7078	TIMP metallopeptidase inhibitor 3
GO	metal ion binding	116	2658	0.989	7490	Wilms tumor 1
GO	metal ion binding	116	2658	0.989	7552	zinc finger protein 711
GO	metal ion binding	116	2658	0.989	767	carbonic anhydrase VIII
GO	metal ion binding	116	2658	0.989	7711	zinc finger protein 155
GO	metal ion binding	116	2658	0.989	79698	zinc finger, matrin type 4
GO	metal ion binding	116	2658	0.989	79710	MORC family CW-type zinc finger 4
GO	metal ion binding	116	2658	0.989	79814	agmatine ureohydrolase (agmatinase)
GO	metal ion binding	116	2658	0.989	81035	collectin sub-family member 12
GO	metal ion binding	116	2658	0.989	81786	tripartite motif-containing 7
GO	metal ion binding	116	2658	0.989	8193	D4, zinc and double PHD fingers family 1
GO	metal ion binding	116	2658	0.989	84083	zinc finger, RAN-binding domain containing 3
GO	metal ion binding	116	2658	0.989	84101	ubiquitin specific peptidase 44
GO	metal ion binding	116	2658	0.989	84168	anthrax toxin receptor 1
GO	metal ion binding	116	2658	0.989	84172	polymerase (RNA) I polypeptide B, 128kDa
GO	metal ion binding	116	2658	0.989	84622	zinc finger protein 594
GO	metal ion binding	116	2658	0.989	84878	zinc finger and BTB domain containing 45
GO	metal ion binding	116	2658	0.989	8626	tumor protein p63
GO	metal ion binding	116	2658	0.989	8728	ADAM metallopeptidase domain 19 (meltrin beta)

GO	metal ion binding	116	2658	0.989	8747	ADAM metallopeptidase domain 21
GO	metal ion binding	116	2658	0.989	8997	kalirin, RhoGEF kinase
GO	metal ion binding	116	2658	0.989	91801	alkB, alkylation repair homolog 8 (E. coli)
GO	metal ion binding	116	2658	0.989	91975	zinc finger protein 300
GO	metal ion binding	116	2658	0.989	92312	mex-3 homolog A (C. elegans)
GO	metal ion binding	116	2658	0.989	9260	PDZ and LIM domain 7 (enigma)
GO	metal ion binding	116	2658	0.989	93474	zinc finger protein 670
GO	metal ion binding	116	2658	0.989	9355	LIM homeobox 2
GO	metal ion binding	116	2658	0.989	9420	cytochrome P450, family 7, subfamily B, polypeptide 1
GO	metal ion binding	116	2658	0.989	9744	ArfGAP with coiled-coil, ankyrin repeat and PH domains 1
GO	metal ion binding	116	2658	0.989	9839	zinc finger E-box binding homeobox 2
GO	metallopeptidase activity	2	88	0.989	10213	proteasome (prosome, macropain) 26S subunit, non-ATPase, 14
GO	metallopeptidase activity	2	88	0.989	8747	ADAM metallopeptidase domain 21
GO	early endosome membrane	1	37	0.989	10254	signal transducing adaptor molecule (SH3 domain and ITAM motif) 2
GO	endosome	6	215	0.989	10254	signal transducing adaptor molecule (SH3 domain and ITAM motif) 2
GO	endosome	6	215	0.989	2534	FYN oncogene related to SRC, FGR, YES
GO	endosome	6	215	0.989	55207	ADP-ribosylation factor-like 8B
GO	endosome	6	215	0.989	6683	spastin
GO	endosome	6	215	0.989	7037	transferrin receptor (p90, CD71)
GO	endosome	6	215	0.989	83930	STARD3 N-terminal like
GO	intracellular protein transport	7	174	0.989	10254	signal transducing adaptor molecule (SH3 domain and ITAM motif) 2
GO	intracellular protein transport	7	174	0.989	1121	choroideremia (Rab escort protein 1)
GO	intracellular protein transport	7	174	0.989	2898	glutamate receptor, ionotropic, kainate 2
GO	intracellular protein transport	7	174	0.989	3836	karyopherin alpha 1 (importin alpha 5)
GO	intracellular protein transport	7	174	0.989	3838	karyopherin alpha 2 (RAG cohort 1, importin alpha 1)
GO	intracellular protein transport	7	174	0.989	54843	synaptotagmin-like 2
GO	intracellular protein transport	7	174	0.989	8905	adaptor-related protein complex 1, sigma 2 subunit
GO	positive regulation of anti-apoptosis	1	32	0.989	1026	cyclin-dependent kinase inhibitor 1A (p21, Cip1)
GO	positive regulation of B cell proliferatior	1	25	0.989	1026	cyclin-dependent kinase inhibitor 1A (p21, Cip1)
GO	cell proliferation	12	286	0.989	10293	TRAF interacting protein
GO	cell proliferation	12	286	0.989	1164	CDC28 protein kinase regulatory subunit 2
GO	cell proliferation	12	286	0.989	1543	cytochrome P450, family 1, subfamily A, polypeptide 1
GO	cell proliferation	12	286	0.989	1841	deoxythymidylate kinase (thymidylate kinase)
GO	cell proliferation	12	286	0.989	2242	feline sarcoma oncogene
GO	cell proliferation	12	286	0.989	2736	GLI family zinc finger 2
GO	cell proliferation	12	286	0.989	29128	ubiquitin-like with PHD and ring finger domains 1

GO	cell proliferation	12	286	0.989	54331	guanine nucleotide binding protein (G protein), gamma 2
GO	cell proliferation	12	286	0.989	55759	WD repeat domain 12
GO	cell proliferation	12	286	0.989	586	branched chain aminotransferase 1, cytosolic
GO	cell proliferation	12	286	0.989	60675	prokineticin 2
GO	cell proliferation	12	286	0.989	6695	sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 1
GO	perinuclear region of cytoplasm	14	309	0.989	10293	TRAF interacting protein
GO	perinuclear region of cytoplasm	14	309	0.989	11226	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltr
GO	perinuclear region of cytoplasm	14	309	0.989	25780	RAS guanyl releasing protein 3 (calcium and DAG-regulated)
GO	perinuclear region of cytoplasm	14	309	0.989	26019	UPF2 regulator of nonsense transcripts homolog (yeast)
GO	perinuclear region of cytoplasm	14	309	0.989	26999	cytoplasmic FMR1 interacting protein 2
GO	perinuclear region of cytoplasm	14	309	0.989	309	annexin A6
GO	perinuclear region of cytoplasm	14	309	0.989	4734	neural precursor cell expressed, developmentally down-regulated 4
GO	perinuclear region of cytoplasm	14	309	0.989	4830	non-metastatic cells 1, protein (NM23A) expressed in
GO	perinuclear region of cytoplasm	14	309	0.989	51191	hect domain and RLD 5
GO	perinuclear region of cytoplasm	14	309	0.989	51499	TP53 regulated inhibitor of apoptosis 1
GO	perinuclear region of cytoplasm	14	309	0.989	6683	spastin
GO	perinuclear region of cytoplasm	14	309	0.989	7037	transferrin receptor (p90, CD71)
GO	perinuclear region of cytoplasm	14	309	0.989	8997	kalirin, RhoGEF kinase
GO	perinuclear region of cytoplasm	14	309	0.989	9053	microtubule-associated protein 7
GO	zinc ion binding	81	1867	0.989	10293	TRAF interacting protein
GO	zinc ion binding	81	1867	0.989	10612	tripartite motif-containing 3
GO	zinc ion binding	81	1867	0.989	10893	matrix metallopeptidase 24 (membrane-inserted)
GO	zinc ion binding	81	1867	0.989	11278	Kruppel-like factor 12
GO	zinc ion binding	81	1867	0.989	114088	tripartite motif-containing 9
GO	zinc ion binding	81	1867	0.989	114804	ring finger protein 157
GO	zinc ion binding	81	1867	0.989	126374	Wilms tumor 1 interacting protein
GO	zinc ion binding	81	1867	0.989	130507	ubiquitin protein ligase E3 component n-recognin 3 (putative)
GO	zinc ion binding	81	1867	0.989	132625	zinc finger protein 42 homolog (mouse)
GO	zinc ion binding	81	1867	0.989	134637	adenosine deaminase, tRNA-specific 2, TAD2 homolog (S. cerevisiae)
GO	zinc ion binding	81	1867	0.989	148213	zinc finger protein 681
GO	zinc ion binding	81	1867	0.989	166336	prickle homolog 2 (Drosophila)
GO	zinc ion binding	81	1867	0.989	1788	DNA (cytosine-5-)-methyltransferase 3 alpha
GO	zinc ion binding	81	1867	0.989	195828	zinc finger protein 367
GO	zinc ion binding	81	1867	0.989	221687	ring finger protein 182
GO	zinc ion binding	81	1867	0.989	2273	four and a half LIM domains 1
GO	zinc ion binding	81	1867	0.989	22891	zinc finger protein 365

GO	zinc ion binding	81	1867	0.989	25953	paroxysmal nonkinesigenic dyskinesia
GO	zinc ion binding	81	1867	0.989	26519	translocase of inner mitochondrial membrane 10 homolog (yeast)
GO	zinc ion binding	81	1867	0.989	26521	translocase of inner mitochondrial membrane 8 homolog B (yeast)
GO	zinc ion binding	81	1867	0.989	2736	GLI family zinc finger 2
GO	zinc ion binding	81	1867	0.989	27445	piccolo (presynaptic cytomatrix protein)
GO	zinc ion binding	81	1867	0.989	284443	zinc finger protein 493
GO	zinc ion binding	81	1867	0.989	286151	F-box protein 43
GO	zinc ion binding	81	1867	0.989	29128	ubiquitin-like with PHD and ring finger domains 1
GO	zinc ion binding	81	1867	0.989	29995	LIM and cysteine-rich domains 1
GO	zinc ion binding	81	1867	0.989	332	baculoviral IAP repeat-containing 5
GO	zinc ion binding	81	1867	0.989	377677	carbonic anhydrase XIII
GO	zinc ion binding	81	1867	0.989	389421	lin-28 homolog B (C. elegans)
GO	zinc ion binding	81	1867	0.989	3975	LIM homeobox 1
GO	zinc ion binding	81	1867	0.989	4312	matrix metallopeptidase 1 (interstitial collagenase)
GO	zinc ion binding	81	1867	0.989	431707	LIM homeobox 8
GO	zinc ion binding	81	1867	0.989	4318	matrix metallopeptidase 9 (gelatinase B, 92kDa gelatinase, 92kDa type IV c
GO	zinc ion binding	81	1867	0.989	4319	matrix metallopeptidase 10 (stromelysin 2)
GO	zinc ion binding	81	1867	0.989	51136	ring finger protein, transmembrane 1
GO	zinc ion binding	81	1867	0.989	5440	polymerase (RNA) II (DNA directed) polypeptide K, 7.0kDa
GO	zinc ion binding	81	1867	0.989	54796	basonuclin 2
GO	zinc ion binding	81	1867	0.989	54843	synaptotagmin-like 2
GO	zinc ion binding	81	1867	0.989	54849	differentially expressed in FDCP 8 homolog (mouse)
GO	zinc ion binding	81	1867	0.989	54993	zinc finger and SCAN domain containing 2
GO	zinc ion binding	81	1867	0.989	55016	membrane-associated ring finger (C3HC4) 1
GO	zinc ion binding	81	1867	0.989	55521	tripartite motif-containing 36
GO	zinc ion binding	81	1867	0.989	55803	ArfGAP with dual PH domains 2
GO	zinc ion binding	81	1867	0.989	55854	zinc finger CCCH-type containing 15
GO	zinc ion binding	81	1867	0.989	56852	RAD18 homolog (S. cerevisiae)
GO	zinc ion binding	81	1867	0.989	57484	ring finger protein 150
GO	zinc ion binding	81	1867	0.989	57574	membrane-associated ring finger (C3HC4) 4
GO	zinc ion binding	81	1867	0.989	57590	WD repeat and FYVE domain containing 1
GO	zinc ion binding	81	1867	0.989	58499	zinc finger protein 462
GO	zinc ion binding	81	1867	0.989	59336	PR domain containing 13
GO	zinc ion binding	81	1867	0.989	619279	zinc finger protein 704
GO	zinc ion binding	81	1867	0.989	6299	sal-like 1 (Drosophila)
GO	zinc ion binding	81	1867	0.989	64393	zinc finger, matrin type 3

