

Cate	Term	Count	Count i	P-value	Gene	Title
GO	extracellular region	181	1730	2.324E-09	#####	chromosome 17 open reading frame 99
GO	extracellular region	181	1730	2.324E-09	10085	EGF-like repeats and discoidin I-like domains 3
GO	extracellular region	181	1730	2.324E-09	10117	enamelin
GO	extracellular region	181	1730	2.324E-09	10216	proteoglycan 4
GO	extracellular region	181	1730	2.324E-09	10417	spondin 2, extracellular matrix protein
GO	extracellular region	181	1730	2.324E-09	10418	spondin 1, extracellular matrix protein
GO	extracellular region	181	1730	2.324E-09	10447	family with sequence similarity 3, member C
GO	extracellular region	181	1730	2.324E-09	10516	fibulin 5
GO	extracellular region	181	1730	2.324E-09	10752	cell adhesion molecule with homology to L1CAM (close homolog of L1)
GO	extracellular region	181	1730	2.324E-09	1114	chromogranin B (secretogranin 1)
GO	extracellular region	181	1730	2.324E-09	1117	chitinase 3-like 2
GO	extracellular region	181	1730	2.324E-09	11202	kallikrein-related peptidase 8
GO	extracellular region	181	1730	2.324E-09	113177	chromosome 19 open reading frame 36
GO	extracellular region	181	1730	2.324E-09	116844	leucine-rich alpha-2-glycoprotein 1
GO	extracellular region	181	1730	2.324E-09	118429	anthrax toxin receptor 2
GO	extracellular region	181	1730	2.324E-09	123	perilipin 2
GO	extracellular region	181	1730	2.324E-09	124220	zymogen granule protein 16 homolog B (rat)
GO	extracellular region	181	1730	2.324E-09	126147	netrin 5
GO	extracellular region	181	1730	2.324E-09	126638	repetin
GO	extracellular region	181	1730	2.324E-09	1295	collagen, type VIII, alpha 1
GO	extracellular region	181	1730	2.324E-09	1363	carboxypeptidase E
GO	extracellular region	181	1730	2.324E-09	1435	colony stimulating factor 1 (macrophage)
GO	extracellular region	181	1730	2.324E-09	1462	versican
GO	extracellular region	181	1730	2.324E-09	1469	cystatin SN
GO	extracellular region	181	1730	2.324E-09	1471	cystatin C
GO	extracellular region	181	1730	2.324E-09	1508	cathepsin B
GO	extracellular region	181	1730	2.324E-09	153218	serine peptidase inhibitor, Kazal type 13 (putative)
GO	extracellular region	181	1730	2.324E-09	157869	chromosome 8 open reading frame 84
GO	extracellular region	181	1730	2.324E-09	168667	BMP binding endothelial regulator
GO	extracellular region	181	1730	2.324E-09	170692	ADAM metallopeptidase with thrombospondin type 1 motif, 18
GO	extracellular region	181	1730	2.324E-09	1755	deleted in malignant brain tumors 1
GO	extracellular region	181	1730	2.324E-09	1803	dipeptidyl-peptidase 4
GO	extracellular region	181	1730	2.324E-09	183	angiotensinogen (serpin peptidase inhibitor, clade A, member 8)
GO	extracellular region	181	1730	2.324E-09	1839	heparin-binding EGF-like growth factor
GO	extracellular region	181	1730	2.324E-09	1906	endothelin 1

GO	extracellular region	181	1730	2.324E-09	1953 multiple EGF-like-domains 6
GO	extracellular region	181	1730	2.324E-09	200504 gastrokine 2
GO	extracellular region	181	1730	2.324E-09	2153 coagulation factor V (proaccelerin, labile factor)
GO	extracellular region	181	1730	2.324E-09	219348 placenta-specific 9
GO	extracellular region	181	1730	2.324E-09	2200 fibrillin 1
GO	extracellular region	181	1730	2.324E-09	2201 fibrillin 2
GO	extracellular region	181	1730	2.324E-09	221806 von Willebrand factor D and EGF domains
GO	extracellular region	181	1730	2.324E-09	223117 sema domain, immunoglobulin domain (Ig), short basic domain, secret
GO	extracellular region	181	1730	2.324E-09	2239 glypican 4
GO	extracellular region	181	1730	2.324E-09	2262 glypican 5
GO	extracellular region	181	1730	2.324E-09	2263 fibroblast growth factor receptor 2
GO	extracellular region	181	1730	2.324E-09	22795 nidogen 2 (osteonidogen)
GO	extracellular region	181	1730	2.324E-09	22915 multimerin 1
GO	extracellular region	181	1730	2.324E-09	22925 phospholipase A2 receptor 1, 180kDa
GO	extracellular region	181	1730	2.324E-09	23145 SCO-spondin homolog (Bos taurus)
GO	extracellular region	181	1730	2.324E-09	2331 fibromodulin
GO	extracellular region	181	1730	2.324E-09	23418 crumbs homolog 1 (Drosophila)
GO	extracellular region	181	1730	2.324E-09	23529 cardiotrophin-like cytokine factor 1
GO	extracellular region	181	1730	2.324E-09	23780 apolipoprotein L, 2
GO	extracellular region	181	1730	2.324E-09	255738 proprotein convertase subtilisin/kexin type 9
GO	extracellular region	181	1730	2.324E-09	255743 nephronectin
GO	extracellular region	181	1730	2.324E-09	2589 UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosami
GO	extracellular region	181	1730	2.324E-09	25890 ABI family, member 3 (NESH) binding protein
GO	extracellular region	181	1730	2.324E-09	25903 olfactomedin-like 2B
GO	extracellular region	181	1730	2.324E-09	26281 fibroblast growth factor 20
GO	extracellular region	181	1730	2.324E-09	2638 group-specific component (vitamin D binding protein)
GO	extracellular region	181	1730	2.324E-09	26998 fetuin B
GO	extracellular region	181	1730	2.324E-09	27123 dickkopf homolog 2 (Xenopus laevis)
GO	extracellular region	181	1730	2.324E-09	283316 CD163 molecule-like 1
GO	extracellular region	181	1730	2.324E-09	2921 chemokine (C-X-C motif) ligand 3
GO	extracellular region	181	1730	2.324E-09	30008 EGF-containing fibulin-like extracellular matrix protein 2
GO	extracellular region	181	1730	2.324E-09	30010 neurexophilin 1
GO	extracellular region	181	1730	2.324E-09	3373 hyaluronoglucosaminidase 1
GO	extracellular region	181	1730	2.324E-09	340654 lipase, family member M
GO	extracellular region	181	1730	2.324E-09	345275 hydroxysteroid (17-beta) dehydrogenase 13
GO	extracellular region	181	1730	2.324E-09	3479 insulin-like growth factor 1 (somatomedin C)

GO	extracellular region	181	1730	2.324E-09	3484 insulin-like growth factor binding protein 1
GO	extracellular region	181	1730	2.324E-09	3486 insulin-like growth factor binding protein 3
GO	extracellular region	181	1730	2.324E-09	3488 insulin-like growth factor binding protein 5
GO	extracellular region	181	1730	2.324E-09	3491 cysteine-rich, angiogenic inducer, 61
GO	extracellular region	181	1730	2.324E-09	3512 immunoglobulin J polypeptide, linker protein for immunoglobulin alpha
GO	extracellular region	181	1730	2.324E-09	3569 interleukin 6 (interferon, beta 2)
GO	extracellular region	181	1730	2.324E-09	3570 interleukin 6 receptor
GO	extracellular region	181	1730	2.324E-09	3601 interleukin 15 receptor, alpha
GO	extracellular region	181	1730	2.324E-09	375790 agrin
GO	extracellular region	181	1730	2.324E-09	3814 KiSS-1 metastasis-suppressor
GO	extracellular region	181	1730	2.324E-09	3827 kininogen 1
GO	extracellular region	181	1730	2.324E-09	390667 pentraxin 4, long
GO	extracellular region	181	1730	2.324E-09	3911 laminin, alpha 5
GO	extracellular region	181	1730	2.324E-09	3913 laminin, beta 2 (laminin S)
GO	extracellular region	181	1730	2.324E-09	3914 laminin, beta 3
GO	extracellular region	181	1730	2.324E-09	3959 lectin, galactoside-binding, soluble, 3 binding protein
GO	extracellular region	181	1730	2.324E-09	4015 lysyl oxidase
GO	extracellular region	181	1730	2.324E-09	404203 serine peptidase inhibitor, Kazal type 6
GO	extracellular region	181	1730	2.324E-09	407738 family with sequence similarity 19 (chemokine (C-C motif)-like), member 1
GO	extracellular region	181	1730	2.324E-09	4246 secretoglobin, family 2A, member 1
GO	extracellular region	181	1730	2.324E-09	4254 KIT ligand
GO	extracellular region	181	1730	2.324E-09	4316 matrix metalloproteinase 7 (matrilysin, uterine)
GO	extracellular region	181	1730	2.324E-09	4582 mucin 1, cell surface associated
GO	extracellular region	181	1730	2.324E-09	4586 mucin 5AC, oligomeric mucus/gel-forming
GO	extracellular region	181	1730	2.324E-09	4588 mucin 6, oligomeric mucus/gel-forming
GO	extracellular region	181	1730	2.324E-09	4684 neural cell adhesion molecule 1
GO	extracellular region	181	1730	2.324E-09	4856 nephroblastoma overexpressed gene
GO	extracellular region	181	1730	2.324E-09	5046 proprotein convertase subtilisin/kexin type 6
GO	extracellular region	181	1730	2.324E-09	50604 interleukin 20
GO	extracellular region	181	1730	2.324E-09	5066 peptidylglycine alpha-amidating monooxygenase
GO	extracellular region	181	1730	2.324E-09	50859 sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican)
GO	extracellular region	181	1730	2.324E-09	51279 complement component 1, r subcomponent-like
GO	extracellular region	181	1730	2.324E-09	5284 polymeric immunoglobulin receptor
GO	extracellular region	181	1730	2.324E-09	5304 prolactin-induced protein
GO	extracellular region	181	1730	2.324E-09	5327 plasminogen activator, tissue
GO	extracellular region	181	1730	2.324E-09	5367 pro-melanin-concentrating hormone

GO	extracellular region	181	1730	2.324E-09	54361 wingless-type MMTV integration site family, member 4
GO	extracellular region	181	1730	2.324E-09	54757 family with sequence similarity 20, member A
GO	extracellular region	181	1730	2.324E-09	55068 ecto-NOX disulfide-thiol exchanger 1
GO	extracellular region	181	1730	2.324E-09	55600 intelectin 1 (galactofuranose binding)
GO	extracellular region	181	1730	2.324E-09	56477 chemokine (C-C motif) ligand 28
GO	extracellular region	181	1730	2.324E-09	5648 mannan-binding lectin serine peptidase 1 (C4/C2 activating component
GO	extracellular region	181	1730	2.324E-09	56547 matrix metallopeptidase 26
GO	extracellular region	181	1730	2.324E-09	5655 kallikrein-related peptidase 10
GO	extracellular region	181	1730	2.324E-09	56944 olfactomedin-like 3
GO	extracellular region	181	1730	2.324E-09	57094 carboxypeptidase A6
GO	extracellular region	181	1730	2.324E-09	5737 prostaglandin F receptor (FP)
GO	extracellular region	181	1730	2.324E-09	57493 HEG homolog 1 (zebrafish)
GO	extracellular region	181	1730	2.324E-09	5768 quiescin Q6 sulfhydryl oxidase 1
GO	extracellular region	181	1730	2.324E-09	5950 retinol binding protein 4, plasma
GO	extracellular region	181	1730	2.324E-09	5972 renin
GO	extracellular region	181	1730	2.324E-09	619518 chromosome 1 open reading frame 191
GO	extracellular region	181	1730	2.324E-09	627 brain-derived neurotrophic factor
GO	extracellular region	181	1730	2.324E-09	629 complement factor B
GO	extracellular region	181	1730	2.324E-09	6343 secretin
GO	extracellular region	181	1730	2.324E-09	6372 chemokine (C-X-C motif) ligand 6 (granulocyte chemotactic protein 2)
GO	extracellular region	181	1730	2.324E-09	6374 chemokine (C-X-C motif) ligand 5
GO	extracellular region	181	1730	2.324E-09	64093 SPARC related modular calcium binding 1
GO	extracellular region	181	1730	2.324E-09	64388 gremlin 2, cysteine knot superfamily, homolog (Xenopus laevis)
GO	extracellular region	181	1730	2.324E-09	6484 ST3 beta-galactoside alpha-2,3-sialyltransferase 4
GO	extracellular region	181	1730	2.324E-09	652 bone morphogenetic protein 4
GO	extracellular region	181	1730	2.324E-09	6590 secretory leukocyte peptidase inhibitor
GO	extracellular region	181	1730	2.324E-09	6690 serine peptidase inhibitor, Kazal type 1
GO	extracellular region	181	1730	2.324E-09	6692 serine peptidase inhibitor, Kunitz type 1
GO	extracellular region	181	1730	2.324E-09	6750 somatostatin
GO	extracellular region	181	1730	2.324E-09	692094 microseminoprotein, prostate associated
GO	extracellular region	181	1730	2.324E-09	6947 transcobalamin I (vitamin B12 binding protein, R binder family)
GO	extracellular region	181	1730	2.324E-09	6948 transcobalamin II; macrocytic anemia
GO	extracellular region	181	1730	2.324E-09	7032 trefoil factor 2
GO	extracellular region	181	1730	2.324E-09	7049 transforming growth factor, beta receptor III
GO	extracellular region	181	1730	2.324E-09	7076 TIMP metallopeptidase inhibitor 1
GO	extracellular region	181	1730	2.324E-09	7092 tolloid-like 1

GO	extracellular region	181	1730	2.324E-09	7133 tumor necrosis factor receptor superfamily, member 1B
GO	extracellular region	181	1730	2.324E-09	715 complement component 1, r subcomponent
GO	extracellular region	181	1730	2.324E-09	717 complement component 2
GO	extracellular region	181	1730	2.324E-09	718 complement component 3
GO	extracellular region	181	1730	2.324E-09	722 complement component 4 binding protein, alpha
GO	extracellular region	181	1730	2.324E-09	725 complement component 4 binding protein, beta
GO	extracellular region	181	1730	2.324E-09	731 complement component 8, alpha polypeptide
GO	extracellular region	181	1730	2.324E-09	7474 wingless-type MMTV integration site family, member 5A
GO	extracellular region	181	1730	2.324E-09	7477 wingless-type MMTV integration site family, member 7B
GO	extracellular region	181	1730	2.324E-09	7869 sema domain, immunoglobulin domain (Ig), short basic domain, secret
GO	extracellular region	181	1730	2.324E-09	7941 phospholipase A2, group VII (platelet-activating factor acetylhydrolase,
GO	extracellular region	181	1730	2.324E-09	79802 HHIP-like 2
GO	extracellular region	181	1730	2.324E-09	79887 phospholipase B domain containing 1
GO	extracellular region	181	1730	2.324E-09	79987 sushi, von Willebrand factor type A, EGF and pentraxin domain contain
GO	extracellular region	181	1730	2.324E-09	8076 microfibrillar associated protein 5
GO	extracellular region	181	1730	2.324E-09	80760 inter-alpha (globulin) inhibitor H5
GO	extracellular region	181	1730	2.324E-09	80763 chromosome 12 open reading frame 39
GO	extracellular region	181	1730	2.324E-09	80830 apolipoprotein L, 6
GO	extracellular region	181	1730	2.324E-09	80833 apolipoprotein L, 3
GO	extracellular region	181	1730	2.324E-09	834 caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, co
GO	extracellular region	181	1730	2.324E-09	83872 hemicentin 1
GO	extracellular region	181	1730	2.324E-09	84171 lysyl oxidase-like 4
GO	extracellular region	181	1730	2.324E-09	8542 apolipoprotein L, 1
GO	extracellular region	181	1730	2.324E-09	8600 tumor necrosis factor (ligand) superfamily, member 11
GO	extracellular region	181	1730	2.324E-09	8635 ribonuclease T2
GO	extracellular region	181	1730	2.324E-09	8646 chordin
GO	extracellular region	181	1730	2.324E-09	8740 tumor necrosis factor (ligand) superfamily, member 14
GO	extracellular region	181	1730	2.324E-09	8839 WNT1 inducible signaling pathway protein 2
GO	extracellular region	181	1730	2.324E-09	885 cholecystokinin
GO	extracellular region	181	1730	2.324E-09	8857 Fc fragment of IgG binding protein
GO	extracellular region	181	1730	2.324E-09	90865 interleukin 33
GO	extracellular region	181	1730	2.324E-09	92304 secretoglobin, family 3A, member 1
GO	extracellular region	181	1730	2.324E-09	92747 chromosome 20 open reading frame 114
GO	extracellular region	181	1730	2.324E-09	929 CD14 molecule
GO	extracellular region	181	1730	2.324E-09	94025 mucin 16, cell surface associated
GO	extracellular region	181	1730	2.324E-09	9510 ADAM metallopeptidase with thrombospondin type 1 motif, 1

GO	extracellular region	181	1730	2.324E-09	9518 growth differentiation factor 15
GO	extracellular region	181	1730	2.324E-09	9966 tumor necrosis factor (ligand) superfamily, member 15
GO	response to glucocorticoid stimulus	17	71	4.225E-06	10076 protein tyrosine phosphatase, receptor type, U
GO	response to glucocorticoid stimulus	17	71	4.225E-06	10081 programmed cell death 7
GO	response to glucocorticoid stimulus	17	71	4.225E-06	1373 carbamoyl-phosphate synthetase 1, mitochondrial
GO	response to glucocorticoid stimulus	17	71	4.225E-06	1843 dual specificity phosphatase 1
GO	response to glucocorticoid stimulus	17	71	4.225E-06	2033 E1A binding protein p300
GO	response to glucocorticoid stimulus	17	71	4.225E-06	35 acyl-Coenzyme A dehydrogenase, C-2 to C-3 short chain
GO	response to glucocorticoid stimulus	17	71	4.225E-06	3569 interleukin 6 (interferon, beta 2)
GO	response to glucocorticoid stimulus	17	71	4.225E-06	3570 interleukin 6 receptor
GO	response to glucocorticoid stimulus	17	71	4.225E-06	3643 insulin receptor
GO	response to glucocorticoid stimulus	17	71	4.225E-06	3845 v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog
GO	response to glucocorticoid stimulus	17	71	4.225E-06	5122 proprotein convertase subtilisin/kexin type 1
GO	response to glucocorticoid stimulus	17	71	4.225E-06	5244 ATP-binding cassette, sub-family B (MDR/TAP), member 4
GO	response to glucocorticoid stimulus	17	71	4.225E-06	5327 plasminogen activator, tissue
GO	response to glucocorticoid stimulus	17	71	4.225E-06	6256 retinoid X receptor, alpha
GO	response to glucocorticoid stimulus	17	71	4.225E-06	652 bone morphogenetic protein 4
GO	response to glucocorticoid stimulus	17	71	4.225E-06	799 calcitonin receptor
GO	response to glucocorticoid stimulus	17	71	4.225E-06	9021 suppressor of cytokine signaling 3
GO	integral to plasma membrane	103	969	4.39E-06	10076 protein tyrosine phosphatase, receptor type, U
GO	integral to plasma membrane	103	969	4.39E-06	10268 receptor (G protein-coupled) activity modifying protein 3
GO	integral to plasma membrane	103	969	4.39E-06	10288 leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM
GO	integral to plasma membrane	103	969	4.39E-06	10312 T-cell, immune regulator 1, ATPase, H <sup>+</sup> transporting, lysosomal VO subu
GO	integral to plasma membrane	103	969	4.39E-06	1048 carcinoembryonic antigen-related cell adhesion molecule 5
GO	integral to plasma membrane	103	969	4.39E-06	10568 solute carrier family 34 (sodium phosphate), member 2
GO	integral to plasma membrane	103	969	4.39E-06	1364 claudin 4
GO	integral to plasma membrane	103	969	4.39E-06	154 adrenergic, beta-2-, receptor, surface
GO	integral to plasma membrane	103	969	4.39E-06	1604 CD55 molecule, decay accelerating factor for complement (Cromer blo
GO	integral to plasma membrane	103	969	4.39E-06	166929 sphingomyelin synthase 2
GO	integral to plasma membrane	103	969	4.39E-06	1813 dopamine receptor D2
GO	integral to plasma membrane	103	969	4.39E-06	1815 dopamine receptor D4
GO	integral to plasma membrane	103	969	4.39E-06	1839 heparin-binding EGF-like growth factor
GO	integral to plasma membrane	103	969	4.39E-06	1902 lysophosphatidic acid receptor 1
GO	integral to plasma membrane	103	969	4.39E-06	1948 ephrin-B2
GO	integral to plasma membrane	103	969	4.39E-06	1969 EPH receptor A2
GO	integral to plasma membrane	103	969	4.39E-06	2015 egf-like module containing, mucin-like, hormone receptor-like 1

GO	integral to plasma membrane	103	969	4.39E-06	2040 stomatin
GO	integral to plasma membrane	103	969	4.39E-06	2044 EPH receptor A5
GO	integral to plasma membrane	103	969	4.39E-06	2205 Fc fragment of IgE, high affinity I, receptor for; alpha polypeptide
GO	integral to plasma membrane	103	969	4.39E-06	2239 glypican 4
GO	integral to plasma membrane	103	969	4.39E-06	2262 glypican 5
GO	integral to plasma membrane	103	969	4.39E-06	22925 phospholipase A2 receptor 1, 180kDa
GO	integral to plasma membrane	103	969	4.39E-06	23208 synaptotagmin XI
GO	integral to plasma membrane	103	969	4.39E-06	23767 fibronectin leucine rich transmembrane protein 3
GO	integral to plasma membrane	103	969	4.39E-06	2564 gamma-aminobutyric acid (GABA) A receptor, epsilon
GO	integral to plasma membrane	103	969	4.39E-06	2615 leucine rich repeat containing 32
GO	integral to plasma membrane	103	969	4.39E-06	27345 potassium large conductance calcium-activated channel, subfamily M,
GO	integral to plasma membrane	103	969	4.39E-06	2861 G protein-coupled receptor 37 (endothelin receptor type B-like)
GO	integral to plasma membrane	103	969	4.39E-06	286133 scavenger receptor class A, member 5 (putative)
GO	integral to plasma membrane	103	969	4.39E-06	2865 free fatty acid receptor 3
GO	integral to plasma membrane	103	969	4.39E-06	2867 free fatty acid receptor 2
GO	integral to plasma membrane	103	969	4.39E-06	28982 feline leukemia virus subgroup C cellular receptor 1
GO	integral to plasma membrane	103	969	4.39E-06	2911 glutamate receptor, metabotropic 1
GO	integral to plasma membrane	103	969	4.39E-06	3355 5-hydroxytryptamine (serotonin) receptor 1F
GO	integral to plasma membrane	103	969	4.39E-06	3561 interleukin 2 receptor, gamma (severe combined immunodeficiency)
GO	integral to plasma membrane	103	969	4.39E-06	358 aquaporin 1 (Colton blood group)
GO	integral to plasma membrane	103	969	4.39E-06	3604 tumor necrosis factor receptor superfamily, member 9
GO	integral to plasma membrane	103	969	4.39E-06	3643 insulin receptor
GO	integral to plasma membrane	103	969	4.39E-06	3732 CD82 molecule
GO	integral to plasma membrane	103	969	4.39E-06	3759 potassium inwardly-rectifying channel, subfamily J, member 2
GO	integral to plasma membrane	103	969	4.39E-06	3949 low density lipoprotein receptor
GO	integral to plasma membrane	103	969	4.39E-06	4065 lymphocyte antigen 75
GO	integral to plasma membrane	103	969	4.39E-06	4179 CD46 molecule, complement regulatory protein
GO	integral to plasma membrane	103	969	4.39E-06	4359 myelin protein zero
GO	integral to plasma membrane	103	969	4.39E-06	4486 macrophage stimulating 1 receptor (c-met-related tyrosine kinase)
GO	integral to plasma membrane	103	969	4.39E-06	4582 mucin 1, cell surface associated
GO	integral to plasma membrane	103	969	4.39E-06	4680 carcinoembryonic antigen-related cell adhesion molecule 6 (non-specif
GO	integral to plasma membrane	103	969	4.39E-06	4853 Notch homolog 2 (Drosophila)
GO	integral to plasma membrane	103	969	4.39E-06	4886 neuropeptide Y receptor Y1
GO	integral to plasma membrane	103	969	4.39E-06	4889 neuropeptide Y receptor Y5
GO	integral to plasma membrane	103	969	4.39E-06	4915 neurotrophic tyrosine kinase, receptor, type 2
GO	integral to plasma membrane	103	969	4.39E-06	493 ATPase, Ca <sup>++</sup> transporting, plasma membrane 4

GO integral to plasma membrane	103	969	4.39E-06	5025 purinergic receptor P2X, ligand-gated ion channel, 4
GO integral to plasma membrane	103	969	4.39E-06	5099 protocadherin 7
GO integral to plasma membrane	103	969	4.39E-06	51280 golgi membrane protein 1
GO integral to plasma membrane	103	969	4.39E-06	5244 ATP-binding cassette, sub-family B (MDR/TAP), member 4
GO integral to plasma membrane	103	969	4.39E-06	5284 polymeric immunoglobulin receptor
GO integral to plasma membrane	103	969	4.39E-06	5349 FXYD domain containing ion transport regulator 3
GO integral to plasma membrane	103	969	4.39E-06	55867 solute carrier family 22 (organic anion/urate transporter), member 11
GO integral to plasma membrane	103	969	4.39E-06	56172 ankylosis, progressive homolog (mouse)
GO integral to plasma membrane	103	969	4.39E-06	5724 platelet-activating factor receptor
GO integral to plasma membrane	103	969	4.39E-06	5732 prostaglandin E receptor 2 (subtype EP2), 53kDa
GO integral to plasma membrane	103	969	4.39E-06	5737 prostaglandin F receptor (FP)
GO integral to plasma membrane	103	969	4.39E-06	5787 protein tyrosine phosphatase, receptor type, B
GO integral to plasma membrane	103	969	4.39E-06	5789 protein tyrosine phosphatase, receptor type, D
GO integral to plasma membrane	103	969	4.39E-06	5794 protein tyrosine phosphatase, receptor type, H
GO integral to plasma membrane	103	969	4.39E-06	5799 protein tyrosine phosphatase, receptor type, N polypeptide 2
GO integral to plasma membrane	103	969	4.39E-06	6006 Rh blood group, CcEe antigens
GO integral to plasma membrane	103	969	4.39E-06	6402 selectin L
GO integral to plasma membrane	103	969	4.39E-06	6505 solute carrier family 1 (neuronal/epithelial high affinity glutamate transp
GO integral to plasma membrane	103	969	4.39E-06	6521 solute carrier family 4, anion exchanger, member 1 (erythrocyte memb
GO integral to plasma membrane	103	969	4.39E-06	6535 solute carrier family 6 (neurotransmitter transporter, creatine), memb
GO integral to plasma membrane	103	969	4.39E-06	6542 solute carrier family 7 (cationic amino acid transporter, $\gamma^+$ system), me
GO integral to plasma membrane	103	969	4.39E-06	6563 solute carrier family 14 (urea transporter), member 1 (Kidd blood group)
GO integral to plasma membrane	103	969	4.39E-06	6564 solute carrier family 15 (oligopeptide transporter), member 1
GO integral to plasma membrane	103	969	4.39E-06	6565 solute carrier family 15 (H <sup>+</sup> /peptide transporter), member 2
GO integral to plasma membrane	103	969	4.39E-06	6653 sortilin-related receptor, L(DLR class) A repeats-containing
GO integral to plasma membrane	103	969	4.39E-06	6751 somatostatin receptor 1
GO integral to plasma membrane	103	969	4.39E-06	684 bone marrow stromal cell antigen 2
GO integral to plasma membrane	103	969	4.39E-06	7049 transforming growth factor, beta receptor III
GO integral to plasma membrane	103	969	4.39E-06	7097 toll-like receptor 2
GO integral to plasma membrane	103	969	4.39E-06	7098 toll-like receptor 3
GO integral to plasma membrane	103	969	4.39E-06	7099 toll-like receptor 4
GO integral to plasma membrane	103	969	4.39E-06	7102 tetraspanin 7
GO integral to plasma membrane	103	969	4.39E-06	7106 tetraspanin 4
GO integral to plasma membrane	103	969	4.39E-06	783 calcium channel, voltage-dependent, beta 2 subunit
GO integral to plasma membrane	103	969	4.39E-06	799 calcitonin receptor
GO integral to plasma membrane	103	969	4.39E-06	8082 sarcospan (Kras oncogene-associated gene)



GO integral to plasma membrane	103	969	4.39E-06	8600 tumor necrosis factor (ligand) superfamily, member 11
GO integral to plasma membrane	103	969	4.39E-06	8645 potassium channel, subfamily K, member 5
GO integral to plasma membrane	103	969	4.39E-06	8671 solute carrier family 4, sodium bicarbonate cotransporter, member 4
GO integral to plasma membrane	103	969	4.39E-06	8794 tumor necrosis factor receptor superfamily, member 10c, decoy withou
GO integral to plasma membrane	103	969	4.39E-06	8842 prominin 1
GO integral to plasma membrane	103	969	4.39E-06	9019 myelin protein zero-like 1
GO integral to plasma membrane	103	969	4.39E-06	91 activin A receptor, type IB
GO integral to plasma membrane	103	969	4.39E-06	9143 synaptogyrin 3
GO integral to plasma membrane	103	969	4.39E-06	9194 solute carrier family 16, member 7 (monocarboxylic acid transporter 2)
GO integral to plasma membrane	103	969	4.39E-06	94 activin A receptor type II-like 1
GO integral to plasma membrane	103	969	4.39E-06	961 CD47 molecule
GO integral to plasma membrane	103	969	4.39E-06	9619 ATP-binding cassette, sub-family G (WHITE), member 1
GO integral to plasma membrane	103	969	4.39E-06	9962 solute carrier family 23 (nucleobase transporters), member 2
GO integral to plasma membrane	103	969	4.39E-06	9966 tumor necrosis factor (ligand) superfamily, member 15
GO extracellular space	75	647	4.613E-06	10439 olfactomedin 1
GO extracellular space	75	647	4.613E-06	1117 chitinase 3-like 2
GO extracellular space	75	647	4.613E-06	11202 kallikrein-related peptidase 8
GO extracellular space	75	647	4.613E-06	1435 colony stimulating factor 1 (macrophage)
GO extracellular space	75	647	4.613E-06	1471 cystatin C
GO extracellular space	75	647	4.613E-06	1508 cathepsin B
GO extracellular space	75	647	4.613E-06	168667 BMP binding endothelial regulator
GO extracellular space	75	647	4.613E-06	183 angiotensinogen (serpin peptidase inhibitor, clade A, member 8)
GO extracellular space	75	647	4.613E-06	1839 heparin-binding EGF-like growth factor
GO extracellular space	75	647	4.613E-06	1906 endothelin 1
GO extracellular space	75	647	4.613E-06	2200 fibrillin 1
GO extracellular space	75	647	4.613E-06	2239 glypican 4
GO extracellular space	75	647	4.613E-06	2262 glypican 5
GO extracellular space	75	647	4.613E-06	22901 arylsulfatase G
GO extracellular space	75	647	4.613E-06	22925 phospholipase A2 receptor 1, 180kDa
GO extracellular space	75	647	4.613E-06	23145 SCO-spondin homolog (Bos taurus)
GO extracellular space	75	647	4.613E-06	23529 cardiotrophin-like cytokine factor 1
GO extracellular space	75	647	4.613E-06	255738 proprotein convertase subtilisin/kexin type 9
GO extracellular space	75	647	4.613E-06	2638 group-specific component (vitamin D binding protein)
GO extracellular space	75	647	4.613E-06	27123 dickkopf homolog 2 (Xenopus laevis)
GO extracellular space	75	647	4.613E-06	2921 chemokine (C-X-C motif) ligand 3
GO extracellular space	75	647	4.613E-06	3373 hyaluronoglucosaminidase 1

GO	extracellular space	75	647	4.613E-06	3479 insulin-like growth factor 1 (somatomedin C)
GO	extracellular space	75	647	4.613E-06	3484 insulin-like growth factor binding protein 1
GO	extracellular space	75	647	4.613E-06	3486 insulin-like growth factor binding protein 3
GO	extracellular space	75	647	4.613E-06	3569 interleukin 6 (interferon, beta 2)
GO	extracellular space	75	647	4.613E-06	3570 interleukin 6 receptor
GO	extracellular space	75	647	4.613E-06	3601 interleukin 15 receptor, alpha
GO	extracellular space	75	647	4.613E-06	375790 agrin
GO	extracellular space	75	647	4.613E-06	3815 v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog
GO	extracellular space	75	647	4.613E-06	3827 kininogen 1
GO	extracellular space	75	647	4.613E-06	3911 laminin, alpha 5
GO	extracellular space	75	647	4.613E-06	3959 lectin, galactoside-binding, soluble, 3 binding protein
GO	extracellular space	75	647	4.613E-06	4015 lysyl oxidase
GO	extracellular space	75	647	4.613E-06	4254 KIT ligand
GO	extracellular space	75	647	4.613E-06	4316 matrix metalloproteinase 7 (matrilysin, uterine)
GO	extracellular space	75	647	4.613E-06	5046 proprotein convertase subtilisin/kexin type 6
GO	extracellular space	75	647	4.613E-06	50604 interleukin 20
GO	extracellular space	75	647	4.613E-06	5122 proprotein convertase subtilisin/kexin type 1
GO	extracellular space	75	647	4.613E-06	51279 complement component 1, r subcomponent-like
GO	extracellular space	75	647	4.613E-06	5327 plasminogen activator, tissue
GO	extracellular space	75	647	4.613E-06	5367 pro-melanin-concentrating hormone
GO	extracellular space	75	647	4.613E-06	55068 ecto-NOX disulfide-thiol exchanger 1
GO	extracellular space	75	647	4.613E-06	56477 chemokine (C-C motif) ligand 28
GO	extracellular space	75	647	4.613E-06	5648 mannan-binding lectin serine peptidase 1 (C4/C2 activating component
GO	extracellular space	75	647	4.613E-06	5768 quiescin Q6 sulfhydryl oxidase 1
GO	extracellular space	75	647	4.613E-06	5950 retinol binding protein 4, plasma
GO	extracellular space	75	647	4.613E-06	5972 renin
GO	extracellular space	75	647	4.613E-06	6372 chemokine (C-X-C motif) ligand 6 (granulocyte chemotactic protein 2)
GO	extracellular space	75	647	4.613E-06	6374 chemokine (C-X-C motif) ligand 5
GO	extracellular space	75	647	4.613E-06	64388 gremlin 2, cysteine knot superfamily, homolog (Xenopus laevis)
GO	extracellular space	75	647	4.613E-06	652 bone morphogenetic protein 4
GO	extracellular space	75	647	4.613E-06	6750 somatostatin
GO	extracellular space	75	647	4.613E-06	6948 transcobalamin II; macrocytic anemia
GO	extracellular space	75	647	4.613E-06	7049 transforming growth factor, beta receptor III
GO	extracellular space	75	647	4.613E-06	717 complement component 2
GO	extracellular space	75	647	4.613E-06	718 complement component 3
GO	extracellular space	75	647	4.613E-06	731 complement component 8, alpha polypeptide

GO extracellular space	75	647	4.613E-06	7474 wingless-type MMTV integration site family, member 5A
GO extracellular space	75	647	4.613E-06	760 carbonic anhydrase II
GO extracellular space	75	647	4.613E-06	7941 phospholipase A2, group VII (platelet-activating factor acetylhydrolase,
GO extracellular space	75	647	4.613E-06	84171 lysyl oxidase-like 4
GO extracellular space	75	647	4.613E-06	8542 apolipoprotein L, 1
GO extracellular space	75	647	4.613E-06	8600 tumor necrosis factor (ligand) superfamily, member 11
GO extracellular space	75	647	4.613E-06	8646 chordin
GO extracellular space	75	647	4.613E-06	8740 tumor necrosis factor (ligand) superfamily, member 14
GO extracellular space	75	647	4.613E-06	8744 tumor necrosis factor (ligand) superfamily, member 9
GO extracellular space	75	647	4.613E-06	885 cholecystokinin
GO extracellular space	75	647	4.613E-06	90865 interleukin 33
GO extracellular space	75	647	4.613E-06	92304 secretoglobulin, family 3A, member 1
GO extracellular space	75	647	4.613E-06	92747 chromosome 20 open reading frame 114
GO extracellular space	75	647	4.613E-06	929 CD14 molecule
GO extracellular space	75	647	4.613E-06	94025 mucin 16, cell surface associated
GO extracellular space	75	647	4.613E-06	9518 growth differentiation factor 15
GO extracellular space	75	647	4.613E-06	9966 tumor necrosis factor (ligand) superfamily, member 15
GO complement activation, classical path	10	27	6.184E-06	1380 complement component (3d/Epstein Barr virus) receptor 2
GO complement activation, classical path	10	27	6.184E-06	1604 CD55 molecule, decay accelerating factor for complement (Cromer blo
GO complement activation, classical path	10	27	6.184E-06	4179 CD46 molecule, complement regulatory protein
GO complement activation, classical path	10	27	6.184E-06	51279 complement component 1, r subcomponent-like
GO complement activation, classical path	10	27	6.184E-06	715 complement component 1, r subcomponent
GO complement activation, classical path	10	27	6.184E-06	717 complement component 2
GO complement activation, classical path	10	27	6.184E-06	718 complement component 3
GO complement activation, classical path	10	27	6.184E-06	722 complement component 4 binding protein, alpha
GO complement activation, classical path	10	27	6.184E-06	725 complement component 4 binding protein, beta
GO complement activation, classical path	10	27	6.184E-06	731 complement component 8, alpha polypeptide
GO cell surface	33	214	9.221E-06	1803 dipeptidyl-peptidase 4
GO cell surface	33	214	9.221E-06	1839 heparin-binding EGF-like growth factor
GO cell surface	33	214	9.221E-06	1902 lysophosphatidic acid receptor 1
GO cell surface	33	214	9.221E-06	222545 G protein-coupled receptor, family C, group 6, member A
GO cell surface	33	214	9.221E-06	2263 fibroblast growth factor receptor 2
GO cell surface	33	214	9.221E-06	2526 fucosyltransferase 4 (alpha (1,3) fucosyltransferase, myeloid-specific)
GO cell surface	33	214	9.221E-06	25825 beta-site APP-cleaving enzyme 2
GO cell surface	33	214	9.221E-06	286133 scavenger receptor class A, member 5 (putative)
GO cell surface	33	214	9.221E-06	3192 heterogeneous nuclear ribonucleoprotein U (scaffold attachment facto

GO	cell surface	33	214	9.221E-06	3306 heat shock 70kDa protein 2
GO	cell surface	33	214	9.221E-06	3570 interleukin 6 receptor
GO	cell surface	33	214	9.221E-06	375790 agrin
GO	cell surface	33	214	9.221E-06	4853 Notch homolog 2 (Drosophila)
GO	cell surface	33	214	9.221E-06	5046 proprotein convertase subtilisin/kexin type 6
GO	cell surface	33	214	9.221E-06	50937 Cdon homolog (mouse)
GO	cell surface	33	214	9.221E-06	51754 transmembrane protein 8B
GO	cell surface	33	214	9.221E-06	5243 ATP-binding cassette, sub-family B (MDR/TAP), member 1
GO	cell surface	33	214	9.221E-06	5327 plasminogen activator, tissue
GO	cell surface	33	214	9.221E-06	57453 Down syndrome cell adhesion molecule like 1
GO	cell surface	33	214	9.221E-06	5801 protein tyrosine phosphatase, receptor type, R
GO	cell surface	33	214	9.221E-06	64127 nucleotide-binding oligomerization domain containing 2
GO	cell surface	33	214	9.221E-06	6710 spectrin, beta, erythrocytic
GO	cell surface	33	214	9.221E-06	7049 transforming growth factor, beta receptor III
GO	cell surface	33	214	9.221E-06	7097 toll-like receptor 2
GO	cell surface	33	214	9.221E-06	7098 toll-like receptor 3
GO	cell surface	33	214	9.221E-06	7852 chemokine (C-X-C motif) receptor 4
GO	cell surface	33	214	9.221E-06	84059 G protein-coupled receptor 98
GO	cell surface	33	214	9.221E-06	8406 sushi-repeat-containing protein, X-linked
GO	cell surface	33	214	9.221E-06	8839 WNT1 inducible signaling pathway protein 2
GO	cell surface	33	214	9.221E-06	8842 prominin 1
GO	cell surface	33	214	9.221E-06	91 activin A receptor, type IB
GO	cell surface	33	214	9.221E-06	94 activin A receptor type II-like 1
GO	cell surface	33	214	9.221E-06	952 CD38 molecule
GO	negative regulation of cell proliferatic	39	287	3.088E-05	10076 protein tyrosine phosphatase, receptor type, U
GO	negative regulation of cell proliferatic	39	287	3.088E-05	10140 transducer of ERBB2, 1
GO	negative regulation of cell proliferatic	39	287	3.088E-05	10252 sprouty homolog 1, antagonist of FGF signaling (Drosophila)
GO	negative regulation of cell proliferatic	39	287	3.088E-05	10253 sprouty homolog 2 (Drosophila)
GO	negative regulation of cell proliferatic	39	287	3.088E-05	10766 transducer of ERBB2, 2
GO	negative regulation of cell proliferatic	39	287	3.088E-05	1741 discs, large homolog 3 (Drosophila)
GO	negative regulation of cell proliferatic	39	287	3.088E-05	1813 dopamine receptor D2
GO	negative regulation of cell proliferatic	39	287	3.088E-05	183 angiotensinogen (serpin peptidase inhibitor, clade A, member 8)
GO	negative regulation of cell proliferatic	39	287	3.088E-05	23371 tensin like C1 domain containing phosphatase (tensin 2)
GO	negative regulation of cell proliferatic	39	287	3.088E-05	2737 GLI family zinc finger 3
GO	negative regulation of cell proliferatic	39	287	3.088E-05	3373 hyaluronoglucosaminidase 1
GO	negative regulation of cell proliferatic	39	287	3.088E-05	3479 insulin-like growth factor 1 (somatomedin C)

GO	negative regulation of cell proliferati	39	287	3.088E-05	3486 insulin-like growth factor binding protein 3
GO	negative regulation of cell proliferati	39	287	3.088E-05	3569 interleukin 6 (interferon, beta 2)
GO	negative regulation of cell proliferati	39	287	3.088E-05	3604 tumor necrosis factor receptor superfamily, member 9
GO	negative regulation of cell proliferati	39	287	3.088E-05	3725 jun oncogene
GO	negative regulation of cell proliferati	39	287	3.088E-05	4087 SMAD family member 2
GO	negative regulation of cell proliferati	39	287	3.088E-05	4194 Mdm4 p53 binding protein homolog (mouse)
GO	negative regulation of cell proliferati	39	287	3.088E-05	4692 necdin homolog (mouse)
GO	negative regulation of cell proliferati	39	287	3.088E-05	4853 Notch homolog 2 (Drosophila)
GO	negative regulation of cell proliferati	39	287	3.088E-05	5371 promyelocytic leukemia
GO	negative regulation of cell proliferati	39	287	3.088E-05	5920 retinoic acid receptor responder (tazarotene induced) 3
GO	negative regulation of cell proliferati	39	287	3.088E-05	604 B-cell CLL/lymphoma 6
GO	negative regulation of cell proliferati	39	287	3.088E-05	6256 retinoid X receptor, alpha
GO	negative regulation of cell proliferati	39	287	3.088E-05	652 bone morphogenetic protein 4
GO	negative regulation of cell proliferati	39	287	3.088E-05	6750 somatostatin
GO	negative regulation of cell proliferati	39	287	3.088E-05	6751 somatostatin receptor 1
GO	negative regulation of cell proliferati	39	287	3.088E-05	7071 Kruppel-like factor 10
GO	negative regulation of cell proliferati	39	287	3.088E-05	8313 axin 2
GO	negative regulation of cell proliferati	39	287	3.088E-05	83595 SRY (sex determining region Y)-box 7
GO	negative regulation of cell proliferati	39	287	3.088E-05	8462 Kruppel-like factor 11
GO	negative regulation of cell proliferati	39	287	3.088E-05	85004 RAS-like, estrogen-regulated, growth inhibitor
GO	negative regulation of cell proliferati	39	287	3.088E-05	8519 interferon induced transmembrane protein 1 (9-27)
GO	negative regulation of cell proliferati	39	287	3.088E-05	85477 scinderin
GO	negative regulation of cell proliferati	39	287	3.088E-05	8839 WNT1 inducible signaling pathway protein 2
GO	negative regulation of cell proliferati	39	287	3.088E-05	9314 Kruppel-like factor 4 (gut)
GO	negative regulation of cell proliferati	39	287	3.088E-05	94 activin A receptor type II-like 1
GO	negative regulation of cell proliferati	39	287	3.088E-05	9510 ADAM metalloproteinase with thrombospondin type 1 motif, 1
GO	negative regulation of cell proliferati	39	287	3.088E-05	9537 tumor protein p53 inducible protein 11
GO	sequence-specific DNA binding	57	487	4.83E-05	10481 homeobox B13
GO	sequence-specific DNA binding	57	487	4.83E-05	116071 basic leucine zipper transcription factor, ATF-like 2
GO	sequence-specific DNA binding	57	487	4.83E-05	116113 forkhead box P4
GO	sequence-specific DNA binding	57	487	4.83E-05	127343 diencephalon/mesencephalon homeobox 1
GO	sequence-specific DNA binding	57	487	4.83E-05	158800 RhoX homeobox family, member 1
GO	sequence-specific DNA binding	57	487	4.83E-05	1628 D site of albumin promoter (albumin D-box) binding protein
GO	sequence-specific DNA binding	57	487	4.83E-05	1958 early growth response 1
GO	sequence-specific DNA binding	57	487	4.83E-05	1999 E74-like factor 3 (ets domain transcription factor, epithelial-specific )
GO	sequence-specific DNA binding	57	487	4.83E-05	2114 v-ets erythroblastosis virus E26 oncogene homolog 2 (avian)

GO	sequence-specific DNA binding	57	487	4.83E-05	2115 ets variant 1
GO	sequence-specific DNA binding	57	487	4.83E-05	2117 ets variant 3
GO	sequence-specific DNA binding	57	487	4.83E-05	2290 forkhead box G1
GO	sequence-specific DNA binding	57	487	4.83E-05	2296 forkhead box C1
GO	sequence-specific DNA binding	57	487	4.83E-05	2303 forkhead box C2 (MFH-1, mesenchyme forkhead 1)
GO	sequence-specific DNA binding	57	487	4.83E-05	2306 forkhead box D2
GO	sequence-specific DNA binding	57	487	4.83E-05	2354 FBJ murine osteosarcoma viral oncogene homolog B
GO	sequence-specific DNA binding	57	487	4.83E-05	2624 GATA binding protein 2
GO	sequence-specific DNA binding	57	487	4.83E-05	26468 LIM homeobox 6
GO	sequence-specific DNA binding	57	487	4.83E-05	2737 GLI family zinc finger 3
GO	sequence-specific DNA binding	57	487	4.83E-05	3131 hepatic leukemia factor
GO	sequence-specific DNA binding	57	487	4.83E-05	3142 H2.0-like homeobox
GO	sequence-specific DNA binding	57	487	4.83E-05	3164 nuclear receptor subfamily 4, group A, member 1
GO	sequence-specific DNA binding	57	487	4.83E-05	3175 one cut homeobox 1
GO	sequence-specific DNA binding	57	487	4.83E-05	3659 interferon regulatory factor 1
GO	sequence-specific DNA binding	57	487	4.83E-05	3726 jun B proto-oncogene
GO	sequence-specific DNA binding	57	487	4.83E-05	4209 myocyte enhancer factor 2D
GO	sequence-specific DNA binding	57	487	4.83E-05	4212 Meis homeobox 2
GO	sequence-specific DNA binding	57	487	4.83E-05	4223 mesenchyme homeobox 2
GO	sequence-specific DNA binding	57	487	4.83E-05	429 achaete-scute complex homolog 1 (Drosophila)
GO	sequence-specific DNA binding	57	487	4.83E-05	4306 nuclear receptor subfamily 3, group C, member 2
GO	sequence-specific DNA binding	57	487	4.83E-05	467 activating transcription factor 3
GO	sequence-specific DNA binding	57	487	4.83E-05	4778 nuclear factor (erythroid-derived 2), 45kDa
GO	sequence-specific DNA binding	57	487	4.83E-05	4783 nuclear factor, interleukin 3 regulated
GO	sequence-specific DNA binding	57	487	4.83E-05	4802 nuclear transcription factor Y, gamma
GO	sequence-specific DNA binding	57	487	4.83E-05	4851 Notch homolog 1, translocation-associated (Drosophila)
GO	sequence-specific DNA binding	57	487	4.83E-05	4929 nuclear receptor subfamily 4, group A, member 2
GO	sequence-specific DNA binding	57	487	4.83E-05	5307 paired-like homeodomain 1
GO	sequence-specific DNA binding	57	487	4.83E-05	5308 paired-like homeodomain 2
GO	sequence-specific DNA binding	57	487	4.83E-05	5396 paired related homeobox 1
GO	sequence-specific DNA binding	57	487	4.83E-05	5460 POU class 5 homeobox 1
GO	sequence-specific DNA binding	57	487	4.83E-05	5463 POU class 6 homeobox 1
GO	sequence-specific DNA binding	57	487	4.83E-05	5465 peroxisome proliferator-activated receptor alpha
GO	sequence-specific DNA binding	57	487	4.83E-05	55810 forkhead box J2
GO	sequence-specific DNA binding	57	487	4.83E-05	57459 GATA zinc finger domain containing 2B
GO	sequence-specific DNA binding	57	487	4.83E-05	57594 homeobox and leucine zipper encoding

GO	sequence-specific DNA binding	57	487	4.83E-05	604 B-cell CLL/lymphoma 6
GO	sequence-specific DNA binding	57	487	4.83E-05	6096 RAR-related orphan receptor B
GO	sequence-specific DNA binding	57	487	4.83E-05	6097 RAR-related orphan receptor C
GO	sequence-specific DNA binding	57	487	4.83E-05	6778 signal transducer and activator of transcription 6, interleukin-4 inducer
GO	sequence-specific DNA binding	57	487	4.83E-05	7008 thyrotrophic embryonic factor
GO	sequence-specific DNA binding	57	487	4.83E-05	7227 trichorhinophalangeal syndrome I
GO	sequence-specific DNA binding	57	487	4.83E-05	8013 nuclear receptor subfamily 4, group A, member 3
GO	sequence-specific DNA binding	57	487	4.83E-05	80714 pre-B-cell leukemia homeobox 4
GO	sequence-specific DNA binding	57	487	4.83E-05	90993 cAMP responsive element binding protein 3-like 1
GO	sequence-specific DNA binding	57	487	4.83E-05	9572 nuclear receptor subfamily 1, group D, member 1
GO	sequence-specific DNA binding	57	487	4.83E-05	9935 v-maf musculoaponeurotic fibrosarcoma oncogene homolog B (avian)
GO	sequence-specific DNA binding	57	487	4.83E-05	9971 nuclear receptor subfamily 1, group H, member 4
GO	transcription factor activity	94	922	5.829E-05	10346 tripartite motif-containing 22
GO	transcription factor activity	94	922	5.829E-05	10481 homeobox B13
GO	transcription factor activity	94	922	5.829E-05	116071 basic leucine zipper transcription factor, ATF-like 2
GO	transcription factor activity	94	922	5.829E-05	116113 forkhead box P4
GO	transcription factor activity	94	922	5.829E-05	127343 diencephalon/mesencephalon homeobox 1
GO	transcription factor activity	94	922	5.829E-05	158800 RhoX homeobox family, member 1
GO	transcription factor activity	94	922	5.829E-05	1628 D site of albumin promoter (albumin D-box) binding protein
GO	transcription factor activity	94	922	5.829E-05	1820 AT rich interactive domain 3A (BRIGHT-like)
GO	transcription factor activity	94	922	5.829E-05	1958 early growth response 1
GO	transcription factor activity	94	922	5.829E-05	1959 early growth response 2
GO	transcription factor activity	94	922	5.829E-05	1960 early growth response 3
GO	transcription factor activity	94	922	5.829E-05	1999 E74-like factor 3 (ets domain transcription factor, epithelial-specific )
GO	transcription factor activity	94	922	5.829E-05	2033 E1A binding protein p300
GO	transcription factor activity	94	922	5.829E-05	2114 v-ets erythroblastosis virus E26 oncogene homolog 2 (avian)
GO	transcription factor activity	94	922	5.829E-05	2115 ets variant 1
GO	transcription factor activity	94	922	5.829E-05	2117 ets variant 3
GO	transcription factor activity	94	922	5.829E-05	2122 MDS1 and EVI1 complex locus
GO	transcription factor activity	94	922	5.829E-05	2290 forkhead box G1
GO	transcription factor activity	94	922	5.829E-05	2296 forkhead box C1
GO	transcription factor activity	94	922	5.829E-05	2303 forkhead box C2 (MFH-1, mesenchyme forkhead 1)
GO	transcription factor activity	94	922	5.829E-05	2306 forkhead box D2
GO	transcription factor activity	94	922	5.829E-05	2353 FBJ murine osteosarcoma viral oncogene homolog
GO	transcription factor activity	94	922	5.829E-05	2354 FBJ murine osteosarcoma viral oncogene homolog B
GO	transcription factor activity	94	922	5.829E-05	23650 tripartite motif-containing 29

GO transcription factor activity	94	922	5.829E-05	2624 GATA binding protein 2
GO transcription factor activity	94	922	5.829E-05	26468 LIM homeobox 6
GO transcription factor activity	94	922	5.829E-05	2737 GLI family zinc finger 3
GO transcription factor activity	94	922	5.829E-05	3131 hepatic leukemia factor
GO transcription factor activity	94	922	5.829E-05	3142 H2.0-like homeobox
GO transcription factor activity	94	922	5.829E-05	3164 nuclear receptor subfamily 4, group A, member 1
GO transcription factor activity	94	922	5.829E-05	3169 forkhead box A1
GO transcription factor activity	94	922	5.829E-05	3175 one cut homeobox 1
GO transcription factor activity	94	922	5.829E-05	3659 interferon regulatory factor 1
GO transcription factor activity	94	922	5.829E-05	3665 interferon regulatory factor 7
GO transcription factor activity	94	922	5.829E-05	3725 jun oncogene
GO transcription factor activity	94	922	5.829E-05	3726 jun B proto-oncogene
GO transcription factor activity	94	922	5.829E-05	4087 SMAD family member 2
GO transcription factor activity	94	922	5.829E-05	4209 myocyte enhancer factor 2D
GO transcription factor activity	94	922	5.829E-05	4212 Meis homeobox 2
GO transcription factor activity	94	922	5.829E-05	4223 mesenchyme homeobox 2
GO transcription factor activity	94	922	5.829E-05	429 achaete-scute complex homolog 1 (Drosophila)
GO transcription factor activity	94	922	5.829E-05	4306 nuclear receptor subfamily 3, group C, member 2
GO transcription factor activity	94	922	5.829E-05	4613 v-myc myelocytomatosis viral related oncogene, neuroblastoma derive
GO transcription factor activity	94	922	5.829E-05	467 activating transcription factor 3
GO transcription factor activity	94	922	5.829E-05	4778 nuclear factor (erythroid-derived 2), 45kDa
GO transcription factor activity	94	922	5.829E-05	4783 nuclear factor, interleukin 3 regulated
GO transcription factor activity	94	922	5.829E-05	4784 nuclear factor I/X (CCAAT-binding transcription factor)
GO transcription factor activity	94	922	5.829E-05	4791 nuclear factor of kappa light polypeptide gene enhancer in B-cells 2 (p4
GO transcription factor activity	94	922	5.829E-05	4802 nuclear transcription factor Y, gamma
GO transcription factor activity	94	922	5.829E-05	4851 Notch homolog 1, translocation-associated (Drosophila)
GO transcription factor activity	94	922	5.829E-05	4929 nuclear receptor subfamily 4, group A, member 2
GO transcription factor activity	94	922	5.829E-05	51085 MLX interacting protein-like
GO transcription factor activity	94	922	5.829E-05	51274 Kruppel-like factor 3 (basic)
GO transcription factor activity	94	922	5.829E-05	5307 paired-like homeodomain 1
GO transcription factor activity	94	922	5.829E-05	5308 paired-like homeodomain 2
GO transcription factor activity	94	922	5.829E-05	5396 paired related homeobox 1
GO transcription factor activity	94	922	5.829E-05	5460 POU class 5 homeobox 1
GO transcription factor activity	94	922	5.829E-05	5463 POU class 6 homeobox 1
GO transcription factor activity	94	922	5.829E-05	5465 peroxisome proliferator-activated receptor alpha
GO transcription factor activity	94	922	5.829E-05	55769 zinc finger protein 83



GO transcription factor activity	94	922	5.829E-05	55810 forkhead box J2
GO transcription factor activity	94	922	5.829E-05	57459 GATA zinc finger domain containing 2B
GO transcription factor activity	94	922	5.829E-05	57594 homeobox and leucine zipper encoding
GO transcription factor activity	94	922	5.829E-05	604 B-cell CLL/lymphoma 6
GO transcription factor activity	94	922	5.829E-05	6096 RAR-related orphan receptor B
GO transcription factor activity	94	922	5.829E-05	6097 RAR-related orphan receptor C
GO transcription factor activity	94	922	5.829E-05	6256 retinoid X receptor, alpha
GO transcription factor activity	94	922	5.829E-05	64651 cysteine-serine-rich nuclear protein 1
GO transcription factor activity	94	922	5.829E-05	6778 signal transducer and activator of transcription 6, interleukin-4 inducible
GO transcription factor activity	94	922	5.829E-05	687 Kruppel-like factor 9
GO transcription factor activity	94	922	5.829E-05	6941 transcription factor 19
GO transcription factor activity	94	922	5.829E-05	7008 thyrotrophic embryonic factor
GO transcription factor activity	94	922	5.829E-05	7022 transcription factor AP-2 gamma (activating enhancer binding protein 2)
GO transcription factor activity	94	922	5.829E-05	7026 nuclear receptor subfamily 2, group F, member 2
GO transcription factor activity	94	922	5.829E-05	7071 Kruppel-like factor 10
GO transcription factor activity	94	922	5.829E-05	7227 trichorhinophalangeal syndrome I
GO transcription factor activity	94	922	5.829E-05	7597 zinc finger and BTB domain containing 25
GO transcription factor activity	94	922	5.829E-05	7706 tripartite motif-containing 25
GO transcription factor activity	94	922	5.829E-05	8013 nuclear receptor subfamily 4, group A, member 3
GO transcription factor activity	94	922	5.829E-05	80714 pre-B-cell leukemia homeobox 4
GO transcription factor activity	94	922	5.829E-05	83595 SRY (sex determining region Y)-box 7
GO transcription factor activity	94	922	5.829E-05	84124 zinc finger protein 394
GO transcription factor activity	94	922	5.829E-05	8462 Kruppel-like factor 11
GO transcription factor activity	94	922	5.829E-05	8531 cold shock domain protein A
GO transcription factor activity	94	922	5.829E-05	8543 LIM domain only 4
GO transcription factor activity	94	922	5.829E-05	8553 basic helix-loop-helix family, member e40
GO transcription factor activity	94	922	5.829E-05	862 runt-related transcription factor 1; translocated to, 1 (cyclin D-related)
GO transcription factor activity	94	922	5.829E-05	8848 TSC22 domain family, member 1
GO transcription factor activity	94	922	5.829E-05	90993 cAMP responsive element binding protein 3-like 1
GO transcription factor activity	94	922	5.829E-05	9314 Kruppel-like factor 4 (gut)
GO transcription factor activity	94	922	5.829E-05	9496 T-box 4
GO transcription factor activity	94	922	5.829E-05	9572 nuclear receptor subfamily 1, group D, member 1
GO transcription factor activity	94	922	5.829E-05	9935 v-maf musculoaponeurotic fibrosarcoma oncogene homolog B (avian)
GO transcription factor activity	94	922	5.829E-05	9971 nuclear receptor subfamily 1, group H, member 4
GO response to lipopolysaccharide	19	105	8.238E-05	10221 tribbles homolog 1 (Drosophila)
GO response to lipopolysaccharide	19	105	8.238E-05	11213 interleukin-1 receptor-associated kinase 3

GO response to lipopolysaccharide	19	105	8.238E-05	1373 carbamoyl-phosphate synthetase 1, mitochondrial
GO response to lipopolysaccharide	19	105	8.238E-05	2353 FBJ murine osteosarcoma viral oncogene homolog
GO response to lipopolysaccharide	19	105	8.238E-05	3570 interleukin 6 receptor
GO response to lipopolysaccharide	19	105	8.238E-05	3587 interleukin 10 receptor, alpha
GO response to lipopolysaccharide	19	105	8.238E-05	3725 jun oncogene
GO response to lipopolysaccharide	19	105	8.238E-05	4129 monoamine oxidase B
GO response to lipopolysaccharide	19	105	8.238E-05	4792 nuclear factor of kappa light polypeptide gene enhancer in B-cells inhib
GO response to lipopolysaccharide	19	105	8.238E-05	5122 proprotein convertase subtilisin/kexin type 1
GO response to lipopolysaccharide	19	105	8.238E-05	5724 platelet-activating factor receptor
GO response to lipopolysaccharide	19	105	8.238E-05	64127 nucleotide-binding oligomerization domain containing 2
GO response to lipopolysaccharide	19	105	8.238E-05	6622 synuclein, alpha (non A4 component of amyloid precursor)
GO response to lipopolysaccharide	19	105	8.238E-05	7001 peroxiredoxin 2
GO response to lipopolysaccharide	19	105	8.238E-05	7097 toll-like receptor 2
GO response to lipopolysaccharide	19	105	8.238E-05	7099 toll-like receptor 4
GO response to lipopolysaccharide	19	105	8.238E-05	834 caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, co
GO response to lipopolysaccharide	19	105	8.238E-05	9021 suppressor of cytokine signaling 3
GO response to lipopolysaccharide	19	105	8.238E-05	9971 nuclear receptor subfamily 1, group H, member 4
GO response to protein stimulus	11	42	8.679E-05	1508 cathepsin B
GO response to protein stimulus	11	42	8.679E-05	1958 early growth response 1
GO response to protein stimulus	11	42	8.679E-05	2033 E1A binding protein p300
GO response to protein stimulus	11	42	8.679E-05	2353 FBJ murine osteosarcoma viral oncogene homolog
GO response to protein stimulus	11	42	8.679E-05	3491 cysteine-rich, angiogenic inducer, 61
GO response to protein stimulus	11	42	8.679E-05	3643 insulin receptor
GO response to protein stimulus	11	42	8.679E-05	4929 nuclear receptor subfamily 4, group A, member 2
GO response to protein stimulus	11	42	8.679E-05	5122 proprotein convertase subtilisin/kexin type 1
GO response to protein stimulus	11	42	8.679E-05	56923 neuromedin U receptor 2
GO response to protein stimulus	11	42	8.679E-05	7071 Kruppel-like factor 10
GO response to protein stimulus	11	42	8.679E-05	7706 tripartite motif-containing 25
GO positive regulation of peptidyl-tyrosin	11	42	8.679E-05	183 angiotensinogen (serpin peptidase inhibitor, clade A, member 8)
GO positive regulation of peptidyl-tyrosin	11	42	8.679E-05	2205 Fc fragment of IgE, high affinity I, receptor for; alpha polypeptide
GO positive regulation of peptidyl-tyrosin	11	42	8.679E-05	3479 insulin-like growth factor 1 (somatomedin C)
GO positive regulation of peptidyl-tyrosin	11	42	8.679E-05	3569 interleukin 6 (interferon, beta 2)
GO positive regulation of peptidyl-tyrosin	11	42	8.679E-05	3570 interleukin 6 receptor
GO positive regulation of peptidyl-tyrosin	11	42	8.679E-05	3678 integrin, alpha 5 (fibronectin receptor, alpha polypeptide)
GO positive regulation of peptidyl-tyrosin	11	42	8.679E-05	4254 KIT ligand
GO positive regulation of peptidyl-tyrosin	11	42	8.679E-05	64127 nucleotide-binding oligomerization domain containing 2

GO	positive regulation of peptidyl-tyrosin	11	42	8.679E-05	6850 spleen tyrosine kinase
GO	positive regulation of peptidyl-tyrosin	11	42	8.679E-05	7099 toll-like receptor 4
GO	positive regulation of peptidyl-tyrosin	11	42	8.679E-05	885 cholecystokinin
GO	membrane	302	3643	8.688E-05	10008 potassium voltage-gated channel, Isk-related family, member 3
GO	membrane	302	3643	8.688E-05	10090 uronyl-2-sulfotransferase
GO	membrane	302	3643	8.688E-05	10103 tetraspanin 1
GO	membrane	302	3643	8.688E-05	10158 PDZK1 interacting protein 1
GO	membrane	302	3643	8.688E-05	10162 lysophosphatidylcholine acyltransferase 3
GO	membrane	302	3643	8.688E-05	10170 dehydrogenase/reductase (SDR family) member 9
GO	membrane	302	3643	8.688E-05	10205 myelin protein zero-like 2
GO	membrane	302	3643	8.688E-05	10282 blocked early in transport 1 homolog ( <i>S. cerevisiae</i> )
GO	membrane	302	3643	8.688E-05	10317 UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 5
GO	membrane	302	3643	8.688E-05	10335 murine retrovirus integration site 1 homolog
GO	membrane	302	3643	8.688E-05	10384 butyrophilin, subfamily 3, member A3
GO	membrane	302	3643	8.688E-05	10435 CDC42 effector protein (Rho GTPase binding) 2
GO	membrane	302	3643	8.688E-05	10568 solute carrier family 34 (sodium phosphate), member 2
GO	membrane	302	3643	8.688E-05	1080 cystic fibrosis transmembrane conductance regulator (ATP-binding cas:
GO	membrane	302	3643	8.688E-05	10826 chromosome 5 open reading frame 4
GO	membrane	302	3643	8.688E-05	10913 ectodysplasin A receptor
GO	membrane	302	3643	8.688E-05	1124 chimerin (chimaerin) 2
GO	membrane	302	3643	8.688E-05	112574 sorting nexin 18
GO	membrane	302	3643	8.688E-05	11273 ataxin 2-like
GO	membrane	302	3643	8.688E-05	11322 transmembrane channel-like 6
GO	membrane	302	3643	8.688E-05	113278 chromosome 20 open reading frame 54
GO	membrane	302	3643	8.688E-05	115273 RAB42, member RAS oncogene family
GO	membrane	302	3643	8.688E-05	116844 leucine-rich alpha-2-glycoprotein 1
GO	membrane	302	3643	8.688E-05	1193 chloride intracellular channel 2
GO	membrane	302	3643	8.688E-05	119467 clarin 3
GO	membrane	302	3643	8.688E-05	120224 transmembrane protein 45B
GO	membrane	302	3643	8.688E-05	121227 leucine-rich repeats and immunoglobulin-like domains 3
GO	membrane	302	3643	8.688E-05	121665 signal peptide peptidase 3
GO	membrane	302	3643	8.688E-05	123096 solute carrier family 25, member 29
GO	membrane	302	3643	8.688E-05	123099 degenerative spermatocyte homolog 2, lipid desaturase ( <i>Drosophila</i> )
GO	membrane	302	3643	8.688E-05	127707 kelch domain containing 7A
GO	membrane	302	3643	8.688E-05	127845 golgi transport 1 homolog A ( <i>S. cerevisiae</i> )
GO	membrane	302	3643	8.688E-05	130367 sphingosine-1-phosphate phosphatase 2

GO membrane	302	3643	8.688E-05	130399 activin A receptor, type IC
GO membrane	302	3643	8.688E-05	137994 leucine zipper-EF-hand containing transmembrane protein 2
GO membrane	302	3643	8.688E-05	143098 membrane protein, palmitoylated 7 (MAGUK p55 subfamily member 7
GO membrane	302	3643	8.688E-05	143425 synaptotagmin IX
GO membrane	302	3643	8.688E-05	1435 colony stimulating factor 1 (macrophage)
GO membrane	302	3643	8.688E-05	144132 dynein heavy chain domain 1
GO membrane	302	3643	8.688E-05	145581 leucine rich repeat and fibronectin type III domain containing 5
GO membrane	302	3643	8.688E-05	147138 transmembrane channel-like 8
GO membrane	302	3643	8.688E-05	147798 transmembrane channel-like 4
GO membrane	302	3643	8.688E-05	148170 CDC42 effector protein (Rho GTPase binding) 5
GO membrane	302	3643	8.688E-05	148229 ATPase, class I, type 8B, member 3
GO membrane	302	3643	8.688E-05	154043 CNKSR family member 3
GO membrane	302	3643	8.688E-05	154141 membrane bound O-acyltransferase domain containing 1
GO membrane	302	3643	8.688E-05	154214 ring finger protein 217
GO membrane	302	3643	8.688E-05	155006 transmembrane protein 213
GO membrane	302	3643	8.688E-05	1558 cytochrome P450, family 2, subfamily C, polypeptide 8
GO membrane	302	3643	8.688E-05	1559 cytochrome P450, family 2, subfamily C, polypeptide 9
GO membrane	302	3643	8.688E-05	1571 cytochrome P450, family 2, subfamily E, polypeptide 1
GO membrane	302	3643	8.688E-05	157506 retinol dehydrogenase 10 (all-trans)
GO membrane	302	3643	8.688E-05	1577 cytochrome P450, family 3, subfamily A, polypeptide 5
GO membrane	302	3643	8.688E-05	157855 potassium channel, subfamily U, member 1
GO membrane	302	3643	8.688E-05	158038 leucine rich repeat and Ig domain containing 2
GO membrane	302	3643	8.688E-05	160518 DENN/MADD domain containing 5B
GO membrane	302	3643	8.688E-05	163590 torsin A interacting protein 2
GO membrane	302	3643	8.688E-05	165679 chromosome 3 open reading frame 57
GO membrane	302	3643	8.688E-05	1755 deleted in malignant brain tumors 1
GO membrane	302	3643	8.688E-05	1815 dopamine receptor D4
GO membrane	302	3643	8.688E-05	192134 UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 6 (core
GO membrane	302	3643	8.688E-05	195814 short chain dehydrogenase/reductase family 16C, member 5
GO membrane	302	3643	8.688E-05	200150 phospholipase D family, member 5
GO membrane	302	3643	8.688E-05	2013 epithelial membrane protein 2
GO membrane	302	3643	8.688E-05	201895 chromosome 4 open reading frame 34
GO membrane	302	3643	8.688E-05	2044 EPH receptor A5
GO membrane	302	3643	8.688E-05	204962 solute carrier family 44, member 5
GO membrane	302	3643	8.688E-05	2055 ceroid-lipofuscinosis, neuronal 8 (epilepsy, progressive with mental ret
GO membrane	302	3643	8.688E-05	2182 acyl-CoA synthetase long-chain family member 4

GO membrane	302	3643	8.688E-05	219623	transmembrane protein 26
GO membrane	302	3643	8.688E-05	221303	family with sequence similarity 162, member B
GO membrane	302	3643	8.688E-05	222223	KIAA1324-like
GO membrane	302	3643	8.688E-05	223117	sema domain, immunoglobulin domain (Ig), short basic domain, secreted
GO membrane	302	3643	8.688E-05	2263	fibroblast growth factor receptor 2
GO membrane	302	3643	8.688E-05	22795	nidogen 2 (osteonidogen)
GO membrane	302	3643	8.688E-05	23035	PH domain and leucine rich repeat protein phosphatase 2
GO membrane	302	3643	8.688E-05	23151	GRAM domain containing 4
GO membrane	302	3643	8.688E-05	23208	synaptotagmin XI
GO membrane	302	3643	8.688E-05	23348	dedicator of cytokinesis 9
GO membrane	302	3643	8.688E-05	23365	Rho guanine nucleotide exchange factor (GEF) 12
GO membrane	302	3643	8.688E-05	23654	plexin B2
GO membrane	302	3643	8.688E-05	23767	fibronectin leucine rich transmembrane protein 3
GO membrane	302	3643	8.688E-05	240	arachidonate 5-lipoxygenase
GO membrane	302	3643	8.688E-05	2525	fucosyltransferase 3 (galactoside 3(4)-L-fucosyltransferase, Lewis blood group antigen synthetase)
GO membrane	302	3643	8.688E-05	2526	fucosyltransferase 4 (alpha (1,3) fucosyltransferase, myeloid-specific)
GO membrane	302	3643	8.688E-05	255104	transmembrane and coiled-coil domains 4
GO membrane	302	3643	8.688E-05	255488	ring finger protein 144B
GO membrane	302	3643	8.688E-05	255743	nephronectin
GO membrane	302	3643	8.688E-05	256987	serine incorporator 5
GO membrane	302	3643	8.688E-05	257019	FERM domain containing 3
GO membrane	302	3643	8.688E-05	25825	beta-site APP-cleaving enzyme 2
GO membrane	302	3643	8.688E-05	2589	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyl transferase 1
GO membrane	302	3643	8.688E-05	259232	sodium leak channel, non-selective
GO membrane	302	3643	8.688E-05	25956	SEC31 homolog B (S. cerevisiae)
GO membrane	302	3643	8.688E-05	26035	glucuronic acid epimerase
GO membrane	302	3643	8.688E-05	26050	SLIT and NTRK-like family, member 5
GO membrane	302	3643	8.688E-05	2615	leucine rich repeat containing 32
GO membrane	302	3643	8.688E-05	26157	GTPase, IMAP family member 2
GO membrane	302	3643	8.688E-05	2635	guanylate binding protein 3
GO membrane	302	3643	8.688E-05	27035	NADPH oxidase 1
GO membrane	302	3643	8.688E-05	27090	ST6 (alpha-N-acetylneuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminyl transferase 6
GO membrane	302	3643	8.688E-05	27242	tumor necrosis factor receptor superfamily, member 21
GO membrane	302	3643	8.688E-05	27345	potassium large conductance calcium-activated channel, subfamily M, member 1
GO membrane	302	3643	8.688E-05	2801	golgin A2
GO membrane	302	3643	8.688E-05	28231	solute carrier organic anion transporter family, member 4A1