GO	zinc ion binding	81	1867	0.989	6591	snail homolog 2 (Drosophila)
GO	zinc ion binding	81	1867	0.989	6615	snail homolog 1 (Drosophila)
GO	zinc ion binding	81	1867	0.989	672	breast cancer 1, early onset
GO	zinc ion binding	81	1867	0.989	7490	Wilms tumor 1
GO	zinc ion binding	81	1867	0.989	7552	zinc finger protein 711
GO	zinc ion binding	81	1867	0.989	767	carbonic anhydrase VIII
GO	zinc ion binding	81	1867	0.989	7711	zinc finger protein 155
GO	zinc ion binding	81	1867	0.989	79698	zinc finger, matrin type 4
GO	zinc ion binding	81	1867	0.989	79710	MORC family CW-type zinc finger 4
GO	zinc ion binding	81	1867	0.989	81786	tripartite motif-containing 7
GO	zinc ion binding	81	1867	0.989	8193	D4, zinc and double PHD fingers family 1
GO	zinc ion binding	81	1867	0.989	84083	zinc finger, RAN-binding domain containing 3
GO	zinc ion binding	81	1867	0.989	84101	ubiquitin specific peptidase 44
GO	zinc ion binding	81	1867	0.989	84206	mex-3 homolog B (C. elegans)
GO	zinc ion binding	81	1867	0.989	8458	transcription termination factor, RNA polymerase II
GO	zinc ion binding	81	1867	0.989	84622	zinc finger protein 594
GO	zinc ion binding	81	1867	0.989	84878	zinc finger and BTB domain containing 45
GO	zinc ion binding	81	1867	0.989	8626	tumor protein p63
GO	zinc ion binding	81	1867	0.989	8728	ADAM metallopeptidase domain 19 (meltrin beta)
GO	zinc ion binding	81	1867	0.989	8747	ADAM metallopeptidase domain 21
GO	zinc ion binding	81	1867	0.989	91975	zinc finger protein 300
GO	zinc ion binding	81	1867	0.989	92312	mex-3 homolog A (C. elegans)
GO	zinc ion binding	81	1867	0.989	9260	PDZ and LIM domain 7 (enigma)
GO	zinc ion binding	81	1867	0.989	93474	zinc finger protein 670
GO	zinc ion binding	81	1867	0.989	9355	LIM homeobox 2
GO	zinc ion binding	81	1867	0.989	9540	tumor protein p53 inducible protein 3
GO	zinc ion binding	81	1867	0.989	9744	ArfGAP with coiled-coil, ankyrin repeat and PH domains 1
GO	zinc ion binding	81	1867	0.989	9839	zinc finger E-box binding homeobox 2
GO	activation of phospholipase C activity	1	22	0.989	10395	deleted in liver cancer 1
GO	focal adhesion	3	86	0.989	10395	deleted in liver cancer 1
GO	focal adhesion	3	86	0.989	30011	SH3-domain kinase binding protein 1
GO	focal adhesion	3	86	0.989	9260	PDZ and LIM domain 7 (enigma)
GO	Rho GTPase activator activity	1	22	0.989	10395	deleted in liver cancer 1
GO	transcriptional repressor complex	1	29	0.989	1045	caudal type homeobox 2
GO	endoplasmic reticulum membrane	21	518	0.989	1047	calmegin
GO	endoplasmic reticulum membrane	21	518	0.989	13	arylacetamide deacetylase (esterase)

GO	endoplasmic reticulum membrane	21	518	0.989	145173	beta 1,3-galactosyltransferase-like
GO	endoplasmic reticulum membrane	21	518	0.989	1543	cytochrome P450, family 1, subfamily A, polypeptide 1
GO	endoplasmic reticulum membrane	21	518	0.989	1733	deiodinase, iodothyronine, type I
GO	endoplasmic reticulum membrane	21	518	0.989	1984	eukaryotic translation initiation factor 5A
GO	endoplasmic reticulum membrane	21	518	0.989	23305	acyl-CoA synthetase long-chain family member 6
GO	endoplasmic reticulum membrane	21	518	0.989	241	arachidonate 5-lipoxygenase-activating protein
GO	endoplasmic reticulum membrane	21	518	0.989	27429	HtrA serine peptidase 2
GO	endoplasmic reticulum membrane	21	518	0.989	51062	atlastin GTPase 1
GO	endoplasmic reticulum membrane	21	518	0.989	581	BCL2-associated X protein
GO	endoplasmic reticulum membrane	21	518	0.989	5924	Ras protein-specific guanine nucleotide-releasing factor 2
GO	endoplasmic reticulum membrane	21	518	0.989	64131	xylosyltransferase I
GO	endoplasmic reticulum membrane	21	518	0.989	6785	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like
GO	endoplasmic reticulum membrane	21	518	0.989	79071	ELOVL family member 6, elongation of long chain fatty acids (FEN1/Elo2, SU
GO	endoplasmic reticulum membrane	21	518	0.989	79669	chromosome 3 open reading frame 52
GO	endoplasmic reticulum membrane	21	518	0.989	79993	ELOVL family member 7, elongation of long chain fatty acids (yeast)
GO	endoplasmic reticulum membrane	21	518	0.989	81562	lectin, mannose-binding 2-like
GO	endoplasmic reticulum membrane	21	518	0.989	84230	leucine rich repeat containing 8 family, member C
GO	endoplasmic reticulum membrane	21	518	0.989	90701	SEC11 homolog C (S. cerevisiae)
GO	endoplasmic reticulum membrane	21	518	0.989	9420	cytochrome P450, family 7, subfamily B, polypeptide 1
GO	endoplasmic reticulum	34	880	0.989	1047	calmegin
GO	endoplasmic reticulum	34	880	0.989	10492	synaptotagmin binding, cytoplasmic RNA interacting protein
GO	endoplasmic reticulum	34	880	0.989	13	arylacetamide deacetylase (esterase)
GO	endoplasmic reticulum	34	880	0.989	145173	beta 1,3-galactosyltransferase-like
GO	endoplasmic reticulum	34	880	0.989	1543	cytochrome P450, family 1, subfamily A, polypeptide 1
GO	endoplasmic reticulum	34	880	0.989	1733	deiodinase, iodothyronine, type I
GO	endoplasmic reticulum	34	880	0.989	1984	eukaryotic translation initiation factor 5A
GO	endoplasmic reticulum	34	880	0.989	2135	exostoses (multiple)-like 2
GO	endoplasmic reticulum	34	880	0.989	23305	acyl-CoA synthetase long-chain family member 6
GO	endoplasmic reticulum	34	880	0.989	23562	claudin 14
GO	endoplasmic reticulum	34	880	0.989	241	arachidonate 5-lipoxygenase-activating protein
GO	endoplasmic reticulum	34	880	0.989	27429	HtrA serine peptidase 2
GO	endoplasmic reticulum	34	880	0.989	283208	prolyl 4-hydroxylase, alpha polypeptide III
GO	endoplasmic reticulum	34	880	0.989	29940	dermatan sulfate epimerase
GO	endoplasmic reticulum	34	880	0.989	341	apolipoprotein C-I
GO	endoplasmic reticulum	34	880	0.989	3778	potassium large conductance calcium-activated channel, subfamily M, alph
GO	endoplasmic reticulum	34	880	0.989	51062	atlastin GTPase 1

GO	endoplasmic reticulum	34	880	0.989	5110	protein-L-isoaspartate (D-aspartate) O-methyltransferase
GO	endoplasmic reticulum	34	880	0.989	5140	phosphodiesterase 3B, cGMP-inhibited
GO	endoplasmic reticulum	34	880	0.989	57333	reticulocalbin 3, EF-hand calcium binding domain
GO	endoplasmic reticulum	34	880	0.989	581	BCL2-associated X protein
GO	endoplasmic reticulum	34	880	0.989	590	butyrylcholinesterase
GO	endoplasmic reticulum	34	880	0.989	5924	Ras protein-specific guanine nucleotide-releasing factor 2
GO	endoplasmic reticulum	34	880	0.989	64131	xylosyltransferase I
GO	endoplasmic reticulum	34	880	0.989	6683	spastin
GO	endoplasmic reticulum	34	880	0.989	6785	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like
GO	endoplasmic reticulum	34	880	0.989	79071	ELOVL family member 6, elongation of long chain fatty acids (FEN1/Elo2, S
GO	endoplasmic reticulum	34	880	0.989	79669	chromosome 3 open reading frame 52
GO	endoplasmic reticulum	34	880	0.989	79993	ELOVL family member 7, elongation of long chain fatty acids (yeast)
GO	endoplasmic reticulum	34	880	0.989	81562	lectin, mannose-binding 2-like
GO	endoplasmic reticulum	34	880	0.989	84230	leucine rich repeat containing 8 family, member C
GO	endoplasmic reticulum	34	880	0.989	90701	SEC11 homolog C (S. cerevisiae)
GO	endoplasmic reticulum	34	880	0.989	9420	cytochrome P450, family 7, subfamily B, polypeptide 1
GO	endoplasmic reticulum	34	880	0.989	9482	syntaxin 8
GO	histone H3 acetylation	1	24	0.989	10474	transcriptional adaptor 3
GO	transcription coactivator activity	7	192	0.989	10474	transcriptional adaptor 3
GO	transcription coactivator activity	7	192	0.989	5469	mediator complex subunit 1
GO	transcription coactivator activity	7	192	0.989	5702	proteasome (prosome, macropain) 26S subunit, ATPase, 3
GO	transcription coactivator activity	7	192	0.989	6672	SP100 nuclear antigen
GO	transcription coactivator activity	7	192	0.989	672	breast cancer 1, early onset
GO	transcription coactivator activity	7	192	0.989	7021	transcription factor AP-2 beta (activating enhancer binding protein 2 beta)
GO	transcription coactivator activity	7	192	0.989	898	cyclin E1
GO	microsome	10	219	0.989	10492	synaptotagmin binding, cytoplasmic RNA interacting protein
GO	microsome	10	219	0.989	13	arylacetamide deacetylase (esterase)
GO	microsome	10	219	0.989	1543	cytochrome P450, family 1, subfamily A, polypeptide 1
GO	microsome	10	219	0.989	1733	deiodinase, iodothyronine, type I
GO	microsome	10	219	0.989	23305	acyl-CoA synthetase long-chain family member 6
GO	microsome	10	219	0.989	4830	non-metastatic cells 1, protein (NM23A) expressed in
GO	microsome	10	219	0.989	51062	atlastin GTPase 1
GO	microsome	10	219	0.989	5140	phosphodiesterase 3B, cGMP-inhibited
GO	microsome	10	219	0.989	90701	SEC11 homolog C (S. cerevisiae)
GO	microsome	10	219	0.989	9420	cytochrome P450, family 7, subfamily B, polypeptide 1
GO	blood vessel remodeling	1	22	0.989	10512	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (

GO	extracellular space	26	647	0.989	10512	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (
GO	extracellular space	26	647	0.989	112616	CKLF-like MARVEL transmembrane domain containing 7
GO	extracellular space	26	647	0.989	123920	CKLF-like MARVEL transmembrane domain containing 3
GO	extracellular space	26	647	0.989	2321	fms-related tyrosine kinase 1 (vascular endothelial growth factor/vascular
GO	extracellular space	26	647	0.989	24147	four jointed box 1 (Drosophila)
GO	extracellular space	26	647	0.989	2878	glutathione peroxidase 3 (plasma)
GO	extracellular space	26	647	0.989	348	apolipoprotein E
GO	extracellular space	26	647	0.989	3557	interleukin 1 receptor antagonist
GO	extracellular space	26	647	0.989	3589	interleukin 11
GO	extracellular space	26	647	0.989	3952	leptin
GO	extracellular space	26	647	0.989	4318	matrix metallopeptidase 9 (gelatinase B, 92kDa gelatinase, 92kDa type IV c
GO	extracellular space	26	647	0.989	4319	matrix metallopeptidase 10 (stromelysin 2)
GO	extracellular space	26	647	0.989	5054	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor t
GO	extracellular space	26	647	0.989	5125	proprotein convertase subtilisin/kexin type 5
GO	extracellular space	26	647	0.989	5228	placental growth factor
GO	extracellular space	26	647	0.989	5654	HtrA serine peptidase 1
GO	extracellular space	26	647	0.989	5744	parathyroid hormone-like hormone
GO	extracellular space	26	647	0.989	57642	collagen, type XX, alpha 1
GO	extracellular space	26	647	0.989	590	butyrylcholinesterase
GO	extracellular space	26	647	0.989	6347	chemokine (C-C motif) ligand 2
GO	extracellular space	26	647	0.989	6422	secreted frizzled-related protein 1
GO	extracellular space	26	647	0.989	6586	slit homolog 3 (Drosophila)
GO	extracellular space	26	647	0.989	7857	secretogranin II (chromogranin C)
GO	extracellular space	26	647	0.989	81029	wingless-type MMTV integration site family, member 5B
GO	extracellular space	26	647	0.989	8788	delta-like 1 homolog (Drosophila)
GO	extracellular space	26	647	0.989	9244	cytokine receptor-like factor 1
GO	immune response	9	303	0.989	10512	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (
GO	immune response	9	303	0.989	2533	FYN binding protein (FYB-120/130)
GO	immune response	9	303	0.989	353091	retinoic acid early transcript 1G
GO	immune response	9	303	0.989	355	Fas (TNF receptor superfamily, member 6)
GO	immune response	9	303	0.989	3557	interleukin 1 receptor antagonist
GO	immune response	9	303	0.989	56241	sushi domain containing 2
GO	immune response	9	303	0.989	57817	hepcidin antimicrobial peptide
GO	immune response	9	303	0.989	729230	chemokine (C-C motif) receptor 2
GO	immune response	9	303	0.989	8482	semaphorin 7A, GPI membrane anchor (John Milton Hagen blood group)
GO	receptor activity	52	1148	0.989	10512	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (

GO	receptor activity	52	1148	0.989	1136	cholinergic receptor, nicotinic, alpha 3
GO	receptor activity	52	1148	0.989	1138	cholinergic receptor, nicotinic, alpha 5
GO	receptor activity	52	1148	0.989	119749	olfactory receptor, family 4, subfamily C, member 46
GO	receptor activity	52	1148	0.989	125962	olfactory receptor, family 7, subfamily G, member 1
GO	receptor activity	52	1148	0.989	131450	CD200 receptor 1
GO	receptor activity	52	1148	0.989	146760	reticulon 4 receptor-like 1
GO	receptor activity	52	1148	0.989	2045	EPH receptor A7
GO	receptor activity	52	1148	0.989	2149	coagulation factor II (thrombin) receptor
GO	receptor activity	52	1148	0.989	2150	coagulation factor II (thrombin) receptor-like 1
GO	receptor activity	52	1148	0.989	2151	coagulation factor II (thrombin) receptor-like 2
GO	receptor activity	52	1148	0.989	2264	fibroblast growth factor receptor 4
GO	receptor activity	52	1148	0.989	22801	integrin, alpha 11
GO	receptor activity	52	1148	0.989	2321	fms-related tyrosine kinase 1 (vascular endothelial growth factor/vascular
GO	receptor activity	52	1148	0.989	23432	G protein-coupled receptor 161
GO	receptor activity	52	1148	0.989	2558	gamma-aminobutyric acid (GABA) A receptor, alpha 5
GO	receptor activity	52	1148	0.989	282770	olfactory receptor, family 10, subfamily AG, member 1
GO	receptor activity	52	1148	0.989	283111	olfactory receptor, family 51, subfamily V, member 1
GO	receptor activity	52	1148	0.989	2842	G protein-coupled receptor 19
GO	receptor activity	52	1148	0.989	2845	G protein-coupled receptor 22
GO	receptor activity	52	1148	0.989	2850	G protein-coupled receptor 27
GO	receptor activity	52	1148	0.989	285659	olfactory receptor, family 2, subfamily V, member 2
GO	receptor activity	52	1148	0.989	2863	G protein-coupled receptor 39
GO	receptor activity	52	1148	0.989	2898	glutamate receptor, ionotropic, kainate 2
GO	receptor activity	52	1148	0.989	2906	glutamate receptor, ionotropic, N-methyl D-aspartate 2D
GO	receptor activity	52	1148	0.989	344838	progestin and adipoQ receptor family member IX
GO	receptor activity	52	1148	0.989	348938	NIPA-like domain containing 4
GO	receptor activity	52	1148	0.989	355	Fas (TNF receptor superfamily, member 6)
GO	receptor activity	52	1148	0.989	3685	integrin, alpha V (vitronectin receptor, alpha polypeptide, antigen CD51)
GO	receptor activity	52	1148	0.989	3694	integrin, beta 6
GO	receptor activity	52	1148	0.989	390061	olfactory receptor, family 51, subfamily Q, member 1
GO	receptor activity	52	1148	0.989	391114	olfactory receptor, family 6, subfamily K, member 3
GO	receptor activity	52	1148	0.989	4158	melanocortin 2 receptor (adrenocorticotropic hormone)
GO	receptor activity	52	1148	0.989	5021	oxytocin receptor
GO	receptor activity	52	1148	0.989	5028	purinergic receptor P2Y, G-protein coupled, 1
GO	receptor activity	52	1148	0.989	5031	pyrimidinergic receptor P2Y, G-protein coupled, 6
GO	receptor activity	52	1148	0.989	53637	sphingosine-1-phosphate receptor 5

GO	receptor activity	52	1148	0.989	54210	triggering receptor expressed on myeloid cells 1
GO	receptor activity	52	1148	0.989	5469	mediator complex subunit 1
GO	receptor activity	52	1148	0.989	54756	interleukin 17 receptor D
GO	receptor activity	52	1148	0.989	558	AXL receptor tyrosine kinase
GO	receptor activity	52	1148	0.989	5754	PTK7 protein tyrosine kinase 7
GO	receptor activity	52	1148	0.989	659	bone morphogenetic protein receptor, type II (serine/threonine kinase)
GO	receptor activity	52	1148	0.989	6833	ATP-binding cassette, sub-family C (CFTR/MRP), member 8
GO	receptor activity	52	1148	0.989	7010	TEK tyrosine kinase, endothelial
GO	receptor activity	52	1148	0.989	7037	transferrin receptor (p90, CD71)
GO	receptor activity	52	1148	0.989	7046	transforming growth factor, beta receptor 1
GO	receptor activity	52	1148	0.989	729230	chemokine (C-C motif) receptor 2
GO	receptor activity	52	1148	0.989	8482	semaphorin 7A, GPI membrane anchor (John Milton Hagen blood group)
GO	receptor activity	52	1148	0.989	91584	plexin A4
GO	receptor activity	52	1148	0.989	9244	cytokine receptor-like factor 1
GO	receptor activity	52	1148	0.989	9568	gamma-aminobutyric acid (GABA) B receptor, 2
GO	cell cortex	2	75	0.989	10539	glutaredoxin 3
GO	cell cortex	2	75	0.989	4734	neural precursor cell expressed, developmentally down-regulated 4
GO	Z disc	2	46	0.989	10539	glutaredoxin 3
GO	Z disc	2	46	0.989	91624	nexilin (F actin binding protein)
GO	protein transport	16	388	0.989	10612	tripartite motif-containing 3
GO	protein transport	16	388	0.989	10890	RAB10, member RAS oncogene family
GO	protein transport	16	388	0.989	11154	adaptor-related protein complex 4, sigma 1 subunit
GO	protein transport	16	388	0.989	1984	eukaryotic translation initiation factor 5A
GO	protein transport	16	388	0.989	26519	translocase of inner mitochondrial membrane 10 homolog (yeast)
GO	protein transport	16	388	0.989	26521	translocase of inner mitochondrial membrane 8 homolog B (yeast)
GO	protein transport	16	388	0.989	29887	sorting nexin 10
GO	protein transport	16	388	0.989	409	arrestin, beta 2
GO	protein transport	16	388	0.989	4928	nucleoporin 98kDa
GO	protein transport	16	388	0.989	55916	nuclear transport factor 2-like export factor 2
GO	protein transport	16	388	0.989	64393	zinc finger, matrin type 3
GO	protein transport	16	388	0.989	729025	solute carrier family 15, member 5
GO	protein transport	16	388	0.989	81562	lectin, mannose-binding 2-like
GO	protein transport	16	388	0.989	83871	RAB34, member RAS oncogene family
GO	protein transport	16	388	0.989	9688	nucleoporin 93kDa
GO	protein transport	16	388	0.989	9744	ArfGAP with coiled-coil, ankyrin repeat and PH domains 1
GO	response to virus	3	105	0.989	10622	polymerase (RNA) III (DNA directed) polypeptide G (32kD)

GO	response to virus	3	105	0.989	1543	cytochrome P450, family 1, subfamily A, polypeptide 1
GO	response to virus	3	105	0.989	59	actin, alpha 2, smooth muscle, aorta
GO	regulation of transcription	37	956	0.989	10656	KH domain containing, RNA binding, signal transduction associated 3
GO	regulation of transcription	37	956	0.989	1161	excision repair cross-complementing rodent repair deficiency, complement
GO	regulation of transcription	37	956	0.989	116931	mediator complex subunit 12-like
GO	regulation of transcription	37	956	0.989	126374	Wilms tumor 1 interacting protein
GO	regulation of transcription	37	956	0.989	132625	zinc finger protein 42 homolog (mouse)
GO	regulation of transcription	37	956	0.989	148213	zinc finger protein 681
GO	regulation of transcription	37	956	0.989	195828	zinc finger protein 367
GO	regulation of transcription	37	956	0.989	2139	eyes absent homolog 2 (Drosophila)
GO	regulation of transcription	37	956	0.989	284443	zinc finger protein 493
GO	regulation of transcription	37	956	0.989	29128	ubiquitin-like with PHD and ring finger domains 1
GO	regulation of transcription	37	956	0.989	2965	general transcription factor IIH, polypeptide 1, 62kDa
GO	regulation of transcription	37	956	0.989	29842	transcription factor CP2-like 1
GO	regulation of transcription	37	956	0.989	29995	LIM and cysteine-rich domains 1
GO	regulation of transcription	37	956	0.989	401265	kelch-like 31 (Drosophila)
GO	regulation of transcription	37	956	0.989	4171	minichromosome maintenance complex component 2
GO	regulation of transcription	37	956	0.989	4287	ataxin 3
GO	regulation of transcription	37	956	0.989	51003	mediator complex subunit 31
GO	regulation of transcription	37	956	0.989	51460	Scm-like with four mbt domains 1
GO	regulation of transcription	37	956	0.989	5245	prohibitin
GO	regulation of transcription	37	956	0.989	5469	mediator complex subunit 1
GO	regulation of transcription	37	956	0.989	54796	basonuclin 2
GO	regulation of transcription	37	956	0.989	58499	zinc finger protein 462
GO	regulation of transcription	37	956	0.989	59336	PR domain containing 13
GO	regulation of transcription	37	956	0.989	6299	sal-like 1 (Drosophila)
GO	regulation of transcription	37	956	0.989	6591	snail homolog 2 (Drosophila)
GO	regulation of transcription	37	956	0.989	7046	transforming growth factor, beta receptor 1
GO	regulation of transcription	37	956	0.989	7552	zinc finger protein 711
GO	regulation of transcription	37	956	0.989	79682	MLF1 interacting protein
GO	regulation of transcription	37	956	0.989	81606	limb bud and heart development homolog (mouse)
GO	regulation of transcription	37	956	0.989	81892	chromosome 14 open reading frame 156
GO	regulation of transcription	37	956	0.989	8193	D4, zinc and double PHD fingers family 1
GO	regulation of transcription	37	956	0.989	83879	cell division cycle associated 7
GO	regulation of transcription	37	956	0.989	8458	transcription termination factor, RNA polymerase II
GO	regulation of transcription	37	956	0.989	84622	zinc finger protein 594

GO	regulation of transcription	37	956	0.989	84878	zinc finger and BTB domain containing 45
GO	regulation of transcription	37	956	0.989	9242	musculin (activated B-cell factor-1)
GO	regulation of transcription	37	956	0.989	93649	myocardin
GO	SH3 domain binding	4	97	0.989	10656	KH domain containing, RNA binding, signal transduction associated 3
GO	SH3 domain binding	4	97	0.989	30011	SH3-domain kinase binding protein 1
GO	SH3 domain binding	4	97	0.989	8728	ADAM metallopeptidase domain 19 (meltrin beta)
GO	SH3 domain binding	4	97	0.989	9732	dedicator of cytokinesis 4
GO	brush border membrane	1	26	0.989	10672	guanine nucleotide binding protein (G protein), alpha 13
GO	G-protein coupled receptor protein sign	27	725	0.989	10672	guanine nucleotide binding protein (G protein), alpha 13
GO	G-protein coupled receptor protein sign	27	725	0.989	119749	olfactory receptor, family 4, subfamily C, member 46
GO	G-protein coupled receptor protein sign	27	725	0.989	125962	olfactory receptor, family 7, subfamily G, member 1
GO	G-protein coupled receptor protein sign	27	725	0.989	2150	coagulation factor II (thrombin) receptor-like 1
GO	G-protein coupled receptor protein sign	27	725	0.989	2151	coagulation factor II (thrombin) receptor-like 2
GO	G-protein coupled receptor protein sign	27	725	0.989	222611	G protein-coupled receptor 111
GO	G-protein coupled receptor protein sign	27	725	0.989	23432	G protein-coupled receptor 161
GO	G-protein coupled receptor protein sign	27	725	0.989	2774	guanine nucleotide binding protein (G protein), alpha activating activity pol
GO	G-protein coupled receptor protein sign	27	725	0.989	282770	olfactory receptor, family 10, subfamily AG, member 1
GO	G-protein coupled receptor protein sign	27	725	0.989	283111	olfactory receptor, family 51, subfamily V, member 1
GO	G-protein coupled receptor protein sign	27	725	0.989	2842	G protein-coupled receptor 19
GO	G-protein coupled receptor protein sign	27	725	0.989	2845	G protein-coupled receptor 22
GO	G-protein coupled receptor protein sign	27	725	0.989	2850	G protein-coupled receptor 27
GO	G-protein coupled receptor protein sign	27	725	0.989	285659	olfactory receptor, family 2, subfamily V, member 2
GO	G-protein coupled receptor protein sign	27	725	0.989	2863	G protein-coupled receptor 39
GO	G-protein coupled receptor protein sign	27	725	0.989	348	apolipoprotein E
GO	G-protein coupled receptor protein sign	27	725	0.989	390061	olfactory receptor, family 51, subfamily Q, member 1
GO	G-protein coupled receptor protein sign	27	725	0.989	391114	olfactory receptor, family 6, subfamily K, member 3
GO	G-protein coupled receptor protein sign	27	725	0.989	4158	melanocortin 2 receptor (adrenocorticotropic hormone)
GO	G-protein coupled receptor protein sign	27	725	0.989	5021	oxytocin receptor
GO	G-protein coupled receptor protein sign	27	725	0.989	53637	sphingosine-1-phosphate receptor 5
GO	G-protein coupled receptor protein sign	27	725	0.989	54331	guanine nucleotide binding protein (G protein), gamma 2
GO	G-protein coupled receptor protein sign	27	725	0.989	60675	prokineticin 2
GO	G-protein coupled receptor protein sign	27	725	0.989	6347	chemokine (C-C motif) ligand 2
GO	G-protein coupled receptor protein sign	27	725	0.989	729230	chemokine (C-C motif) receptor 2
GO	G-protein coupled receptor protein sign	27	725	0.989	8325	frizzled homolog 8 (Drosophila)
GO	G-protein coupled receptor protein sign	27	725	0.989	9568	gamma-aminobutyric acid (GABA) B receptor, 2
GO	in utero embryonic development	6	136	0.989	10672	guanine nucleotide binding protein (G protein), alpha 13

GO	in utero embryonic development	6	136	0.989	2736	GLI family zinc finger 2
GO	in utero embryonic development	6	136	0.989	3276	protein arginine methyltransferase 1
GO	in utero embryonic development	6	136	0.989	4436	mutS homolog 2, colon cancer, nonpolyposis type 1 (E. coli)
GO	in utero embryonic development	6	136	0.989	7046	transforming growth factor, beta receptor 1
GO	in utero embryonic development	6	136	0.989	8533	COP9 constitutive photomorphogenic homolog subunit 3 (Arabidopsis)
GO	molecular_function	19	577	0.989	10761	placenta-specific 1
GO	molecular_function	19	577	0.989	10777	cyclic AMP-regulated phosphoprotein, 21 kD
GO	molecular_function	19	577	0.989	10962	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophi
GO	molecular_function	19	577	0.989	11249	neurexophilin 2
GO	molecular_function	19	577	0.989	11259	filamin A interacting protein 1-like
GO	molecular_function	19	577	0.989	1290	collagen, type V, alpha 2
GO	molecular_function	19	577	0.989	132851	spermatogenesis associated 4
GO	molecular_function	19	577	0.989	2273	four and a half LIM domains 1
GO	molecular_function	19	577	0.989	266727	MAM domain containing glycosylphosphatidylinositol anchor 1
GO	molecular_function	19	577	0.989	27241	Bardet-Biedl syndrome 9
GO	molecular_function	19	577	0.989	54726	OTU domain containing 4
GO	molecular_function	19	577	0.989	54733	solute carrier family 35, member F2
GO	molecular_function	19	577	0.989	56651	chromosome 18 open reading frame 2
GO	molecular_function	19	577	0.989	64208	popeye domain containing 3
GO	molecular_function	19	577	0.989	66000	transmembrane protein 108
GO	molecular_function	19	577	0.989	7840	Alstrom syndrome 1
GO	molecular_function	19	577	0.989	8788	delta-like 1 homolog (Drosophila)
GO	molecular_function	19	577	0.989	93323	HAUS augmin-like complex, subunit 8
GO	molecular_function	19	577	0.989	9805	secernin 1
GO	response to unfolded protein	2	49	0.989	10808	heat shock 105kDa/110kDa protein 1
GO	response to unfolded protein	2	49	0.989	3336	heat shock 10kDa protein 1 (chaperonin 10)
GO	Golgi apparatus	34	784	0.989	10890	RAB10, member RAS oncogene family
GO	Golgi apparatus	34	784	0.989	11154	adaptor-related protein complex 4, sigma 1 subunit
GO	Golgi apparatus	34	784	0.989	11226	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltr
GO	Golgi apparatus	34	784	0.989	11227	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltr
GO	Golgi apparatus	34	784	0.989	114805	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltr
GO	Golgi apparatus	34	784	0.989	152007	GLI pathogenesis-related 2
GO	Golgi apparatus	34	784	0.989	1730	diaphanous homolog 2 (Drosophila)
GO	Golgi apparatus	34	784	0.989	2149	coagulation factor II (thrombin) receptor
GO	Golgi apparatus	34	784	0.989	2150	coagulation factor II (thrombin) receptor-like 1
GO	Golgi apparatus	34	784	0.989	23057	nicotinamide nucleotide adenylyltransferase 2

GO	Golgi apparatus	34	784	0.989	27065	DNA segment on chromosome 4 (unique) 234 expressed sequence
GO	Golgi apparatus	34	784	0.989	29940	dermatan sulfate epimerase
GO	Golgi apparatus	34	784	0.989	348	apolipoprotein E
GO	Golgi apparatus	34	784	0.989	3763	potassium inwardly-rectifying channel, subfamily J, member 6
GO	Golgi apparatus	34	784	0.989	3932	lymphocyte-specific protein tyrosine kinase
GO	Golgi apparatus	34	784	0.989	411	arylsulfatase B
GO	Golgi apparatus	34	784	0.989	4893	neuroblastoma RAS viral (v-ras) oncogene homolog
GO	Golgi apparatus	34	784	0.989	51062	atlastin GTPase 1
GO	Golgi apparatus	34	784	0.989	5125	proprotein convertase subtilisin/kexin type 5
GO	Golgi apparatus	34	784	0.989	5140	phosphodiesterase 3B, cGMP-inhibited
GO	Golgi apparatus	34	784	0.989	54331	guanine nucleotide binding protein (G protein), gamma 2
GO	Golgi apparatus	34	784	0.989	54756	interleukin 17 receptor D
GO	Golgi apparatus	34	784	0.989	57574	membrane-associated ring finger (C3HC4) 4
GO	Golgi apparatus	34	784	0.989	64131	xylosyltransferase I
GO	Golgi apparatus	34	784	0.989	79623	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltr
GO	Golgi apparatus	34	784	0.989	79929	MAP6 domain containing 1
GO	Golgi apparatus	34	784	0.989	81562	lectin, mannose-binding 2-like
GO	Golgi apparatus	34	784	0.989	83871	RAB34, member RAS oncogene family
GO	Golgi apparatus	34	784	0.989	84620	ST6 beta-galactosamide alpha-2,6-sialyltranferase 2
GO	Golgi apparatus	34	784	0.989	84752	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 9
GO	Golgi apparatus	34	784	0.989	8905	adaptor-related protein complex 1, sigma 2 subunit
GO	Golgi apparatus	34	784	0.989	9215	like-glycosyltransferase
GO	Golgi apparatus	34	784	0.989	9653	heparan sulfate 2-O-sulfotransferase 1
GO	Golgi apparatus	34	784	0.989	9910	RAB GTPase activating protein 1-like
GO	proteolysis	18	423	0.989	10893	matrix metallopeptidase 24 (membrane-inserted)
GO	proteolysis	18	423	0.989	132724	transmembrane protease, serine 11B
GO	proteolysis	18	423	0.989	25827	F-box and leucine-rich repeat protein 2
GO	proteolysis	18	423	0.989	27429	HtrA serine peptidase 2
GO	proteolysis	18	423	0.989	344805	transmembrane protease, serine 7
GO	proteolysis	18	423	0.989	4312	matrix metallopeptidase 1 (interstitial collagenase)
GO	proteolysis	18	423	0.989	4318	matrix metallopeptidase 9 (gelatinase B, 92kDa gelatinase, 92kDa type IV c
GO	proteolysis	18	423	0.989	4319	matrix metallopeptidase 10 (stromelysin 2)
GO	proteolysis	18	423	0.989	5125	proprotein convertase subtilisin/kexin type 5
GO	proteolysis	18	423	0.989	5184	peptidase D
GO	proteolysis	18	423	0.989	5624	protein C (inactivator of coagulation factors Va and VIIIa)
GO	proteolysis	18	423	0.989	5654	HtrA serine peptidase 1

GO	proteolysis	18	423	0.989	7037	transferrin receptor (p90, CD71)
GO	proteolysis	18	423	0.989	7113	transmembrane protease, serine 2
GO	proteolysis	18	423	0.989	8728	ADAM metallopeptidase domain 19 (meltrin beta)
GO	proteolysis	18	423	0.989	8747	ADAM metallopeptidase domain 21
GO	proteolysis	18	423	0.989	90701	SEC11 homolog C (S. cerevisiae)
GO	proteolysis	18	423	0.989	9805	secernin 1
GO	vesicle-mediated transport	3	165	0.989	11149	blood vessel epicardial substance
GO	vesicle-mediated transport	3	165	0.989	54843	synaptotagmin-like 2
GO	vesicle-mediated transport	3	165	0.989	8997	kalirin, RhoGEF kinase
GO	response to stimulus	14	477	0.989	1121	choroideremia (Rab escort protein 1)
GO	response to stimulus	14	477	0.989	119749	olfactory receptor, family 4, subfamily C, member 46
GO	response to stimulus	14	477	0.989	125962	olfactory receptor, family 7, subfamily G, member 1
GO	response to stimulus	14	477	0.989	27241	Bardet-Biedl syndrome 9
GO	response to stimulus	14	477	0.989	282770	olfactory receptor, family 10, subfamily AG, member 1
GO	response to stimulus	14	477	0.989	283111	olfactory receptor, family 51, subfamily V, member 1
GO	response to stimulus	14	477	0.989	285659	olfactory receptor, family 2, subfamily V, member 2
GO	response to stimulus	14	477	0.989	390061	olfactory receptor, family 51, subfamily Q, member 1
GO	response to stimulus	14	477	0.989	391114	olfactory receptor, family 6, subfamily K, member 3
GO	response to stimulus	14	477	0.989	5145	phosphodiesterase 6A, cGMP-specific, rod, alpha
GO	response to stimulus	14	477	0.989	5264	phytanoyl-CoA 2-hydroxylase
GO	response to stimulus	14	477	0.989	6785	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like
GO	response to stimulus	14	477	0.989	7078	TIMP metallopeptidase inhibitor 3
GO	response to stimulus	14	477	0.989	7840	Alstrom syndrome 1
GO	sugar binding	6	161	0.989	11226	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltr
GO	sugar binding	6	161	0.989	11227	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltr
GO	sugar binding	6	161	0.989	114805	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltr
GO	sugar binding	6	161	0.989	79623	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltr
GO	sugar binding	6	161	0.989	81035	collectin sub-family member 12
GO	sugar binding	6	161	0.989	81562	lectin, mannose-binding 2-like
GO	SH3/SH2 adaptor activity	2	50	0.989	1123	chimerin (chimaerin) 1
GO	SH3/SH2 adaptor activity	2	50	0.989	8835	suppressor of cytokine signaling 2
GO	neuropeptide signaling pathway	3	85	0.989	11249	neurexophilin 2
GO	neuropeptide signaling pathway	3	85	0.989	222611	G protein-coupled receptor 111
GO	neuropeptide signaling pathway	3	85	0.989	60675	prokineticin 2
GO	chemotaxis	5	117	0.989	112616	CKLF-like MARVEL transmembrane domain containing 7
GO	chemotaxis	5	117	0.989	123920	CKLF-like MARVEL transmembrane domain containing 3