GO membrane	302	3643	8.688E-05	283417 dpy-19-like 2 (C. elegans)
GO membrane	302	3643	8.688E-05	283537 solute carrier family 46, member 3
GO membrane	302	3643	8.688E-05	284021 chromosome 17 open reading frame 60
GO membrane	302	3643	8.688E-05	284353 NTPase, KAP family P-loop domain containing 1
GO membrane	302	3643	8.688E-05	286144 chromosome 8 open reading frame 83
GO membrane	302	3643	8.688E-05	28959 transmembrane protein 176B
GO membrane	302	3643	8.688E-05	29015 solute carrier family 43, member 3
GO membrane	302	3643	8.688E-05	29103 DnaJ (Hsp40) homolog, subfamily C, member 15
GO membrane	302	3643	8.688E-05	30008 EGF-containing fibulin-like extracellular matrix protein 2
GO membrane	302	3643	8.688E-05	3134 major histocompatibility complex, class I, F
GO membrane	302	3643	8.688E-05	3294 hydroxysteroid (17-beta) dehydrogenase 2
GO membrane	302	3643	8.688E-05	3429 interferon, alpha-inducible protein 27
GO membrane	302	3643	8.688E-05	3561 interleukin 2 receptor, gamma (severe combined immunodeficiency)
GO membrane	302	3643	8.688E-05	3601 interleukin 15 receptor, alpha
GO membrane	302	3643	8.688E-05	3604 tumor necrosis factor receptor superfamily, member 9
GO membrane	302	3643	8.688E-05	3643 insulin receptor
GO membrane	302	3643	8.688E-05	3687 integrin, alpha X (complement component 3 receptor 4 subunit)
GO membrane	302	3643	8.688E-05	3696 integrin, beta 8
GO membrane	302	3643	8.688E-05	3709 inositol 1,4,5-triphosphate receptor, type 2
GO membrane	302	3643	8.688E-05	374378 UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosami
GO membrane	302	3643	8.688E-05	375056 melanoma inhibitory activity family, member 3
GO membrane	302	3643	8.688E-05	3759 potassium inwardly-rectifying channel, subfamily J, member 2
GO membrane	302	3643	8.688E-05	3773 potassium inwardly-rectifying channel, subfamily J, member 16
GO membrane	302	3643	8.688E-05	3775 potassium channel, subfamily K, member 1
GO membrane	302	3643	8.688E-05	3783 potassium intermediate/small conductance calcium-activated channel,
GO membrane	302	3643	8.688E-05	3786 potassium voltage-gated channel, KQT-like subfamily, member 3
GO membrane	302	3643	8.688E-05	378925 ring finger protein 148
GO membrane	302	3643	8.688E-05	3815 v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog
GO membrane	302	3643	8.688E-05	3823 killer cell lectin-like receptor subfamily C, member 3
GO membrane	302	3643	8.688E-05	387496 RAS-like, family 11, member A
GO membrane	302	3643	8.688E-05	387923 stress-associated endoplasmic reticulum protein family 2 member 2
GO membrane	302	3643	8.688E-05	388633 low density lipoprotein receptor class A domain containing 1
GO membrane	302	3643	8.688E-05	3959 lectin, galactoside-binding, soluble, 3 binding protein
GO membrane	302	3643	8.688E-05	4038 low density lipoprotein receptor-related protein 4
GO membrane	302	3643	8.688E-05	4056 leukotriene C4 synthase
GO membrane	302	3643	8.688E-05	405753 dual oxidase maturation factor 2

GO membrane	302	3643	8.688E-05	4065 lymphocyte antigen 75
GO membrane	302	3643	8.688E-05	4121 mannosidase, alpha, class 1A, member 1
GO membrane	302	3643	8.688E-05	4128 monoamine oxidase A
GO membrane	302	3643	8.688E-05	4129 monoamine oxidase B
GO membrane	302	3643	8.688E-05	4170 myeloid cell leukemia sequence 1 (BCL2-related)
GO membrane	302	3643	8.688E-05	4306 nuclear receptor subfamily 3, group C, member 2
GO membrane	302	3643	8.688E-05	4915 neurotrophic tyrosine kinase, receptor, type 2
GO membrane	302	3643	8.688E-05	4939 2'-5'-oligoadenylate synthetase 2, 69/71kDa
GO membrane	302	3643	8.688E-05	5025 purinergic receptor P2X, ligand-gated ion channel, 4
GO membrane	302	3643	8.688E-05	5046 proprotein convertase subtilisin/kexin type 6
GO membrane	302	3643	8.688E-05	5066 peptidylglycine alpha-amidating monooxygenase
GO membrane	302	3643	8.688E-05	50937 Cdon homolog (mouse)
GO membrane	302	3643	8.688E-05	51063 calcium homeostasis modulator 2
GO membrane	302	3643	8.688E-05	51093 chromosome 1 open reading frame 66
GO membrane	302	3643	8.688E-05	51228 glycolipid transfer protein
GO membrane	302	3643	8.688E-05	51272 blocked early in transport 1 homolog ( <i>S. cerevisiae</i> )-like
GO membrane	302	3643	8.688E-05	51280 golgi membrane protein 1
GO membrane	302	3643	8.688E-05	51285 RAS-like, family 12
GO membrane	302	3643	8.688E-05	51303 FK506 binding protein 11, 19 kDa
GO membrane	302	3643	8.688E-05	51309 armadillo repeat containing, X-linked 1
GO membrane	302	3643	8.688E-05	51313 family with sequence similarity 198, member B
GO membrane	302	3643	8.688E-05	5158 phosphodiesterase 6B, cGMP-specific, rod, beta
GO membrane	302	3643	8.688E-05	51703 acyl-CoA synthetase long-chain family member 5
GO membrane	302	3643	8.688E-05	5243 ATP-binding cassette, sub-family B (MDR/TAP), member 1
GO membrane	302	3643	8.688E-05	53373 two pore segment channel 1
GO membrane	302	3643	8.688E-05	53405 chloride intracellular channel 5
GO membrane	302	3643	8.688E-05	5349 FXYD domain containing ion transport regulator 3
GO membrane	302	3643	8.688E-05	5351 procollagen-lysine 1, 2-oxoglutarate 5-dioxygenase 1
GO membrane	302	3643	8.688E-05	53827 FXYD domain containing ion transport regulator 5
GO membrane	302	3643	8.688E-05	53947 alpha 1,4-galactosyltransferase
GO membrane	302	3643	8.688E-05	54463 family with sequence similarity 134, member B
GO membrane	302	3643	8.688E-05	54664 transmembrane protein 106B
GO membrane	302	3643	8.688E-05	54681 prolyl 4-hydroxylase, transmembrane (endoplasmic reticulum)
GO membrane	302	3643	8.688E-05	54852 progesterin and adipoQ receptor family member V
GO membrane	302	3643	8.688E-05	54894 ring finger protein 43
GO membrane	302	3643	8.688E-05	54933 rhomboid, veinlet-like 2 ( <i>Drosophila</i> )

GO membrane	302	3643	8.688E-05	54947 lysophosphatidylcholine acyltransferase 2
GO membrane	302	3643	8.688E-05	55061 sushi domain containing 4
GO membrane	302	3643	8.688E-05	55076 transmembrane protein 45A
GO membrane	302	3643	8.688E-05	55275 vacuolar protein sorting 53 homolog ( <i>S. cerevisiae</i> )
GO membrane	302	3643	8.688E-05	55281 transmembrane protein 140
GO membrane	302	3643	8.688E-05	55304 serine palmitoyltransferase, long chain base subunit 3
GO membrane	302	3643	8.688E-05	55332 DNA-damage regulated autophagy modulator 1
GO membrane	302	3643	8.688E-05	55365 transmembrane protein 176A
GO membrane	302	3643	8.688E-05	55638 Golgi-localized protein
GO membrane	302	3643	8.688E-05	55714 odz, odd Oz/ten-m homolog 3 ( <i>Drosophila</i> )
GO membrane	302	3643	8.688E-05	55754 transmembrane protein 30A
GO membrane	302	3643	8.688E-05	55799 calcium channel, voltage-dependent, alpha 2/delta subunit 3
GO membrane	302	3643	8.688E-05	55808 ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalact
GO membrane	302	3643	8.688E-05	56605 ERO1-like beta ( <i>S. cerevisiae</i> )
GO membrane	302	3643	8.688E-05	56649 transmembrane protease, serine 4
GO membrane	302	3643	8.688E-05	56654 neural proliferation, differentiation and control, 1
GO membrane	302	3643	8.688E-05	56913 core 1 synthase, glycoprotein-N-acetylgalactosamine 3-beta-galactosyl
GO membrane	302	3643	8.688E-05	57132 chromatin modifying protein 1B
GO membrane	302	3643	8.688E-05	57134 mannosidase, alpha, class 1C, member 1
GO membrane	302	3643	8.688E-05	57146 transmembrane protein 159
GO membrane	302	3643	8.688E-05	57161 pellino homolog 2 ( <i>Drosophila</i> )
GO membrane	302	3643	8.688E-05	57185 NIPA-like domain containing 3
GO membrane	302	3643	8.688E-05	57210 solute carrier family 45, member 4
GO membrane	302	3643	8.688E-05	57221 KIAA1244
GO membrane	302	3643	8.688E-05	5724 platelet-activating factor receptor
GO membrane	302	3643	8.688E-05	57458 transmembrane and coiled-coil domain family 3
GO membrane	302	3643	8.688E-05	57493 HEG homolog 1 (zebrafish)
GO membrane	302	3643	8.688E-05	57535 KIAA1324
GO membrane	302	3643	8.688E-05	57537 sortilin-related VPS10 domain containing receptor 2
GO membrane	302	3643	8.688E-05	57670 KIAA1549
GO membrane	302	3643	8.688E-05	5768 quiescin Q6 sulfhydryl oxidase 1
GO membrane	302	3643	8.688E-05	5787 protein tyrosine phosphatase, receptor type, B
GO membrane	302	3643	8.688E-05	5789 protein tyrosine phosphatase, receptor type, D
GO membrane	302	3643	8.688E-05	5794 protein tyrosine phosphatase, receptor type, H
GO membrane	302	3643	8.688E-05	5799 protein tyrosine phosphatase, receptor type, N polypeptide 2
GO membrane	302	3643	8.688E-05	5873 RAB27A, member RAS oncogene family



GO membrane	302	3643	8.688E-05	59271 chromosome 21 open reading frame 63
GO membrane	302	3643	8.688E-05	5972 renin
GO membrane	302	3643	8.688E-05	6006 Rh blood group, CcEe antigens
GO membrane	302	3643	8.688E-05	6238 ribosome binding protein 1 homolog 180kDa (dog)
GO membrane	302	3643	8.688E-05	63027 solute carrier family 22, member 23
GO membrane	302	3643	8.688E-05	6330 sodium channel, voltage-gated, type IV, beta
GO membrane	302	3643	8.688E-05	63982 anoctamin 3
GO membrane	302	3643	8.688E-05	64108 receptor (chemosensory) transporter protein 4
GO membrane	302	3643	8.688E-05	64116 solute carrier family 39 (zinc transporter), member 8
GO membrane	302	3643	8.688E-05	646658 transmembrane protein 90A
GO membrane	302	3643	8.688E-05	64699 transmembrane protease, serine 3
GO membrane	302	3643	8.688E-05	6484 ST3 beta-galactoside alpha-2,3-sialyltransferase 4
GO membrane	302	3643	8.688E-05	6489 ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 1
GO membrane	302	3643	8.688E-05	6494 signal-induced proliferation-associated 1
GO membrane	302	3643	8.688E-05	6505 solute carrier family 1 (neuronal/epithelial high affinity glutamate transp
GO membrane	302	3643	8.688E-05	6521 solute carrier family 4, anion exchanger, member 1 (erythrocyte memb
GO membrane	302	3643	8.688E-05	6535 solute carrier family 6 (neurotransmitter transporter, creatine), memb
GO membrane	302	3643	8.688E-05	6542 solute carrier family 7 (cationic amino acid transporter, y+ system), me
GO membrane	302	3643	8.688E-05	654463 fer-1-like 6 (C. elegans)
GO membrane	302	3643	8.688E-05	6564 solute carrier family 15 (oligopeptide transporter), member 1
GO membrane	302	3643	8.688E-05	6565 solute carrier family 15 (H+/peptide transporter), member 2
GO membrane	302	3643	8.688E-05	6653 sortilin-related receptor, L(DLR class) A repeats-containing
GO membrane	302	3643	8.688E-05	6916 thromboxane A synthase 1 (platelet)
GO membrane	302	3643	8.688E-05	7098 toll-like receptor 3
GO membrane	302	3643	8.688E-05	7102 tetraspanin 7
GO membrane	302	3643	8.688E-05	7111 tropomodulin 1
GO membrane	302	3643	8.688E-05	727910 TLC domain containing 2
GO membrane	302	3643	8.688E-05	728215 family with sequence similarity 155, member A
GO membrane	302	3643	8.688E-05	731 complement component 8, alpha polypeptide
GO membrane	302	3643	8.688E-05	771 carbonic anhydrase XII
GO membrane	302	3643	8.688E-05	7869 sema domain, immunoglobulin domain (Ig), short basic domain, secret
GO membrane	302	3643	8.688E-05	79152 fatty acid 2-hydroxylase
GO membrane	302	3643	8.688E-05	79180 EF-hand domain family, member D2
GO membrane	302	3643	8.688E-05	79695 UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosami
GO membrane	302	3643	8.688E-05	79789 calmin (calponin-like, transmembrane)
GO membrane	302	3643	8.688E-05	79820 cation channel, sperm-associated, beta

GO membrane	302	3643	8.688E-05	79838 transmembrane channel-like 5
GO membrane	302	3643	8.688E-05	79895 ATPase, class I, type 8B, member 4
GO membrane	302	3643	8.688E-05	79932 KIAA0319-like
GO membrane	302	3643	8.688E-05	79956 endoplasmic reticulum metalloproteinase 1
GO membrane	302	3643	8.688E-05	79957 progesterin and adiponectin receptor family member VI
GO membrane	302	3643	8.688E-05	79971 wntless homolog (Drosophila)
GO membrane	302	3643	8.688E-05	79987 sushi, von Willebrand factor type A, EGF and pentraxin domain contain
GO membrane	302	3643	8.688E-05	80223 RAB11 family interacting protein 1 (class I)
GO membrane	302	3643	8.688E-05	81544 glycerophosphodiester phosphodiesterase domain containing 5
GO membrane	302	3643	8.688E-05	81615 transmembrane protein 163
GO membrane	302	3643	8.688E-05	81693 amnionless homolog (mouse)
GO membrane	302	3643	8.688E-05	819 calcium modulating ligand
GO membrane	302	3643	8.688E-05	83394 PITPNM family member 3
GO membrane	302	3643	8.688E-05	83661 membrane-spanning 4-domains, subfamily A, member 8B
GO membrane	302	3643	8.688E-05	83857 transmembrane and tetratricopeptide repeat containing 1
GO membrane	302	3643	8.688E-05	83890 spermatogenesis associated 9
GO membrane	302	3643	8.688E-05	84059 G protein-coupled receptor 98
GO membrane	302	3643	8.688E-05	8406 sushi-repeat-containing protein, X-linked
GO membrane	302	3643	8.688E-05	84171 lysyl oxidase-like 4
GO membrane	302	3643	8.688E-05	84561 solute carrier family 12 (potassium/chloride transporters), member 8
GO membrane	302	3643	8.688E-05	84879 major facilitator superfamily domain containing 2A
GO membrane	302	3643	8.688E-05	84976 dispatched homolog 1 (Drosophila)
GO membrane	302	3643	8.688E-05	85004 RAS-like, estrogen-regulated, growth inhibitor
GO membrane	302	3643	8.688E-05	8509 N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 2
GO membrane	302	3643	8.688E-05	8645 potassium channel, subfamily K, member 5
GO membrane	302	3643	8.688E-05	8673 vesicle-associated membrane protein 8 (endobrevin)
GO membrane	302	3643	8.688E-05	8706 beta-1,3-N-acetylgalactosaminyltransferase 1 (globoside blood group)
GO membrane	302	3643	8.688E-05	8751 ADAM metalloproteinase domain 15
GO membrane	302	3643	8.688E-05	8793 tumor necrosis factor receptor superfamily, member 10d, decoy with t
GO membrane	302	3643	8.688E-05	8796 sciellin
GO membrane	302	3643	8.688E-05	8911 calcium channel, voltage-dependent, T type, alpha 1I subunit
GO membrane	302	3643	8.688E-05	89801 protein phosphatase 1, regulatory (inhibitor) subunit 3F
GO membrane	302	3643	8.688E-05	89866 SEC16 homolog B (S. cerevisiae)
GO membrane	302	3643	8.688E-05	8992 ATPase, H <sup>+</sup> transporting, lysosomal 9kDa, V0 subunit e1
GO membrane	302	3643	8.688E-05	9019 myelin protein zero-like 1
GO membrane	302	3643	8.688E-05	9050 proline-serine-threonine phosphatase interacting protein 2

GO membrane	302	3643	8.688E-05	90993 cAMP responsive element binding protein 3-like 1
GO membrane	302	3643	8.688E-05	91 activin A receptor, type IB
GO membrane	302	3643	8.688E-05	9143 synaptogyrin 3
GO membrane	302	3643	8.688E-05	9214 Fas apoptotic inhibitory molecule 3
GO membrane	302	3643	8.688E-05	92691 transmembrane protein 169
GO membrane	302	3643	8.688E-05	92840 receptor accessory protein 6
GO membrane	302	3643	8.688E-05	93273 LEM domain containing 1
GO membrane	302	3643	8.688E-05	93589 calcium channel, voltage-dependent, alpha 2/delta subunit 4
GO membrane	302	3643	8.688E-05	94 activin A receptor type II-like 1
GO membrane	302	3643	8.688E-05	9435 carbohydrate (N-acetylglucosamine-6-O) sulfotransferase 2
GO membrane	302	3643	8.688E-05	9445 integral membrane protein 2B
GO membrane	302	3643	8.688E-05	9452 integral membrane protein 2A
GO membrane	302	3643	8.688E-05	9481 solute carrier family 25, member 27
GO membrane	302	3643	8.688E-05	9537 tumor protein p53 inducible protein 11
GO membrane	302	3643	8.688E-05	9804 translocase of outer mitochondrial membrane 20 homolog (yeast)
GO membrane	302	3643	8.688E-05	9823 armadillo repeat containing, X-linked 2
GO membrane	302	3643	8.688E-05	9914 ATPase, Ca <sup>++</sup> transporting, type 2C, member 2
GO transmembrane receptor protein tyrosine kinase	7	18	0.0001116	10076 protein tyrosine phosphatase, receptor type, U
GO transmembrane receptor protein tyrosine kinase	7	18	0.0001116	5787 protein tyrosine phosphatase, receptor type, B
GO transmembrane receptor protein tyrosine kinase	7	18	0.0001116	5789 protein tyrosine phosphatase, receptor type, D
GO transmembrane receptor protein tyrosine kinase	7	18	0.0001116	5791 protein tyrosine phosphatase, receptor type, E
GO transmembrane receptor protein tyrosine kinase	7	18	0.0001116	5794 protein tyrosine phosphatase, receptor type, H
GO transmembrane receptor protein tyrosine kinase	7	18	0.0001116	5799 protein tyrosine phosphatase, receptor type, N polypeptide 2
GO transmembrane receptor protein tyrosine kinase	7	18	0.0001116	5801 protein tyrosine phosphatase, receptor type, R
GO response to progesterone stimulus	8	24	0.0001275	10628 thioredoxin interacting protein
GO response to progesterone stimulus	8	24	0.0001275	2066 v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian)
GO response to progesterone stimulus	8	24	0.0001275	2353 FBJ murine osteosarcoma viral oncogene homolog
GO response to progesterone stimulus	8	24	0.0001275	3726 jun B proto-oncogene
GO response to progesterone stimulus	8	24	0.0001275	7097 toll-like receptor 2
GO response to progesterone stimulus	8	24	0.0001275	7099 toll-like receptor 4
GO response to progesterone stimulus	8	24	0.0001275	9021 suppressor of cytokine signaling 3
GO response to progesterone stimulus	8	24	0.0001275	952 CD38 molecule
GO innate immune response	19	109	0.0001382	10417 spondin 2, extracellular matrix protein
GO innate immune response	19	109	0.0001382	1380 complement component (3d/Epstein Barr virus) receptor 2
GO innate immune response	19	109	0.0001382	1604 CD55 molecule, decay accelerating factor for complement (Cromer blood group)
GO innate immune response	19	109	0.0001382	1755 deleted in malignant brain tumors 1

GO innate immune response	19	109	0.0001382	4179 CD46 molecule, complement regulatory protein
GO innate immune response	19	109	0.0001382	51279 complement component 1, r subcomponent-like
GO innate immune response	19	109	0.0001382	64127 nucleotide-binding oligomerization domain containing 2
GO innate immune response	19	109	0.0001382	64135 interferon induced with helicase C domain 1
GO innate immune response	19	109	0.0001382	7097 toll-like receptor 2
GO innate immune response	19	109	0.0001382	7098 toll-like receptor 3
GO innate immune response	19	109	0.0001382	7099 toll-like receptor 4
GO innate immune response	19	109	0.0001382	7100 toll-like receptor 5
GO innate immune response	19	109	0.0001382	715 complement component 1, r subcomponent
GO innate immune response	19	109	0.0001382	722 complement component 4 binding protein, alpha
GO innate immune response	19	109	0.0001382	725 complement component 4 binding protein, beta
GO innate immune response	19	109	0.0001382	7706 tripartite motif-containing 25
GO innate immune response	19	109	0.0001382	79132 DEXH (Asp-Glu-X-His) box polypeptide 58
GO innate immune response	19	109	0.0001382	8542 apolipoprotein L, 1
GO innate immune response	19	109	0.0001382	929 CD14 molecule
GO negative regulation of ERK1 and ERK2	5	9	0.0001478	10252 sprouty homolog 1, antagonist of FGF signaling (Drosophila)
GO negative regulation of ERK1 and ERK2	5	9	0.0001478	10253 sprouty homolog 2 (Drosophila)
GO negative regulation of ERK1 and ERK2	5	9	0.0001478	154043 CNKSR family member 3
GO negative regulation of ERK1 and ERK2	5	9	0.0001478	3479 insulin-like growth factor 1 (somatomedin C)
GO negative regulation of ERK1 and ERK2	5	9	0.0001478	7099 toll-like receptor 4
GO Rho guanyl-nucleotide exchange factor	14	68	0.0001702	152273 FYVE, RhoGEF and PH domain containing 5
GO Rho guanyl-nucleotide exchange factor	14	68	0.0001702	221178 spermatogenesis associated 13
GO Rho guanyl-nucleotide exchange factor	14	68	0.0001702	23263 MCF.2 cell line derived transforming sequence-like
GO Rho guanyl-nucleotide exchange factor	14	68	0.0001702	23348 dedicator of cytokinesis 9
GO Rho guanyl-nucleotide exchange factor	14	68	0.0001702	23365 Rho guanine nucleotide exchange factor (GEF) 12
GO Rho guanyl-nucleotide exchange factor	14	68	0.0001702	26030 pleckstrin homology domain containing, family G (with RhoGef domain)
GO Rho guanyl-nucleotide exchange factor	14	68	0.0001702	389337 Rho guanine nucleotide exchange factor (GEF) 37
GO Rho guanyl-nucleotide exchange factor	14	68	0.0001702	440107 pleckstrin homology domain containing, family G (with RhoGef domain)
GO Rho guanyl-nucleotide exchange factor	14	68	0.0001702	54848 Rho guanine nucleotide exchange factor (GEF) 38
GO Rho guanyl-nucleotide exchange factor	14	68	0.0001702	55160 Rho guanine nucleotide exchange factor (GEF) 10-like
GO Rho guanyl-nucleotide exchange factor	14	68	0.0001702	55200 pleckstrin homology domain containing, family G (with RhoGef domain)
GO Rho guanyl-nucleotide exchange factor	14	68	0.0001702	7984 Rho guanine nucleotide exchange factor (GEF) 5
GO Rho guanyl-nucleotide exchange factor	14	68	0.0001702	84033 obscurin, cytoskeletal calmodulin and titin-interacting RhoGEF
GO Rho guanyl-nucleotide exchange factor	14	68	0.0001702	9459 Rac/Cdc42 guanine nucleotide exchange factor (GEF) 6
GO integral to membrane	315	3857	0.0001793	10008 potassium voltage-gated channel, Isk-related family, member 3
GO integral to membrane	315	3857	0.0001793	1004 cadherin 6, type 2, K-cadherin (fetal kidney)

GO integral to membrane	315	3857	0.0001793	1009 cadherin 11, type 2, OB-cadherin (osteoblast)
GO integral to membrane	315	3857	0.0001793	10090 uronyl-2-sulfotransferase
GO integral to membrane	315	3857	0.0001793	10103 tetraspanin 1
GO integral to membrane	315	3857	0.0001793	1014 cadherin 16, KSP-cadherin
GO integral to membrane	315	3857	0.0001793	10158 PDZK1 interacting protein 1
GO integral to membrane	315	3857	0.0001793	1016 cadherin 18, type 2
GO integral to membrane	315	3857	0.0001793	10162 lysophosphatidylcholine acyltransferase 3
GO integral to membrane	315	3857	0.0001793	10205 myelin protein zero-like 2
GO integral to membrane	315	3857	0.0001793	10282 blocked early in transport 1 homolog ( <i>S. cerevisiae</i> )
GO integral to membrane	315	3857	0.0001793	10317 UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 5
GO integral to membrane	315	3857	0.0001793	10335 murine retrovirus integration site 1 homolog
GO integral to membrane	315	3857	0.0001793	10384 butyrophilin, subfamily 3, member A3
GO integral to membrane	315	3857	0.0001793	10410 interferon induced transmembrane protein 3 (1-8U)
GO integral to membrane	315	3857	0.0001793	10507 sema domain, immunoglobulin domain (Ig), transmembrane domain (T
GO integral to membrane	315	3857	0.0001793	10568 solute carrier family 34 (sodium phosphate), member 2
GO integral to membrane	315	3857	0.0001793	10752 cell adhesion molecule with homology to L1CAM (close homolog of L1)
GO integral to membrane	315	3857	0.0001793	1080 cystic fibrosis transmembrane conductance regulator (ATP-binding cas:
GO integral to membrane	315	3857	0.0001793	10826 chromosome 5 open reading frame 4
GO integral to membrane	315	3857	0.0001793	1087 carcinoembryonic antigen-related cell adhesion molecule 7
GO integral to membrane	315	3857	0.0001793	10913 ectodysplasin A receptor
GO integral to membrane	315	3857	0.0001793	112 adenylate cyclase 6
GO integral to membrane	315	3857	0.0001793	11322 transmembrane channel-like 6
GO integral to membrane	315	3857	0.0001793	113235 solute carrier family 46 (folate transporter), member 1
GO integral to membrane	315	3857	0.0001793	113278 chromosome 20 open reading frame 54
GO integral to membrane	315	3857	0.0001793	1139 cholinergic receptor, nicotinic, alpha 7
GO integral to membrane	315	3857	0.0001793	114569 mal, T-cell differentiation protein 2
GO integral to membrane	315	3857	0.0001793	115330 G protein-coupled receptor 146
GO integral to membrane	315	3857	0.0001793	118429 anthrax toxin receptor 2
GO integral to membrane	315	3857	0.0001793	1193 chloride intracellular channel 2
GO integral to membrane	315	3857	0.0001793	119467 clarin 3
GO integral to membrane	315	3857	0.0001793	120224 transmembrane protein 45B
GO integral to membrane	315	3857	0.0001793	121130 olfactory receptor, family 10, subfamily P, member 1
GO integral to membrane	315	3857	0.0001793	121227 leucine-rich repeats and immunoglobulin-like domains 3
GO integral to membrane	315	3857	0.0001793	121665 signal peptide peptidase 3
GO integral to membrane	315	3857	0.0001793	123096 solute carrier family 25, member 29
GO integral to membrane	315	3857	0.0001793	123099 degenerative spermatocyte homolog 2, lipid desaturase ( <i>Drosophila</i> )

GO integral to membrane	315	3857	0.0001793	127707 kelch domain containing 7A
GO integral to membrane	315	3857	0.0001793	127845 golgi transport 1 homolog A ( <i>S. cerevisiae</i> )
GO integral to membrane	315	3857	0.0001793	130367 sphingosine-1-phosphate phosphotase 2
GO integral to membrane	315	3857	0.0001793	130399 activin A receptor, type IC
GO integral to membrane	315	3857	0.0001793	137994 leucine zipper-EF-hand containing transmembrane protein 2
GO integral to membrane	315	3857	0.0001793	1380 complement component (3d/Epstein Barr virus) receptor 2
GO integral to membrane	315	3857	0.0001793	143425 synaptotagmin IX
GO integral to membrane	315	3857	0.0001793	1435 colony stimulating factor 1 (macrophage)
GO integral to membrane	315	3857	0.0001793	143503 olfactory receptor, family 51, subfamily E, member 1
GO integral to membrane	315	3857	0.0001793	144132 dynein heavy chain domain 1
GO integral to membrane	315	3857	0.0001793	145581 leucine rich repeat and fibronectin type III domain containing 5
GO integral to membrane	315	3857	0.0001793	147138 transmembrane channel-like 8
GO integral to membrane	315	3857	0.0001793	147798 transmembrane channel-like 4
GO integral to membrane	315	3857	0.0001793	148229 ATPase, class I, type 8B, member 3
GO integral to membrane	315	3857	0.0001793	151473 solute carrier family 16, member 14 (monocarboxylic acid transporter)
GO integral to membrane	315	3857	0.0001793	154141 membrane bound O-acyltransferase domain containing 1
GO integral to membrane	315	3857	0.0001793	154214 ring finger protein 217
GO integral to membrane	315	3857	0.0001793	155006 transmembrane protein 213
GO integral to membrane	315	3857	0.0001793	157506 retinol dehydrogenase 10 (all-trans)
GO integral to membrane	315	3857	0.0001793	157855 potassium channel, subfamily U, member 1
GO integral to membrane	315	3857	0.0001793	158038 leucine rich repeat and Ig domain containing 2
GO integral to membrane	315	3857	0.0001793	160518 DENN/MADD domain containing 5B
GO integral to membrane	315	3857	0.0001793	163590 torsin A interacting protein 2
GO integral to membrane	315	3857	0.0001793	165679 chromosome 3 open reading frame 57
GO integral to membrane	315	3857	0.0001793	1803 dipeptidyl-peptidase 4
GO integral to membrane	315	3857	0.0001793	1901 sphingosine-1-phosphate receptor 1
GO integral to membrane	315	3857	0.0001793	192134 UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 6 (core
GO integral to membrane	315	3857	0.0001793	195814 short chain dehydrogenase/reductase family 16C, member 5
GO integral to membrane	315	3857	0.0001793	200150 phospholipase D family, member 5
GO integral to membrane	315	3857	0.0001793	2013 epithelial membrane protein 2
GO integral to membrane	315	3857	0.0001793	201895 chromosome 4 open reading frame 34
GO integral to membrane	315	3857	0.0001793	2044 EPH receptor A5
GO integral to membrane	315	3857	0.0001793	204962 solute carrier family 44, member 5
GO integral to membrane	315	3857	0.0001793	2055 ceroid-lipofuscinosis, neuronal 8 (epilepsy, progressive with mental ret
GO integral to membrane	315	3857	0.0001793	2066 v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian)
GO integral to membrane	315	3857	0.0001793	2182 acyl-CoA synthetase long-chain family member 4

GO integral to membrane	315	3857	0.0001793	219623	transmembrane protein 26
GO integral to membrane	315	3857	0.0001793	221303	family with sequence similarity 162, member B
GO integral to membrane	315	3857	0.0001793	222223	KIAA1324-like
GO integral to membrane	315	3857	0.0001793	222545	G protein-coupled receptor, family C, group 6, member A
GO integral to membrane	315	3857	0.0001793	2263	fibroblast growth factor receptor 2
GO integral to membrane	315	3857	0.0001793	22859	latrophilin 1
GO integral to membrane	315	3857	0.0001793	23151	GRAM domain containing 4
GO integral to membrane	315	3857	0.0001793	23266	latrophilin 2
GO integral to membrane	315	3857	0.0001793	23284	latrophilin 3
GO integral to membrane	315	3857	0.0001793	23418	crumbs homolog 1 (Drosophila)
GO integral to membrane	315	3857	0.0001793	23654	plexin B2
GO integral to membrane	315	3857	0.0001793	2525	fucosyltransferase 3 (galactoside 3(4)-L-fucosyltransferase, Lewis blood
GO integral to membrane	315	3857	0.0001793	2526	fucosyltransferase 4 (alpha (1,3) fucosyltransferase, myeloid-specific)
GO integral to membrane	315	3857	0.0001793	255104	transmembrane and coiled-coil domains 4
GO integral to membrane	315	3857	0.0001793	255488	ring finger protein 144B
GO integral to membrane	315	3857	0.0001793	256987	serine incorporator 5
GO integral to membrane	315	3857	0.0001793	257019	FERM domain containing 3
GO integral to membrane	315	3857	0.0001793	25825	beta-site APP-cleaving enzyme 2
GO integral to membrane	315	3857	0.0001793	2589	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosami
GO integral to membrane	315	3857	0.0001793	259232	sodium leak channel, non-selective
GO integral to membrane	315	3857	0.0001793	26035	glucuronic acid epimerase
GO integral to membrane	315	3857	0.0001793	26050	SLIT and NTRK-like family, member 5
GO integral to membrane	315	3857	0.0001793	26157	GTPase, IMAP family member 2
GO integral to membrane	315	3857	0.0001793	2635	guanylate binding protein 3
GO integral to membrane	315	3857	0.0001793	2642	glucagon receptor
GO integral to membrane	315	3857	0.0001793	26507	cyclin M1
GO integral to membrane	315	3857	0.0001793	266675	bestrophin 4
GO integral to membrane	315	3857	0.0001793	27035	NADPH oxidase 1
GO integral to membrane	315	3857	0.0001793	2706	gap junction protein, beta 2, 26kDa
GO integral to membrane	315	3857	0.0001793	2707	gap junction protein, beta 3, 31kDa
GO integral to membrane	315	3857	0.0001793	27076	LY6/PLAUR domain containing 3
GO integral to membrane	315	3857	0.0001793	27090	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalact
GO integral to membrane	315	3857	0.0001793	27202	G protein-coupled receptor 77
GO integral to membrane	315	3857	0.0001793	27242	tumor necrosis factor receptor superfamily, member 21
GO integral to membrane	315	3857	0.0001793	28231	solute carrier organic anion transporter family, member 4A1
GO integral to membrane	315	3857	0.0001793	283316	CD163 molecule-like 1