GO	chemotaxis	5	117	0.989	60675	prokineticin 2
GO	chemotaxis	5	117	0.989	6347	chemokine (C-C motif) ligand 2
GO	chemotaxis	5	117	0.989	729230	chemokine (C-C motif) receptor 2
GO	cytokine activity	6	143	0.989	112616	CKLF-like MARVEL transmembrane domain containing 7
GO	cytokine activity	6	143	0.989	123920	CKLF-like MARVEL transmembrane domain containing 3
GO	cytokine activity	6	143	0.989	3557	interleukin 1 receptor antagonist
GO	cytokine activity	6	143	0.989	3589	interleukin 11
GO	cytokine activity	6	143	0.989	3624	inhibin, beta A
GO	cytokine activity	6	143	0.989	7857	secretogranin II (chromogranin C)
GO	heme binding	4	110	0.989	114757	cytoglobin
GO	heme binding	4	110	0.989	1543	cytochrome P450, family 1, subfamily A, polypeptide 1
GO	heme binding	4	110	0.989	339761	cytochrome P450, family 27, subfamily C, polypeptide 1
GO	heme binding	4	110	0.989	9420	cytochrome P450, family 7, subfamily B, polypeptide 1
GO	anchored to membrane	2	109	0.989	116372	LY6/PLAUR domain containing 1
GO	anchored to membrane	2	109	0.989	8482	semaphorin 7A, GPI membrane anchor (John Milton Hagen blood group)
GO	olfactory receptor activity	7	290	0.989	119749	olfactory receptor, family 4, subfamily C, member 46
GO	olfactory receptor activity	7	290	0.989	125962	olfactory receptor, family 7, subfamily G, member 1
GO	olfactory receptor activity	7	290	0.989	282770	olfactory receptor, family 10, subfamily AG, member 1
GO	olfactory receptor activity	7	290	0.989	283111	olfactory receptor, family 51, subfamily V, member 1
GO	olfactory receptor activity	7	290	0.989	285659	olfactory receptor, family 2, subfamily V, member 2
GO	olfactory receptor activity	7	290	0.989	390061	olfactory receptor, family 51, subfamily Q, member 1
GO	olfactory receptor activity	7	290	0.989	391114	olfactory receptor, family 6, subfamily K, member 3
GO	sensory perception of smell	8	305	0.989	119749	olfactory receptor, family 4, subfamily C, member 46
GO	sensory perception of smell	8	305	0.989	125962	olfactory receptor, family 7, subfamily G, member 1
GO	sensory perception of smell	8	305	0.989	130507	ubiquitin protein ligase E3 component n-recognin 3 (putative)
GO	sensory perception of smell	8	305	0.989	282770	olfactory receptor, family 10, subfamily AG, member 1
GO	sensory perception of smell	8	305	0.989	283111	olfactory receptor, family 51, subfamily V, member 1
GO	sensory perception of smell	8	305	0.989	285659	olfactory receptor, family 2, subfamily V, member 2
GO	sensory perception of smell	8	305	0.989	390061	olfactory receptor, family 51, subfamily Q, member 1
GO	sensory perception of smell	8	305	0.989	391114	olfactory receptor, family 6, subfamily K, member 3
GO	inflammatory response	8	222	0.989	12	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), me
GO	inflammatory response	8	222	0.989	2149	coagulation factor II (thrombin) receptor
GO	inflammatory response	8	222	0.989	3557	interleukin 1 receptor antagonist
GO	inflammatory response	8	222	0.989	3694	integrin, beta 6
GO	inflammatory response	8	222	0.989	60675	prokineticin 2
GO	inflammatory response	8	222	0.989	6347	chemokine (C-C motif) ligand 2

GO	inflammatory response	8	222	0.989	729230	chemokine (C-C motif) receptor 2
GO	inflammatory response	8	222	0.989	7857	secretogranin II (chromogranin C)
GO	serine-type endopeptidase inhibitor act	2	90	0.989	12	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), me
GO	serine-type endopeptidase inhibitor act	2	90	0.989	5054	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor t
GO	positive regulation of NF-kappaB transc	1	47	0.989	121268	Ras homolog enriched in brain like 1
GO	protein amino acid dephosphorylation	3	120	0.989	128853	dual specificity phosphatase 15
GO	protein amino acid dephosphorylation	3	120	0.989	5494	protein phosphatase, Mg2+/Mn2+ dependent, 1A
GO	protein amino acid dephosphorylation	3	120	0.989	5795	protein tyrosine phosphatase, receptor type, J
GO	protein tyrosine phosphatase activity	2	82	0.989	128853	dual specificity phosphatase 15
GO	protein tyrosine phosphatase activity	2	82	0.989	2139	eyes absent homolog 2 (Drosophila)
GO	protein tyrosine/serine/threonine phos	1	30	0.989	128853	dual specificity phosphatase 15
GO	catalytic activity	5	114	0.989	13	arylacetamide deacetylase (esterase)
GO	catalytic activity	5	114	0.989	3248	hydroxyprostaglandin dehydrogenase 15-(NAD)
GO	catalytic activity	5	114	0.989	3778	potassium large conductance calcium-activated channel, subfamily M, alph
GO	catalytic activity	5	114	0.989	5264	phytanoyl-CoA 2-hydroxylase
GO	catalytic activity	5	114	0.989	590	butyrylcholinesterase
GO	carbohydrate metabolic process	8	198	0.989	145173	beta 1,3-galactosyltransferase-like
GO	carbohydrate metabolic process	8	198	0.989	23171	glycerol-3-phosphate dehydrogenase 1-like
GO	carbohydrate metabolic process	8	198	0.989	283209	phosphoglucomutase 2-like 1
GO	carbohydrate metabolic process	8	198	0.989	6120	ribulose-5-phosphate-3-epimerase
GO	carbohydrate metabolic process	8	198	0.989	64080	ribokinase
GO	carbohydrate metabolic process	8	198	0.989	6518	solute carrier family 2 (facilitated glucose/fructose transporter), member 5
GO	carbohydrate metabolic process	8	198	0.989	669	2,3-bisphosphoglycerate mutase
GO	carbohydrate metabolic process	8	198	0.989	6833	ATP-binding cassette, sub-family C (CFTR/MRP), member 8
GO	external side of plasma membrane	5	121	0.989	146760	reticulon 4 receptor-like 1
GO	external side of plasma membrane	5	121	0.989	3685	integrin, alpha V (vitronectin receptor, alpha polypeptide, antigen CD51)
GO	external side of plasma membrane	5	121	0.989	3778	potassium large conductance calcium-activated channel, subfamily M, alph
GO	external side of plasma membrane	5	121	0.989	4897	neuronal cell adhesion molecule
GO	external side of plasma membrane	5	121	0.989	8788	delta-like 1 homolog (Drosophila)
GO	phosphoprotein phosphatase activity	1	36	0.989	147699	protein phosphatase, Mg2+/Mn2+ dependent, 1N (putative)
GO	structural constituent of cytoskeleton	3	73	0.989	1496	catenin (cadherin-associated protein), alpha 2
GO	structural constituent of cytoskeleton	3	73	0.989	6711	spectrin, beta, non-erythrocytic 1
GO	structural constituent of cytoskeleton	3	73	0.989	7168	tropomyosin 1 (alpha)
GO	enzyme binding	5	114	0.989	1543	cytochrome P450, family 1, subfamily A, polypeptide 1
GO	enzyme binding	5	114	0.989	241	arachidonate 5-lipoxygenase-activating protein
GO	enzyme binding	5	114	0.989	332	baculoviral IAP repeat-containing 5

GO	enzyme binding	5	114	0.989	590	butyrylcholinesterase
GO	enzyme binding	5	114	0.989	672	breast cancer 1, early onset
GO	response to lipopolysaccharide	3	105	0.989	1543	cytochrome P450, family 1, subfamily A, polypeptide 1
GO	response to lipopolysaccharide	3	105	0.989	2149	coagulation factor II (thrombin) receptor
GO	response to lipopolysaccharide	3	105	0.989	6347	chemokine (C-C motif) ligand 2
GO	acyltransferase activity	3	133	0.989	157570	establishment of cohesion 1 homolog 2 (S. cerevisiae)
GO	acyltransferase activity	3	133	0.989	57678	glycerol-3-phosphate acyltransferase, mitochondrial
GO	acyltransferase activity	3	133	0.989	8520	histone acetyltransferase 1
GO	cytoplasmic vesicle	9	229	0.989	157753	transmembrane protein 74
GO	cytoplasmic vesicle	9	229	0.989	23138	Nedd4 binding protein 3
GO	cytoplasmic vesicle	9	229	0.989	30011	SH3-domain kinase binding protein 1
GO	cytoplasmic vesicle	9	229	0.989	409	arrestin, beta 2
GO	cytoplasmic vesicle	9	229	0.989	4884	neuronal pentraxin I
GO	cytoplasmic vesicle	9	229	0.989	528	ATPase, H+ transporting, lysosomal 42kDa, V1 subunit C1
GO	cytoplasmic vesicle	9	229	0.989	55016	membrane-associated ring finger (C3HC4) 1
GO	cytoplasmic vesicle	9	229	0.989	55521	tripartite motif-containing 36
GO	cytoplasmic vesicle	9	229	0.989	8905	adaptor-related protein complex 1, sigma 2 subunit
GO	lysosomal membrane	2	83	0.989	157753	transmembrane protein 74
GO	lysosomal membrane	2	83	0.989	55207	ADP-ribosylation factor-like 8B
GO	intracellular membrane-bounded organ	2	127	0.989	1730	diaphanous homolog 2 (Drosophila)
GO	intracellular membrane-bounded organ	2	127	0.989	25758	chromosome 11 open reading frame 41
GO	microtubule motor activity	3	76	0.989	1781	dynein, cytoplasmic 1, intermediate chain 2
GO	microtubule motor activity	3	76	0.989	3797	kinesin family member 3C
GO	microtubule motor activity	3	76	0.989	3800	kinesin family member 5C
GO	chromatin modification	5	204	0.989	1788	DNA (cytosine-5-)-methyltransferase 3 alpha
GO	chromatin modification	5	204	0.989	2139	eyes absent homolog 2 (Drosophila)
GO	chromatin modification	5	204	0.989	50485	SWI/SNF related, matrix associated, actin dependent regulator of chromati
GO	chromatin modification	5	204	0.989	55506	H2A histone family, member Y2
GO	chromatin modification	5	204	0.989	8520	histone acetyltransferase 1
GO	growth factor activity	7	152	0.989	182	jagged 1 (Alagille syndrome)
GO	growth factor activity	7	152	0.989	3589	interleukin 11
GO	growth factor activity	7	152	0.989	3624	inhibin, beta A
GO	growth factor activity	7	152	0.989	3952	leptin
GO	growth factor activity	7	152	0.989	5228	placental growth factor
GO	growth factor activity	7	152	0.989	9535	glia maturation factor, gamma
GO	growth factor activity	7	152	0.989	9542	neuregulin 2

GO	keratinocyte differentiation	1	29	0.989	182	jagged 1 (Alagille syndrome)
GO	membrane fraction	15	472	0.989	1836	solute carrier family 26 (sulfate transporter), member 2
GO	membrane fraction	15	472	0.989	2027	enolase 3 (beta, muscle)
GO	membrane fraction	15	472	0.989	25789	transmembrane protein 59-like
GO	membrane fraction	15	472	0.989	2736	GLI family zinc finger 2
GO	membrane fraction	15	472	0.989	2898	glutamate receptor, ionotropic, kainate 2
GO	membrane fraction	15	472	0.989	4893	neuroblastoma RAS viral (v-ras) oncogene homolog
GO	membrane fraction	15	472	0.989	5341	pleckstrin
GO	membrane fraction	15	472	0.989	54843	synaptotagmin-like 2
GO	membrane fraction	15	472	0.989	5494	protein phosphatase, Mg2+/Mn2+ dependent, 1A
GO	membrane fraction	15	472	0.989	5588	protein kinase C, theta
GO	membrane fraction	15	472	0.989	57099	apoptosis, caspase activation inhibitor
GO	membrane fraction	15	472	0.989	590	butyrylcholinesterase
GO	membrane fraction	15	472	0.989	6546	solute carrier family 8 (sodium/calcium exchanger), member 1
GO	membrane fraction	15	472	0.989	6580	solute carrier family 22 (organic cation transporter), member 1
GO	membrane fraction	15	472	0.989	6586	slit homolog 3 (Drosophila)
GO	regulation of translational initiation	1	24	0.989	1983	eukaryotic translation initiation factor 5
GO	translation initiation factor activity	1	49	0.989	1983	eukaryotic translation initiation factor 5
GO	translational initiation	1	36	0.989	1983	eukaryotic translation initiation factor 5
GO	positive regulation of cell proliferation	13	290	0.989	1984	eukaryotic translation initiation factor 5A
GO	positive regulation of cell proliferation	13	290	0.989	2149	coagulation factor II (thrombin) receptor
GO	positive regulation of cell proliferation	13	290	0.989	2264	fibroblast growth factor receptor 4
GO	positive regulation of cell proliferation	13	290	0.989	2305	forkhead box M1
GO	positive regulation of cell proliferation	13	290	0.989	2321	fms-related tyrosine kinase 1 (vascular endothelial growth factor/vascular
GO	positive regulation of cell proliferation	13	290	0.989	2736	GLI family zinc finger 2
GO	positive regulation of cell proliferation	13	290	0.989	3589	interleukin 11
GO	positive regulation of cell proliferation	13	290	0.989	4893	neuroblastoma RAS viral (v-ras) oncogene homolog
GO	positive regulation of cell proliferation	13	290	0.989	5228	placental growth factor
GO	positive regulation of cell proliferation	13	290	0.989	5744	parathyroid hormone-like hormone
GO	positive regulation of cell proliferation	13	290	0.989	6659	SRY (sex determining region Y)-box 4
GO	positive regulation of cell proliferation	13	290	0.989	7046	transforming growth factor, beta receptor 1
GO	positive regulation of cell proliferation	13	290	0.989	8872	cell division cycle 123 homolog (S. cerevisiae)
GO	protein N-terminus binding	2	72	0.989	1984	eukaryotic translation initiation factor 5A
GO	protein N-terminus binding	2	72	0.989	241	arachidonate 5-lipoxygenase-activating protein
GO	chloride channel complex	2	54	0.989	200959	gamma-aminobutyric acid (GABA) receptor, rho 3
GO	chloride channel complex	2	54	0.989	2558	gamma-aminobutyric acid (GABA) A receptor, alpha 5

GO	activation of protein kinase C activity by	1	34	0.989	2149	coagulation factor II (thrombin) receptor
GO	anatomical structure morphogenesis	4	101	0.989	2149	coagulation factor II (thrombin) receptor
GO	anatomical structure morphogenesis	4	101	0.989	5081	paired box 7
GO	anatomical structure morphogenesis	4	101	0.989	6422	secreted frizzled-related protein 1
GO	anatomical structure morphogenesis	4	101	0.989	7481	wingless-type MMTV integration site family, member 11
GO	positive regulation of I-kappaB kinase/N	2	109	0.989	2149	coagulation factor II (thrombin) receptor
GO	positive regulation of I-kappaB kinase/N	2	109	0.989	5494	protein phosphatase, Mg2+/Mn2+ dependent, 1A
GO	blood coagulation	3	71	0.989	2151	coagulation factor II (thrombin) receptor-like 2
GO	blood coagulation	3	71	0.989	5028	purinergic receptor P2Y, G-protein coupled, 1
GO	blood coagulation	3	71	0.989	953	ectonucleoside triphosphate diphosphohydrolase 1
GO	phosphoinositide phospholipase C activ	1	26	0.989	2151	coagulation factor II (thrombin) receptor-like 2
GO	epidermis development	3	75	0.989	2171	fatty acid binding protein 5 (psoriasis-associated)
GO	epidermis development	3	75	0.989	3918	laminin, gamma 2
GO	epidermis development	3	75	0.989	5744	parathyroid hormone-like hormone
GO	electron transport chain	2	86	0.989	2232	ferredoxin reductase
GO	electron transport chain	2	86	0.989	4709	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 3, 12kDa
GO	generation of precursor metabolites and	1	55	0.989	2232	ferredoxin reductase
GO	mitochondrial matrix	5	147	0.989	2232	ferredoxin reductase
GO	mitochondrial matrix	5	147	0.989	26275	3-hydroxyisobutyryl-Coenzyme A hydrolase
GO	mitochondrial matrix	5	147	0.989	3336	heat shock 10kDa protein 1 (chaperonin 10)
GO	mitochondrial matrix	5	147	0.989	5303	protein (peptidylprolyl cis/trans isomerase) NIMA-interacting, 4 (parvulin)
GO	mitochondrial matrix	5	147	0.989	8659	aldehyde dehydrogenase 4 family, member A1
GO	fibroblast growth factor receptor signali	1	33	0.989	2264	fibroblast growth factor receptor 4
GO	cell-matrix adhesion	3	68	0.989	22801	integrin, alpha 11
GO	cell-matrix adhesion	3	68	0.989	3685	integrin, alpha V (vitronectin receptor, alpha polypeptide, antigen CD51)
GO	cell-matrix adhesion	3	68	0.989	3694	integrin, beta 6
GO	insulin secretion	1	23	0.989	2281	FK506 binding protein 1B, 12.6 kDa
GO	mitochondrial outer membrane	3	81	0.989	23305	acyl-CoA synthetase long-chain family member 6
GO	mitochondrial outer membrane	3	81	0.989	57678	glycerol-3-phosphate acyltransferase, mitochondrial
GO	mitochondrial outer membrane	3	81	0.989	581	BCL2-associated X protein
GO	peroxisome	4	92	0.989	23305	acyl-CoA synthetase long-chain family member 6
GO	peroxisome	4	92	0.989	255027	MPV17 mitochondrial membrane protein-like
GO	peroxisome	4	92	0.989	26061	2-hydroxyacyl-CoA lyase 1
GO	peroxisome	4	92	0.989	5264	phytanoyl-CoA 2-hydroxylase
GO	synaptic vesicle	2	46	0.989	23705	cell adhesion molecule 1
GO	synaptic vesicle	2	46	0.989	27445	piccolo (presynaptic cytomatrix protein)

GO	cell surface receptor linked signaling pa	7	161	0.989	2534	FYN oncogene related to SRC, FGR, YES
GO	cell surface receptor linked signaling pa	7	161	0.989	3276	protein arginine methyltransferase 1
GO	cell surface receptor linked signaling pa	7	161	0.989	3624	inhibin, beta A
GO	cell surface receptor linked signaling pa	7	161	0.989	5021	oxytocin receptor
GO	cell surface receptor linked signaling pa	7	161	0.989	5028	purinergic receptor P2Y, G-protein coupled, 1
GO	cell surface receptor linked signaling pa	7	161	0.989	6347	chemokine (C-C motif) ligand 2
GO	cell surface receptor linked signaling pa	7	161	0.989	8685	macrophage receptor with collagenous structure
GO	feeding behavior	1	25	0.989	2534	FYN oncogene related to SRC, FGR, YES
GO	T cell receptor signaling pathway	1	22	0.989	2534	FYN oncogene related to SRC, FGR, YES
GO	chloride transport	2	50	0.989	2558	gamma-aminobutyric acid (GABA) A receptor, alpha 5
GO	chloride transport	2	50	0.989	9635	chloride channel accessory 2
GO	nuclear-transcribed mRNA catabolic prc	1	28	0.989	26019	UPF2 regulator of nonsense transcripts homolog (yeast)
GO	guanyl-nucleotide exchange factor activ	4	120	0.989	26230	T-cell lymphoma invasion and metastasis 2
GO	guanyl-nucleotide exchange factor activ	4	120	0.989	5924	Ras protein-specific guanine nucleotide-releasing factor 2
GO	guanyl-nucleotide exchange factor activ	4	120	0.989	8997	kalirin, RhoGEF kinase
GO	guanyl-nucleotide exchange factor activ	4	120	0.989	9732	dedicator of cytokinesis 4
GO	mitochondrial inner membrane	7	231	0.989	2628	glycine amidinotransferase (L-arginine:glycine amidinotransferase)
GO	mitochondrial inner membrane	7	231	0.989	4709	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 3, 12kDa
GO	mitochondrial inner membrane	7	231	0.989	516	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit C1 (subu
GO	mitochondrial inner membrane	7	231	0.989	5245	prohibitin
GO	mitochondrial inner membrane	7	231	0.989	57678	glycerol-3-phosphate acyltransferase, mitochondrial
GO	mitochondrial inner membrane	7	231	0.989	60386	solute carrier family 25 (mitochondrial thiamine pyrophosphate carrier), m
GO	mitochondrial inner membrane	7	231	0.989	8604	solute carrier family 25 (mitochondrial carrier, Aralar), member 12
GO	microtubule cytoskeleton	2	53	0.989	26586	cytoskeleton associated protein 2
GO	microtubule cytoskeleton	2	53	0.989	6683	spastin
GO	cilium	2	90	0.989	27241	Bardet-Biedl syndrome 9
GO	cilium	2	90	0.989	7840	Alstrom syndrome 1
GO	actin filament organization	1	28	0.989	27289	Rho family GTPase 1
GO	lung development	2	60	0.989	2736	GLI family zinc finger 2
GO	lung development	2	60	0.989	7046	transforming growth factor, beta receptor 1
GO	mammary gland development	1	25	0.989	2736	GLI family zinc finger 2
GO	promoter binding	4	101	0.989	2736	GLI family zinc finger 2
GO	promoter binding	4	101	0.989	6657	SRY (sex determining region Y)-box 2
GO	promoter binding	4	101	0.989	6662	SRY (sex determining region Y)-box 9
GO	promoter binding	4	101	0.989	7490	Wilms tumor 1
GO	transcription activator activity	9	227	0.989	2736	GLI family zinc finger 2

GO	transcription activator activity	9	227	0.989	4603	v-myb myeloblastosis viral oncogene homolog (avian)-like 1
GO	transcription activator activity	9	227	0.989	5245	prohibitin
GO	transcription activator activity	9	227	0.989	5469	mediator complex subunit 1
GO	transcription activator activity	9	227	0.989	6299	sal-like 1 (Drosophila)
GO	transcription activator activity	9	227	0.989	6662	SRY (sex determining region Y)-box 9
GO	transcription activator activity	9	227	0.989	672	breast cancer 1, early onset
GO	transcription activator activity	9	227	0.989	7490	Wilms tumor 1
GO	transcription activator activity	9	227	0.989	8626	tumor protein p63
GO	mitochondrial membrane	2	51	0.989	27429	HtrA serine peptidase 2
GO	mitochondrial membrane	2	51	0.989	65055	receptor accessory protein 1
GO	mitochondrion organization	1	25	0.989	27429	HtrA serine peptidase 2
GO	response to stress	4	112	0.989	27429	HtrA serine peptidase 2
GO	response to stress	4	112	0.989	65009	NDRG family member 4
GO	response to stress	4	112	0.989	94241	tumor protein p53 inducible nuclear protein 1
GO	response to stress	4	112	0.989	9448	mitogen-activated protein kinase kinase kinase kinase 4
GO	inhibition of adenylate cyclase activity b	1	30	0.989	2774	guanine nucleotide binding protein (G protein), alpha activating activity pol
GO	endoplasmic reticulum lumen	3	68	0.989	283208	prolyl 4-hydroxylase, alpha polypeptide III
GO	endoplasmic reticulum lumen	3	68	0.989	57333	reticulocalbin 3, EF-hand calcium binding domain
GO	endoplasmic reticulum lumen	3	68	0.989	590	butyrylcholinesterase
GO	iron ion binding	1	65	0.989	283208	prolyl 4-hydroxylase, alpha polypeptide III
GO	transcription factor binding	4	170	0.989	2878	glutathione peroxidase 3 (plasma)
GO	transcription factor binding	4	170	0.989	6672	SP100 nuclear antigen
GO	transcription factor binding	4	170	0.989	7029	transcription factor Dp-2 (E2F dimerization partner 2)
GO	transcription factor binding	4	170	0.989	93649	myocardin
GO	general RNA polymerase II transcription	1	22	0.989	2965	general transcription factor IIH, polypeptide 1, 62kDa
GO	RNA elongation from RNA polymerase I	2	47	0.989	2965	general transcription factor IIH, polypeptide 1, 62kDa
GO	RNA elongation from RNA polymerase I	2	47	0.989	5440	polymerase (RNA) II (DNA directed) polypeptide K, 7.0kDa
GO	cell morphogenesis	1	30	0.989	29842	transcription factor CP2-like 1
GO	phosphoinositide binding	1	56	0.989	29887	sorting nexin 10
GO	cell-cell signaling	8	238	0.989	30011	SH3-domain kinase binding protein 1
GO	cell-cell signaling	8	238	0.989	3589	interleukin 11
GO	cell-cell signaling	8	238	0.989	3624	inhibin, beta A
GO	cell-cell signaling	8	238	0.989	5125	proprotein convertase subtilisin/kexin type 5
GO	cell-cell signaling	8	238	0.989	5228	placental growth factor
GO	cell-cell signaling	8	238	0.989	5744	parathyroid hormone-like hormone
GO	cell-cell signaling	8	238	0.989	5795	protein tyrosine phosphatase, receptor type, J