GO integral to membrane	315	3857	0.0001793	283383 G protein-coupled receptor 133
GO integral to membrane	315	3857	0.0001793	283417 dpy-19-like 2 (C. elegans)
GO integral to membrane	315	3857	0.0001793	283537 solute carrier family 46, member 3
GO integral to membrane	315	3857	0.0001793	284021 chromosome 17 open reading frame 60
GO integral to membrane	315	3857	0.0001793	284353 NTPase, KAP family P-loop domain containing 1
GO integral to membrane	315	3857	0.0001793	286144 chromosome 8 open reading frame 83
GO integral to membrane	315	3857	0.0001793	286183 Na <sup>+</sup> /K <sup>+</sup> transporting ATPase interacting 3
GO integral to membrane	315	3857	0.0001793	28959 transmembrane protein 176B
GO integral to membrane	315	3857	0.0001793	29015 solute carrier family 43, member 3
GO integral to membrane	315	3857	0.0001793	29103 DnaJ (Hsp40) homolog, subfamily C, member 15
GO integral to membrane	315	3857	0.0001793	29126 CD274 molecule
GO integral to membrane	315	3857	0.0001793	3134 major histocompatibility complex, class I, F
GO integral to membrane	315	3857	0.0001793	3294 hydroxysteroid (17-beta) dehydrogenase 2
GO integral to membrane	315	3857	0.0001793	338557 G protein-coupled receptor 120
GO integral to membrane	315	3857	0.0001793	342035 gliomedin
GO integral to membrane	315	3857	0.0001793	3429 interferon, alpha-inducible protein 27
GO integral to membrane	315	3857	0.0001793	343450 potassium channel, subfamily T, member 2
GO integral to membrane	315	3857	0.0001793	353345 G protein-coupled receptor 141
GO integral to membrane	315	3857	0.0001793	3570 interleukin 6 receptor
GO integral to membrane	315	3857	0.0001793	3587 interleukin 10 receptor, alpha
GO integral to membrane	315	3857	0.0001793	3601 interleukin 15 receptor, alpha
GO integral to membrane	315	3857	0.0001793	3678 integrin, alpha 5 (fibronectin receptor, alpha polypeptide)
GO integral to membrane	315	3857	0.0001793	368 ATP-binding cassette, sub-family C (CFTR/MRP), member 6
GO integral to membrane	315	3857	0.0001793	3687 integrin, alpha X (complement component 3 receptor 4 subunit)
GO integral to membrane	315	3857	0.0001793	3689 integrin, beta 2 (complement component 3 receptor 3 and 4 subunit)
GO integral to membrane	315	3857	0.0001793	3691 integrin, beta 4
GO integral to membrane	315	3857	0.0001793	3696 integrin, beta 8
GO integral to membrane	315	3857	0.0001793	3709 inositol 1,4,5-triphosphate receptor, type 2
GO integral to membrane	315	3857	0.0001793	374378 UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosami
GO integral to membrane	315	3857	0.0001793	375056 melanoma inhibitory activity family, member 3
GO integral to membrane	315	3857	0.0001793	3773 potassium inwardly-rectifying channel, subfamily J, member 16
GO integral to membrane	315	3857	0.0001793	3775 potassium channel, subfamily K, member 1
GO integral to membrane	315	3857	0.0001793	3782 potassium intermediate/small conductance calcium-activated channel,
GO integral to membrane	315	3857	0.0001793	3783 potassium intermediate/small conductance calcium-activated channel,
GO integral to membrane	315	3857	0.0001793	3786 potassium voltage-gated channel, KQT-like subfamily, member 3
GO integral to membrane	315	3857	0.0001793	378925 ring finger protein 148



GO integral to membrane	315	3857	0.0001793	3790 potassium voltage-gated channel, delayed-rectifier, subfamily S, memb
GO integral to membrane	315	3857	0.0001793	3815 v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog
GO integral to membrane	315	3857	0.0001793	3823 killer cell lectin-like receptor subfamily C, member 3
GO integral to membrane	315	3857	0.0001793	387509 G protein-coupled receptor 153
GO integral to membrane	315	3857	0.0001793	387923 stress-associated endoplasmic reticulum protein family member 2
GO integral to membrane	315	3857	0.0001793	388633 low density lipoprotein receptor class A domain containing 1
GO integral to membrane	315	3857	0.0001793	392392 olfactory receptor, family 1, subfamily K, member 1
GO integral to membrane	315	3857	0.0001793	402415 XK, Kell blood group complex subunit-related, X-linked
GO integral to membrane	315	3857	0.0001793	4038 low density lipoprotein receptor-related protein 4
GO integral to membrane	315	3857	0.0001793	4056 leukotriene C4 synthase
GO integral to membrane	315	3857	0.0001793	405753 dual oxidase maturation factor 2
GO integral to membrane	315	3857	0.0001793	412 steroid sulfatase (microsomal), isozyme S
GO integral to membrane	315	3857	0.0001793	4121 mannosidase, alpha, class 1A, member 1
GO integral to membrane	315	3857	0.0001793	4128 monoamine oxidase A
GO integral to membrane	315	3857	0.0001793	4129 monoamine oxidase B
GO integral to membrane	315	3857	0.0001793	4170 myeloid cell leukemia sequence 1 (BCL2-related)
GO integral to membrane	315	3857	0.0001793	4254 KIT ligand
GO integral to membrane	315	3857	0.0001793	4684 neural cell adhesion molecule 1
GO integral to membrane	315	3857	0.0001793	4851 Notch homolog 1, translocation-associated (Drosophila)
GO integral to membrane	315	3857	0.0001793	50617 ATPase, H+ transporting, lysosomal V0 subunit a4
GO integral to membrane	315	3857	0.0001793	5066 peptidylglycine alpha-amidating monooxygenase
GO integral to membrane	315	3857	0.0001793	50937 Cdon homolog (mouse)
GO integral to membrane	315	3857	0.0001793	51063 calcium homeostasis modulator 2
GO integral to membrane	315	3857	0.0001793	51093 chromosome 1 open reading frame 66
GO integral to membrane	315	3857	0.0001793	51272 blocked early in transport 1 homolog (S. cerevisiae)-like
GO integral to membrane	315	3857	0.0001793	51303 FK506 binding protein 11, 19 kDa
GO integral to membrane	315	3857	0.0001793	51309 armadillo repeat containing, X-linked 1
GO integral to membrane	315	3857	0.0001793	51313 family with sequence similarity 198, member B
GO integral to membrane	315	3857	0.0001793	51703 acyl-CoA synthetase long-chain family member 5
GO integral to membrane	315	3857	0.0001793	51754 transmembrane protein 8B
GO integral to membrane	315	3857	0.0001793	5243 ATP-binding cassette, sub-family B (MDR/TAP), member 1
GO integral to membrane	315	3857	0.0001793	5318 plakophilin 2
GO integral to membrane	315	3857	0.0001793	53373 two pore segment channel 1
GO integral to membrane	315	3857	0.0001793	53405 chloride intracellular channel 5
GO integral to membrane	315	3857	0.0001793	5362 plexin A2
GO integral to membrane	315	3857	0.0001793	53827 FXFD domain containing ion transport regulator 5

GO integral to membrane	315	3857	0.0001793	53947 alpha 1,4-galactosyltransferase
GO integral to membrane	315	3857	0.0001793	54463 family with sequence similarity 134, member B
GO integral to membrane	315	3857	0.0001793	54664 transmembrane protein 106B
GO integral to membrane	315	3857	0.0001793	54681 prolyl 4-hydroxylase, transmembrane (endoplasmic reticulum)
GO integral to membrane	315	3857	0.0001793	54852 progesterin and adipoQ receptor family member V
GO integral to membrane	315	3857	0.0001793	54894 ring finger protein 43
GO integral to membrane	315	3857	0.0001793	54933 rhomboid, veinlet-like 2 (Drosophila)
GO integral to membrane	315	3857	0.0001793	54947 lysophosphatidylcholine acyltransferase 2
GO integral to membrane	315	3857	0.0001793	55061 sushi domain containing 4
GO integral to membrane	315	3857	0.0001793	55076 transmembrane protein 45A
GO integral to membrane	315	3857	0.0001793	55080 TAP binding protein-like
GO integral to membrane	315	3857	0.0001793	55281 transmembrane protein 140
GO integral to membrane	315	3857	0.0001793	55304 serine palmitoyltransferase, long chain base subunit 3
GO integral to membrane	315	3857	0.0001793	55332 DNA-damage regulated autophagy modulator 1
GO integral to membrane	315	3857	0.0001793	55365 transmembrane protein 176A
GO integral to membrane	315	3857	0.0001793	55638 Golgi-localized protein
GO integral to membrane	315	3857	0.0001793	55714 odz, odd Oz/ten-m homolog 3 (Drosophila)
GO integral to membrane	315	3857	0.0001793	55754 transmembrane protein 30A
GO integral to membrane	315	3857	0.0001793	55799 calcium channel, voltage-dependent, alpha 2/delta subunit 3
GO integral to membrane	315	3857	0.0001793	55808 ST6 (alpha-N-acetyl-neuraminy-2,3-beta-galactosyl-1,3)-N-acetylgalact
GO integral to membrane	315	3857	0.0001793	55824 phosphoprotein associated with glycosphingolipid microdomains 1
GO integral to membrane	315	3857	0.0001793	56172 ankylosis, progressive homolog (mouse)
GO integral to membrane	315	3857	0.0001793	56649 transmembrane protease, serine 4
GO integral to membrane	315	3857	0.0001793	56654 neural proliferation, differentiation and control, 1
GO integral to membrane	315	3857	0.0001793	56913 core 1 synthase, glycoprotein-N-acetylgalactosamine 3-beta-galactosyl
GO integral to membrane	315	3857	0.0001793	56923 neuromedin U receptor 2
GO integral to membrane	315	3857	0.0001793	57104 patatin-like phospholipase domain containing 2
GO integral to membrane	315	3857	0.0001793	57134 mannosidase, alpha, class 1C, member 1
GO integral to membrane	315	3857	0.0001793	57146 transmembrane protein 159
GO integral to membrane	315	3857	0.0001793	57185 NIPA-like domain containing 3
GO integral to membrane	315	3857	0.0001793	57210 solute carrier family 45, member 4
GO integral to membrane	315	3857	0.0001793	57221 KIAA1244
GO integral to membrane	315	3857	0.0001793	5724 platelet-activating factor receptor
GO integral to membrane	315	3857	0.0001793	5734 prostaglandin E receptor 4 (subtype EP4)
GO integral to membrane	315	3857	0.0001793	57453 Down syndrome cell adhesion molecule like 1
GO integral to membrane	315	3857	0.0001793	57458 transmembrane and coiled-coil domain family 3

GO integral to membrane	315	3857	0.0001793	57488 extended synaptotagmin-like protein 2
GO integral to membrane	315	3857	0.0001793	57493 HEG homolog 1 (zebrafish)
GO integral to membrane	315	3857	0.0001793	57512 G protein-coupled receptor 158
GO integral to membrane	315	3857	0.0001793	57535 KIAA1324
GO integral to membrane	315	3857	0.0001793	57537 sortilin-related VPS10 domain containing receptor 2
GO integral to membrane	315	3857	0.0001793	57620 stromal interaction molecule 2
GO integral to membrane	315	3857	0.0001793	57670 KIAA1549
GO integral to membrane	315	3857	0.0001793	5768 quiescin Q6 sulfhydryl oxidase 1
GO integral to membrane	315	3857	0.0001793	57863 cell adhesion molecule 3
GO integral to membrane	315	3857	0.0001793	5791 protein tyrosine phosphatase, receptor type, E
GO integral to membrane	315	3857	0.0001793	5801 protein tyrosine phosphatase, receptor type, R
GO integral to membrane	315	3857	0.0001793	59271 chromosome 21 open reading frame 63
GO integral to membrane	315	3857	0.0001793	6238 ribosome binding protein 1 homolog 180kDa (dog)
GO integral to membrane	315	3857	0.0001793	63027 solute carrier family 22, member 23
GO integral to membrane	315	3857	0.0001793	6330 sodium channel, voltage-gated, type IV, beta
GO integral to membrane	315	3857	0.0001793	63982 anoctamin 3
GO integral to membrane	315	3857	0.0001793	64108 receptor (chemosensory) transporter protein 4
GO integral to membrane	315	3857	0.0001793	64116 solute carrier family 39 (zinc transporter), member 8
GO integral to membrane	315	3857	0.0001793	646658 transmembrane protein 90A
GO integral to membrane	315	3857	0.0001793	64699 transmembrane protease, serine 3
GO integral to membrane	315	3857	0.0001793	6484 ST3 beta-galactoside alpha-2,3-sialyltransferase 4
GO integral to membrane	315	3857	0.0001793	6489 ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 1
GO integral to membrane	315	3857	0.0001793	6535 solute carrier family 6 (neurotransmitter transporter, creatine), member 1
GO integral to membrane	315	3857	0.0001793	654463 fer-1-like 6 (C. elegans)
GO integral to membrane	315	3857	0.0001793	682 basigin (Ok blood group)
GO integral to membrane	315	3857	0.0001793	6857 synaptotagmin I
GO integral to membrane	315	3857	0.0001793	6916 thromboxane A synthase 1 (platelet)
GO integral to membrane	315	3857	0.0001793	7100 toll-like receptor 5
GO integral to membrane	315	3857	0.0001793	7133 tumor necrosis factor receptor superfamily, member 1B
GO integral to membrane	315	3857	0.0001793	7223 transient receptor potential cation channel, subfamily C, member 4
GO integral to membrane	315	3857	0.0001793	727910 TLC domain containing 2
GO integral to membrane	315	3857	0.0001793	728215 family with sequence similarity 155, member A
GO integral to membrane	315	3857	0.0001793	729993 shisa homolog 9 (Xenopus laevis)
GO integral to membrane	315	3857	0.0001793	731 complement component 8, alpha polypeptide
GO integral to membrane	315	3857	0.0001793	771 carbonic anhydrase XII
GO integral to membrane	315	3857	0.0001793	774 calcium channel, voltage-dependent, N type, alpha 1B subunit

GO integral to membrane	315	3857	0.0001793	7852 chemokine (C-X-C motif) receptor 4
GO integral to membrane	315	3857	0.0001793	79152 fatty acid 2-hydroxylase
GO integral to membrane	315	3857	0.0001793	79689 STEAP family member 4
GO integral to membrane	315	3857	0.0001793	79695 UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosami
GO integral to membrane	315	3857	0.0001793	79789 calmin (calponin-like, transmembrane)
GO integral to membrane	315	3857	0.0001793	79820 cation channel, sperm-associated, beta
GO integral to membrane	315	3857	0.0001793	79838 transmembrane channel-like 5
GO integral to membrane	315	3857	0.0001793	79895 ATPase, class I, type 8B, member 4
GO integral to membrane	315	3857	0.0001793	79932 KIAA0319-like
GO integral to membrane	315	3857	0.0001793	79956 endoplasmic reticulum metalloproteinase 1
GO integral to membrane	315	3857	0.0001793	79957 progesterin and adipoQ receptor family member VI
GO integral to membrane	315	3857	0.0001793	79971 wntless homolog (Drosophila)
GO integral to membrane	315	3857	0.0001793	81285 olfactory receptor, family 51, subfamily E, member 2
GO integral to membrane	315	3857	0.0001793	81470 olfactory receptor, family 2, subfamily G, member 2
GO integral to membrane	315	3857	0.0001793	81544 glycerophosphodiester phosphodiesterase domain containing 5
GO integral to membrane	315	3857	0.0001793	81615 transmembrane protein 163
GO integral to membrane	315	3857	0.0001793	81693 amnionless homolog (mouse)
GO integral to membrane	315	3857	0.0001793	819 calcium modulating ligand
GO integral to membrane	315	3857	0.0001793	83394 PITPNM family member 3
GO integral to membrane	315	3857	0.0001793	83604 transmembrane protein 47
GO integral to membrane	315	3857	0.0001793	83661 membrane-spanning 4-domains, subfamily A, member 8B
GO integral to membrane	315	3857	0.0001793	83857 transmembrane and tetratricopeptide repeat containing 1
GO integral to membrane	315	3857	0.0001793	83890 spermatogenesis associated 9
GO integral to membrane	315	3857	0.0001793	84059 G protein-coupled receptor 98
GO integral to membrane	315	3857	0.0001793	84561 solute carrier family 12 (potassium/chloride transporters), member 8
GO integral to membrane	315	3857	0.0001793	84879 major facilitator superfamily domain containing 2A
GO integral to membrane	315	3857	0.0001793	84976 dispatched homolog 1 (Drosophila)
GO integral to membrane	315	3857	0.0001793	8509 N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 2
GO integral to membrane	315	3857	0.0001793	8514 potassium voltage-gated channel, shaker-related subfamily, beta mem
GO integral to membrane	315	3857	0.0001793	8519 interferon induced transmembrane protein 1 (9-27)
GO integral to membrane	315	3857	0.0001793	8673 vesicle-associated membrane protein 8 (endobrevin)
GO integral to membrane	315	3857	0.0001793	8706 beta-1,3-N-acetylgalactosaminyltransferase 1 (globoside blood group)
GO integral to membrane	315	3857	0.0001793	8740 tumor necrosis factor (ligand) superfamily, member 14
GO integral to membrane	315	3857	0.0001793	8744 tumor necrosis factor (ligand) superfamily, member 9
GO integral to membrane	315	3857	0.0001793	8751 ADAM metalloproteinase domain 15
GO integral to membrane	315	3857	0.0001793	8793 tumor necrosis factor receptor superfamily, member 10d, decoy with t

GO integral to membrane	315	3857	0.0001793	8911 calcium channel, voltage-dependent, T type, alpha 1I subunit
GO integral to membrane	315	3857	0.0001793	8912 calcium channel, voltage-dependent, T type, alpha 1H subunit
GO integral to membrane	315	3857	0.0001793	8973 cholinergic receptor, nicotinic, alpha 6
GO integral to membrane	315	3857	0.0001793	89801 protein phosphatase 1, regulatory (inhibitor) subunit 3F
GO integral to membrane	315	3857	0.0001793	8992 ATPase, H+ transporting, lysosomal 9kDa, V0 subunit e1
GO integral to membrane	315	3857	0.0001793	9071 claudin 10
GO integral to membrane	315	3857	0.0001793	90993 cAMP responsive element binding protein 3-like 1
GO integral to membrane	315	3857	0.0001793	91653 Boc homolog (mouse)
GO integral to membrane	315	3857	0.0001793	9214 Fas apoptotic inhibitory molecule 3
GO integral to membrane	315	3857	0.0001793	92691 transmembrane protein 169
GO integral to membrane	315	3857	0.0001793	92840 receptor accessory protein 6
GO integral to membrane	315	3857	0.0001793	93273 LEM domain containing 1
GO integral to membrane	315	3857	0.0001793	93589 calcium channel, voltage-dependent, alpha 2/delta subunit 4
GO integral to membrane	315	3857	0.0001793	94025 mucin 16, cell surface associated
GO integral to membrane	315	3857	0.0001793	9435 carbohydrate (N-acetylglucosamine-6-O) sulfotransferase 2
GO integral to membrane	315	3857	0.0001793	9445 integral membrane protein 2B
GO integral to membrane	315	3857	0.0001793	9452 integral membrane protein 2A
GO integral to membrane	315	3857	0.0001793	9481 solute carrier family 25, member 27
GO integral to membrane	315	3857	0.0001793	952 CD38 molecule
GO integral to membrane	315	3857	0.0001793	9537 tumor protein p53 inducible protein 11
GO integral to membrane	315	3857	0.0001793	9804 translocase of outer mitochondrial membrane 20 homolog (yeast)
GO integral to membrane	315	3857	0.0001793	9823 armadillo repeat containing, X-linked 2
GO integral to membrane	315	3857	0.0001793	9914 ATPase, Ca++ transporting, type 2C, member 2
GO integral to membrane	315	3857	0.0001793	9962 solute carrier family 23 (nucleobase transporters), member 2
GO integral to membrane	315	3857	0.0001793	9966 tumor necrosis factor (ligand) superfamily, member 15
GO rhythmic process	6	14	0.0001877	1628 D site of albumin promoter (albumin D-box) binding protein
GO rhythmic process	6	14	0.0001877	3131 hepatic leukemia factor
GO rhythmic process	6	14	0.0001877	4783 nuclear factor, interleukin 3 regulated
GO rhythmic process	6	14	0.0001877	55068 ecto-NOX disulfide-thiol exchanger 1
GO rhythmic process	6	14	0.0001877	7008 thyrotrophic embryonic factor
GO rhythmic process	6	14	0.0001877	8863 period homolog 3 (Drosophila)
GO steroid hormone receptor activity	11	46	0.0002101	3164 nuclear receptor subfamily 4, group A, member 1
GO steroid hormone receptor activity	11	46	0.0002101	4306 nuclear receptor subfamily 3, group C, member 2
GO steroid hormone receptor activity	11	46	0.0002101	4929 nuclear receptor subfamily 4, group A, member 2
GO steroid hormone receptor activity	11	46	0.0002101	5465 peroxisome proliferator-activated receptor alpha
GO steroid hormone receptor activity	11	46	0.0002101	6096 RAR-related orphan receptor B

GO steroid hormone receptor activity	11	46	0.0002101	6097 RAR-related orphan receptor C
GO steroid hormone receptor activity	11	46	0.0002101	6256 retinoid X receptor, alpha
GO steroid hormone receptor activity	11	46	0.0002101	7026 nuclear receptor subfamily 2, group F, member 2
GO steroid hormone receptor activity	11	46	0.0002101	8013 nuclear receptor subfamily 4, group A, member 3
GO steroid hormone receptor activity	11	46	0.0002101	9572 nuclear receptor subfamily 1, group D, member 1
GO steroid hormone receptor activity	11	46	0.0002101	9971 nuclear receptor subfamily 1, group H, member 4
GO positive regulation of NF-kappaB trans	11	47	0.0002576	11213 interleukin-1 receptor-associated kinase 3
GO positive regulation of NF-kappaB trans	11	47	0.0002576	183 angiotensinogen (serpin peptidase inhibitor, clade A, member 8)
GO positive regulation of NF-kappaB trans	11	47	0.0002576	29108 PYD and CARD domain containing
GO positive regulation of NF-kappaB trans	11	47	0.0002576	3569 interleukin 6 (interferon, beta 2)
GO positive regulation of NF-kappaB trans	11	47	0.0002576	3570 interleukin 6 receptor
GO positive regulation of NF-kappaB trans	11	47	0.0002576	3845 v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog
GO positive regulation of NF-kappaB trans	11	47	0.0002576	64127 nucleotide-binding oligomerization domain containing 2
GO positive regulation of NF-kappaB trans	11	47	0.0002576	7097 toll-like receptor 2
GO positive regulation of NF-kappaB trans	11	47	0.0002576	7098 toll-like receptor 3
GO positive regulation of NF-kappaB trans	11	47	0.0002576	7099 toll-like receptor 4
GO positive regulation of NF-kappaB trans	11	47	0.0002576	7474 wntless-type MMTV integration site family, member 5A
GO negative regulation of fibroblast growth	4	6	0.0002914	10252 sprouty homolog 1, antagonist of FGF signaling (Drosophila)
GO negative regulation of fibroblast growth	4	6	0.0002914	10253 sprouty homolog 2 (Drosophila)
GO negative regulation of fibroblast growth	4	6	0.0002914	54361 wntless-type MMTV integration site family, member 4
GO negative regulation of fibroblast growth	4	6	0.0002914	7474 wntless-type MMTV integration site family, member 5A
GO cardiac muscle cell proliferation	4	6	0.0002914	2296 forkhead box C1
GO cardiac muscle cell proliferation	4	6	0.0002914	2303 forkhead box C2 (MFH-1, mesenchyme forkhead 1)
GO cardiac muscle cell proliferation	4	6	0.0002914	6256 retinoid X receptor, alpha
GO cardiac muscle cell proliferation	4	6	0.0002914	7049 transforming growth factor, beta receptor III
GO pathogen-associated molecular pattern	4	6	0.0002914	7097 toll-like receptor 2
GO pathogen-associated molecular pattern	4	6	0.0002914	7098 toll-like receptor 3
GO pathogen-associated molecular pattern	4	6	0.0002914	7099 toll-like receptor 4
GO pathogen-associated molecular pattern	4	6	0.0002914	7100 toll-like receptor 5
GO transcription repressor activity	25	173	0.0003036	116113 forkhead box P4
GO transcription repressor activity	25	173	0.0003036	127343 diencephalon/mesencephalon homeobox 1
GO transcription repressor activity	25	173	0.0003036	150094 salt-inducible kinase 1
GO transcription repressor activity	25	173	0.0003036	1999 E74-like factor 3 (ets domain transcription factor, epithelial-specific )
GO transcription repressor activity	25	173	0.0003036	2117 ets variant 3
GO transcription repressor activity	25	173	0.0003036	2290 forkhead box G1
GO transcription repressor activity	25	173	0.0003036	22904 strawberry notch homolog 2 (Drosophila)

GO transcription repressor activity	25	173	0.0003036	2737 GLI family zinc finger 3
GO transcription repressor activity	25	173	0.0003036	3400 inhibitor of DNA binding 4, dominant negative helix-loop-helix protein
GO transcription repressor activity	25	173	0.0003036	3428 interferon, gamma-inducible protein 16
GO transcription repressor activity	25	173	0.0003036	3725 jun oncogene
GO transcription repressor activity	25	173	0.0003036	4204 methyl CpG binding protein 2 (Rett syndrome)
GO transcription repressor activity	25	173	0.0003036	5083 paired box 9
GO transcription repressor activity	25	173	0.0003036	51085 MLX interacting protein-like
GO transcription repressor activity	25	173	0.0003036	5371 promyelocytic leukemia
GO transcription repressor activity	25	173	0.0003036	5396 paired related homeobox 1
GO transcription repressor activity	25	173	0.0003036	604 B-cell CLL/lymphoma 6
GO transcription repressor activity	25	173	0.0003036	652 bone morphogenetic protein 4
GO transcription repressor activity	25	173	0.0003036	7227 trichorhinophalangeal syndrome I
GO transcription repressor activity	25	173	0.0003036	83595 SRY (sex determining region Y)-box 7
GO transcription repressor activity	25	173	0.0003036	84159 AT rich interactive domain 5B (MRF1-like)
GO transcription repressor activity	25	173	0.0003036	84911 zinc finger protein 382
GO transcription repressor activity	25	173	0.0003036	8553 basic helix-loop-helix family, member e40
GO transcription repressor activity	25	173	0.0003036	9314 Kruppel-like factor 4 (gut)
GO transcription repressor activity	25	173	0.0003036	9734 histone deacetylase 9
GO piRNA binding	3	3	0.0003186	143689 piwi-like 4 (Drosophila)
GO piRNA binding	3	3	0.0003186	55124 piwi-like 2 (Drosophila)
GO piRNA binding	3	3	0.0003186	9271 piwi-like 1 (Drosophila)
GO insulin-like growth factor binding pro	3	3	0.0003186	3479 insulin-like growth factor 1 (somatomedin C)
GO insulin-like growth factor binding pro	3	3	0.0003186	3486 insulin-like growth factor binding protein 3
GO insulin-like growth factor binding pro	3	3	0.0003186	3488 insulin-like growth factor binding protein 5
GO mesodermal cell fate determination	3	3	0.0003186	652 bone morphogenetic protein 4
GO mesodermal cell fate determination	3	3	0.0003186	89870 tripartite motif-containing 15
GO mesodermal cell fate determination	3	3	0.0003186	9314 Kruppel-like factor 4 (gut)
GO positive regulation of macrophage cy	3	3	0.0003186	7097 toll-like receptor 2
GO positive regulation of macrophage cy	3	3	0.0003186	7099 toll-like receptor 4
GO positive regulation of macrophage cy	3	3	0.0003186	7474 wingless-type MMTV integration site family, member 5A
GO response to glucose stimulus	12	57	0.0003935	10628 thioredoxin interacting protein
GO response to glucose stimulus	12	57	0.0003935	130399 activin A receptor, type IC
GO response to glucose stimulus	12	57	0.0003935	1508 cathepsin B
GO response to glucose stimulus	12	57	0.0003935	1958 early growth response 1
GO response to glucose stimulus	12	57	0.0003935	2033 E1A binding protein p300
GO response to glucose stimulus	12	57	0.0003935	2752 glutamate-ammonia ligase (glutamine synthetase)

GO response to glucose stimulus	12	57	0.0003935	3643 insulin receptor
GO response to glucose stimulus	12	57	0.0003935	4087 SMAD family member 2
GO response to glucose stimulus	12	57	0.0003935	5122 proprotein convertase subtilisin/kexin type 1
GO response to glucose stimulus	12	57	0.0003935	51703 acyl-CoA synthetase long-chain family member 5
GO response to glucose stimulus	12	57	0.0003935	8660 insulin receptor substrate 2
GO response to glucose stimulus	12	57	0.0003935	9971 nuclear receptor subfamily 1, group H, member 4
GO ligand-dependent nuclear receptor a	8	28	0.0004214	3164 nuclear receptor subfamily 4, group A, member 1
GO ligand-dependent nuclear receptor a	8	28	0.0004214	4929 nuclear receptor subfamily 4, group A, member 2
GO ligand-dependent nuclear receptor a	8	28	0.0004214	5465 peroxisome proliferator-activated receptor alpha
GO ligand-dependent nuclear receptor a	8	28	0.0004214	6096 RAR-related orphan receptor B
GO ligand-dependent nuclear receptor a	8	28	0.0004214	6097 RAR-related orphan receptor C
GO ligand-dependent nuclear receptor a	8	28	0.0004214	7026 nuclear receptor subfamily 2, group F, member 2
GO ligand-dependent nuclear receptor a	8	28	0.0004214	9572 nuclear receptor subfamily 1, group D, member 1
GO ligand-dependent nuclear receptor a	8	28	0.0004214	9971 nuclear receptor subfamily 1, group H, member 4
GO response to light stimulus	6	16	0.0004444	1813 dopamine receptor D2
GO response to light stimulus	6	16	0.0004444	1843 dual specificity phosphatase 1
GO response to light stimulus	6	16	0.0004444	2353 FBJ murine osteosarcoma viral oncogene homolog
GO response to light stimulus	6	16	0.0004444	3726 jun B proto-oncogene
GO response to light stimulus	6	16	0.0004444	5187 period homolog 1 (Drosophila)
GO response to light stimulus	6	16	0.0004444	8553 basic helix-loop-helix family, member e40
GO positive regulation of gene-specific tr	16	92	0.0004655	10014 histone deacetylase 5
GO positive regulation of gene-specific tr	16	92	0.0004655	22807 IKAROS family zinc finger 2 (Helios)
GO positive regulation of gene-specific tr	16	92	0.0004655	2624 GATA binding protein 2
GO positive regulation of gene-specific tr	16	92	0.0004655	2737 GLI family zinc finger 3
GO positive regulation of gene-specific tr	16	92	0.0004655	3169 forkhead box A1
GO positive regulation of gene-specific tr	16	92	0.0004655	3175 one cut homeobox 1
GO positive regulation of gene-specific tr	16	92	0.0004655	3479 insulin-like growth factor 1 (somatomedin C)
GO positive regulation of gene-specific tr	16	92	0.0004655	4784 nuclear factor I/X (CCAAT-binding transcription factor)
GO positive regulation of gene-specific tr	16	92	0.0004655	4792 nuclear factor of kappa light polypeptide gene enhancer in B-cells inhib
GO positive regulation of gene-specific tr	16	92	0.0004655	51085 MLX interacting protein-like
GO positive regulation of gene-specific tr	16	92	0.0004655	5460 POU class 5 homeobox 1
GO positive regulation of gene-specific tr	16	92	0.0004655	6256 retinoid X receptor, alpha
GO positive regulation of gene-specific tr	16	92	0.0004655	652 bone morphogenetic protein 4
GO positive regulation of gene-specific tr	16	92	0.0004655	7097 toll-like receptor 2
GO positive regulation of gene-specific tr	16	92	0.0004655	7098 toll-like receptor 3
GO positive regulation of gene-specific tr	16	92	0.0004655	7099 toll-like receptor 4



GO	positive regulation of smooth muscle	8	29	0.0005473	1906 endothelin 1
GO	positive regulation of smooth muscle	8	29	0.0005473	27035 NADPH oxidase 1
GO	positive regulation of smooth muscle	8	29	0.0005473	3479 insulin-like growth factor 1 (somatomedin C)
GO	positive regulation of smooth muscle	8	29	0.0005473	3569 interleukin 6 (interferon, beta 2)
GO	positive regulation of smooth muscle	8	29	0.0005473	3570 interleukin 6 receptor
GO	positive regulation of smooth muscle	8	29	0.0005473	3725 jun oncogene
GO	positive regulation of smooth muscle	8	29	0.0005473	4889 neuropeptide Y receptor Y5
GO	positive regulation of smooth muscle	8	29	0.0005473	652 bone morphogenetic protein 4
GO	positive regulation of osteoclast diffe	4	7	0.000643	1435 colony stimulating factor 1 (macrophage)
GO	positive regulation of osteoclast diffe	4	7	0.000643	7071 Kruppel-like factor 10
GO	positive regulation of osteoclast diffe	4	7	0.000643	760 carbonic anhydrase II
GO	positive regulation of osteoclast diffe	4	7	0.000643	8600 tumor necrosis factor (ligand) superfamily, member 11
GO	negative regulation of cell death	4	7	0.000643	1508 cathepsin B
GO	negative regulation of cell death	4	7	0.000643	4851 Notch homolog 1, translocation-associated (Drosophila)
GO	negative regulation of cell death	4	7	0.000643	5071 Parkinson disease (autosomal recessive, juvenile) 2, parkin
GO	negative regulation of cell death	4	7	0.000643	652 bone morphogenetic protein 4
GO	cellular response to lipopolysaccharic	4	7	0.000643	4056 leukotriene C4 synthase
GO	cellular response to lipopolysaccharic	4	7	0.000643	7099 toll-like receptor 4
GO	cellular response to lipopolysaccharic	4	7	0.000643	7474 wingless-type MMTV integration site family, member 5A
GO	cellular response to lipopolysaccharic	4	7	0.000643	929 CD14 molecule
GO	microglial cell activation during immu	4	7	0.000643	7097 toll-like receptor 2
GO	microglial cell activation during immu	4	7	0.000643	7098 toll-like receptor 3
GO	microglial cell activation during immu	4	7	0.000643	7099 toll-like receptor 4
GO	microglial cell activation during immu	4	7	0.000643	7100 toll-like receptor 5
GO	signal transduction	157	1796	0.0006537	10156 RAS p21 protein activator 4
GO	signal transduction	157	1796	0.0006537	10253 sprouty homolog 2 (Drosophila)
GO	signal transduction	157	1796	0.0006537	10752 cell adhesion molecule with homology to L1CAM (close homolog of L1)
GO	signal transduction	157	1796	0.0006537	10913 ectodysplasin A receptor
GO	signal transduction	157	1796	0.0006537	11213 interleukin-1 receptor-associated kinase 3
GO	signal transduction	157	1796	0.0006537	11228 Ras association (RalGDS/AF-6) domain family (N-terminal) member 8
GO	signal transduction	157	1796	0.0006537	1124 chimerin (chimaerin) 2
GO	signal transduction	157	1796	0.0006537	1139 cholinergic receptor, nicotinic, alpha 7
GO	signal transduction	157	1796	0.0006537	115330 G protein-coupled receptor 146
GO	signal transduction	157	1796	0.0006537	116984 ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 2
GO	signal transduction	157	1796	0.0006537	1193 chloride intracellular channel 2
GO	signal transduction	157	1796	0.0006537	121130 olfactory receptor, family 10, subfamily P, member 1

GO signal transduction	157	1796	0.0006537	1382 cellular retinoic acid binding protein 2
GO signal transduction	157	1796	0.0006537	143503 olfactory receptor, family 51, subfamily E, member 1
GO signal transduction	157	1796	0.0006537	154 adrenergic, beta-2-, receptor, surface
GO signal transduction	157	1796	0.0006537	1612 death-associated protein kinase 1
GO signal transduction	157	1796	0.0006537	1785 dynamin 2
GO signal transduction	157	1796	0.0006537	1813 dopamine receptor D2
GO signal transduction	157	1796	0.0006537	1815 dopamine receptor D4
GO signal transduction	157	1796	0.0006537	1839 heparin-binding EGF-like growth factor
GO signal transduction	157	1796	0.0006537	1901 sphingosine-1-phosphate receptor 1
GO signal transduction	157	1796	0.0006537	1902 lysophosphatidic acid receptor 1
GO signal transduction	157	1796	0.0006537	1969 EPH receptor A2
GO signal transduction	157	1796	0.0006537	2015 egf-like module containing, mucin-like, hormone receptor-like 1
GO signal transduction	157	1796	0.0006537	2066 v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian)
GO signal transduction	157	1796	0.0006537	2205 Fc fragment of IgE, high affinity I, receptor for; alpha polypeptide
GO signal transduction	157	1796	0.0006537	222545 G protein-coupled receptor, family C, group 6, member A
GO signal transduction	157	1796	0.0006537	22859 latrophilin 1
GO signal transduction	157	1796	0.0006537	23092 Rho GTPase activating protein 26
GO signal transduction	157	1796	0.0006537	23179 ral guanine nucleotide dissociation stimulator-like 1
GO signal transduction	157	1796	0.0006537	23266 latrophilin 2
GO signal transduction	157	1796	0.0006537	23284 latrophilin 3
GO signal transduction	157	1796	0.0006537	23303 kinesin family member 13B
GO signal transduction	157	1796	0.0006537	23654 plexin B2
GO signal transduction	157	1796	0.0006537	26191 protein tyrosine phosphatase, non-receptor type 22 (lymphoid)
GO signal transduction	157	1796	0.0006537	26281 fibroblast growth factor 20
GO signal transduction	157	1796	0.0006537	2642 glucagon receptor
GO signal transduction	157	1796	0.0006537	27035 NADPH oxidase 1
GO signal transduction	157	1796	0.0006537	27202 G protein-coupled receptor 77
GO signal transduction	157	1796	0.0006537	27242 tumor necrosis factor receptor superfamily, member 21
GO signal transduction	157	1796	0.0006537	2769 guanine nucleotide binding protein (G protein), alpha 15 (Gq class)
GO signal transduction	157	1796	0.0006537	283383 G protein-coupled receptor 133
GO signal transduction	157	1796	0.0006537	285704 RGM domain family, member B
GO signal transduction	157	1796	0.0006537	2861 G protein-coupled receptor 37 (endothelin receptor type B-like)
GO signal transduction	157	1796	0.0006537	2865 free fatty acid receptor 3
GO signal transduction	157	1796	0.0006537	2867 free fatty acid receptor 2
GO signal transduction	157	1796	0.0006537	29108 PYD and CARD domain containing
GO signal transduction	157	1796	0.0006537	2911 glutamate receptor, metabotropic 1