GO	cell-cell signaling	8	238	0.989	7010	TEK tyrosine kinase, endothelial
GO	steroid binding	1	23	0.989	3028	hydroxysteroid (17-beta) dehydrogenase 10
GO	cholesterol biosynthetic process	1	25	0.989	3157	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 (soluble)
GO	transcription repressor activity	5	173	0.989	3224	homeobox C8
GO	transcription repressor activity	5	173	0.989	5245	prohibitin
GO	transcription repressor activity	5	173	0.989	6299	sal-like 1 (Drosophila)
GO	transcription repressor activity	5	173	0.989	7490	Wilms tumor 1
GO	transcription repressor activity	5	173	0.989	8626	tumor protein p63
GO	embryonic skeletal system morphogene	1	36	0.989	3236	homeobox D10
GO	fatty acid metabolic process	2	75	0.989	3248	hydroxyprostaglandin dehydrogenase 15-(NAD)
GO	fatty acid metabolic process	2	75	0.989	57678	glycerol-3-phosphate acyltransferase, mitochondrial
GO	cysteine-type endopeptidase inhibitor a	1	22	0.989	332	baculoviral IAP repeat-containing 5
GO	monooxygenase activity	2	52	0.989	339761	cytochrome P450, family 27, subfamily C, polypeptide 1
GO	monooxygenase activity	2	52	0.989	9420	cytochrome P450, family 7, subfamily B, polypeptide 1
GO	late endosome	1	43	0.989	348	apolipoprotein E
GO	negative regulation of inflammatory res	1	24	0.989	348	apolipoprotein E
GO	phospholipid binding	2	49	0.989	348	apolipoprotein E
GO	phospholipid binding	2	49	0.989	83851	synaptotagmin XVI
GO	negative regulation of transcription, DN	3	91	0.989	3516	recombination signal binding protein for immunoglobulin kappa J region
GO	negative regulation of transcription, DN	3	91	0.989	6662	SRY (sex determining region Y)-box 9
GO	negative regulation of transcription, DN	3	91	0.989	8626	tumor protein p63
GO	antigen processing and presentation	1	28	0.989	353091	retinoic acid early transcript 1G
GO	activation of pro-apoptotic gene produc	1	22	0.989	355	Fas (TNF receptor superfamily, member 6)
GO	transmembrane receptor activity	5	108	0.989	355	Fas (TNF receptor superfamily, member 6)
GO	transmembrane receptor activity	5	108	0.989	5026	purinergic receptor P2X, ligand-gated ion channel, 5
GO	transmembrane receptor activity	5	108	0.989	84168	anthrax toxin receptor 1
GO	transmembrane receptor activity	5	108	0.989	8685	macrophage receptor with collagenous structure
GO	transmembrane receptor activity	5	108	0.989	92737	delta/notch-like EGF repeat containing
GO	positive regulation of peptidyl-tyrosine	1	42	0.989	3589	interleukin 11
GO	defense response	2	63	0.989	3624	inhibin, beta A
GO	defense response	2	63	0.989	81035	collectin sub-family member 12
GO	erythrocyte differentiation	1	23	0.989	3624	inhibin, beta A
GO	ovarian follicle development	1	36	0.989	3624	inhibin, beta A
GO	cell surface	4	214	0.989	3751	potassium voltage-gated channel, Shal-related subfamily, member 2
GO	cell surface	4	214	0.989	3763	potassium inwardly-rectifying channel, subfamily J, member 6
GO	cell surface	4	214	0.989	659	bone morphogenetic protein receptor, type II (serine/threonine kinase)

GO	cell surface	4	214	0.989	7010	TEK tyrosine kinase, endothelial
GO	potassium channel activity	1	33	0.989	3754	potassium voltage-gated channel, subfamily F, member 1
GO	cell maturation	1	23	0.989	3778	potassium large conductance calcium-activated channel, subfamily M, alph
GO	histone deacetylase binding	1	39	0.989	3838	karyopherin alpha 2 (RAG cohort 1, importin alpha 1)
GO	intermediate filament	2	80	0.989	3883	keratin 33A
GO	intermediate filament	2	80	0.989	4830	non-metastatic cells 1, protein (NM23A) expressed in
GO	keratin filament	1	64	0.989	3887	keratin 81
GO	gene silencing by RNA	1	30	0.989	389421	lin-28 homolog B (C. elegans)
GO	post-translational protein modification	1	27	0.989	389898	ubiquitin-conjugating enzyme E2N-like
GO	response to insulin stimulus	2	51	0.989	3952	leptin
GO	response to insulin stimulus	2	51	0.989	5588	protein kinase C, theta
GO	transcription factor complex	3	140	0.989	406	aryl hydrocarbon receptor nuclear translocator-like
GO	transcription factor complex	3	140	0.989	6657	SRY (sex determining region Y)-box 2
GO	transcription factor complex	3	140	0.989	7029	transcription factor Dp-2 (E2F dimerization partner 2)
GO	negative regulation of NF-kappaB transc	1	22	0.989	409	arrestin, beta 2
GO	lysosome organization	1	22	0.989	411	arylsulfatase B
GO	lysosome	2	144	0.989	411	arylsulfatase B
GO	lysosome	2	144	0.989	57599	WD repeat domain 48
GO	mitochondrial electron transport, NADH	1	36	0.989	4709	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 3, 12kDa
GO	mitochondrial respiratory chain comple	1	39	0.989	4709	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 3, 12kDa
GO	respiratory chain	1	42	0.989	4709	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 3, 12kDa
GO	peripheral nervous system developmen	1	24	0.989	4763	neurofibromin 1
GO	pigmentation	1	22	0.989	4763	neurofibromin 1
GO	wound healing	2	49	0.989	4763	neurofibromin 1
GO	wound healing	2	49	0.989	7168	tropomyosin 1 (alpha)
GO	ATP biosynthetic process	1	53	0.989	479	ATPase, H+/K+ transporting, nongastric, alpha polypeptide
GO	hydrolase activity, acting on acid anhydr	2	47	0.989	479	ATPase, H+/K+ transporting, nongastric, alpha polypeptide
GO	hydrolase activity, acting on acid anhydr	2	47	0.989	528	ATPase, H+ transporting, lysosomal 42kDa, V1 subunit C1
GO	centrosome	4	117	0.989	4830	non-metastatic cells 1, protein (NM23A) expressed in
GO	centrosome	4	117	0.989	7840	Alstrom syndrome 1
GO	centrosome	4	117	0.989	8409	ubiquitously-expressed transcript
GO	centrosome	4	117	0.989	898	cyclin E1
GO	response to cAMP	2	46	0.989	4830	non-metastatic cells 1, protein (NM23A) expressed in
GO	response to cAMP	2	46	0.989	9420	cytochrome P450, family 7, subfamily B, polypeptide 1
GO	excretion	1	35	0.989	4867	nephronophthisis 1 (juvenile)
GO	transport vesicle	1	39	0.989	4884	neuronal pentraxin I

GO	kinetochore	2	49	0.989	4928	nucleoporin 98kDa
GO	kinetochore	2	49	0.989	54984	PIN2-interacting protein 1
GO	hydrolase activity, acting on glycosyl bo	1	44	0.989	4968	8-oxoguanine DNA glycosylase
GO	peptide hormone binding	1	22	0.989	5021	oxytocin receptor
GO	protease binding	1	23	0.989	5054	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor t
GO	translational elongation	4	87	0.989	51121	ribosomal protein L26-like 1
GO	translational elongation	4	87	0.989	6133	ribosomal protein L9
GO	translational elongation	4	87	0.989	6154	ribosomal protein L26
GO	translational elongation	4	87	0.989	6204	ribosomal protein S10
GO	secretory granule	1	51	0.989	5125	proprotein convertase subtilisin/kexin type 5
GO	Wnt receptor signaling pathway	3	90	0.989	51339	dapper, antagonist of beta-catenin, homolog 1 (Xenopus laevis)
GO	Wnt receptor signaling pathway	3	90	0.989	5494	protein phosphatase, Mg2+/Mn2+ dependent, 1A
GO	Wnt receptor signaling pathway	3	90	0.989	81029	wingless-type MMTV integration site family, member 5B
GO	drug binding	1	44	0.989	5140	phosphodiesterase 3B, cGMP-inhibited
GO	insoluble fraction	1	39	0.989	5140	phosphodiesterase 3B, cGMP-inhibited
GO	aminopeptidase activity	1	28	0.989	5184	peptidase D
GO	cellular amino acid metabolic process	1	36	0.989	5184	peptidase D
GO	metallocarboxypeptidase activity	1	25	0.989	5184	peptidase D
GO	positive regulation of cell division	1	37	0.989	5228	placental growth factor
GO	negative regulation of transcription	6	148	0.989	5245	prohibitin
GO	negative regulation of transcription	6	148	0.989	6672	SP100 nuclear antigen
GO	negative regulation of transcription	6	148	0.989	672	breast cancer 1, early onset
GO	negative regulation of transcription	6	148	0.989	7341	SMT3 suppressor of mif two 3 homolog 1 (S. cerevisiae)
GO	negative regulation of transcription	6	148	0.989	7490	Wilms tumor 1
GO	negative regulation of transcription	6	148	0.989	9839	zinc finger E-box binding homeobox 2
GO	apical part of cell	1	42	0.989	528	ATPase, H+ transporting, lysosomal 42kDa, V1 subunit C1
GO	cell projection organization	1	28	0.989	5341	pleckstrin
GO	calcium channel activity	2	44	0.989	54822	transient receptor potential cation channel, subfamily M, member 7
GO	calcium channel activity	2	44	0.989	7220	transient receptor potential cation channel, subfamily C, member 1
GO	exocytosis	2	47	0.989	54843	synaptotagmin-like 2
GO	exocytosis	2	47	0.989	9805	secernin 1
GO	amino acid transmembrane transporter	1	26	0.989	55117	solute carrier family 6 (neutral amino acid transporter), member 15
GO	amino acid transport	1	46	0.989	55117	solute carrier family 6 (neutral amino acid transporter), member 15
GO	neurotransmitter transport	1	40	0.989	55117	solute carrier family 6 (neutral amino acid transporter), member 15
GO	GDP binding	1	26	0.989	55207	ADP-ribosylation factor-like 8B
GO	late endosome membrane	2	51	0.989	55207	ADP-ribosylation factor-like 8B

GO	late endosome membrane	2	51	0.989	83930	STARD3 N-terminal like
GO	acrosomal vesicle	1	33	0.989	55521	tripartite motif-containing 36
GO	phagocytosis	1	27	0.989	55531	ELMO/CED-12 domain containing 1
GO	4 iron, 4 sulfur cluster binding	1	25	0.989	5558	primase, DNA, polypeptide 2 (58kDa)
GO	positive regulation of T cell proliferatior	1	27	0.989	5588	protein kinase C, theta
GO	response to heat	2	47	0.989	5588	protein kinase C, theta
GO	response to heat	2	47	0.989	6347	chemokine (C-C motif) ligand 2
GO	negative regulation of transforming gro	1	28	0.989	5654	HtrA serine peptidase 1
GO	endomembrane system	2	77	0.989	57099	apoptosis, caspase activation inhibitor
GO	endomembrane system	2	77	0.989	9732	dedicator of cytokinesis 4
GO	integral to endoplasmic reticulum mem	2	46	0.989	57168	aspartate beta-hydroxylase domain containing 2
GO	integral to endoplasmic reticulum mem	2	46	0.989	79071	ELOVL family member 6, elongation of long chain fatty acids (FEN1/Elo2, SU
GO	cilium axoneme	1	26	0.989	57560	intraflagellar transport 80 homolog (Chlamydomonas)
GO	positive regulation of multicellular orga	1	23	0.989	57678	glycerol-3-phosphate acyltransferase, mitochondrial
GO	reciprocal meiotic recombination	1	22	0.989	5889	RAD51 homolog C (S. cerevisiae)
GO	regulation of blood pressure	1	49	0.989	59	actin, alpha 2, smooth muscle, aorta
GO	activation of MAPK activity	1	53	0.989	60675	prokineticin 2
GO	rRNA binding	1	23	0.989	6133	ribosomal protein L9
GO	cytosolic large ribosomal subunit	1	33	0.989	6154	ribosomal protein L26
GO	cytosolic small ribosomal subunit	1	34	0.989	6204	ribosomal protein S10
GO	chemokine activity	1	42	0.989	6347	chemokine (C-C motif) ligand 2
GO	response to gamma radiation	1	24	0.989	6347	chemokine (C-C motif) ligand 2
GO	response to interleukin-1	1	24	0.989	64131	xylosyltransferase I
GO	regulation of growth	2	51	0.989	64393	zinc finger, matrin type 3
GO	regulation of growth	2	51	0.989	8091	high mobility group AT-hook 2
GO	glucose transport	1	22	0.989	6518	solute carrier family 2 (facilitated glucose/fructose transporter), member 5
GO	heat shock protein binding	1	62	0.989	6546	solute carrier family 8 (sodium/calcium exchanger), member 1
GO	response to hydrogen peroxide	1	40	0.989	6546	solute carrier family 8 (sodium/calcium exchanger), member 1
GO	cation transport	1	65	0.989	6549	solute carrier family 9 (sodium/hydrogen exchanger), member 2
GO	protein localization	1	54	0.989	6549	solute carrier family 9 (sodium/hydrogen exchanger), member 2
GO	negative regulation of gene expression	1	23	0.989	6586	slit homolog 3 (Drosophila)
GO	BMP signaling pathway	1	43	0.989	659	bone morphogenetic protein receptor, type II (serine/threonine kinase)
GO	mesoderm formation	1	22	0.989	659	bone morphogenetic protein receptor, type II (serine/threonine kinase)
GO	negative regulation of epithelial cell pro	1	26	0.989	6657	SRY (sex determining region Y)-box 2
GO	negative regulation of neuron differenti	1	27	0.989	6657	SRY (sex determining region Y)-box 2
GO	protein stabilization	1	31	0.989	6659	SRY (sex determining region Y)-box 4