GO signal transduction	157	1796	0.0006537	29126 CD274 molecule
GO signal transduction	157	1796	0.0006537	3164 nuclear receptor subfamily 4, group A, member 1
GO signal transduction	157	1796	0.0006537	3355 5-hydroxytryptamine (serotonin) receptor 1F
GO signal transduction	157	1796	0.0006537	338557 G protein-coupled receptor 120
GO signal transduction	157	1796	0.0006537	3479 insulin-like growth factor 1 (somatomedin C)
GO signal transduction	157	1796	0.0006537	3484 insulin-like growth factor binding protein 1
GO signal transduction	157	1796	0.0006537	3488 insulin-like growth factor binding protein 5
GO signal transduction	157	1796	0.0006537	353345 G protein-coupled receptor 141
GO signal transduction	157	1796	0.0006537	3561 interleukin 2 receptor, gamma (severe combined immunodeficiency)
GO signal transduction	157	1796	0.0006537	3601 interleukin 15 receptor, alpha
GO signal transduction	157	1796	0.0006537	3709 inositol 1,4,5-triphosphate receptor, type 2
GO signal transduction	157	1796	0.0006537	375790 agrin
GO signal transduction	157	1796	0.0006537	3815 v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog
GO signal transduction	157	1796	0.0006537	3845 v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog
GO signal transduction	157	1796	0.0006537	387496 RAS-like, family 11, member A
GO signal transduction	157	1796	0.0006537	387509 G protein-coupled receptor 153
GO signal transduction	157	1796	0.0006537	392392 olfactory receptor, family 1, subfamily K, member 1
GO signal transduction	157	1796	0.0006537	395 Rho GTPase activating protein 6
GO signal transduction	157	1796	0.0006537	3959 lectin, galactoside-binding, soluble, 3 binding protein
GO signal transduction	157	1796	0.0006537	4163 mutated in colorectal cancers
GO signal transduction	157	1796	0.0006537	4254 KIT ligand
GO signal transduction	157	1796	0.0006537	4306 nuclear receptor subfamily 3, group C, member 2
GO signal transduction	157	1796	0.0006537	4486 macrophage stimulating 1 receptor (c-met-related tyrosine kinase)
GO signal transduction	157	1796	0.0006537	4599 myxovirus (influenza virus) resistance 1, interferon-inducible protein p1
GO signal transduction	157	1796	0.0006537	4680 carcinoembryonic antigen-related cell adhesion molecule 6 (non-specific)
GO signal transduction	157	1796	0.0006537	4791 nuclear factor of kappa light polypeptide gene enhancer in B-cells 2 (p4)
GO signal transduction	157	1796	0.0006537	4886 neuropeptide Y receptor Y1
GO signal transduction	157	1796	0.0006537	4889 neuropeptide Y receptor Y5
GO signal transduction	157	1796	0.0006537	4929 nuclear receptor subfamily 4, group A, member 2
GO signal transduction	157	1796	0.0006537	5025 purinergic receptor P2X, ligand-gated ion channel, 4
GO signal transduction	157	1796	0.0006537	51285 RAS-like, family 12
GO signal transduction	157	1796	0.0006537	5129 cyclin-dependent kinase 18
GO signal transduction	157	1796	0.0006537	5136 phosphodiesterase 1A, calmodulin-dependent
GO signal transduction	157	1796	0.0006537	5152 phosphodiesterase 9A
GO signal transduction	157	1796	0.0006537	5158 phosphodiesterase 6B, cGMP-specific, rod, beta
GO signal transduction	157	1796	0.0006537	51655 RAS, dexamethasone-induced 1

GO signal transduction	157	1796	0.0006537	5187 period homolog 1 (Drosophila)
GO signal transduction	157	1796	0.0006537	5295 phosphoinositide-3-kinase, regulatory subunit 1 (alpha)
GO signal transduction	157	1796	0.0006537	5362 plexin A2
GO signal transduction	157	1796	0.0006537	5367 pro-melanin-concentrating hormone
GO signal transduction	157	1796	0.0006537	54769 DIRAS family, GTP-binding RAS-like 2
GO signal transduction	157	1796	0.0006537	54933 rhomboid, veinlet-like 2 (Drosophila)
GO signal transduction	157	1796	0.0006537	55600 intelectin 1 (galactofuranose binding)
GO signal transduction	157	1796	0.0006537	55714 odz, odd Oz/ten-m homolog 3 (Drosophila)
GO signal transduction	157	1796	0.0006537	5577 protein kinase, cAMP-dependent, regulatory, type II, beta
GO signal transduction	157	1796	0.0006537	55824 phosphoprotein associated with glycosphingolipid microdomains 1
GO signal transduction	157	1796	0.0006537	5608 mitogen-activated protein kinase kinase 6
GO signal transduction	157	1796	0.0006537	56923 neuromedin U receptor 2
GO signal transduction	157	1796	0.0006537	57139 ral guanine nucleotide dissociation stimulator-like 3
GO signal transduction	157	1796	0.0006537	5724 platelet-activating factor receptor
GO signal transduction	157	1796	0.0006537	5732 prostaglandin E receptor 2 (subtype EP2), 53kDa
GO signal transduction	157	1796	0.0006537	5734 prostaglandin E receptor 4 (subtype EP4)
GO signal transduction	157	1796	0.0006537	5737 prostaglandin F receptor (FP)
GO signal transduction	157	1796	0.0006537	57512 G protein-coupled receptor 158
GO signal transduction	157	1796	0.0006537	57524 CASK interacting protein 1
GO signal transduction	157	1796	0.0006537	57636 Rho GTPase activating protein 23
GO signal transduction	157	1796	0.0006537	5900 ral guanine nucleotide dissociation stimulator
GO signal transduction	157	1796	0.0006537	60485 salvador homolog 1 (Drosophila)
GO signal transduction	157	1796	0.0006537	6238 ribosome binding protein 1 homolog 180kDa (dog)
GO signal transduction	157	1796	0.0006537	6372 chemokine (C-X-C motif) ligand 6 (granulocyte chemotactic protein 2)
GO signal transduction	157	1796	0.0006537	6374 chemokine (C-X-C motif) ligand 5
GO signal transduction	157	1796	0.0006537	6452 SH3-domain binding protein 2
GO signal transduction	157	1796	0.0006537	6494 signal-induced proliferation-associated 1
GO signal transduction	157	1796	0.0006537	6751 somatostatin receptor 1
GO signal transduction	157	1796	0.0006537	6778 signal transducer and activator of transcription 6, interleukin-4 inducer
GO signal transduction	157	1796	0.0006537	7026 nuclear receptor subfamily 2, group F, member 2
GO signal transduction	157	1796	0.0006537	7089 transducin-like enhancer of split 2 (E(sp1) homolog, Drosophila)
GO signal transduction	157	1796	0.0006537	7090 transducin-like enhancer of split 3 (E(sp1) homolog, Drosophila)
GO signal transduction	157	1796	0.0006537	7097 toll-like receptor 2
GO signal transduction	157	1796	0.0006537	7098 toll-like receptor 3
GO signal transduction	157	1796	0.0006537	7099 toll-like receptor 4
GO signal transduction	157	1796	0.0006537	7100 toll-like receptor 5

GO signal transduction	157	1796	0.0006537	718 complement component 3
GO signal transduction	157	1796	0.0006537	726 calpain 5
GO signal transduction	157	1796	0.0006537	7852 chemokine (C-X-C motif) receptor 4
GO signal transduction	157	1796	0.0006537	799 calcitonin receptor
GO signal transduction	157	1796	0.0006537	80115 BAI1-associated protein 2-like 2
GO signal transduction	157	1796	0.0006537	81285 olfactory receptor, family 51, subfamily E, member 2
GO signal transduction	157	1796	0.0006537	81470 olfactory receptor, family 2, subfamily G, member 2
GO signal transduction	157	1796	0.0006537	819 calcium modulating ligand
GO signal transduction	157	1796	0.0006537	8313 axin 2
GO signal transduction	157	1796	0.0006537	834 caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, co
GO signal transduction	157	1796	0.0006537	83593 Ras association (RalGDS/AF-6) domain family member 5
GO signal transduction	157	1796	0.0006537	83937 Ras association (RalGDS/AF-6) domain family member 4
GO signal transduction	157	1796	0.0006537	84059 G protein-coupled receptor 98
GO signal transduction	157	1796	0.0006537	85004 RAS-like, estrogen-regulated, growth inhibitor
GO signal transduction	157	1796	0.0006537	8527 diacylglycerol kinase, delta 130kDa
GO signal transduction	157	1796	0.0006537	8622 phosphodiesterase 8B
GO signal transduction	157	1796	0.0006537	8660 insulin receptor substrate 2
GO signal transduction	157	1796	0.0006537	8740 tumor necrosis factor (ligand) superfamily, member 14
GO signal transduction	157	1796	0.0006537	8744 tumor necrosis factor (ligand) superfamily, member 9
GO signal transduction	157	1796	0.0006537	8793 tumor necrosis factor receptor superfamily, member 10d, decoy with t
GO signal transduction	157	1796	0.0006537	8794 tumor necrosis factor receptor superfamily, member 10c, decoy witho
GO signal transduction	157	1796	0.0006537	8839 WNT1 inducible signaling pathway protein 2
GO signal transduction	157	1796	0.0006537	885 cholecystokinin
GO signal transduction	157	1796	0.0006537	8863 period homolog 3 (Drosophila)
GO signal transduction	157	1796	0.0006537	8864 period homolog 2 (Drosophila)
GO signal transduction	157	1796	0.0006537	8911 calcium channel, voltage-dependent, T type, alpha 1I subunit
GO signal transduction	157	1796	0.0006537	8973 cholinergic receptor, nicotinic, alpha 6
GO signal transduction	157	1796	0.0006537	9064 mitogen-activated protein kinase kinase kinase 6
GO signal transduction	157	1796	0.0006537	91 activin A receptor, type IB
GO signal transduction	157	1796	0.0006537	9182 Ras association (RalGDS/AF-6) domain family (N-terminal) member 9
GO signal transduction	157	1796	0.0006537	94 activin A receptor type II-like 1
GO signal transduction	157	1796	0.0006537	9518 growth differentiation factor 15
GO signal transduction	157	1796	0.0006537	952 CD38 molecule
GO signal transduction	157	1796	0.0006537	9567 GTP binding protein 1
GO signal transduction	157	1796	0.0006537	9788 metastasis suppressor 1
GO signal transduction	157	1796	0.0006537	9966 tumor necrosis factor (ligand) superfamily, member 15

GO signal transduction	157	1796	0.0006537	9971 nuclear receptor subfamily 1, group H, member 4
GO regulation of apoptosis	18	114	0.0007103	10116 fem-1 homolog b (C. elegans)
GO regulation of apoptosis	18	114	0.0007103	130399 activin A receptor, type IC
GO regulation of apoptosis	18	114	0.0007103	1508 cathepsin B
GO regulation of apoptosis	18	114	0.0007103	2737 GLI family zinc finger 3
GO regulation of apoptosis	18	114	0.0007103	29108 PYD and CARD domain containing
GO regulation of apoptosis	18	114	0.0007103	3569 interleukin 6 (interferon, beta 2)
GO regulation of apoptosis	18	114	0.0007103	3570 interleukin 6 receptor
GO regulation of apoptosis	18	114	0.0007103	4170 myeloid cell leukemia sequence 1 (BCL2-related)
GO regulation of apoptosis	18	114	0.0007103	5025 purinergic receptor P2X, ligand-gated ion channel, 4
GO regulation of apoptosis	18	114	0.0007103	57118 calcium/calmodulin-dependent protein kinase ID
GO regulation of apoptosis	18	114	0.0007103	64127 nucleotide-binding oligomerization domain containing 2
GO regulation of apoptosis	18	114	0.0007103	64135 interferon induced with helicase C domain 1
GO regulation of apoptosis	18	114	0.0007103	64798 DEP domain containing 6
GO regulation of apoptosis	18	114	0.0007103	7001 peroxiredoxin 2
GO regulation of apoptosis	18	114	0.0007103	79092 caspase recruitment domain family, member 14
GO regulation of apoptosis	18	114	0.0007103	837 caspase 4, apoptosis-related cysteine peptidase
GO regulation of apoptosis	18	114	0.0007103	84674 caspase recruitment domain family, member 6
GO regulation of apoptosis	18	114	0.0007103	8996 nucleolar protein 3 (apoptosis repressor with CARD domain)
GO ion transport	54	505	0.0007212	10008 potassium voltage-gated channel, Isk-related family, member 3
GO ion transport	54	505	0.0007212	10312 T-cell, immune regulator 1, ATPase, H <sup>+</sup> transporting, lysosomal V0 subunit
GO ion transport	54	505	0.0007212	10568 solute carrier family 34 (sodium phosphate), member 2
GO ion transport	54	505	0.0007212	1080 cystic fibrosis transmembrane conductance regulator (ATP-binding cassette)
GO ion transport	54	505	0.0007212	1139 cholinergic receptor, nicotinic, alpha 7
GO ion transport	54	505	0.0007212	1193 chloride intracellular channel 2
GO ion transport	54	505	0.0007212	157855 potassium channel, subfamily U, member 1
GO ion transport	54	505	0.0007212	2564 gamma-aminobutyric acid (GABA) A receptor, epsilon
GO ion transport	54	505	0.0007212	259232 sodium leak channel, non-selective
GO ion transport	54	505	0.0007212	26507 cyclin M1
GO ion transport	54	505	0.0007212	266675 bestrophin 4
GO ion transport	54	505	0.0007212	27035 NADPH oxidase 1
GO ion transport	54	505	0.0007212	27345 potassium large conductance calcium-activated channel, subfamily M, member 1
GO ion transport	54	505	0.0007212	28231 solute carrier organic anion transporter family, member 4A1
GO ion transport	54	505	0.0007212	286133 scavenger receptor class A, member 5 (putative)
GO ion transport	54	505	0.0007212	343450 potassium channel, subfamily T, member 2
GO ion transport	54	505	0.0007212	3709 inositol 1,4,5-triphosphate receptor, type 2

GO ion transport	54	505	0.0007212	3759 potassium inwardly-rectifying channel, subfamily J, member 2
GO ion transport	54	505	0.0007212	3773 potassium inwardly-rectifying channel, subfamily J, member 16
GO ion transport	54	505	0.0007212	3775 potassium channel, subfamily K, member 1
GO ion transport	54	505	0.0007212	3782 potassium intermediate/small conductance calcium-activated channel,
GO ion transport	54	505	0.0007212	3783 potassium intermediate/small conductance calcium-activated channel,
GO ion transport	54	505	0.0007212	3786 potassium voltage-gated channel, KQT-like subfamily, member 3
GO ion transport	54	505	0.0007212	3790 potassium voltage-gated channel, delayed-rectifier, subfamily S, memb
GO ion transport	54	505	0.0007212	498 ATP synthase, H <sup>+</sup> transporting, mitochondrial F1 complex, alpha subun
GO ion transport	54	505	0.0007212	5025 purinergic receptor P2X, ligand-gated ion channel, 4
GO ion transport	54	505	0.0007212	50617 ATPase, H <sup>+</sup> transporting, lysosomal V0 subunit a4
GO ion transport	54	505	0.0007212	53373 two pore segment channel 1
GO ion transport	54	505	0.0007212	53405 chloride intracellular channel 5
GO ion transport	54	505	0.0007212	5349 FXYP domain containing ion transport regulator 3
GO ion transport	54	505	0.0007212	53827 FXYP domain containing ion transport regulator 5
GO ion transport	54	505	0.0007212	55799 calcium channel, voltage-dependent, alpha 2/delta subunit 3
GO ion transport	54	505	0.0007212	55867 solute carrier family 22 (organic anion/urate transporter), member 11
GO ion transport	54	505	0.0007212	57620 stromal interaction molecule 2
GO ion transport	54	505	0.0007212	63027 solute carrier family 22, member 23
GO ion transport	54	505	0.0007212	6330 sodium channel, voltage-gated, type IV, beta
GO ion transport	54	505	0.0007212	63982 anoctamin 3
GO ion transport	54	505	0.0007212	64116 solute carrier family 39 (zinc transporter), member 8
GO ion transport	54	505	0.0007212	6535 solute carrier family 6 (neurotransmitter transporter, creatine), memb
GO ion transport	54	505	0.0007212	6947 transcobalamin I (vitamin B12 binding protein, R binder family)
GO ion transport	54	505	0.0007212	6948 transcobalamin II; macrocytic anemia
GO ion transport	54	505	0.0007212	7223 transient receptor potential cation channel, subfamily C, member 4
GO ion transport	54	505	0.0007212	774 calcium channel, voltage-dependent, N type, alpha 1B subunit
GO ion transport	54	505	0.0007212	783 calcium channel, voltage-dependent, beta 2 subunit
GO ion transport	54	505	0.0007212	79689 STEAP family member 4
GO ion transport	54	505	0.0007212	84561 solute carrier family 12 (potassium/chloride transporters), member 8
GO ion transport	54	505	0.0007212	8514 potassium voltage-gated channel, shaker-related subfamily, beta mem
GO ion transport	54	505	0.0007212	8645 potassium channel, subfamily K, member 5
GO ion transport	54	505	0.0007212	8911 calcium channel, voltage-dependent, T type, alpha 1I subunit
GO ion transport	54	505	0.0007212	8912 calcium channel, voltage-dependent, T type, alpha 1H subunit
GO ion transport	54	505	0.0007212	8973 cholinergic receptor, nicotinic, alpha 6
GO ion transport	54	505	0.0007212	8992 ATPase, H <sup>+</sup> transporting, lysosomal 9kDa, V0 subunit e1
GO ion transport	54	505	0.0007212	93589 calcium channel, voltage-dependent, alpha 2/delta subunit 4

GO ion transport	54	505	0.0007212	9962 solute carrier family 23 (nucleobase transporters), member 2
GO positive regulation of tumor necrosis	5	12	0.0007808	64127 nucleotide-binding oligomerization domain containing 2
GO positive regulation of tumor necrosis	5	12	0.0007808	7097 toll-like receptor 2
GO positive regulation of tumor necrosis	5	12	0.0007808	7098 toll-like receptor 3
GO positive regulation of tumor necrosis	5	12	0.0007808	7099 toll-like receptor 4
GO positive regulation of tumor necrosis	5	12	0.0007808	929 CD14 molecule
GO lipoprotein metabolic process	6	18	0.000915	23780 apolipoprotein L, 2
GO lipoprotein metabolic process	6	18	0.000915	255738 proprotein convertase subtilisin/kexin type 9
GO lipoprotein metabolic process	6	18	0.000915	5465 peroxisome proliferator-activated receptor alpha
GO lipoprotein metabolic process	6	18	0.000915	80830 apolipoprotein L, 6
GO lipoprotein metabolic process	6	18	0.000915	80833 apolipoprotein L, 3
GO lipoprotein metabolic process	6	18	0.000915	8542 apolipoprotein L, 1
GO regulation of Rho protein signal trans	13	71	0.0009389	152273 FYVE, RhoGEF and PH domain containing 5
GO regulation of Rho protein signal trans	13	71	0.0009389	221178 spermatogenesis associated 13
GO regulation of Rho protein signal trans	13	71	0.0009389	23263 MCF.2 cell line derived transforming sequence-like
GO regulation of Rho protein signal trans	13	71	0.0009389	23365 Rho guanine nucleotide exchange factor (GEF) 12
GO regulation of Rho protein signal trans	13	71	0.0009389	26030 pleckstrin homology domain containing, family G (with RhoGef domain
GO regulation of Rho protein signal trans	13	71	0.0009389	389337 Rho guanine nucleotide exchange factor (GEF) 37
GO regulation of Rho protein signal trans	13	71	0.0009389	440107 pleckstrin homology domain containing, family G (with RhoGef domain
GO regulation of Rho protein signal trans	13	71	0.0009389	54848 Rho guanine nucleotide exchange factor (GEF) 38
GO regulation of Rho protein signal trans	13	71	0.0009389	55160 Rho guanine nucleotide exchange factor (GEF) 10-like
GO regulation of Rho protein signal trans	13	71	0.0009389	55200 pleckstrin homology domain containing, family G (with RhoGef domain
GO regulation of Rho protein signal trans	13	71	0.0009389	7984 Rho guanine nucleotide exchange factor (GEF) 5
GO regulation of Rho protein signal trans	13	71	0.0009389	84033 obscurin, cytoskeletal calmodulin and titin-interacting RhoGEF
GO regulation of Rho protein signal trans	13	71	0.0009389	9459 Rac/Cdc42 guanine nucleotide exchange factor (GEF) 6
GO plasma membrane	228	2763	0.0010189	1004 cadherin 6, type 2, K-cadherin (fetal kidney)
GO plasma membrane	228	2763	0.0010189	10076 protein tyrosine phosphatase, receptor type, U
GO plasma membrane	228	2763	0.0010189	1009 cadherin 11, type 2, OB-cadherin (osteoblast)
GO plasma membrane	228	2763	0.0010189	1014 cadherin 16, KSP-cadherin
GO plasma membrane	228	2763	0.0010189	10156 RAS p21 protein activator 4
GO plasma membrane	228	2763	0.0010189	1016 cadherin 18, type 2
GO plasma membrane	228	2763	0.0010189	10252 sprouty homolog 1, antagonist of FGF signaling (Drosophila)
GO plasma membrane	228	2763	0.0010189	10253 sprouty homolog 2 (Drosophila)
GO plasma membrane	228	2763	0.0010189	10268 receptor (G protein-coupled) activity modifying protein 3
GO plasma membrane	228	2763	0.0010189	10288 leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM
GO plasma membrane	228	2763	0.0010189	10312 T-cell, immune regulator 1, ATPase, H+ transporting, lysosomal V0 sub



GO plasma membrane	228	2763	0.0010189	10397 N-myc downstream regulated 1
GO plasma membrane	228	2763	0.0010189	10410 interferon induced transmembrane protein 3 (1-8U)
GO plasma membrane	228	2763	0.0010189	10435 CDC42 effector protein (Rho GTPase binding) 2
GO plasma membrane	228	2763	0.0010189	1048 carcinoembryonic antigen-related cell adhesion molecule 5
GO plasma membrane	228	2763	0.0010189	10507 sema domain, immunoglobulin domain (Ig), transmembrane domain (T
GO plasma membrane	228	2763	0.0010189	10752 cell adhesion molecule with homology to L1CAM (close homolog of L1)
GO plasma membrane	228	2763	0.0010189	10811 NADPH oxidase activator 1
GO plasma membrane	228	2763	0.0010189	1087 carcinoembryonic antigen-related cell adhesion molecule 7
GO plasma membrane	228	2763	0.0010189	10942 protease, serine, 21 (testisin)
GO plasma membrane	228	2763	0.0010189	11156 protein tyrosine phosphatase type IVA, member 3
GO plasma membrane	228	2763	0.0010189	112 adenylate cyclase 6
GO plasma membrane	228	2763	0.0010189	113235 solute carrier family 46 (folate transporter), member 1
GO plasma membrane	228	2763	0.0010189	1139 cholinergic receptor, nicotinic, alpha 7
GO plasma membrane	228	2763	0.0010189	114569 mal, T-cell differentiation protein 2
GO plasma membrane	228	2763	0.0010189	115330 G protein-coupled receptor 146
GO plasma membrane	228	2763	0.0010189	118429 anthrax toxin receptor 2
GO plasma membrane	228	2763	0.0010189	121130 olfactory receptor, family 10, subfamily P, member 1
GO plasma membrane	228	2763	0.0010189	123 perilipin 2
GO plasma membrane	228	2763	0.0010189	130576 LY6/PLAUR domain containing 6B
GO plasma membrane	228	2763	0.0010189	1363 carboxypeptidase E
GO plasma membrane	228	2763	0.0010189	1364 claudin 4
GO plasma membrane	228	2763	0.0010189	1368 carboxypeptidase M
GO plasma membrane	228	2763	0.0010189	1380 complement component (3d/Epstein Barr virus) receptor 2
GO plasma membrane	228	2763	0.0010189	1435 colony stimulating factor 1 (macrophage)
GO plasma membrane	228	2763	0.0010189	143503 olfactory receptor, family 51, subfamily E, member 1
GO plasma membrane	228	2763	0.0010189	148170 CDC42 effector protein (Rho GTPase binding) 5
GO plasma membrane	228	2763	0.0010189	151473 solute carrier family 16, member 14 (monocarboxylic acid transporter :
GO plasma membrane	228	2763	0.0010189	154 adrenergic, beta-2-, receptor, surface
GO plasma membrane	228	2763	0.0010189	157638 family with sequence similarity 84, member B
GO plasma membrane	228	2763	0.0010189	1604 CD55 molecule, decay accelerating factor for complement (Cromer blo
GO plasma membrane	228	2763	0.0010189	166929 sphingomyelin synthase 2
GO plasma membrane	228	2763	0.0010189	1741 discs, large homolog 3 (Drosophila)
GO plasma membrane	228	2763	0.0010189	1785 dynamin 2
GO plasma membrane	228	2763	0.0010189	1803 dipeptidyl-peptidase 4
GO plasma membrane	228	2763	0.0010189	1813 dopamine receptor D2
GO plasma membrane	228	2763	0.0010189	1815 dopamine receptor D4

GO plasma membrane	228	2763	0.0010189	1821 dystrophin related protein 2
GO plasma membrane	228	2763	0.0010189	1839 heparin-binding EGF-like growth factor
GO plasma membrane	228	2763	0.0010189	1901 sphingosine-1-phosphate receptor 1
GO plasma membrane	228	2763	0.0010189	1902 lysophosphatidic acid receptor 1
GO plasma membrane	228	2763	0.0010189	1948 ephrin-B2
GO plasma membrane	228	2763	0.0010189	1969 EPH receptor A2
GO plasma membrane	228	2763	0.0010189	2015 egf-like module containing, mucin-like, hormone receptor-like 1
GO plasma membrane	228	2763	0.0010189	2026 enolase 2 (gamma, neuronal)
GO plasma membrane	228	2763	0.0010189	2040 stomatin
GO plasma membrane	228	2763	0.0010189	2066 v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian)
GO plasma membrane	228	2763	0.0010189	2153 coagulation factor V (proaccelerin, labile factor)
GO plasma membrane	228	2763	0.0010189	2205 Fc fragment of IgE, high affinity I, receptor for; alpha polypeptide
GO plasma membrane	228	2763	0.0010189	222545 G protein-coupled receptor, family C, group 6, member A
GO plasma membrane	228	2763	0.0010189	2239 glypican 4
GO plasma membrane	228	2763	0.0010189	2262 glypican 5
GO plasma membrane	228	2763	0.0010189	2263 fibroblast growth factor receptor 2
GO plasma membrane	228	2763	0.0010189	22859 latrophilin 1
GO plasma membrane	228	2763	0.0010189	22925 phospholipase A2 receptor 1, 180kDa
GO plasma membrane	228	2763	0.0010189	23048 formin binding protein 1
GO plasma membrane	228	2763	0.0010189	23180 raftlin, lipid raft linker 1
GO plasma membrane	228	2763	0.0010189	23263 MCF.2 cell line derived transforming sequence-like
GO plasma membrane	228	2763	0.0010189	23266 latrophilin 2
GO plasma membrane	228	2763	0.0010189	23284 latrophilin 3
GO plasma membrane	228	2763	0.0010189	23371 tensin like C1 domain containing phosphatase (tensin 2)
GO plasma membrane	228	2763	0.0010189	23418 crumbs homolog 1 (Drosophila)
GO plasma membrane	228	2763	0.0010189	23682 RAB38, member RAS oncogene family
GO plasma membrane	228	2763	0.0010189	2564 gamma-aminobutyric acid (GABA) A receptor, epsilon
GO plasma membrane	228	2763	0.0010189	25837 RAB26, member RAS oncogene family
GO plasma membrane	228	2763	0.0010189	2633 guanylate binding protein 1, interferon-inducible, 67kDa
GO plasma membrane	228	2763	0.0010189	2634 guanylate binding protein 2, interferon-inducible
GO plasma membrane	228	2763	0.0010189	2642 glucagon receptor
GO plasma membrane	228	2763	0.0010189	26507 cyclin M1
GO plasma membrane	228	2763	0.0010189	266675 bestrophin 4
GO plasma membrane	228	2763	0.0010189	2706 gap junction protein, beta 2, 26kDa
GO plasma membrane	228	2763	0.0010189	2707 gap junction protein, beta 3, 31kDa
GO plasma membrane	228	2763	0.0010189	27076 LY6/PLAUR domain containing 3

GO plasma membrane	228	2763	0.0010189	27134 tight junction protein 3 (zona occludens 3)
GO plasma membrane	228	2763	0.0010189	27202 G protein-coupled receptor 77
GO plasma membrane	228	2763	0.0010189	2769 guanine nucleotide binding protein (G protein), alpha 15 (Gq class)
GO plasma membrane	228	2763	0.0010189	283316 CD163 molecule-like 1
GO plasma membrane	228	2763	0.0010189	283383 G protein-coupled receptor 133
GO plasma membrane	228	2763	0.0010189	285704 RGM domain family, member B
GO plasma membrane	228	2763	0.0010189	2861 G protein-coupled receptor 37 (endothelin receptor type B-like)
GO plasma membrane	228	2763	0.0010189	286133 scavenger receptor class A, member 5 (putative)
GO plasma membrane	228	2763	0.0010189	286183 Na <sup>+</sup> /K <sup>+</sup> transporting ATPase interacting 3
GO plasma membrane	228	2763	0.0010189	2865 free fatty acid receptor 3
GO plasma membrane	228	2763	0.0010189	2867 free fatty acid receptor 2
GO plasma membrane	228	2763	0.0010189	28982 feline leukemia virus subgroup C cellular receptor 1
GO plasma membrane	228	2763	0.0010189	2911 glutamate receptor, metabotropic 1
GO plasma membrane	228	2763	0.0010189	29126 CD274 molecule
GO plasma membrane	228	2763	0.0010189	29760 B-cell linker
GO plasma membrane	228	2763	0.0010189	3355 5-hydroxytryptamine (serotonin) receptor 1F
GO plasma membrane	228	2763	0.0010189	338557 G protein-coupled receptor 120
GO plasma membrane	228	2763	0.0010189	342035 gliomedin
GO plasma membrane	228	2763	0.0010189	343450 potassium channel, subfamily T, member 2
GO plasma membrane	228	2763	0.0010189	353345 G protein-coupled receptor 141
GO plasma membrane	228	2763	0.0010189	3570 interleukin 6 receptor
GO plasma membrane	228	2763	0.0010189	358 aquaporin 1 (Colton blood group)
GO plasma membrane	228	2763	0.0010189	3587 interleukin 10 receptor, alpha
GO plasma membrane	228	2763	0.0010189	3643 insulin receptor
GO plasma membrane	228	2763	0.0010189	3678 integrin, alpha 5 (fibronectin receptor, alpha polypeptide)
GO plasma membrane	228	2763	0.0010189	368 ATP-binding cassette, sub-family C (CFTR/MRP), member 6
GO plasma membrane	228	2763	0.0010189	3689 integrin, beta 2 (complement component 3 receptor 3 and 4 subunit)
GO plasma membrane	228	2763	0.0010189	3691 integrin, beta 4
GO plasma membrane	228	2763	0.0010189	3732 CD82 molecule
GO plasma membrane	228	2763	0.0010189	3782 potassium intermediate/small conductance calcium-activated channel,
GO plasma membrane	228	2763	0.0010189	3790 potassium voltage-gated channel, delayed-rectifier, subfamily S, memb
GO plasma membrane	228	2763	0.0010189	3845 v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog
GO plasma membrane	228	2763	0.0010189	387509 G protein-coupled receptor 153
GO plasma membrane	228	2763	0.0010189	392392 olfactory receptor, family 1, subfamily K, member 1
GO plasma membrane	228	2763	0.0010189	3949 low density lipoprotein receptor
GO plasma membrane	228	2763	0.0010189	3958 lectin, galactoside-binding, soluble, 3

GO plasma membrane	228	2763	0.0010189	399694 SHC (Src homology 2 domain containing) family, member 4
GO plasma membrane	228	2763	0.0010189	402415 XK, Kell blood group complex subunit-related, X-linked
GO plasma membrane	228	2763	0.0010189	412 steroid sulfatase (microsomal), isozyme S
GO plasma membrane	228	2763	0.0010189	4163 mutated in colorectal cancers
GO plasma membrane	228	2763	0.0010189	4179 CD46 molecule, complement regulatory protein
GO plasma membrane	228	2763	0.0010189	4254 KIT ligand
GO plasma membrane	228	2763	0.0010189	4359 myelin protein zero
GO plasma membrane	228	2763	0.0010189	4486 macrophage stimulating 1 receptor (c-met-related tyrosine kinase)
GO plasma membrane	228	2763	0.0010189	4582 mucin 1, cell surface associated
GO plasma membrane	228	2763	0.0010189	4680 carcinoembryonic antigen-related cell adhesion molecule 6 (non-specif
GO plasma membrane	228	2763	0.0010189	4684 neural cell adhesion molecule 1
GO plasma membrane	228	2763	0.0010189	4851 Notch homolog 1, translocation-associated (Drosophila)
GO plasma membrane	228	2763	0.0010189	4853 Notch homolog 2 (Drosophila)
GO plasma membrane	228	2763	0.0010189	4886 neuropeptide Y receptor Y1
GO plasma membrane	228	2763	0.0010189	4889 neuropeptide Y receptor Y5
GO plasma membrane	228	2763	0.0010189	493 ATPase, Ca <sup>++</sup> transporting, plasma membrane 4
GO plasma membrane	228	2763	0.0010189	498 ATP synthase, H <sup>+</sup> transporting, mitochondrial F1 complex, alpha subun
GO plasma membrane	228	2763	0.0010189	5025 purinergic receptor P2X, ligand-gated ion channel, 4
GO plasma membrane	228	2763	0.0010189	50617 ATPase, H <sup>+</sup> transporting, lysosomal V0 subunit a4
GO plasma membrane	228	2763	0.0010189	5099 protocadherin 7
GO plasma membrane	228	2763	0.0010189	51299 neuritin 1
GO plasma membrane	228	2763	0.0010189	5152 phosphodiesterase 9A
GO plasma membrane	228	2763	0.0010189	51655 RAS, dexamethasone-induced 1
GO plasma membrane	228	2763	0.0010189	51754 transmembrane protein 8B
GO plasma membrane	228	2763	0.0010189	5218 cyclin-dependent kinase 14
GO plasma membrane	228	2763	0.0010189	5244 ATP-binding cassette, sub-family B (MDR/TAP), member 4
GO plasma membrane	228	2763	0.0010189	5284 polymeric immunoglobulin receptor
GO plasma membrane	228	2763	0.0010189	5318 plakophilin 2
GO plasma membrane	228	2763	0.0010189	5362 plexin A2
GO plasma membrane	228	2763	0.0010189	54769 DIRAS family, GTP-binding RAS-like 2
GO plasma membrane	228	2763	0.0010189	55068 ecto-NOX disulfide-thiol exchanger 1
GO plasma membrane	228	2763	0.0010189	55080 TAP binding protein-like
GO plasma membrane	228	2763	0.0010189	55600 intelectin 1 (galactofuranose binding)
GO plasma membrane	228	2763	0.0010189	55824 phosphoprotein associated with glycosphingolipid microdomains 1
GO plasma membrane	228	2763	0.0010189	55867 solute carrier family 22 (organic anion/urate transporter), member 11
GO plasma membrane	228	2763	0.0010189	56288 par-3 partitioning defective 3 homolog (C. elegans)

GO plasma membrane	228	2763	0.0010189	56923 neuromedin U receptor 2
GO plasma membrane	228	2763	0.0010189	57104 patatin-like phospholipase domain containing 2
GO plasma membrane	228	2763	0.0010189	5724 platelet-activating factor receptor
GO plasma membrane	228	2763	0.0010189	5732 prostaglandin E receptor 2 (subtype EP2), 53kDa
GO plasma membrane	228	2763	0.0010189	5734 prostaglandin E receptor 4 (subtype EP4)
GO plasma membrane	228	2763	0.0010189	5737 prostaglandin F receptor (FP)
GO plasma membrane	228	2763	0.0010189	5742 prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and
GO plasma membrane	228	2763	0.0010189	57453 Down syndrome cell adhesion molecule like 1
GO plasma membrane	228	2763	0.0010189	57488 extended synaptotagmin-like protein 2
GO plasma membrane	228	2763	0.0010189	57512 G protein-coupled receptor 158
GO plasma membrane	228	2763	0.0010189	57620 stromal interaction molecule 2
GO plasma membrane	228	2763	0.0010189	5774 protein tyrosine phosphatase, non-receptor type 3
GO plasma membrane	228	2763	0.0010189	57799 RAB40C, member RAS oncogene family
GO plasma membrane	228	2763	0.0010189	57863 cell adhesion molecule 3
GO plasma membrane	228	2763	0.0010189	5791 protein tyrosine phosphatase, receptor type, E
GO plasma membrane	228	2763	0.0010189	5801 protein tyrosine phosphatase, receptor type, R
GO plasma membrane	228	2763	0.0010189	629 complement factor B
GO plasma membrane	228	2763	0.0010189	6402 selectin L
GO plasma membrane	228	2763	0.0010189	64083 golgi phosphoprotein 3 (coat-protein)
GO plasma membrane	228	2763	0.0010189	64127 nucleotide-binding oligomerization domain containing 2
GO plasma membrane	228	2763	0.0010189	6446 serum/glucocorticoid regulated kinase 1
GO plasma membrane	228	2763	0.0010189	6563 solute carrier family 14 (urea transporter), member 1 (Kidd blood group)
GO plasma membrane	228	2763	0.0010189	6622 synuclein, alpha (non A4 component of amyloid precursor)
GO plasma membrane	228	2763	0.0010189	6751 somatostatin receptor 1
GO plasma membrane	228	2763	0.0010189	6812 syntaxin binding protein 1
GO plasma membrane	228	2763	0.0010189	682 basigin (Ok blood group)
GO plasma membrane	228	2763	0.0010189	684 bone marrow stromal cell antigen 2
GO plasma membrane	228	2763	0.0010189	6857 synaptotagmin I
GO plasma membrane	228	2763	0.0010189	7049 transforming growth factor, beta receptor III
GO plasma membrane	228	2763	0.0010189	7097 toll-like receptor 2
GO plasma membrane	228	2763	0.0010189	7099 toll-like receptor 4
GO plasma membrane	228	2763	0.0010189	7100 toll-like receptor 5
GO plasma membrane	228	2763	0.0010189	7106 tetraspanin 4
GO plasma membrane	228	2763	0.0010189	7133 tumor necrosis factor receptor superfamily, member 1B
GO plasma membrane	228	2763	0.0010189	7223 transient receptor potential cation channel, subfamily C, member 4
GO plasma membrane	228	2763	0.0010189	729993 shisa homolog 9 ( <i>Xenopus laevis</i> )

GO plasma membrane	228	2763	0.0010189	731 complement component 8, alpha polypeptide
GO plasma membrane	228	2763	0.0010189	774 calcium channel, voltage-dependent, N type, alpha 1B subunit
GO plasma membrane	228	2763	0.0010189	7852 chemokine (C-X-C motif) receptor 4
GO plasma membrane	228	2763	0.0010189	79092 caspase recruitment domain family, member 14
GO plasma membrane	228	2763	0.0010189	79689 STEAP family member 4
GO plasma membrane	228	2763	0.0010189	799 calcitonin receptor
GO plasma membrane	228	2763	0.0010189	81285 olfactory receptor, family 51, subfamily E, member 2
GO plasma membrane	228	2763	0.0010189	81470 olfactory receptor, family 2, subfamily G, member 2
GO plasma membrane	228	2763	0.0010189	83604 transmembrane protein 47
GO plasma membrane	228	2763	0.0010189	84059 G protein-coupled receptor 98
GO plasma membrane	228	2763	0.0010189	8434 reversion-inducing-cysteine-rich protein with kazal motifs
GO plasma membrane	228	2763	0.0010189	8519 interferon induced transmembrane protein 1 (9-27)
GO plasma membrane	228	2763	0.0010189	8527 diacylglycerol kinase, delta 130kDa
GO plasma membrane	228	2763	0.0010189	8600 tumor necrosis factor (ligand) superfamily, member 11
GO plasma membrane	228	2763	0.0010189	8631 src kinase associated phosphoprotein 1
GO plasma membrane	228	2763	0.0010189	8660 insulin receptor substrate 2
GO plasma membrane	228	2763	0.0010189	8671 solute carrier family 4, sodium bicarbonate cotransporter, member 4
GO plasma membrane	228	2763	0.0010189	8740 tumor necrosis factor (ligand) superfamily, member 14
GO plasma membrane	228	2763	0.0010189	8744 tumor necrosis factor (ligand) superfamily, member 9
GO plasma membrane	228	2763	0.0010189	8794 tumor necrosis factor receptor superfamily, member 10c, decoy without
GO plasma membrane	228	2763	0.0010189	8839 WNT1 inducible signaling pathway protein 2
GO plasma membrane	228	2763	0.0010189	8842 prominin 1
GO plasma membrane	228	2763	0.0010189	8875 vanin 2
GO plasma membrane	228	2763	0.0010189	8912 calcium channel, voltage-dependent, T type, alpha 1H subunit
GO plasma membrane	228	2763	0.0010189	8973 cholinergic receptor, nicotinic, alpha 6
GO plasma membrane	228	2763	0.0010189	9071 claudin 10
GO plasma membrane	228	2763	0.0010189	91653 Boc homolog (mouse)
GO plasma membrane	228	2763	0.0010189	9194 solute carrier family 16, member 7 (monocarboxylic acid transporter 2)
GO plasma membrane	228	2763	0.0010189	929 CD14 molecule
GO plasma membrane	228	2763	0.0010189	94025 mucin 16, cell surface associated
GO plasma membrane	228	2763	0.0010189	9414 tight junction protein 2 (zona occludens 2)
GO plasma membrane	228	2763	0.0010189	952 CD38 molecule
GO plasma membrane	228	2763	0.0010189	961 CD47 molecule
GO plasma membrane	228	2763	0.0010189	9619 ATP-binding cassette, sub-family G (WHITE), member 1
GO plasma membrane	228	2763	0.0010189	9892 synaptosomal-associated protein, 91kDa homolog (mouse)
GO plasma membrane	228	2763	0.0010189	9962 solute carrier family 23 (nucleobase transporters), member 2

GO plasma membrane	228	2763	0.0010189	9966 tumor necrosis factor (ligand) superfamily, member 15
GO voltage-gated ion channel activity	21	147	0.0010346	10008 potassium voltage-gated channel, Isk-related family, member 3
GO voltage-gated ion channel activity	21	147	0.0010346	1193 chloride intracellular channel 2
GO voltage-gated ion channel activity	21	147	0.0010346	157855 potassium channel, subfamily U, member 1
GO voltage-gated ion channel activity	21	147	0.0010346	259232 sodium leak channel, non-selective
GO voltage-gated ion channel activity	21	147	0.0010346	27035 NADPH oxidase 1
GO voltage-gated ion channel activity	21	147	0.0010346	3759 potassium inwardly-rectifying channel, subfamily J, member 2
GO voltage-gated ion channel activity	21	147	0.0010346	3773 potassium inwardly-rectifying channel, subfamily J, member 16
GO voltage-gated ion channel activity	21	147	0.0010346	3775 potassium channel, subfamily K, member 1
GO voltage-gated ion channel activity	21	147	0.0010346	3786 potassium voltage-gated channel, KQT-like subfamily, member 3
GO voltage-gated ion channel activity	21	147	0.0010346	3790 potassium voltage-gated channel, delayed-rectifier, subfamily S, memb
GO voltage-gated ion channel activity	21	147	0.0010346	53373 two pore segment channel 1
GO voltage-gated ion channel activity	21	147	0.0010346	53405 chloride intracellular channel 5
GO voltage-gated ion channel activity	21	147	0.0010346	55799 calcium channel, voltage-dependent, alpha 2/delta subunit 3
GO voltage-gated ion channel activity	21	147	0.0010346	6330 sodium channel, voltage-gated, type IV, beta
GO voltage-gated ion channel activity	21	147	0.0010346	774 calcium channel, voltage-dependent, N type, alpha 1B subunit
GO voltage-gated ion channel activity	21	147	0.0010346	783 calcium channel, voltage-dependent, beta 2 subunit
GO voltage-gated ion channel activity	21	147	0.0010346	8514 potassium voltage-gated channel, shaker-related subfamily, beta memi
GO voltage-gated ion channel activity	21	147	0.0010346	8645 potassium channel, subfamily K, member 5
GO voltage-gated ion channel activity	21	147	0.0010346	8911 calcium channel, voltage-dependent, T type, alpha 1I subunit
GO voltage-gated ion channel activity	21	147	0.0010346	8912 calcium channel, voltage-dependent, T type, alpha 1H subunit
GO voltage-gated ion channel activity	21	147	0.0010346	93589 calcium channel, voltage-dependent, alpha 2/delta subunit 4
GO anchored to membrane	17	109	0.0011358	1048 carcinoembryonic antigen-related cell adhesion molecule 5
GO anchored to membrane	17	109	0.0011358	1087 carcinoembryonic antigen-related cell adhesion molecule 7
GO anchored to membrane	17	109	0.0011358	10942 protease, serine, 21 (testisin)
GO anchored to membrane	17	109	0.0011358	130576 LY6/PLAUR domain containing 6B
GO anchored to membrane	17	109	0.0011358	1368 carboxypeptidase M
GO anchored to membrane	17	109	0.0011358	1604 CD55 molecule, decay accelerating factor for complement (Cromer blo
GO anchored to membrane	17	109	0.0011358	2239 glypican 4
GO anchored to membrane	17	109	0.0011358	2262 glypican 5
GO anchored to membrane	17	109	0.0011358	4680 carcinoembryonic antigen-related cell adhesion molecule 6 (non-specif
GO anchored to membrane	17	109	0.0011358	4684 neural cell adhesion molecule 1
GO anchored to membrane	17	109	0.0011358	51299 neuritin 1
GO anchored to membrane	17	109	0.0011358	55600 intelectin 1 (galactofuranose binding)
GO anchored to membrane	17	109	0.0011358	684 bone marrow stromal cell antigen 2
GO anchored to membrane	17	109	0.0011358	8434 reversion-inducing-cysteine-rich protein with kazal motifs

GO anchored to membrane	17	109	0.0011358	8794 tumor necrosis factor receptor superfamily, member 10c, decoy withou
GO anchored to membrane	17	109	0.0011358	8875 vanin 2
GO anchored to membrane	17	109	0.0011358	929 CD14 molecule
GO positive regulation of chemokine pro	5	13	0.0011977	3569 interleukin 6 (interferon, beta 2)
GO positive regulation of chemokine pro	5	13	0.0011977	3570 interleukin 6 receptor
GO positive regulation of chemokine pro	5	13	0.0011977	7097 toll-like receptor 2
GO positive regulation of chemokine pro	5	13	0.0011977	7098 toll-like receptor 3
GO positive regulation of chemokine pro	5	13	0.0011977	7099 toll-like receptor 4
GO epithelial cell maturation involved in	3	4	0.0012092	10116 fem-1 homolog b (C. elegans)
GO epithelial cell maturation involved in	3	4	0.0012092	10481 homeobox B13
GO epithelial cell maturation involved in	3	4	0.0012092	3169 forkhead box A1
GO activin receptor activity, type I	3	4	0.0012092	130399 activin A receptor, type IC
GO activin receptor activity, type I	3	4	0.0012092	91 activin A receptor, type IB
GO activin receptor activity, type I	3	4	0.0012092	94 activin A receptor type II-like 1
GO secretory columnar luminal epithelial	3	4	0.0012092	3169 forkhead box A1
GO secretory columnar luminal epithelial	3	4	0.0012092	4851 Notch homolog 1, translocation-associated (Drosophila)
GO secretory columnar luminal epithelial	3	4	0.0012092	6256 retinoid X receptor, alpha
GO positive regulation of toll-like receptc	3	4	0.0012092	7097 toll-like receptor 2
GO positive regulation of toll-like receptc	3	4	0.0012092	7098 toll-like receptor 3
GO positive regulation of toll-like receptc	3	4	0.0012092	7100 toll-like receptor 5
GO apical plasma membrane	22	159	0.0012219	10312 T-cell, immune regulator 1, ATPase, H+ transporting, lysosomal V0 subu
GO apical plasma membrane	22	159	0.0012219	10568 solute carrier family 34 (sodium phosphate), member 2
GO apical plasma membrane	22	159	0.0012219	1080 cystic fibrosis transmembrane conductance regulator (ATP-binding cas:
GO apical plasma membrane	22	159	0.0012219	113235 solute carrier family 46 (folate transporter), member 1
GO apical plasma membrane	22	159	0.0012219	114569 mal, T-cell differentiation protein 2
GO apical plasma membrane	22	159	0.0012219	1508 cathepsin B
GO apical plasma membrane	22	159	0.0012219	154 adrenergic, beta-2-, receptor, surface
GO apical plasma membrane	22	159	0.0012219	1803 dipeptidyl-peptidase 4
GO apical plasma membrane	22	159	0.0012219	23418 crumbs homolog 1 (Drosophila)
GO apical plasma membrane	22	159	0.0012219	3570 interleukin 6 receptor
GO apical plasma membrane	22	159	0.0012219	358 aquaporin 1 (Colton blood group)
GO apical plasma membrane	22	159	0.0012219	368 ATP-binding cassette, sub-family C (CFTR/MRP), member 6
GO apical plasma membrane	22	159	0.0012219	3775 potassium channel, subfamily K, member 1
GO apical plasma membrane	22	159	0.0012219	4008 LIM domain 7
GO apical plasma membrane	22	159	0.0012219	4582 mucin 1, cell surface associated
GO apical plasma membrane	22	159	0.0012219	50617 ATPase, H+ transporting, lysosomal V0 subunit a4



GO	apical plasma membrane	22	159	0.0012219	5244 ATP-binding cassette, sub-family B (MDR/TAP), member 4
GO	apical plasma membrane	22	159	0.0012219	55867 solute carrier family 22 (organic anion/urate transporter), member 11
GO	apical plasma membrane	22	159	0.0012219	57619 shroom family member 3
GO	apical plasma membrane	22	159	0.0012219	5873 RAB27A, member RAS oncogene family
GO	apical plasma membrane	22	159	0.0012219	8842 prominin 1
GO	apical plasma membrane	22	159	0.0012219	9962 solute carrier family 23 (nucleobase transporters), member 2
GO	immune response	35	303	0.0016375	10216 proteoglycan 4
GO	immune response	35	303	0.0016375	10288 leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM
GO	immune response	35	303	0.0016375	10346 tripartite motif-containing 22
GO	immune response	35	303	0.0016375	10410 interferon induced transmembrane protein 3 (1-8U)
GO	immune response	35	303	0.0016375	10507 sema domain, immunoglobulin domain (Ig), transmembrane domain (T
GO	immune response	35	303	0.0016375	10964 interferon-induced protein 44-like
GO	immune response	35	303	0.0016375	1380 complement component (3d/Epstein Barr virus) receptor 2
GO	immune response	35	303	0.0016375	157869 chromosome 8 open reading frame 84
GO	immune response	35	303	0.0016375	2634 guanylate binding protein 2, interferon-inducible
GO	immune response	35	303	0.0016375	29126 CD274 molecule
GO	immune response	35	303	0.0016375	2921 chemokine (C-X-C motif) ligand 3
GO	immune response	35	303	0.0016375	3134 major histocompatibility complex, class I, F
GO	immune response	35	303	0.0016375	3512 immunoglobulin J polypeptide, linker protein for immunoglobulin alpha;
GO	immune response	35	303	0.0016375	3561 interleukin 2 receptor, gamma (severe combined immunodeficiency)
GO	immune response	35	303	0.0016375	4065 lymphocyte antigen 75
GO	immune response	35	303	0.0016375	4783 nuclear factor, interleukin 3 regulated
GO	immune response	35	303	0.0016375	4851 Notch homolog 1, translocation-associated (Drosophila)
GO	immune response	35	303	0.0016375	4939 2'-5'-oligoadenylate synthetase 2, 69/71kDa
GO	immune response	35	303	0.0016375	56477 chemokine (C-C motif) ligand 28
GO	immune response	35	303	0.0016375	5724 platelet-activating factor receptor
GO	immune response	35	303	0.0016375	5734 prostaglandin E receptor 4 (subtype EP4)
GO	immune response	35	303	0.0016375	6372 chemokine (C-X-C motif) ligand 6 (granulocyte chemotactic protein 2)
GO	immune response	35	303	0.0016375	6374 chemokine (C-X-C motif) ligand 5
GO	immune response	35	303	0.0016375	7049 transforming growth factor, beta receptor III
GO	immune response	35	303	0.0016375	7097 toll-like receptor 2
GO	immune response	35	303	0.0016375	7099 toll-like receptor 4
GO	immune response	35	303	0.0016375	7133 tumor necrosis factor receptor superfamily, member 1B
GO	immune response	35	303	0.0016375	715 complement component 1, r subcomponent
GO	immune response	35	303	0.0016375	718 complement component 3
GO	immune response	35	303	0.0016375	731 complement component 8, alpha polypeptide

GO immune response	35	303	0.0016375	8600 tumor necrosis factor (ligand) superfamily, member 11
GO immune response	35	303	0.0016375	8740 tumor necrosis factor (ligand) superfamily, member 14
GO immune response	35	303	0.0016375	8744 tumor necrosis factor (ligand) superfamily, member 9
GO immune response	35	303	0.0016375	9567 GTP binding protein 1
GO immune response	35	303	0.0016375	9966 tumor necrosis factor (ligand) superfamily, member 15
GO response to retinoic acid	8	34	0.0017063	1843 dual specificity phosphatase 1
GO response to retinoic acid	8	34	0.0017063	2033 E1A binding protein p300
GO response to retinoic acid	8	34	0.0017063	3294 hydroxysteroid (17-beta) dehydrogenase 2
GO response to retinoic acid	8	34	0.0017063	429 achaete-scute complex homolog 1 (Drosophila)
GO response to retinoic acid	8	34	0.0017063	5950 retinol binding protein 4, plasma
GO response to retinoic acid	8	34	0.0017063	6256 retinoid X receptor, alpha
GO response to retinoic acid	8	34	0.0017063	652 bone morphogenetic protein 4
GO response to retinoic acid	8	34	0.0017063	952 CD38 molecule
GO response to cytokine stimulus	10	50	0.0017843	1080 cystic fibrosis transmembrane conductance regulator (ATP-binding cas:
GO response to cytokine stimulus	10	50	0.0017843	10906 TRAF-type zinc finger domain containing 1
GO response to cytokine stimulus	10	50	0.0017843	2353 FBJ murine osteosarcoma viral oncogene homolog
GO response to cytokine stimulus	10	50	0.0017843	3570 interleukin 6 receptor
GO response to cytokine stimulus	10	50	0.0017843	3725 jun oncogene
GO response to cytokine stimulus	10	50	0.0017843	3726 jun B proto-oncogene
GO response to cytokine stimulus	10	50	0.0017843	4170 myeloid cell leukemia sequence 1 (BCL2-related)
GO response to cytokine stimulus	10	50	0.0017843	5371 promyelocytic leukemia
GO response to cytokine stimulus	10	50	0.0017843	6778 signal transducer and activator of transcription 6, interleukin-4 inducec
GO response to cytokine stimulus	10	50	0.0017843	9021 suppressor of cytokine signaling 3
GO positive regulation of transcription fr	34	295	0.0019637	10891 peroxisome proliferator-activated receptor gamma, coactivator 1 alpha
GO positive regulation of transcription fr	34	295	0.0019637	154 adrenergic, beta-2-, receptor, surface
GO positive regulation of transcription fr	34	295	0.0019637	1958 early growth response 1
GO positive regulation of transcription fr	34	295	0.0019637	1959 early growth response 2
GO positive regulation of transcription fr	34	295	0.0019637	2033 E1A binding protein p300
GO positive regulation of transcription fr	34	295	0.0019637	2296 forkhead box C1
GO positive regulation of transcription fr	34	295	0.0019637	2303 forkhead box C2 (MFH-1, mesenchyme forkhead 1)
GO positive regulation of transcription fr	34	295	0.0019637	23373 CREB regulated transcription coactivator 1
GO positive regulation of transcription fr	34	295	0.0019637	2353 FBJ murine osteosarcoma viral oncogene homolog
GO positive regulation of transcription fr	34	295	0.0019637	2737 GLI family zinc finger 3
GO positive regulation of transcription fr	34	295	0.0019637	28996 homeodomain interacting protein kinase 2
GO positive regulation of transcription fr	34	295	0.0019637	3164 nuclear receptor subfamily 4, group A, member 1
GO positive regulation of transcription fr	34	295	0.0019637	3569 interleukin 6 (interferon, beta 2)

GO	positive regulation of transcription fr	34	295	0.0019637	3659 interferon regulatory factor 1
GO	positive regulation of transcription fr	34	295	0.0019637	3725 jun oncogene
GO	positive regulation of transcription fr	34	295	0.0019637	375790 agrin
GO	positive regulation of transcription fr	34	295	0.0019637	4087 SMAD family member 2
GO	positive regulation of transcription fr	34	295	0.0019637	4212 Meis homeobox 2
GO	positive regulation of transcription fr	34	295	0.0019637	4286 microphthalmia-associated transcription factor
GO	positive regulation of transcription fr	34	295	0.0019637	429 achaete-scute complex homolog 1 (Drosophila)
GO	positive regulation of transcription fr	34	295	0.0019637	4851 Notch homolog 1, translocation-associated (Drosophila)
GO	positive regulation of transcription fr	34	295	0.0019637	4929 nuclear receptor subfamily 4, group A, member 2
GO	positive regulation of transcription fr	34	295	0.0019637	5083 paired box 9
GO	positive regulation of transcription fr	34	295	0.0019637	51621 Kruppel-like factor 13
GO	positive regulation of transcription fr	34	295	0.0019637	5325 pleiomorphic adenoma gene-like 1
GO	positive regulation of transcription fr	34	295	0.0019637	5465 peroxisome proliferator-activated receptor alpha
GO	positive regulation of transcription fr	34	295	0.0019637	6256 retinoid X receptor, alpha
GO	positive regulation of transcription fr	34	295	0.0019637	64651 cysteine-serine-rich nuclear protein 1
GO	positive regulation of transcription fr	34	295	0.0019637	6778 signal transducer and activator of transcription 6, interleukin-4 inducible
GO	positive regulation of transcription fr	34	295	0.0019637	8013 nuclear receptor subfamily 4, group A, member 3
GO	positive regulation of transcription fr	34	295	0.0019637	8631 src kinase associated phosphoprotein 1
GO	positive regulation of transcription fr	34	295	0.0019637	91 activin A receptor, type IB
GO	positive regulation of transcription fr	34	295	0.0019637	9935 v-maf musculoaponeurotic fibrosarcoma oncogene homolog B (avian)
GO	positive regulation of transcription fr	34	295	0.0019637	9971 nuclear receptor subfamily 1, group H, member 4
GO	retinol metabolic process	4	9	0.0020714	10170 dehydrogenase/reductase (SDR family) member 9
GO	retinol metabolic process	4	9	0.0020714	157506 retinol dehydrogenase 10 (all-trans)
GO	retinol metabolic process	4	9	0.0020714	195814 short chain dehydrogenase/reductase family 16C, member 5
GO	retinol metabolic process	4	9	0.0020714	5950 retinol binding protein 4, plasma
GO	response to fatty acid	4	9	0.0020714	2033 E1A binding protein p300
GO	response to fatty acid	4	9	0.0020714	5122 proprotein convertase subtilisin/kexin type 1
GO	response to fatty acid	4	9	0.0020714	7097 toll-like receptor 2
GO	response to fatty acid	4	9	0.0020714	7099 toll-like receptor 4
GO	ligand-regulated transcription factor	4	9	0.0020714	4853 Notch homolog 2 (Drosophila)
GO	ligand-regulated transcription factor	4	9	0.0020714	5465 peroxisome proliferator-activated receptor alpha
GO	ligand-regulated transcription factor	4	9	0.0020714	6256 retinoid X receptor, alpha
GO	ligand-regulated transcription factor	4	9	0.0020714	7026 nuclear receptor subfamily 2, group F, member 2
GO	positive regulation of interleukin-12 p70 production	4	9	0.0020714	64127 nucleotide-binding oligomerization domain containing 2
GO	positive regulation of interleukin-12 p70 production	4	9	0.0020714	7097 toll-like receptor 2
GO	positive regulation of interleukin-12 p70 production	4	9	0.0020714	7098 toll-like receptor 3

GO positive regulation of interleukin-12 p	4	9	0.0020714	7099 toll-like receptor 4
GO circadian rhythm	8	35	0.0020813	1960 early growth response 3
GO circadian rhythm	8	35	0.0020813	3725 jun oncogene
GO circadian rhythm	8	35	0.0020813	50865 heme binding protein 1
GO circadian rhythm	8	35	0.0020813	5187 period homolog 1 (Drosophila)
GO circadian rhythm	8	35	0.0020813	6096 RAR-related orphan receptor B
GO circadian rhythm	8	35	0.0020813	8553 basic helix-loop-helix family, member e40
GO circadian rhythm	8	35	0.0020813	8864 period homolog 2 (Drosophila)
GO circadian rhythm	8	35	0.0020813	9572 nuclear receptor subfamily 1, group D, member 1
GO positive regulation of interleukin-6 pr	6	21	0.0022406	3569 interleukin 6 (interferon, beta 2)
GO positive regulation of interleukin-6 pr	6	21	0.0022406	3570 interleukin 6 receptor
GO positive regulation of interleukin-6 pr	6	21	0.0022406	64127 nucleotide-binding oligomerization domain containing 2
GO positive regulation of interleukin-6 pr	6	21	0.0022406	7097 toll-like receptor 2
GO positive regulation of interleukin-6 pr	6	21	0.0022406	7098 toll-like receptor 3
GO positive regulation of interleukin-6 pr	6	21	0.0022406	7099 toll-like receptor 4
GO multicellular organismal developmen	83	890	0.0023224	10085 EGF-like repeats and discoidin I-like domains 3
GO multicellular organismal developmen	83	890	0.0023224	10252 sprouty homolog 1, antagonist of FGF signaling (Drosophila)
GO multicellular organismal developmen	83	890	0.0023224	10253 sprouty homolog 2 (Drosophila)
GO multicellular organismal developmen	83	890	0.0023224	10439 olfactomedin 1
GO multicellular organismal developmen	83	890	0.0023224	10481 homeobox B13
GO multicellular organismal developmen	83	890	0.0023224	10507 sema domain, immunoglobulin domain (Ig), transmembrane domain (T
GO multicellular organismal developmen	83	890	0.0023224	10752 cell adhesion molecule with homology to L1CAM (close homolog of L1)
GO multicellular organismal developmen	83	890	0.0023224	10912 growth arrest and DNA-damage-inducible, gamma
GO multicellular organismal developmen	83	890	0.0023224	10913 ectodysplasin A receptor
GO multicellular organismal developmen	83	890	0.0023224	127343 diencephalon/mesencephalon homeobox 1
GO multicellular organismal developmen	83	890	0.0023224	143689 piwi-like 4 (Drosophila)
GO multicellular organismal developmen	83	890	0.0023224	1462 versican
GO multicellular organismal developmen	83	890	0.0023224	150094 salt-inducible kinase 1
GO multicellular organismal developmen	83	890	0.0023224	158800 RhoX homeobox family, member 1
GO multicellular organismal developmen	83	890	0.0023224	1755 deleted in malignant brain tumors 1
GO multicellular organismal developmen	83	890	0.0023224	1948 ephrin-B2
GO multicellular organismal developmen	83	890	0.0023224	1969 EPH receptor A2
GO multicellular organismal developmen	83	890	0.0023224	1999 E74-like factor 3 (ets domain transcription factor, epithelial-specific )
GO multicellular organismal developmen	83	890	0.0023224	2122 MDS1 and EVI1 complex locus
GO multicellular organismal developmen	83	890	0.0023224	222171 proline rich 15
GO multicellular organismal developmen	83	890	0.0023224	222546 regulatory factor X, 6

GO multicellular organismal developmen	83	890	0.0023224	223117 sema domain, immunoglobulin domain (Ig), short basic domain, secret
GO multicellular organismal developmen	83	890	0.0023224	2290 forkhead box G1
GO multicellular organismal developmen	83	890	0.0023224	2303 forkhead box C2 (MFH-1, mesenchyme forkhead 1)
GO multicellular organismal developmen	83	890	0.0023224	2354 FBJ murine osteosarcoma viral oncogene homolog B
GO multicellular organismal developmen	83	890	0.0023224	23654 plexin B2
GO multicellular organismal developmen	83	890	0.0023224	23780 apolipoprotein L, 2
GO multicellular organismal developmen	83	890	0.0023224	255743 nephronectin
GO multicellular organismal developmen	83	890	0.0023224	26468 LIM homeobox 6
GO multicellular organismal developmen	83	890	0.0023224	27123 dickkopf homolog 2 ( <i>Xenopus laevis</i> )
GO multicellular organismal developmen	83	890	0.0023224	28982 feline leukemia virus subgroup C cellular receptor 1
GO multicellular organismal developmen	83	890	0.0023224	3131 hepatic leukemia factor
GO multicellular organismal developmen	83	890	0.0023224	3142 H2.0-like homeobox
GO multicellular organismal developmen	83	890	0.0023224	3169 forkhead box A1
GO multicellular organismal developmen	83	890	0.0023224	342035 gliomedin
GO multicellular organismal developmen	83	890	0.0023224	4005 LIM domain only 2 (rhombotin-like 1)
GO multicellular organismal developmen	83	890	0.0023224	4170 myeloid cell leukemia sequence 1 (BCL2-related)
GO multicellular organismal developmen	83	890	0.0023224	4209 myocyte enhancer factor 2D
GO multicellular organismal developmen	83	890	0.0023224	4223 mesenchyme homeobox 2
GO multicellular organismal developmen	83	890	0.0023224	4286 microphthalmia-associated transcription factor
GO multicellular organismal developmen	83	890	0.0023224	4486 macrophage stimulating 1 receptor (c-met-related tyrosine kinase)
GO multicellular organismal developmen	83	890	0.0023224	4616 growth arrest and DNA-damage-inducible, beta
GO multicellular organismal developmen	83	890	0.0023224	4778 nuclear factor (erythroid-derived 2), 45kDa
GO multicellular organismal developmen	83	890	0.0023224	4853 Notch homolog 2 ( <i>Drosophila</i> )
GO multicellular organismal developmen	83	890	0.0023224	4915 neurotrophic tyrosine kinase, receptor, type 2
GO multicellular organismal developmen	83	890	0.0023224	5063 p21 protein (Cdc42/Rac)-activated kinase 3
GO multicellular organismal developmen	83	890	0.0023224	5083 paired box 9
GO multicellular organismal developmen	83	890	0.0023224	51274 Kruppel-like factor 3 (basic)
GO multicellular organismal developmen	83	890	0.0023224	51314 thioredoxin domain containing 3 (spermatzoa)
GO multicellular organismal developmen	83	890	0.0023224	5307 paired-like homeodomain 1
GO multicellular organismal developmen	83	890	0.0023224	5308 paired-like homeodomain 2
GO multicellular organismal developmen	83	890	0.0023224	5362 plexin A2
GO multicellular organismal developmen	83	890	0.0023224	5367 pro-melanin-concentrating hormone
GO multicellular organismal developmen	83	890	0.0023224	5396 paired related homeobox 1
GO multicellular organismal developmen	83	890	0.0023224	54361 wingless-type MMTV integration site family, member 4
GO multicellular organismal developmen	83	890	0.0023224	54852 progesterin and adipoQ receptor family member V
GO multicellular organismal developmen	83	890	0.0023224	55124 piwi-like 2 ( <i>Drosophila</i> )

GO multicellular organismal developmen	83	890	0.0023224	56913 core 1 synthase, glycoprotein-N-acetylgalactosamine 3-beta-galactosyl
GO multicellular organismal developmen	83	890	0.0023224	56944 olfactomedin-like 3
GO multicellular organismal developmen	83	890	0.0023224	6096 RAR-related orphan receptor B
GO multicellular organismal developmen	83	890	0.0023224	6239 ras responsive element binding protein 1
GO multicellular organismal developmen	83	890	0.0023224	64359 nucleoredoxin
GO multicellular organismal developmen	83	890	0.0023224	684 bone marrow stromal cell antigen 2
GO multicellular organismal developmen	83	890	0.0023224	7092 tolloid-like 1
GO multicellular organismal developmen	83	890	0.0023224	7477 wingless-type MMTV integration site family, member 7B
GO multicellular organismal developmen	83	890	0.0023224	7546 Zic family member 2 (odd-paired homolog, Drosophila)
GO multicellular organismal developmen	83	890	0.0023224	7869 sema domain, immunoglobulin domain (Ig), short basic domain, secret
GO multicellular organismal developmen	83	890	0.0023224	79820 cation channel, sperm-associated, beta
GO multicellular organismal developmen	83	890	0.0023224	79971 wntless homolog (Drosophila)
GO multicellular organismal developmen	83	890	0.0023224	81693 amnionless homolog (mouse)
GO multicellular organismal developmen	83	890	0.0023224	8313 axin 2
GO multicellular organismal developmen	83	890	0.0023224	8382 non-metastatic cells 5, protein expressed in (nucleoside-diphosphate k
GO multicellular organismal developmen	83	890	0.0023224	83890 spermatogenesis associated 9
GO multicellular organismal developmen	83	890	0.0023224	84033 obscurin, cytoskeletal calmodulin and titin-interacting RhoGEF
GO multicellular organismal developmen	83	890	0.0023224	8527 diacylglycerol kinase, delta 130kDa
GO multicellular organismal developmen	83	890	0.0023224	85416 Zic family member 5 (odd-paired homolog, Drosophila)
GO multicellular organismal developmen	83	890	0.0023224	8600 tumor necrosis factor (ligand) superfamily, member 11
GO multicellular organismal developmen	83	890	0.0023224	91461 protein kinase domain containing, cytoplasmic homolog (mouse)
GO multicellular organismal developmen	83	890	0.0023224	9271 piwi-like 1 (Drosophila)
GO multicellular organismal developmen	83	890	0.0023224	9435 carbohydrate (N-acetylglucosamine-6-O) sulfotransferase 2
GO multicellular organismal developmen	83	890	0.0023224	9496 T-box 4
GO multicellular organismal developmen	83	890	0.0023224	9633 metallothionein-like 5, testis-specific (tesmin)
GO multicellular organismal developmen	83	890	0.0023224	9904 RNA binding motif protein 19
GO filopodium assembly	5	15	0.0024909	152273 FYVE, RhoGEF and PH domain containing 5
GO filopodium assembly	5	15	0.0024909	23092 Rho GTPase activating protein 26
GO filopodium assembly	5	15	0.0024909	3691 integrin, beta 4
GO filopodium assembly	5	15	0.0024909	80115 BAI1-associated protein 2-like 2
GO filopodium assembly	5	15	0.0024909	9788 metastasis suppressor 1
GO cell adhesion	53	522	0.0025144	1004 cadherin 6, type 2, K-cadherin (fetal kidney)
GO cell adhesion	53	522	0.0025144	10076 protein tyrosine phosphatase, receptor type, U
GO cell adhesion	53	522	0.0025144	10085 EGF-like repeats and discoidin I-like domains 3
GO cell adhesion	53	522	0.0025144	1009 cadherin 11, type 2, OB-cadherin (osteoblast)
GO cell adhesion	53	522	0.0025144	1014 cadherin 16, KSP-cadherin