GO	protein dimerization activity	2	84	0.989	666	BCL2-related ovarian killer
GO	protein dimerization activity	2	84	0.989	7021	transcription factor AP-2 beta (activating enhancer binding protein 2 beta)
GO	specific RNA polymerase II transcription	1	33	0.989	6662	SRY (sex determining region Y)-box 9
GO	positive regulation of transcription facto	1	25	0.989	6672	SP100 nuclear antigen
GO	respiratory gaseous exchange	1	29	0.989	669	2,3-bisphosphoglycerate mutase
GO	positive regulation of gene-specific tran	2	92	0.989	672	breast cancer 1, early onset
GO	positive regulation of gene-specific tran	2	92	0.989	93649	myocardin
GO	positive regulation of protein ubiquitina	1	25	0.989	672	breast cancer 1, early onset
GO	mRNA binding	1	41	0.989	6741	Sjogren syndrome antigen B (autoantigen La)
GO	tRNA binding	1	24	0.989	6741	Sjogren syndrome antigen B (autoantigen La)
GO	palate development	1	34	0.989	7046	transforming growth factor, beta receptor 1
GO	peptidyl-serine phosphorylation	1	26	0.989	7046	transforming growth factor, beta receptor 1
GO	positive regulation of cell growth	1	34	0.989	7046	transforming growth factor, beta receptor 1
GO	platelet alpha granule lumen	1	34	0.989	7058	thrombospondin 2
GO	enzyme inhibitor activity	1	27	0.989	7078	TIMP metallopeptidase inhibitor 3
GO	response to hormone stimulus	1	44	0.989	7078	TIMP metallopeptidase inhibitor 3
GO	calcium-dependent protein binding	1	31	0.989	7137	troponin I type 3 (cardiac)
GO	regulation of heart contraction	1	32	0.989	7168	tropomyosin 1 (alpha)
GO	ubiquitin-specific protease activity	1	28	0.989	7353	ubiquitin fusion degradation 1 like (yeast)
GO	positive regulation of gene-specific tran	1	39	0.989	7490	Wilms tumor 1
GO	transcription regulator activity	1	102	0.989	7552	zinc finger protein 711
GO	voltage-gated calcium channel activity	1	23	0.989	773	calcium channel, voltage-dependent, P/Q type, alpha 1A subunit
GO	calcium-mediated signaling	1	33	0.989	7840	Alstrom syndrome 1
GO	cilium assembly	1	24	0.989	7840	Alstrom syndrome 1
GO	spermatid development	1	32	0.989	7840	Alstrom syndrome 1
GO	regulation of cell cycle	1	42	0.989	80712	ESX homeobox 1
GO	innate immune response	2	109	0.989	81035	collectin sub-family member 12
GO	innate immune response	2	109	0.989	8685	macrophage receptor with collagenous structure
GO	Golgi cisterna membrane	1	63	0.989	84620	ST6 beta-galactosamide alpha-2,6-sialyltranferase 2
GO	integral to Golgi membrane	2	45	0.989	84620	ST6 beta-galactosamide alpha-2,6-sialyltranferase 2
GO	integral to Golgi membrane	2	45	0.989	9215	like-glycosyltransferase
GO	protein amino acid glycosylation	3	65	0.989	84620	ST6 beta-galactosamide alpha-2,6-sialyltranferase 2
GO	protein amino acid glycosylation	3	65	0.989	84752	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 9
GO	protein amino acid glycosylation	3	65	0.989	9215	like-glycosyltransferase
GO	galactosyltransferase activity	1	23	0.989	84752	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 9
GO	cellular membrane organization	1	53	0.989	8905	adaptor-related protein complex 1, sigma 2 subunit

GO	post-Golgi vesicle-mediated transport	1	37	0.989	8905	adaptor-related protein complex 1, sigma 2 subunit
GO	microtubule associated complex	1	25	0.989	9053	microtubule-associated protein 7
GO	myelination	1	29	0.989	9076	claudin 1
GO	small GTPase regulator activity	1	28	0.989	9448	mitogen-activated protein kinase kinase kinase kinase 4
GO	sulfotransferase activity	1	34	0.989	9653	heparan sulfate 2-O-sulfotransferase 1

semaphorin) 3C

a)

permeability factor receptor)

synthetase, phosphoribosylaminoimidazole synthetase

a member 1

:ation group 8

ermeability factor receptor)

semaphorin) 3C

ype 1), member 1

a member 1

ermeability factor receptor)

:ation group 8

n, subfamily a-like 1

·ansferase 6 (GalNAc-T6)
·ansferase 5 (GalNAc-T5)
·ansferase 13 (GalNAc-T13)
·ansferase 14 (GalNAc-T14)

e)

ype 1), member 1

synthetase, phosphoribosylaminoimidazole synthetase

ollagenase)

a member 1

ype 1), member 1

e)

:ation group 8

:mber 3

ining

synthetase, phosphoribosylaminoimidazole synthetase

a member 1

ollagenase)

ype 1), member 1

ype 1), member 1

ermeability factor receptor)

a member 1

ɔermeability factor receptor)

ation group 8

ation group 8

ation group 8

ollagenase)

ype 1), member 1

ype 1), member 1

ype 1), member 1

ining

nding protein)

nit 9)

synthetase, phosphoribosylaminoimidazole synthetase

synthetase, phosphoribosylaminoimidazole synthetase

synthetase, phosphoribosylaminoimidazole synthetase

a member 1
a member 1
a member 1
a member 1
a member 1
a member 1
a member 1

ype 1), member 1
ype 1), member 1
ype 1), member 1

ember 19
ember 19

JR4/Elo3-like, yeast)

a member 1

synthetase, phosphoribosylaminoimidazole synthetase

:ation group 8
n, subfamily a-like 1

:ation group 8

n, subfamily a-like 1

a member 1

ermeability factor receptor)

a member 1

e)

e)

e)

a member 1

a member 1

ollagenase)

a)

ermeability factor receptor)

synthetase, phosphoribosylaminoimidazole synthetase

e)

n, subfamily a-like 1

a member 1

a member 1

nit 9)

ember 19

semaphorin) 3C

ermeability factor receptor)

ansferase 5 (GalNAc-T5)

a member 1

semaphorin) 3C
semaphorin) 3C
semaphorin) 3C

nding protein)

a member 1

ype 1), member 1

a member 1

ype 1), member 1

a)

ermeability factor receptor)

synthetase, phosphoribosylaminoimidazole synthetase

lypeptide, olfactory type
e)

n, subfamily a-like 1

a member 1

e)

ation group 8

ation group 8

unit 9)

semaphorin) 3C

:ation group 8

permeability factor receptor)

synthetase, phosphoribosylaminoimidazole synthetase
synthetase, phosphoribosylaminoimidazole synthetase

a member 1
a member 1

ype 1), member 1
ype 1), member 1
ype 1), member 1

JR4/Elo3-like, yeast)

a member 1

:ation group 8

ation group 8

mber 3

ining

n, subfamily a-like 1

semaphorin) 3C

nding protein)

ollagenase)

ermeability factor receptor)

ermeability factor receptor)

:ation group 8

ollagenase)

a member 1

ining

n, subfamily a-like 1

synthetase, phosphoribosylaminoimidazole synthetase

ollagenase)

ype 1), member 1

e)

ɔermeability factor receptor)

lypeptide, olfactory type

:ation group 8

synthetase, phosphoribosylaminoimidazole synthetase

synthetase, phosphoribosylaminoimidazole synthetase

ype 1), member 1

ype 1), member 1

a member 1

a member 1

ember 19

ermeability factor receptor)

lypeptide, olfactory type

a member 1

ype 1), member 1

lypeptide, olfactory type

semaphorin) 3C
semaphorin) 3C

cation group 8

synthetase, phosphoribosylaminoimidazole synthetase

ype 1), member 1

n, subfamily a-like 1

ype 1), member 1

ype 1), member 1

synthetase, phosphoribosylaminoimidazole synthetase

ember 4B

permeability factor receptor)

semaphorin) 3C

unit 9)

ember 3

nit 9)

4

semaphorin) 3C

lypeptide, olfactory type

ransferase 6 (GalNAc-T6)
ransferase 5 (GalNAc-T5)
ransferase 13 (GalNAc-T13)

ransferase 14 (GalNAc-T14)

a)

lypeptide, olfactory type

a)

permeability factor receptor)

synthetase, phosphoribosylaminoimidazole synthetase

e)

a member 1

ype 1), member 1

a member 1

semaphorin) 3C

ember 3

permeability factor receptor)

5

ollagenase)

ype 1), member 1

ermeability factor receptor)

a member 1

nit 9)

ation group 8

ermeability factor receptor)

ila); translocated to, 11
ansferase 5 (GalNAc-T5)

4

synthetase, phosphoribosylaminoimidazole synthetase

a member 1

ollagenase)

ermeability factor receptor)

a member 1

ype 1), member 1

ollagenase)

ype 1), member 1

ember 3

ype 1), member 1

a member 1

ining

ype 1), member 1
ype 1), member 1
ype 1), member 1

4

a member 1
ollagenase)

ember 4B

permeability factor receptor)

cation group 8

ype 1), member 1

ermeability factor receptor)

lypeptide, olfactory type

ollagenase)

ation group 8

ype 1), member 1

ember 3

ermeability factor receptor)

a member 1
a member 1

nit 9)

ember 19

R4/Elo3-like, yeast)

mber 3

ember 3

ining

n, subfamily a-like 1

:ation group 8

lypeptide, olfactory type

ype 1), member 1

ransferase 6 (GalNAc-T6)
ransferase 5 (GalNAc-T5)
ransferase 13 (GalNAc-T13)

ransferase 14 (GalNAc-T14)

ype 1), member 1

unit 9)

ransferase 6 (GalNAc-T6)

ınit 9)

ype 1), member 1

ransferase 6 (GalNAc-T6)
ransferase 5 (GalNAc-T5)

ransferase 13 (GalNAc-T13)

a member 1

unit 9)

ember 19

4

JR4/Elo3-like, yeast)

ansferase 14 (GalNAc-T14)

a)

semaphorin) 3C

ransferase 6 (GalNAc-T6)
ransferase 5 (GalNAc-T5)

ransferase 13 (GalNAc-T13)

5

nit 9)

ember 19

4

JR4/Elo3-like, yeast)

ansferase 14 (GalNAc-T14)

)

)

)

lypeptide, olfactory type

nding protein)

a member 1

ollagenase)

ember 3

ember 4B

ember 19

n, subfamily a-like 1

synthetase, phosphoribosylaminoimidazole synthetase

e)

a member 1

ollagenase)

ansferase 6 (GalNAc-T6)

ollagenase)

4
JR4/Elo3-like, yeast)

a member 1

4
JR4/Elo3-like, yeast)

semaphorin) 3C

semaphorin) 3C

ermeability factor receptor)

ollagenase)

ype 1), member 1

semaphorin) 3C

semaphorin) 3C

permeability factor receptor)

ation group 8

lypeptide, olfactory type

ila); translocated to, 11

ransferase 6 (GalNAc-T6)
ransferase 5 (GalNAc-T5)
ransferase 13 (GalNAc-T13)

ansferase 14 (GalNAc-T14)

ollagenase)

4

ansferase 6 (GalNAc-T6)
ansferase 5 (GalNAc-T5)
ansferase 13 (GalNAc-T13)
ansferase 14 (GalNAc-T14)

ember 3

ember 3
ype 1), member 1

a member 1

a member 1

n, subfamily a-like 1

ermeability factor receptor)

ınit 9)

ember 19

lypeptide, olfactory type

a member 1

ype 1), member 1

JR4/Elo3-like, yeast)