GO cell adhesion	53	522	0.0025144	1016 cadherin 18, type 2
GO cell adhesion	53	522	0.0025144	10205 myelin protein zero-like 2
GO cell adhesion	53	522	0.0025144	10417 spondin 2, extracellular matrix protein
GO cell adhesion	53	522	0.0025144	10418 spondin 1, extracellular matrix protein
GO cell adhesion	53	522	0.0025144	10507 sema domain, immunoglobulin domain (Ig), transmembrane domain (T
GO cell adhesion	53	522	0.0025144	10516 fibulin 5
GO cell adhesion	53	522	0.0025144	10752 cell adhesion molecule with homology to L1CAM (close homolog of L1)
GO cell adhesion	53	522	0.0025144	11187 plakophilin 3
GO cell adhesion	53	522	0.0025144	1295 collagen, type VIII, alpha 1
GO cell adhesion	53	522	0.0025144	1462 versican
GO cell adhesion	53	522	0.0025144	1803 dipeptidyl-peptidase 4
GO cell adhesion	53	522	0.0025144	1901 sphingosine-1-phosphate receptor 1
GO cell adhesion	53	522	0.0025144	2015 egf-like module containing, mucin-like, hormone receptor-like 1
GO cell adhesion	53	522	0.0025144	2153 coagulation factor V (proaccelerin, labile factor)
GO cell adhesion	53	522	0.0025144	22795 nidogen 2 (osteonidogen)
GO cell adhesion	53	522	0.0025144	22915 multimerin 1
GO cell adhesion	53	522	0.0025144	23145 SCO-spondin homolog (Bos taurus)
GO cell adhesion	53	522	0.0025144	23767 fibronectin leucine rich transmembrane protein 3
GO cell adhesion	53	522	0.0025144	255743 nephronectin
GO cell adhesion	53	522	0.0025144	285704 RGM domain family, member B
GO cell adhesion	53	522	0.0025144	3491 cysteine-rich, angiogenic inducer, 61
GO cell adhesion	53	522	0.0025144	3678 integrin, alpha 5 (fibronectin receptor, alpha polypeptide)
GO cell adhesion	53	522	0.0025144	3687 integrin, alpha X (complement component 3 receptor 4 subunit)
GO cell adhesion	53	522	0.0025144	3689 integrin, beta 2 (complement component 3 receptor 3 and 4 subunit)
GO cell adhesion	53	522	0.0025144	3691 integrin, beta 4
GO cell adhesion	53	522	0.0025144	3696 integrin, beta 8
GO cell adhesion	53	522	0.0025144	3913 laminin, beta 2 (laminin 5)
GO cell adhesion	53	522	0.0025144	3914 laminin, beta 3
GO cell adhesion	53	522	0.0025144	3959 lectin, galactoside-binding, soluble, 3 binding protein
GO cell adhesion	53	522	0.0025144	4254 KIT ligand
GO cell adhesion	53	522	0.0025144	4586 mucin 5AC, oligomeric mucus/gel-forming
GO cell adhesion	53	522	0.0025144	4684 neural cell adhesion molecule 1
GO cell adhesion	53	522	0.0025144	50937 Cdon homolog (mouse)
GO cell adhesion	53	522	0.0025144	5099 protocadherin 7
GO cell adhesion	53	522	0.0025144	51754 transmembrane protein 8B
GO cell adhesion	53	522	0.0025144	5239 phosphoglucomutase 5

GO cell adhesion	53	522	0.0025144	57453 Down syndrome cell adhesion molecule like 1
GO cell adhesion	53	522	0.0025144	57863 cell adhesion molecule 3
GO cell adhesion	53	522	0.0025144	6402 selectin L
GO cell adhesion	53	522	0.0025144	79987 sushi, von Willebrand factor type A, EGF and pentraxin domain contain
GO cell adhesion	53	522	0.0025144	8082 sarcospan (Kras oncogene-associated gene)
GO cell adhesion	53	522	0.0025144	8406 sushi-repeat-containing protein, X-linked
GO cell adhesion	53	522	0.0025144	8839 WNT1 inducible signaling pathway protein 2
GO cell adhesion	53	522	0.0025144	9071 claudin 10
GO cell adhesion	53	522	0.0025144	91653 Boc homolog (mouse)
GO cell adhesion	53	522	0.0025144	94025 mucin 16, cell surface associated
GO cell adhesion	53	522	0.0025144	961 CD47 molecule
GO cell adhesion	53	522	0.0025144	9788 metastasis suppressor 1
GO scavenger receptor activity	9	44	0.0025403	10216 proteoglycan 4
GO scavenger receptor activity	9	44	0.0025403	157869 chromosome 8 open reading frame 84
GO scavenger receptor activity	9	44	0.0025403	1755 deleted in malignant brain tumors 1
GO scavenger receptor activity	9	44	0.0025403	283316 CD163 molecule-like 1
GO scavenger receptor activity	9	44	0.0025403	286133 scavenger receptor class A, member 5 (putative)
GO scavenger receptor activity	9	44	0.0025403	3959 lectin, galactoside-binding, soluble, 3 binding protein
GO scavenger receptor activity	9	44	0.0025403	56649 transmembrane protease, serine 4
GO scavenger receptor activity	9	44	0.0025403	64699 transmembrane protease, serine 3
GO scavenger receptor activity	9	44	0.0025403	84171 lysyl oxidase-like 4
GO negative regulation of nerve growth f	3	5	0.0028689	10252 sprouty homolog 1, antagonist of FGF signaling (Drosophila)
GO negative regulation of nerve growth f	3	5	0.0028689	10253 sprouty homolog 2 (Drosophila)
GO negative regulation of nerve growth f	3	5	0.0028689	183 angiotensinogen (serpin peptidase inhibitor, clade A, member 8)
GO insulin binding	3	5	0.0028689	3643 insulin receptor
GO insulin binding	3	5	0.0028689	5122 proprotein convertase subtilisin/kexin type 1
GO insulin binding	3	5	0.0028689	5295 phosphoinositide-3-kinase, regulatory subunit 1 (alpha)
GO placenta blood vessel development	3	5	0.0028689	3696 integrin, beta 8
GO placenta blood vessel development	3	5	0.0028689	6692 serine peptidase inhibitor, Kunitz type 1
GO placenta blood vessel development	3	5	0.0028689	9021 suppressor of cytokine signaling 3
GO lipopolysaccharide receptor activity	3	5	0.0028689	5724 platelet-activating factor receptor
GO lipopolysaccharide receptor activity	3	5	0.0028689	7097 toll-like receptor 2
GO lipopolysaccharide receptor activity	3	5	0.0028689	7099 toll-like receptor 4
GO regulation of transcription, DNA-depe	92	1013	0.0030092	10346 tripartite motif-containing 22
GO regulation of transcription, DNA-depe	92	1013	0.0030092	10481 homeobox B13
GO regulation of transcription, DNA-depe	92	1013	0.0030092	10838 zinc finger protein 275



GO	regulation of transcription, DNA-depe	92	1013	0.0030092	115196 zinc finger protein 554
GO	regulation of transcription, DNA-depe	92	1013	0.0030092	116071 basic leucine zipper transcription factor, ATF-like 2
GO	regulation of transcription, DNA-depe	92	1013	0.0030092	116113 forkhead box P4
GO	regulation of transcription, DNA-depe	92	1013	0.0030092	127343 diencephalon/mesencephalon homeobox 1
GO	regulation of transcription, DNA-depe	92	1013	0.0030092	1382 cellular retinoic acid binding protein 2
GO	regulation of transcription, DNA-depe	92	1013	0.0030092	147694 zinc finger protein 548
GO	regulation of transcription, DNA-depe	92	1013	0.0030092	147923 zinc finger protein 420
GO	regulation of transcription, DNA-depe	92	1013	0.0030092	158800 Rhox homeobox family, member 1
GO	regulation of transcription, DNA-depe	92	1013	0.0030092	162962 zinc finger protein 836
GO	regulation of transcription, DNA-depe	92	1013	0.0030092	163050 zinc finger protein 564
GO	regulation of transcription, DNA-depe	92	1013	0.0030092	1820 AT rich interactive domain 3A (BRIGHT-like)
GO	regulation of transcription, DNA-depe	92	1013	0.0030092	1959 early growth response 2
GO	regulation of transcription, DNA-depe	92	1013	0.0030092	1999 E74-like factor 3 (ets domain transcription factor, epithelial-specific )
GO	regulation of transcription, DNA-depe	92	1013	0.0030092	2115 ets variant 1
GO	regulation of transcription, DNA-depe	92	1013	0.0030092	2117 ets variant 3
GO	regulation of transcription, DNA-depe	92	1013	0.0030092	222546 regulatory factor X, 6
GO	regulation of transcription, DNA-depe	92	1013	0.0030092	2290 forkhead box G1
GO	regulation of transcription, DNA-depe	92	1013	0.0030092	2296 forkhead box C1
GO	regulation of transcription, DNA-depe	92	1013	0.0030092	2306 forkhead box D2
GO	regulation of transcription, DNA-depe	92	1013	0.0030092	2354 FBJ murine osteosarcoma viral oncogene homolog B
GO	regulation of transcription, DNA-depe	92	1013	0.0030092	256051 zinc finger protein 549
GO	regulation of transcription, DNA-depe	92	1013	0.0030092	2624 GATA binding protein 2
GO	regulation of transcription, DNA-depe	92	1013	0.0030092	26468 LIM homeobox 6
GO	regulation of transcription, DNA-depe	92	1013	0.0030092	3131 hepatic leukemia factor
GO	regulation of transcription, DNA-depe	92	1013	0.0030092	3142 H2.0-like homeobox
GO	regulation of transcription, DNA-depe	92	1013	0.0030092	3164 nuclear receptor subfamily 4, group A, member 1
GO	regulation of transcription, DNA-depe	92	1013	0.0030092	3169 forkhead box A1
GO	regulation of transcription, DNA-depe	92	1013	0.0030092	3175 one cut homeobox 1
GO	regulation of transcription, DNA-depe	92	1013	0.0030092	3428 interferon, gamma-inducible protein 16
GO	regulation of transcription, DNA-depe	92	1013	0.0030092	342908 zinc finger protein 404
GO	regulation of transcription, DNA-depe	92	1013	0.0030092	345462 zinc finger protein 879
GO	regulation of transcription, DNA-depe	92	1013	0.0030092	3665 interferon regulatory factor 7
GO	regulation of transcription, DNA-depe	92	1013	0.0030092	3725 jun oncogene
GO	regulation of transcription, DNA-depe	92	1013	0.0030092	388536 zinc finger protein 790
GO	regulation of transcription, DNA-depe	92	1013	0.0030092	388558 zinc finger protein 808
GO	regulation of transcription, DNA-depe	92	1013	0.0030092	400713 zinc finger protein 880

GO	regulation of transcription, DNA-depe	92	1013	0.0030092	4209	myocyte enhancer factor 2D
GO	regulation of transcription, DNA-depe	92	1013	0.0030092	4212	Meis homeobox 2
GO	regulation of transcription, DNA-depe	92	1013	0.0030092	4223	mesenchyme homeobox 2
GO	regulation of transcription, DNA-depe	92	1013	0.0030092	4286	microphthalmia-associated transcription factor
GO	regulation of transcription, DNA-depe	92	1013	0.0030092	4306	nuclear receptor subfamily 3, group C, member 2
GO	regulation of transcription, DNA-depe	92	1013	0.0030092	467	activating transcription factor 3
GO	regulation of transcription, DNA-depe	92	1013	0.0030092	4692	necdin homolog (mouse)
GO	regulation of transcription, DNA-depe	92	1013	0.0030092	4783	nuclear factor, interleukin 3 regulated
GO	regulation of transcription, DNA-depe	92	1013	0.0030092	4784	nuclear factor I/X (CCAAT-binding transcription factor)
GO	regulation of transcription, DNA-depe	92	1013	0.0030092	4791	nuclear factor of kappa light polypeptide gene enhancer in B-cells 2 (p4
GO	regulation of transcription, DNA-depe	92	1013	0.0030092	4802	nuclear transcription factor Y, gamma
GO	regulation of transcription, DNA-depe	92	1013	0.0030092	4853	Notch homolog 2 (Drosophila)
GO	regulation of transcription, DNA-depe	92	1013	0.0030092	4929	nuclear receptor subfamily 4, group A, member 2
GO	regulation of transcription, DNA-depe	92	1013	0.0030092	5083	paired box 9
GO	regulation of transcription, DNA-depe	92	1013	0.0030092	51085	MLX interacting protein-like
GO	regulation of transcription, DNA-depe	92	1013	0.0030092	51710	zinc finger protein 44
GO	regulation of transcription, DNA-depe	92	1013	0.0030092	5187	period homolog 1 (Drosophila)
GO	regulation of transcription, DNA-depe	92	1013	0.0030092	5307	paired-like homeodomain 1
GO	regulation of transcription, DNA-depe	92	1013	0.0030092	5308	paired-like homeodomain 2
GO	regulation of transcription, DNA-depe	92	1013	0.0030092	5396	paired related homeobox 1
GO	regulation of transcription, DNA-depe	92	1013	0.0030092	5460	POU class 5 homeobox 1
GO	regulation of transcription, DNA-depe	92	1013	0.0030092	5463	POU class 6 homeobox 1
GO	regulation of transcription, DNA-depe	92	1013	0.0030092	5465	peroxisome proliferator-activated receptor alpha
GO	regulation of transcription, DNA-depe	92	1013	0.0030092	55762	zinc finger protein 701
GO	regulation of transcription, DNA-depe	92	1013	0.0030092	55769	zinc finger protein 83
GO	regulation of transcription, DNA-depe	92	1013	0.0030092	55810	forkhead box J2
GO	regulation of transcription, DNA-depe	92	1013	0.0030092	55893	zinc finger protein 395
GO	regulation of transcription, DNA-depe	92	1013	0.0030092	57459	GATA zinc finger domain containing 2B
GO	regulation of transcription, DNA-depe	92	1013	0.0030092	57594	homeobox and leucine zipper encoding
GO	regulation of transcription, DNA-depe	92	1013	0.0030092	6096	RAR-related orphan receptor B
GO	regulation of transcription, DNA-depe	92	1013	0.0030092	6097	RAR-related orphan receptor C
GO	regulation of transcription, DNA-depe	92	1013	0.0030092	6239	ras responsive element binding protein 1
GO	regulation of transcription, DNA-depe	92	1013	0.0030092	64651	cysteine-serine-rich nuclear protein 1
GO	regulation of transcription, DNA-depe	92	1013	0.0030092	7090	transducin-like enhancer of split 3 (E(sp1) homolog, Drosophila)
GO	regulation of transcription, DNA-depe	92	1013	0.0030092	7565	zinc finger protein 17
GO	regulation of transcription, DNA-depe	92	1013	0.0030092	7678	zinc finger protein 124

GO	regulation of transcription, DNA-depe	92	1013	0.0030092	8013 nuclear receptor subfamily 4, group A, member 3
GO	regulation of transcription, DNA-depe	92	1013	0.0030092	80714 pre-B-cell leukemia homeobox 4
GO	regulation of transcription, DNA-depe	92	1013	0.0030092	84124 zinc finger protein 394
GO	regulation of transcription, DNA-depe	92	1013	0.0030092	84911 zinc finger protein 382
GO	regulation of transcription, DNA-depe	92	1013	0.0030092	8531 cold shock domain protein A
GO	regulation of transcription, DNA-depe	92	1013	0.0030092	8553 basic helix-loop-helix family, member e40
GO	regulation of transcription, DNA-depe	92	1013	0.0030092	862 runt-related transcription factor 1; translocated to, 1 (cyclin D-related)
GO	regulation of transcription, DNA-depe	92	1013	0.0030092	8622 phosphodiesterase 8B
GO	regulation of transcription, DNA-depe	92	1013	0.0030092	8848 TSC22 domain family, member 1
GO	regulation of transcription, DNA-depe	92	1013	0.0030092	8863 period homolog 3 (Drosophila)
GO	regulation of transcription, DNA-depe	92	1013	0.0030092	8864 period homolog 2 (Drosophila)
GO	regulation of transcription, DNA-depe	92	1013	0.0030092	90592 zinc finger protein 700
GO	regulation of transcription, DNA-depe	92	1013	0.0030092	90993 cAMP responsive element binding protein 3-like 1
GO	regulation of transcription, DNA-depe	92	1013	0.0030092	92283 zinc finger protein 461
GO	regulation of transcription, DNA-depe	92	1013	0.0030092	9422 zinc finger protein 264
GO	regulation of transcription, DNA-depe	92	1013	0.0030092	9496 T-box 4
GO	regulation of transcription, DNA-depe	92	1013	0.0030092	9572 nuclear receptor subfamily 1, group D, member 1
GO	response to drug	27	225	0.0031121	10628 thioredoxin interacting protein
GO	response to drug	27	225	0.0031121	1080 cystic fibrosis transmembrane conductance regulator (ATP-binding cas:
GO	response to drug	27	225	0.0031121	123 perilipin 2
GO	response to drug	27	225	0.0031121	1373 carbamoyl-phosphate synthetase 1, mitochondrial
GO	response to drug	27	225	0.0031121	1813 dopamine receptor D2
GO	response to drug	27	225	0.0031121	2026 enolase 2 (gamma, neuronal)
GO	response to drug	27	225	0.0031121	2033 E1A binding protein p300
GO	response to drug	27	225	0.0031121	2066 v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian)
GO	response to drug	27	225	0.0031121	2353 FBJ murine osteosarcoma viral oncogene homolog
GO	response to drug	27	225	0.0031121	2564 gamma-aminobutyric acid (GABA) A receptor, epsilon
GO	response to drug	27	225	0.0031121	358 aquaporin 1 (Colton blood group)
GO	response to drug	27	225	0.0031121	368 ATP-binding cassette, sub-family C (CFTR/MRP), member 6
GO	response to drug	27	225	0.0031121	3725 jun oncogene
GO	response to drug	27	225	0.0031121	3726 jun B proto-oncogene
GO	response to drug	27	225	0.0031121	4015 lysyl oxidase
GO	response to drug	27	225	0.0031121	4056 leukotriene C4 synthase
GO	response to drug	27	225	0.0031121	4129 monoamine oxidase B
GO	response to drug	27	225	0.0031121	5122 proprotein convertase subtilisin/kexin type 1
GO	response to drug	27	225	0.0031121	5243 ATP-binding cassette, sub-family B (MDR/TAP), member 1

GO response to drug	27	225	0.0031121	5244 ATP-binding cassette, sub-family B (MDR/TAP), member 4
GO response to drug	27	225	0.0031121	5608 mitogen-activated protein kinase kinase 6
GO response to drug	27	225	0.0031121	5972 renin
GO response to drug	27	225	0.0031121	627 brain-derived neurotrophic factor
GO response to drug	27	225	0.0031121	6622 synuclein, alpha (non A4 component of amyloid precursor)
GO response to drug	27	225	0.0031121	6750 somatostatin
GO response to drug	27	225	0.0031121	834 caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, co
GO response to drug	27	225	0.0031121	9021 suppressor of cytokine signaling 3
GO positive regulation of Ras protein sigl	4	10	0.0032664	1435 colony stimulating factor 1 (macrophage)
GO positive regulation of Ras protein sigl	4	10	0.0032664	3479 insulin-like growth factor 1 (somatomedin C)
GO positive regulation of Ras protein sigl	4	10	0.0032664	4254 KIT ligand
GO positive regulation of Ras protein sigl	4	10	0.0032664	4853 Notch homolog 2 (Drosophila)
GO receptor signaling protein tyrosine ki	4	10	0.0032664	2066 v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian)
GO receptor signaling protein tyrosine ki	4	10	0.0032664	3643 insulin receptor
GO receptor signaling protein tyrosine ki	4	10	0.0032664	3815 v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog
GO receptor signaling protein tyrosine ki	4	10	0.0032664	6850 spleen tyrosine kinase
GO positive regulation of tyrosine phospl	4	10	0.0032664	23529 cardiotrophin-like cytokine factor 1
GO positive regulation of tyrosine phospl	4	10	0.0032664	3569 interleukin 6 (interferon, beta 2)
GO positive regulation of tyrosine phospl	4	10	0.0032664	3570 interleukin 6 receptor
GO positive regulation of tyrosine phospl	4	10	0.0032664	50604 interleukin 20
GO positive regulation of interleukin-8 pr	4	10	0.0032664	7097 toll-like receptor 2
GO positive regulation of interleukin-8 pr	4	10	0.0032664	7098 toll-like receptor 3
GO positive regulation of interleukin-8 pr	4	10	0.0032664	7099 toll-like receptor 4
GO positive regulation of interleukin-8 pr	4	10	0.0032664	7100 toll-like receptor 5
GO response to cAMP	9	46	0.0034918	1373 carbamoyl-phosphate synthetase 1, mitochondrial
GO response to cAMP	9	46	0.0034918	1843 dual specificity phosphatase 1
GO response to cAMP	9	46	0.0034918	2353 FBJ murine osteosarcoma viral oncogene homolog
GO response to cAMP	9	46	0.0034918	3570 interleukin 6 receptor
GO response to cAMP	9	46	0.0034918	3725 jun oncogene
GO response to cAMP	9	46	0.0034918	3726 jun B proto-oncogene
GO response to cAMP	9	46	0.0034918	5327 plasminogen activator, tissue
GO response to cAMP	9	46	0.0034918	5972 renin
GO response to cAMP	9	46	0.0034918	682 basigin (Ok blood group)
GO potassium channel regulator activity	6	23	0.0037057	10008 potassium voltage-gated channel, Isk-related family, member 3
GO potassium channel regulator activity	6	23	0.0037057	154 adrenergic, beta-2-, receptor, surface
GO potassium channel regulator activity	6	23	0.0037057	1813 dopamine receptor D2

GO potassium channel regulator activity	6	23	0.0037057	1815 dopamine receptor D4
GO potassium channel regulator activity	6	23	0.0037057	3790 potassium voltage-gated channel, delayed-rectifier, subfamily S, memb
GO potassium channel regulator activity	6	23	0.0037057	8514 potassium voltage-gated channel, shaker-related subfamily, beta mem
GO odontogenesis	6	23	0.0037057	10117 enamelin
GO odontogenesis	6	23	0.0037057	1435 colony stimulating factor 1 (macrophage)
GO odontogenesis	6	23	0.0037057	2066 v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian)
GO odontogenesis	6	23	0.0037057	2331 fibromodulin
GO odontogenesis	6	23	0.0037057	358 aquaporin 1 (Colton blood group)
GO odontogenesis	6	23	0.0037057	652 bone morphogenetic protein 4
GO regulation of cell proliferation	12	73	0.0037325	10628 thioredoxin interacting protein
GO regulation of cell proliferation	12	73	0.0037325	1628 D site of albumin promoter (albumin D-box) binding protein
GO regulation of cell proliferation	12	73	0.0037325	183 angiotensinogen (serpin peptidase inhibitor, clade A, member 8)
GO regulation of cell proliferation	12	73	0.0037325	3911 laminin, alpha 5
GO regulation of cell proliferation	12	73	0.0037325	4286 microphthalmia-associated transcription factor
GO regulation of cell proliferation	12	73	0.0037325	4316 matrix metalloproteinase 7 (matrilysin, uterine)
GO regulation of cell proliferation	12	73	0.0037325	4792 nuclear factor of kappa light polypeptide gene enhancer in B-cells inhib
GO regulation of cell proliferation	12	73	0.0037325	5732 prostaglandin E receptor 2 (subtype EP2), 53kDa
GO regulation of cell proliferation	12	73	0.0037325	5742 prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase a
GO regulation of cell proliferation	12	73	0.0037325	6778 signal transducer and activator of transcription 6, interleukin-4 inducec
GO regulation of cell proliferation	12	73	0.0037325	8744 tumor necrosis factor (ligand) superfamily, member 9
GO regulation of cell proliferation	12	73	0.0037325	92304 secretoglobulin, family 3A, member 1
GO response to organic cyclic substance	14	92	0.0037721	123 perilipin 2
GO response to organic cyclic substance	14	92	0.0037721	1508 cathepsin B
GO response to organic cyclic substance	14	92	0.0037721	2026 enolase 2 (gamma, neuronal)
GO response to organic cyclic substance	14	92	0.0037721	2033 E1A binding protein p300
GO response to organic cyclic substance	14	92	0.0037721	205 adenylate kinase 3-like 1
GO response to organic cyclic substance	14	92	0.0037721	2353 FBJ murine osteosarcoma viral oncogene homolog
GO response to organic cyclic substance	14	92	0.0037721	3725 jun oncogene
GO response to organic cyclic substance	14	92	0.0037721	3726 jun B proto-oncogene
GO response to organic cyclic substance	14	92	0.0037721	412 steroid sulfatase (microsomal), isozyme S
GO response to organic cyclic substance	14	92	0.0037721	5122 proprotein convertase subtilisin/kexin type 1
GO response to organic cyclic substance	14	92	0.0037721	6256 retinoid X receptor, alpha
GO response to organic cyclic substance	14	92	0.0037721	652 bone morphogenetic protein 4
GO response to organic cyclic substance	14	92	0.0037721	834 caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, co
GO response to organic cyclic substance	14	92	0.0037721	9021 suppressor of cytokine signaling 3
GO membrane raft	15	103	0.0042491	112 adenylate cyclase 6

GO membrane raft	15	103	0.0042491	1604 CD55 molecule, decay accelerating factor for complement (Cromer blo
GO membrane raft	15	103	0.0042491	1803 dipeptidyl-peptidase 4
GO membrane raft	15	103	0.0042491	2040 stomatin
GO membrane raft	15	103	0.0042491	285704 RGM domain family, member B
GO membrane raft	15	103	0.0042491	3845 v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog
GO membrane raft	15	103	0.0042491	55600 intelectin 1 (galactofuranose binding)
GO membrane raft	15	103	0.0042491	5577 protein kinase, cAMP-dependent, regulatory, type II, beta
GO membrane raft	15	103	0.0042491	55824 phosphoprotein associated with glycosphingolipid microdomains 1
GO membrane raft	15	103	0.0042491	6004 regulator of G-protein signaling 16
GO membrane raft	15	103	0.0042491	682 basigin (Ok blood group)
GO membrane raft	15	103	0.0042491	7099 toll-like receptor 4
GO membrane raft	15	103	0.0042491	7133 tumor necrosis factor receptor superfamily, member 1B
GO membrane raft	15	103	0.0042491	79180 EF-hand domain family, member D2
GO membrane raft	15	103	0.0042491	929 CD14 molecule
GO regulation of long-term neuronal syn	5	17	0.004577	1813 dopamine receptor D2
GO regulation of long-term neuronal syn	5	17	0.004577	183 angiotensinogen (serpin peptidase inhibitor, clade A, member 8)
GO regulation of long-term neuronal syn	5	17	0.004577	1958 early growth response 1
GO regulation of long-term neuronal syn	5	17	0.004577	3845 v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog
GO regulation of long-term neuronal syn	5	17	0.004577	6622 synuclein, alpha (non A4 component of amyloid precursor)
GO negative regulation of Ras GTPase ac	2	2	0.0046681	10252 sprouty homolog 1, antagonist of FGF signaling (Drosophila)
GO negative regulation of Ras GTPase ac	2	2	0.0046681	10253 sprouty homolog 2 (Drosophila)
GO bud elongation involved in lung bran	2	2	0.0046681	157506 retinol dehydrogenase 10 (all-trans)
GO bud elongation involved in lung bran	2	2	0.0046681	652 bone morphogenetic protein 4
GO blood vessel endothelial cell prolifera	2	2	0.0046681	168667 BMP binding endothelial regulator
GO blood vessel endothelial cell prolifera	2	2	0.0046681	652 bone morphogenetic protein 4
GO positive regulation of dopamine upta	2	2	0.0046681	1813 dopamine receptor D2
GO positive regulation of dopamine upta	2	2	0.0046681	1815 dopamine receptor D4
GO establishment of blood-nerve barrier	2	2	0.0046681	183 angiotensinogen (serpin peptidase inhibitor, clade A, member 8)
GO establishment of blood-nerve barrier	2	2	0.0046681	2947 glutathione S-transferase mu 3 (brain)
GO lymph vessel development	2	2	0.0046681	1948 ephrin-B2
GO lymph vessel development	2	2	0.0046681	2296 forkhead box C1
GO positive regulation of glycoprotein bi	2	2	0.0046681	2033 E1A binding protein p300
GO positive regulation of glycoprotein bi	2	2	0.0046681	3643 insulin receptor
GO positive regulation of interleukin-3 bi	2	2	0.0046681	2205 Fc fragment of IgE, high affinity I, receptor for; alpha polypeptide
GO positive regulation of interleukin-3 bi	2	2	0.0046681	6850 spleen tyrosine kinase
GO serotonin secretion	2	2	0.0046681	2205 Fc fragment of IgE, high affinity I, receptor for; alpha polypeptide

GO	serotonin secretion	2	2	0.0046681	6850 spleen tyrosine kinase
GO	Ral guanyl-nucleotide exchange factc	2	2	0.0046681	23179 ral guanine nucleotide dissociation stimulator-like 1
GO	Ral guanyl-nucleotide exchange factc	2	2	0.0046681	57139 ral guanine nucleotide dissociation stimulator-like 3
GO	regulation of low-density lipoprotein	2	2	0.0046681	255738 proprotein convertase subtilisin/kexin type 9
GO	regulation of low-density lipoprotein	2	2	0.0046681	29116 myosin regulatory light chain interacting protein
GO	prostate gland stromal morphogenes	2	2	0.0046681	3169 forkhead box A1
GO	prostate gland stromal morphogenes	2	2	0.0046681	3479 insulin-like growth factor 1 (somatomedin C)
GO	hepatic immune response	2	2	0.0046681	3569 interleukin 6 (interferon, beta 2)
GO	hepatic immune response	2	2	0.0046681	3570 interleukin 6 receptor
GO	response to iron(II) ion	2	2	0.0046681	48 aconitase 1, soluble
GO	response to iron(II) ion	2	2	0.0046681	6622 synuclein, alpha (non A4 component of amyloid precursor)
GO	axon target recognition	2	2	0.0046681	627 brain-derived neurotrophic factor
GO	axon target recognition	2	2	0.0046681	6812 syntaxin binding protein 1
GO	RNA destabilization	2	2	0.0046681	7133 tumor necrosis factor receptor superfamily, member 1B
GO	RNA destabilization	2	2	0.0046681	7538 zinc finger protein 36, C3H type, homolog (mouse)
GO	response to exogenous dsRNA	4	11	0.0048571	11213 interleukin-1 receptor-associated kinase 3
GO	response to exogenous dsRNA	4	11	0.0048571	4792 nuclear factor of kappa light polypeptide gene enhancer in B-cells inhib
GO	response to exogenous dsRNA	4	11	0.0048571	64127 nucleotide-binding oligomerization domain containing 2
GO	response to exogenous dsRNA	4	11	0.0048571	7098 toll-like receptor 3
GO	neural crest cell development	4	11	0.0048571	157506 retinol dehydrogenase 10 (all-trans)
GO	neural crest cell development	4	11	0.0048571	1906 endothelin 1
GO	neural crest cell development	4	11	0.0048571	2296 forkhead box C1
GO	neural crest cell development	4	11	0.0048571	2303 forkhead box C2 (MFH-1, mesenchyme forkhead 1)
GO	cell fate determination	4	11	0.0048571	2624 GATA binding protein 2
GO	cell fate determination	4	11	0.0048571	4170 myeloid cell leukemia sequence 1 (BCL2-related)
GO	cell fate determination	4	11	0.0048571	4853 Notch homolog 2 (Drosophila)
GO	cell fate determination	4	11	0.0048571	57453 Down syndrome cell adhesion molecule like 1
GO	myoblast fusion	4	11	0.0048571	4842 nitric oxide synthase 1 (neuronal)
GO	myoblast fusion	4	11	0.0048571	50937 Cdon homolog (mouse)
GO	myoblast fusion	4	11	0.0048571	834 caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, co
GO	myoblast fusion	4	11	0.0048571	8912 calcium channel, voltage-dependent, T type, alpha 1H subunit
GO	proteinaceous extracellular matrix	26	223	0.0053803	10117 enamelin
GO	proteinaceous extracellular matrix	26	223	0.0053803	10417 spondin 2, extracellular matrix protein
GO	proteinaceous extracellular matrix	26	223	0.0053803	10418 spondin 1, extracellular matrix protein
GO	proteinaceous extracellular matrix	26	223	0.0053803	10516 fibulin 5
GO	proteinaceous extracellular matrix	26	223	0.0053803	10752 cell adhesion molecule with homology to L1CAM (close homolog of L1)

GO	proteinaceous extracellular matrix	26	223	0.0053803	126638	repetin
GO	proteinaceous extracellular matrix	26	223	0.0053803	1462	versican
GO	proteinaceous extracellular matrix	26	223	0.0053803	170692	ADAM metallopeptidase with thrombospondin type 1 motif, 18
GO	proteinaceous extracellular matrix	26	223	0.0053803	2200	fibrillin 1
GO	proteinaceous extracellular matrix	26	223	0.0053803	2201	fibrillin 2
GO	proteinaceous extracellular matrix	26	223	0.0053803	2239	glypican 4
GO	proteinaceous extracellular matrix	26	223	0.0053803	2262	glypican 5
GO	proteinaceous extracellular matrix	26	223	0.0053803	2331	fibromodulin
GO	proteinaceous extracellular matrix	26	223	0.0053803	23767	fibronectin leucine rich transmembrane protein 3
GO	proteinaceous extracellular matrix	26	223	0.0053803	255743	nephronectin
GO	proteinaceous extracellular matrix	26	223	0.0053803	3958	lectin, galactoside-binding, soluble, 3
GO	proteinaceous extracellular matrix	26	223	0.0053803	3959	lectin, galactoside-binding, soluble, 3 binding protein
GO	proteinaceous extracellular matrix	26	223	0.0053803	4316	matrix metallopeptidase 7 (matrilysin, uterine)
GO	proteinaceous extracellular matrix	26	223	0.0053803	50859	sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican)
GO	proteinaceous extracellular matrix	26	223	0.0053803	54361	wingless-type MMTV integration site family, member 4
GO	proteinaceous extracellular matrix	26	223	0.0053803	56547	matrix metallopeptidase 26
GO	proteinaceous extracellular matrix	26	223	0.0053803	652	bone morphogenetic protein 4
GO	proteinaceous extracellular matrix	26	223	0.0053803	7076	TIMP metallopeptidase inhibitor 1
GO	proteinaceous extracellular matrix	26	223	0.0053803	7474	wingless-type MMTV integration site family, member 5A
GO	proteinaceous extracellular matrix	26	223	0.0053803	7477	wingless-type MMTV integration site family, member 7B
GO	proteinaceous extracellular matrix	26	223	0.0053803	8076	microfibrillar associated protein 5
GO	regulation of blood pressure	9	49	0.005419	183	angiotensinogen (serpin peptidase inhibitor, clade A, member 8)
GO	regulation of blood pressure	9	49	0.005419	1906	endothelin 1
GO	regulation of blood pressure	9	49	0.005419	2642	glucagon receptor
GO	regulation of blood pressure	9	49	0.005419	27035	NADPH oxidase 1
GO	regulation of blood pressure	9	49	0.005419	4886	neuropeptide Y receptor Y1
GO	regulation of blood pressure	9	49	0.005419	5025	purinergic receptor P2X, ligand-gated ion channel, 4
GO	regulation of blood pressure	9	49	0.005419	5742	prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and
GO	regulation of blood pressure	9	49	0.005419	5972	renin
GO	regulation of blood pressure	9	49	0.005419	94	activin A receptor type II-like 1
GO	regulation of hydrogen peroxide met	3	6	0.0054465	10811	NADPH oxidase activator 1
GO	regulation of hydrogen peroxide met	3	6	0.0054465	3643	insulin receptor
GO	regulation of hydrogen peroxide met	3	6	0.0054465	7001	peroxiredoxin 2
GO	response to peptidoglycan	3	6	0.0054465	11213	interleukin-1 receptor-associated kinase 3
GO	response to peptidoglycan	3	6	0.0054465	3569	interleukin 6 (interferon, beta 2)
GO	response to peptidoglycan	3	6	0.0054465	7097	toll-like receptor 2



GO positive regulation of organ growth	3	6	0.0054465	183 angiotensinogen (serpin peptidase inhibitor, clade A, member 8)
GO positive regulation of organ growth	3	6	0.0054465	3142 H2.0-like homeobox
GO positive regulation of organ growth	3	6	0.0054465	8531 cold shock domain protein A
GO chromatin DNA binding	3	6	0.0054465	2303 forkhead box C2 (MFH-1, mesenchyme forkhead 1)
GO chromatin DNA binding	3	6	0.0054465	4851 Notch homolog 1, translocation-associated (Drosophila)
GO chromatin DNA binding	3	6	0.0054465	604 B-cell CLL/lymphoma 6
GO insulin-like growth factor I binding	3	6	0.0054465	3486 insulin-like growth factor binding protein 3
GO insulin-like growth factor I binding	3	6	0.0054465	3488 insulin-like growth factor binding protein 5
GO insulin-like growth factor I binding	3	6	0.0054465	3643 insulin receptor
GO lipid binding	16	116	0.0055177	1382 cellular retinoic acid binding protein 2
GO lipid binding	16	116	0.0055177	23048 formin binding protein 1
GO lipid binding	16	116	0.0055177	23780 apolipoprotein L, 2
GO lipid binding	16	116	0.0055177	2865 free fatty acid receptor 3
GO lipid binding	16	116	0.0055177	2867 free fatty acid receptor 2
GO lipid binding	16	116	0.0055177	4056 leukotriene C4 synthase
GO lipid binding	16	116	0.0055177	51228 glycolipid transfer protein
GO lipid binding	16	116	0.0055177	5346 perilipin 1
GO lipid binding	16	116	0.0055177	5465 peroxisome proliferator-activated receptor alpha
GO lipid binding	16	116	0.0055177	56288 par-3 partitioning defective 3 homolog (C. elegans)
GO lipid binding	16	116	0.0055177	5742 prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase a)
GO lipid binding	16	116	0.0055177	80830 apolipoprotein L, 6
GO lipid binding	16	116	0.0055177	80833 apolipoprotein L, 3
GO lipid binding	16	116	0.0055177	83394 PITPNM family member 3
GO lipid binding	16	116	0.0055177	8542 apolipoprotein L, 1
GO lipid binding	16	116	0.0055177	92747 chromosome 20 open reading frame 114
GO phosphatidylinositol binding	5	18	0.0059855	5295 phosphoinositide-3-kinase, regulatory subunit 1 (alpha)
GO phosphatidylinositol binding	5	18	0.0059855	6857 synaptotagmin I
GO phosphatidylinositol binding	5	18	0.0059855	85477 scinderin
GO phosphatidylinositol binding	5	18	0.0059855	91404 SEC14 and spectrin domains 1
GO phosphatidylinositol binding	5	18	0.0059855	9892 synaptosomal-associated protein, 91kDa homolog (mouse)
GO metal ion binding	213	2658	0.0060111	10106 CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) sma
GO metal ion binding	213	2658	0.0060111	10156 RAS p21 protein activator 4
GO metal ion binding	213	2658	0.0060111	10346 tripartite motif-containing 22
GO metal ion binding	213	2658	0.0060111	104 adenosine deaminase, RNA-specific, B1 (RED1 homolog rat)
GO metal ion binding	213	2658	0.0060111	10417 spondin 2, extracellular matrix protein
GO metal ion binding	213	2658	0.0060111	10838 zinc finger protein 275

GO metal ion binding	213	2658	0.0060111	10906 TRAF-type zinc finger domain containing 1
GO metal ion binding	213	2658	0.0060111	11043 midline 2
GO metal ion binding	213	2658	0.0060111	11074 tripartite motif-containing 31
GO metal ion binding	213	2658	0.0060111	11155 LIM domain binding 3
GO metal ion binding	213	2658	0.0060111	112 adenylate cyclase 6
GO metal ion binding	213	2658	0.0060111	11200 CHK2 checkpoint homolog ( <i>S. pombe</i> )
GO metal ion binding	213	2658	0.0060111	11238 carbonic anhydrase VB, mitochondrial
GO metal ion binding	213	2658	0.0060111	1124 chimerin (chimaerin) 2
GO metal ion binding	213	2658	0.0060111	11279 Kruppel-like factor 8
GO metal ion binding	213	2658	0.0060111	115196 zinc finger protein 554
GO metal ion binding	213	2658	0.0060111	116113 forkhead box P4
GO metal ion binding	213	2658	0.0060111	116984 ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 2
GO metal ion binding	213	2658	0.0060111	118429 anthrax toxin receptor 2
GO metal ion binding	213	2658	0.0060111	118987 PDZ domain containing 8
GO metal ion binding	213	2658	0.0060111	124 alcohol dehydrogenase 1A (class I), alpha polypeptide
GO metal ion binding	213	2658	0.0060111	125 alcohol dehydrogenase 1B (class I), beta polypeptide
GO metal ion binding	213	2658	0.0060111	130399 activin A receptor, type IC
GO metal ion binding	213	2658	0.0060111	134218 DnaJ (Hsp40) homolog, subfamily C, member 21
GO metal ion binding	213	2658	0.0060111	135644 tripartite motif-containing 40
GO metal ion binding	213	2658	0.0060111	1363 carboxypeptidase E
GO metal ion binding	213	2658	0.0060111	1368 carboxypeptidase M
GO metal ion binding	213	2658	0.0060111	143425 synaptotagmin IX
GO metal ion binding	213	2658	0.0060111	147694 zinc finger protein 548
GO metal ion binding	213	2658	0.0060111	147923 zinc finger protein 420
GO metal ion binding	213	2658	0.0060111	151636 deltex 3-like ( <i>Drosophila</i> )
GO metal ion binding	213	2658	0.0060111	152273 FYVE, RhoGEF and PH domain containing 5
GO metal ion binding	213	2658	0.0060111	154214 ring finger protein 217
GO metal ion binding	213	2658	0.0060111	1558 cytochrome P450, family 2, subfamily C, polypeptide 8
GO metal ion binding	213	2658	0.0060111	1559 cytochrome P450, family 2, subfamily C, polypeptide 9
GO metal ion binding	213	2658	0.0060111	1571 cytochrome P450, family 2, subfamily E, polypeptide 1
GO metal ion binding	213	2658	0.0060111	1577 cytochrome P450, family 3, subfamily A, polypeptide 5
GO metal ion binding	213	2658	0.0060111	162962 zinc finger protein 836
GO metal ion binding	213	2658	0.0060111	163050 zinc finger protein 564
GO metal ion binding	213	2658	0.0060111	163115 zinc finger protein 781
GO metal ion binding	213	2658	0.0060111	170692 ADAM metallopeptidase with thrombospondin type 1 motif, 18
GO metal ion binding	213	2658	0.0060111	1958 early growth response 1

GO metal ion binding	213	2658	0.0060111	1959 early growth response 2
GO metal ion binding	213	2658	0.0060111	1960 early growth response 3
GO metal ion binding	213	2658	0.0060111	201501 zinc finger and BTB domain containing 7C
GO metal ion binding	213	2658	0.0060111	2033 E1A binding protein p300
GO metal ion binding	213	2658	0.0060111	2122 MDS1 and EVI1 complex locus
GO metal ion binding	213	2658	0.0060111	2153 coagulation factor V (proaccelerin, labile factor)
GO metal ion binding	213	2658	0.0060111	220441 ring finger protein 152
GO metal ion binding	213	2658	0.0060111	22807 IKAROS family zinc finger 2 (Helios)
GO metal ion binding	213	2658	0.0060111	22901 arylsulfatase G
GO metal ion binding	213	2658	0.0060111	22998 LIM and calponin homology domains 1
GO metal ion binding	213	2658	0.0060111	23035 PH domain and leucine rich repeat protein phosphatase 2
GO metal ion binding	213	2658	0.0060111	23081 lysine (K)-specific demethylase 4C
GO metal ion binding	213	2658	0.0060111	23099 zinc finger and BTB domain containing 43
GO metal ion binding	213	2658	0.0060111	23119 hypermethylated in cancer 2
GO metal ion binding	213	2658	0.0060111	23338 PHD finger protein 15
GO metal ion binding	213	2658	0.0060111	23371 tensin like C1 domain containing phosphatase (tensin 2)
GO metal ion binding	213	2658	0.0060111	23650 tripartite motif-containing 29
GO metal ion binding	213	2658	0.0060111	23774 bromodomain containing 1
GO metal ion binding	213	2658	0.0060111	240 arachidonate 5-lipoxygenase
GO metal ion binding	213	2658	0.0060111	2521 fused in sarcoma
GO metal ion binding	213	2658	0.0060111	254295 phytanoyl-CoA dioxygenase domain containing 1
GO metal ion binding	213	2658	0.0060111	255488 ring finger protein 144B
GO metal ion binding	213	2658	0.0060111	256051 zinc finger protein 549
GO metal ion binding	213	2658	0.0060111	25862 ubiquitin specific peptidase 49
GO metal ion binding	213	2658	0.0060111	25946 zinc finger protein 385A
GO metal ion binding	213	2658	0.0060111	2624 GATA binding protein 2
GO metal ion binding	213	2658	0.0060111	26468 LIM homeobox 6
GO metal ion binding	213	2658	0.0060111	27035 NADPH oxidase 1
GO metal ion binding	213	2658	0.0060111	27246 ring finger protein 115
GO metal ion binding	213	2658	0.0060111	27295 PDZ and LIM domain 3
GO metal ion binding	213	2658	0.0060111	2737 GLI family zinc finger 3
GO metal ion binding	213	2658	0.0060111	27434 polymerase (DNA directed), mu
GO metal ion binding	213	2658	0.0060111	284346 zinc finger protein 575
GO metal ion binding	213	2658	0.0060111	284716 ribosomal modification protein rimK-like family member A
GO metal ion binding	213	2658	0.0060111	29116 myosin regulatory light chain interacting protein
GO metal ion binding	213	2658	0.0060111	316 aldehyde oxidase 1

GO metal ion binding	213	2658	0.0060111	3164 nuclear receptor subfamily 4, group A, member 1
GO metal ion binding	213	2658	0.0060111	3268 ArfGAP with FG repeats 2
GO metal ion binding	213	2658	0.0060111	342908 zinc finger protein 404
GO metal ion binding	213	2658	0.0060111	345462 zinc finger protein 879
GO metal ion binding	213	2658	0.0060111	3486 insulin-like growth factor binding protein 3
GO metal ion binding	213	2658	0.0060111	3643 insulin receptor
GO metal ion binding	213	2658	0.0060111	376940 zinc finger CCCH-type containing 6
GO metal ion binding	213	2658	0.0060111	378925 ring finger protein 148
GO metal ion binding	213	2658	0.0060111	388536 zinc finger protein 790
GO metal ion binding	213	2658	0.0060111	388558 zinc finger protein 808
GO metal ion binding	213	2658	0.0060111	388567 zinc finger protein 749
GO metal ion binding	213	2658	0.0060111	388591 ring finger protein 207
GO metal ion binding	213	2658	0.0060111	389058 Sp5 transcription factor
GO metal ion binding	213	2658	0.0060111	390667 pentraxin 4, long
GO metal ion binding	213	2658	0.0060111	3983 actin binding LIM protein 1
GO metal ion binding	213	2658	0.0060111	4005 LIM domain only 2 (rhombotin-like 1)
GO metal ion binding	213	2658	0.0060111	4007 prickle homolog 3 (Drosophila)
GO metal ion binding	213	2658	0.0060111	400713 zinc finger protein 880
GO metal ion binding	213	2658	0.0060111	4008 LIM domain 7
GO metal ion binding	213	2658	0.0060111	4015 lysyl oxidase
GO metal ion binding	213	2658	0.0060111	412 steroid sulfatase (microsomal), isozyme S
GO metal ion binding	213	2658	0.0060111	4151 myoglobin
GO metal ion binding	213	2658	0.0060111	4194 Mdm4 p53 binding protein homolog (mouse)
GO metal ion binding	213	2658	0.0060111	4306 nuclear receptor subfamily 3, group C, member 2
GO metal ion binding	213	2658	0.0060111	4316 matrix metallopeptidase 7 (matrilysin, uterine)
GO metal ion binding	213	2658	0.0060111	4638 myosin light chain kinase
GO metal ion binding	213	2658	0.0060111	48 aconitase 1, soluble
GO metal ion binding	213	2658	0.0060111	4842 nitric oxide synthase 1 (neuronal)
GO metal ion binding	213	2658	0.0060111	4929 nuclear receptor subfamily 4, group A, member 2
GO metal ion binding	213	2658	0.0060111	493 ATPase, Ca <sup>++</sup> transporting, plasma membrane 4
GO metal ion binding	213	2658	0.0060111	5053 phenylalanine hydroxylase
GO metal ion binding	213	2658	0.0060111	5063 p21 protein (Cdc42/Rac)-activated kinase 3
GO metal ion binding	213	2658	0.0060111	5066 peptidylglycine alpha-amidating monooxygenase
GO metal ion binding	213	2658	0.0060111	5071 Parkinson disease (autosomal recessive, juvenile) 2, parkin
GO metal ion binding	213	2658	0.0060111	51274 Kruppel-like factor 3 (basic)
GO metal ion binding	213	2658	0.0060111	5136 phosphodiesterase 1A, calmodulin-dependent

GO metal ion binding	213	2658	0.0060111	5152 phosphodiesterase 9A
GO metal ion binding	213	2658	0.0060111	51523 CXXC finger 5
GO metal ion binding	213	2658	0.0060111	5158 phosphodiesterase 6B, cGMP-specific, rod, beta
GO metal ion binding	213	2658	0.0060111	51621 Kruppel-like factor 13
GO metal ion binding	213	2658	0.0060111	51710 zinc finger protein 44
GO metal ion binding	213	2658	0.0060111	5325 pleiomorphic adenoma gene-like 1
GO metal ion binding	213	2658	0.0060111	5351 procollagen-lysine 1, 2-oxoglutarate 5-dioxygenase 1
GO metal ion binding	213	2658	0.0060111	5371 promyelocytic leukemia
GO metal ion binding	213	2658	0.0060111	54511 3-hydroxymethyl-3-methylglutaryl-Coenzyme A lyase-like 1
GO metal ion binding	213	2658	0.0060111	5465 peroxisome proliferator-activated receptor alpha
GO metal ion binding	213	2658	0.0060111	54739 XIAP associated factor 1
GO metal ion binding	213	2658	0.0060111	54877 zinc finger, CCHC domain containing 2
GO metal ion binding	213	2658	0.0060111	54894 ring finger protein 43
GO metal ion binding	213	2658	0.0060111	54904 Wolf-Hirschhorn syndrome candidate 1-like 1
GO metal ion binding	213	2658	0.0060111	55140 elongation protein 3 homolog ( <i>S. cerevisiae</i> )
GO metal ion binding	213	2658	0.0060111	55432 YOD1 OTU deubiquinating enzyme 1 homolog ( <i>S. cerevisiae</i> )
GO metal ion binding	213	2658	0.0060111	55616 ArfGAP with SH3 domain, ankyrin repeat and PH domain 3
GO metal ion binding	213	2658	0.0060111	55657 zinc finger protein 692
GO metal ion binding	213	2658	0.0060111	55693 lysine (K)-specific demethylase 4D
GO metal ion binding	213	2658	0.0060111	55762 zinc finger protein 701
GO metal ion binding	213	2658	0.0060111	55769 zinc finger protein 83
GO metal ion binding	213	2658	0.0060111	55799 calcium channel, voltage-dependent, alpha 2/delta subunit 3
GO metal ion binding	213	2658	0.0060111	55870 ash1 (absent, small, or homeotic)-like ( <i>Drosophila</i> )
GO metal ion binding	213	2658	0.0060111	55893 zinc finger protein 395
GO metal ion binding	213	2658	0.0060111	56547 matrix metalloproteinase 26
GO metal ion binding	213	2658	0.0060111	56913 core 1 synthase, glycoprotein-N-acetylgalactosamine 3-beta-galactosyl
GO metal ion binding	213	2658	0.0060111	56978 PR domain containing 8
GO metal ion binding	213	2658	0.0060111	57094 carboxypeptidase A6
GO metal ion binding	213	2658	0.0060111	57379 activation-induced cytidine deaminase
GO metal ion binding	213	2658	0.0060111	5742 prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase a
GO metal ion binding	213	2658	0.0060111	57459 GATA zinc finger domain containing 2B
GO metal ion binding	213	2658	0.0060111	57494 ribosomal modification protein rimK-like family member B
GO metal ion binding	213	2658	0.0060111	57643 zinc finger, SWIM-type containing 5
GO metal ion binding	213	2658	0.0060111	59344 arachidonate lipoxygenase 3
GO metal ion binding	213	2658	0.0060111	604 B-cell CLL/lymphoma 6
GO metal ion binding	213	2658	0.0060111	6096 RAR-related orphan receptor B

GO metal ion binding	213	2658	0.0060111	6097 RAR-related orphan receptor C
GO metal ion binding	213	2658	0.0060111	6239 ras responsive element binding protein 1
GO metal ion binding	213	2658	0.0060111	6256 retinoid X receptor, alpha
GO metal ion binding	213	2658	0.0060111	64135 interferon induced with helicase C domain 1
GO metal ion binding	213	2658	0.0060111	687 Kruppel-like factor 9
GO metal ion binding	213	2658	0.0060111	6916 thromboxane A synthase 1 (platelet)
GO metal ion binding	213	2658	0.0060111	6941 transcription factor 19
GO metal ion binding	213	2658	0.0060111	7026 nuclear receptor subfamily 2, group F, member 2
GO metal ion binding	213	2658	0.0060111	7071 Kruppel-like factor 10
GO metal ion binding	213	2658	0.0060111	7076 TIMP metalloproteinase inhibitor 1
GO metal ion binding	213	2658	0.0060111	7227 trichorhinophalangeal syndrome I
GO metal ion binding	213	2658	0.0060111	7404 ubiquitously transcribed tetratricopeptide repeat gene, Y-linked
GO metal ion binding	213	2658	0.0060111	7538 zinc finger protein 36, C3H type, homolog (mouse)
GO metal ion binding	213	2658	0.0060111	7546 Zic family member 2 (odd-paired homolog, Drosophila)
GO metal ion binding	213	2658	0.0060111	7565 zinc finger protein 17
GO metal ion binding	213	2658	0.0060111	7597 zinc finger and BTB domain containing 25
GO metal ion binding	213	2658	0.0060111	760 carbonic anhydrase II
GO metal ion binding	213	2658	0.0060111	7678 zinc finger protein 124
GO metal ion binding	213	2658	0.0060111	7706 tripartite motif-containing 25
GO metal ion binding	213	2658	0.0060111	771 carbonic anhydrase XII
GO metal ion binding	213	2658	0.0060111	79132 DEXH (Asp-Glu-X-His) box polypeptide 58
GO metal ion binding	213	2658	0.0060111	79152 fatty acid 2-hydroxylase
GO metal ion binding	213	2658	0.0060111	79444 baculoviral IAP repeat-containing 7
GO metal ion binding	213	2658	0.0060111	79673 zinc finger protein 329
GO metal ion binding	213	2658	0.0060111	79689 STEAP family member 4
GO metal ion binding	213	2658	0.0060111	79872 Cas-Br-M (murine) ecotropic retroviral transforming sequence-like 1
GO metal ion binding	213	2658	0.0060111	79894 zinc finger protein 672
GO metal ion binding	213	2658	0.0060111	79956 endoplasmic reticulum metalloproteinase 1
GO metal ion binding	213	2658	0.0060111	8013 nuclear receptor subfamily 4, group A, member 3
GO metal ion binding	213	2658	0.0060111	81603 tripartite motif-containing 8
GO metal ion binding	213	2658	0.0060111	81844 tripartite motif-containing 56
GO metal ion binding	213	2658	0.0060111	83593 Ras association (RalGDS/AF-6) domain family member 5
GO metal ion binding	213	2658	0.0060111	84033 obscurin, cytoskeletal calmodulin and titin-interacting RhoGEF
GO metal ion binding	213	2658	0.0060111	84124 zinc finger protein 394
GO metal ion binding	213	2658	0.0060111	84171 lysyl oxidase-like 4
GO metal ion binding	213	2658	0.0060111	8462 Kruppel-like factor 11

GO metal ion binding	213	2658	0.0060111	84858 zinc finger protein 503
GO metal ion binding	213	2658	0.0060111	84911 zinc finger protein 382
GO metal ion binding	213	2658	0.0060111	8527 diacylglycerol kinase, delta 130kDa
GO metal ion binding	213	2658	0.0060111	85416 Zic family member 5 (odd-paired homolog, Drosophila)
GO metal ion binding	213	2658	0.0060111	8543 LIM domain only 4
GO metal ion binding	213	2658	0.0060111	85441 peroxisomal proliferator-activated receptor A interacting complex 285
GO metal ion binding	213	2658	0.0060111	862 runt-related transcription factor 1; translocated to, 1 (cyclin D-related)
GO metal ion binding	213	2658	0.0060111	8622 phosphodiesterase 8B
GO metal ion binding	213	2658	0.0060111	8751 ADAM metallopeptidase domain 15
GO metal ion binding	213	2658	0.0060111	8796 sciellin
GO metal ion binding	213	2658	0.0060111	89870 tripartite motif-containing 15
GO metal ion binding	213	2658	0.0060111	90592 zinc finger protein 700
GO metal ion binding	213	2658	0.0060111	91 activin A receptor, type IB
GO metal ion binding	213	2658	0.0060111	92283 zinc finger protein 461
GO metal ion binding	213	2658	0.0060111	92822 zinc finger protein 276
GO metal ion binding	213	2658	0.0060111	9314 Kruppel-like factor 4 (gut)
GO metal ion binding	213	2658	0.0060111	93349 SP140 nuclear body protein-like
GO metal ion binding	213	2658	0.0060111	93589 calcium channel, voltage-dependent, alpha 2/delta subunit 4
GO metal ion binding	213	2658	0.0060111	94 activin A receptor type II-like 1
GO metal ion binding	213	2658	0.0060111	94059 leukocyte receptor cluster (LRC) member 9
GO metal ion binding	213	2658	0.0060111	9422 zinc finger protein 264
GO metal ion binding	213	2658	0.0060111	9510 ADAM metallopeptidase with thrombospondin type 1 motif, 1
GO metal ion binding	213	2658	0.0060111	9572 nuclear receptor subfamily 1, group D, member 1
GO metal ion binding	213	2658	0.0060111	9615 guanine deaminase
GO metal ion binding	213	2658	0.0060111	9633 metallothionein-like 5, testis-specific (tesmin)
GO metal ion binding	213	2658	0.0060111	9914 ATPase, Ca <sup>++</sup> transporting, type 2C, member 2
GO metal ion binding	213	2658	0.0060111	9971 nuclear receptor subfamily 1, group H, member 4
GO sarcolemma	10	59	0.0062544	112 adenylate cyclase 6
GO sarcolemma	10	59	0.0062544	1508 cathepsin B
GO sarcolemma	10	59	0.0062544	154 adrenergic, beta-2-, receptor, surface
GO sarcolemma	10	59	0.0062544	240 arachidonate 5-lipoxygenase
GO sarcolemma	10	59	0.0062544	358 aquaporin 1 (Colton blood group)
GO sarcolemma	10	59	0.0062544	4842 nitric oxide synthase 1 (neuronal)
GO sarcolemma	10	59	0.0062544	5239 phosphoglucomutase 5
GO sarcolemma	10	59	0.0062544	682 basigin (Ok blood group)
GO sarcolemma	10	59	0.0062544	783 calcium channel, voltage-dependent, beta 2 subunit

GO sarcolemma	10	59	0.0062544	8082 sarcospan (Kras oncogene-associated gene)
GO positive regulation of apoptosis	15	108	0.0066353	10628 thioredoxin interacting protein
GO positive regulation of apoptosis	15	108	0.0066353	154 adrenergic, beta-2-, receptor, surface
GO positive regulation of apoptosis	15	108	0.0066353	1785 dynamin 2
GO positive regulation of apoptosis	15	108	0.0066353	183 angiotensinogen (serpin peptidase inhibitor, clade A, member 8)
GO positive regulation of apoptosis	15	108	0.0066353	1843 dual specificity phosphatase 1
GO positive regulation of apoptosis	15	108	0.0066353	3486 insulin-like growth factor binding protein 3
GO positive regulation of apoptosis	15	108	0.0066353	3827 kininogen 1
GO positive regulation of apoptosis	15	108	0.0066353	4851 Notch homolog 1, translocation-associated (Drosophila)
GO positive regulation of apoptosis	15	108	0.0066353	5608 mitogen-activated protein kinase kinase 6
GO positive regulation of apoptosis	15	108	0.0066353	604 B-cell CLL/lymphoma 6
GO positive regulation of apoptosis	15	108	0.0066353	6256 retinoid X receptor, alpha
GO positive regulation of apoptosis	15	108	0.0066353	652 bone morphogenetic protein 4
GO positive regulation of apoptosis	15	108	0.0066353	7099 toll-like receptor 4
GO positive regulation of apoptosis	15	108	0.0066353	85477 scinderin
GO positive regulation of apoptosis	15	108	0.0066353	885 cholecystokinin
GO cell-cell signaling	27	238	0.0066554	10253 sprouty homolog 2 (Drosophila)
GO cell-cell signaling	27	238	0.0066554	10288 leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM
GO cell-cell signaling	27	238	0.0066554	183 angiotensinogen (serpin peptidase inhibitor, clade A, member 8)
GO cell-cell signaling	27	238	0.0066554	1906 endothelin 1
GO cell-cell signaling	27	238	0.0066554	1948 ephrin-B2
GO cell-cell signaling	27	238	0.0066554	23418 crumbs homolog 1 (Drosophila)
GO cell-cell signaling	27	238	0.0066554	26281 fibroblast growth factor 20
GO cell-cell signaling	27	238	0.0066554	2706 gap junction protein, beta 2, 26kDa
GO cell-cell signaling	27	238	0.0066554	3689 integrin, beta 2 (complement component 3 receptor 3 and 4 subunit)
GO cell-cell signaling	27	238	0.0066554	4680 carcinoembryonic antigen-related cell adhesion molecule 6 (non-specif
GO cell-cell signaling	27	238	0.0066554	5122 proprotein convertase subtilisin/kexin type 1
GO cell-cell signaling	27	238	0.0066554	54361 wingless-type MMTV integration site family, member 4
GO cell-cell signaling	27	238	0.0066554	55870 ash1 (absent, small, or homeotic)-like (Drosophila)
GO cell-cell signaling	27	238	0.0066554	56923 neuromedin U receptor 2
GO cell-cell signaling	27	238	0.0066554	6372 chemokine (C-X-C motif) ligand 6 (granulocyte chemotactic protein 2)
GO cell-cell signaling	27	238	0.0066554	6374 chemokine (C-X-C motif) ligand 5
GO cell-cell signaling	27	238	0.0066554	6750 somatostatin
GO cell-cell signaling	27	238	0.0066554	6751 somatostatin receptor 1
GO cell-cell signaling	27	238	0.0066554	684 bone marrow stromal cell antigen 2
GO cell-cell signaling	27	238	0.0066554	7022 transcription factor AP-2 gamma (activating enhancer binding protein 2)



GO cell-cell signaling	27	238	0.0066554	7071 Kruppel-like factor 10
GO cell-cell signaling	27	238	0.0066554	7477 wingless-type MMTV integration site family, member 7B
GO cell-cell signaling	27	238	0.0066554	7869 sema domain, immunoglobulin domain (Ig), short basic domain, secret
GO cell-cell signaling	27	238	0.0066554	8744 tumor necrosis factor (ligand) superfamily, member 9
GO cell-cell signaling	27	238	0.0066554	8839 WNT1 inducible signaling pathway protein 2
GO cell-cell signaling	27	238	0.0066554	9019 myelin protein zero-like 1
GO cell-cell signaling	27	238	0.0066554	9518 growth differentiation factor 15
GO lung development	10	60	0.0070569	1080 cystic fibrosis transmembrane conductance regulator (ATP-binding cas:
GO lung development	10	60	0.0070569	2033 E1A binding protein p300
GO lung development	10	60	0.0070569	2737 GLI family zinc finger 3
GO lung development	10	60	0.0070569	3169 forkhead box A1
GO lung development	10	60	0.0070569	3911 laminin, alpha 5
GO lung development	10	60	0.0070569	4015 lysyl oxidase
GO lung development	10	60	0.0070569	4087 SMAD family member 2
GO lung development	10	60	0.0070569	4851 Notch homolog 1, translocation-associated (Drosophila)
GO lung development	10	60	0.0070569	5950 retinol binding protein 4, plasma
GO lung development	10	60	0.0070569	7474 wingless-type MMTV integration site family, member 5A
GO response to hypoxia	18	140	0.0070871	1139 cholinergic receptor, nicotinic, alpha 7
GO response to hypoxia	18	140	0.0070871	1803 dipeptidyl-peptidase 4
GO response to hypoxia	18	140	0.0070871	1906 endothelin 1
GO response to hypoxia	18	140	0.0070871	2033 E1A binding protein p300
GO response to hypoxia	18	140	0.0070871	3709 inositol 1,4,5-triphosphate receptor, type 2
GO response to hypoxia	18	140	0.0070871	4151 myoglobin
GO response to hypoxia	18	140	0.0070871	4842 nitric oxide synthase 1 (neuronal)
GO response to hypoxia	18	140	0.0070871	4929 nuclear receptor subfamily 4, group A, member 2
GO response to hypoxia	18	140	0.0070871	5327 plasminogen activator, tissue
GO response to hypoxia	18	140	0.0070871	5351 procollagen-lysine 1, 2-oxoglutarate 5-dioxygenase 1
GO response to hypoxia	18	140	0.0070871	5371 promyelocytic leukemia
GO response to hypoxia	18	140	0.0070871	5465 peroxisome proliferator-activated receptor alpha
GO response to hypoxia	18	140	0.0070871	7097 toll-like receptor 2
GO response to hypoxia	18	140	0.0070871	7099 toll-like receptor 4
GO response to hypoxia	18	140	0.0070871	7852 chemokine (C-X-C motif) receptor 4
GO response to hypoxia	18	140	0.0070871	834 caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, co
GO response to hypoxia	18	140	0.0070871	9021 suppressor of cytokine signaling 3
GO response to hypoxia	18	140	0.0070871	952 CD38 molecule
GO zinc ion binding	154	1867	0.0071938	10346 tripartite motif-containing 22

GO zinc ion binding	154	1867	0.0071938	10838 zinc finger protein 275
GO zinc ion binding	154	1867	0.0071938	10906 TRAF-type zinc finger domain containing 1
GO zinc ion binding	154	1867	0.0071938	11043 midline 2
GO zinc ion binding	154	1867	0.0071938	11074 tripartite motif-containing 31
GO zinc ion binding	154	1867	0.0071938	11155 LIM domain binding 3
GO zinc ion binding	154	1867	0.0071938	11238 carbonic anhydrase VB, mitochondrial
GO zinc ion binding	154	1867	0.0071938	11279 Kruppel-like factor 8
GO zinc ion binding	154	1867	0.0071938	115196 zinc finger protein 554
GO zinc ion binding	154	1867	0.0071938	116113 forkhead box P4
GO zinc ion binding	154	1867	0.0071938	116984 ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 2
GO zinc ion binding	154	1867	0.0071938	124 alcohol dehydrogenase 1A (class I), alpha polypeptide
GO zinc ion binding	154	1867	0.0071938	125 alcohol dehydrogenase 1B (class I), beta polypeptide
GO zinc ion binding	154	1867	0.0071938	134218 DnaJ (Hsp40) homolog, subfamily C, member 21
GO zinc ion binding	154	1867	0.0071938	135644 tripartite motif-containing 40
GO zinc ion binding	154	1867	0.0071938	1363 carboxypeptidase E
GO zinc ion binding	154	1867	0.0071938	1368 carboxypeptidase M
GO zinc ion binding	154	1867	0.0071938	147694 zinc finger protein 548
GO zinc ion binding	154	1867	0.0071938	147923 zinc finger protein 420
GO zinc ion binding	154	1867	0.0071938	151636 deltex 3-like (Drosophila)
GO zinc ion binding	154	1867	0.0071938	152273 FYVE, RhoGEF and PH domain containing 5
GO zinc ion binding	154	1867	0.0071938	154214 ring finger protein 217
GO zinc ion binding	154	1867	0.0071938	162962 zinc finger protein 836
GO zinc ion binding	154	1867	0.0071938	163050 zinc finger protein 564
GO zinc ion binding	154	1867	0.0071938	163115 zinc finger protein 781
GO zinc ion binding	154	1867	0.0071938	170692 ADAM metallopeptidase with thrombospondin type 1 motif, 18
GO zinc ion binding	154	1867	0.0071938	1821 dystrophin related protein 2
GO zinc ion binding	154	1867	0.0071938	1958 early growth response 1
GO zinc ion binding	154	1867	0.0071938	1959 early growth response 2
GO zinc ion binding	154	1867	0.0071938	1960 early growth response 3
GO zinc ion binding	154	1867	0.0071938	201501 zinc finger and BTB domain containing 7C
GO zinc ion binding	154	1867	0.0071938	2033 E1A binding protein p300
GO zinc ion binding	154	1867	0.0071938	2122 MDS1 and EVI1 complex locus
GO zinc ion binding	154	1867	0.0071938	220441 ring finger protein 152
GO zinc ion binding	154	1867	0.0071938	22807 IKAROS family zinc finger 2 (Helios)
GO zinc ion binding	154	1867	0.0071938	22998 LIM and calponin homology domains 1
GO zinc ion binding	154	1867	0.0071938	23081 lysine (K)-specific demethylase 4C

GO zinc ion binding	154	1867	0.0071938	23099 zinc finger and BTB domain containing 43
GO zinc ion binding	154	1867	0.0071938	23119 hypermethylated in cancer 2
GO zinc ion binding	154	1867	0.0071938	23338 PHD finger protein 15
GO zinc ion binding	154	1867	0.0071938	23650 tripartite motif-containing 29
GO zinc ion binding	154	1867	0.0071938	23774 bromodomain containing 1
GO zinc ion binding	154	1867	0.0071938	2521 fused in sarcoma
GO zinc ion binding	154	1867	0.0071938	255488 ring finger protein 144B
GO zinc ion binding	154	1867	0.0071938	256051 zinc finger protein 549
GO zinc ion binding	154	1867	0.0071938	25862 ubiquitin specific peptidase 49
GO zinc ion binding	154	1867	0.0071938	25946 zinc finger protein 385A
GO zinc ion binding	154	1867	0.0071938	2624 GATA binding protein 2
GO zinc ion binding	154	1867	0.0071938	26468 LIM homeobox 6
GO zinc ion binding	154	1867	0.0071938	27246 ring finger protein 115
GO zinc ion binding	154	1867	0.0071938	27295 PDZ and LIM domain 3
GO zinc ion binding	154	1867	0.0071938	2737 GLI family zinc finger 3
GO zinc ion binding	154	1867	0.0071938	284346 zinc finger protein 575
GO zinc ion binding	154	1867	0.0071938	29116 myosin regulatory light chain interacting protein
GO zinc ion binding	154	1867	0.0071938	3164 nuclear receptor subfamily 4, group A, member 1
GO zinc ion binding	154	1867	0.0071938	3268 ArfGAP with FG repeats 2
GO zinc ion binding	154	1867	0.0071938	342908 zinc finger protein 404
GO zinc ion binding	154	1867	0.0071938	345462 zinc finger protein 879
GO zinc ion binding	154	1867	0.0071938	376940 zinc finger CCCH-type containing 6
GO zinc ion binding	154	1867	0.0071938	378925 ring finger protein 148
GO zinc ion binding	154	1867	0.0071938	3827 kininogen 1
GO zinc ion binding	154	1867	0.0071938	388536 zinc finger protein 790
GO zinc ion binding	154	1867	0.0071938	388558 zinc finger protein 808
GO zinc ion binding	154	1867	0.0071938	388567 zinc finger protein 749
GO zinc ion binding	154	1867	0.0071938	388591 ring finger protein 207
GO zinc ion binding	154	1867	0.0071938	389058 Sp5 transcription factor
GO zinc ion binding	154	1867	0.0071938	3983 actin binding LIM protein 1
GO zinc ion binding	154	1867	0.0071938	4005 LIM domain only 2 (rhombotin-like 1)
GO zinc ion binding	154	1867	0.0071938	4007 prickle homolog 3 (Drosophila)
GO zinc ion binding	154	1867	0.0071938	400713 zinc finger protein 880
GO zinc ion binding	154	1867	0.0071938	4008 LIM domain 7
GO zinc ion binding	154	1867	0.0071938	4194 Mdm4 p53 binding protein homolog (mouse)
GO zinc ion binding	154	1867	0.0071938	4306 nuclear receptor subfamily 3, group C, member 2

GO zinc ion binding	154	1867	0.0071938	4316 matrix metallopeptidase 7 (matrilysin, uterine)
GO zinc ion binding	154	1867	0.0071938	4929 nuclear receptor subfamily 4, group A, member 2
GO zinc ion binding	154	1867	0.0071938	5025 purinergic receptor P2X, ligand-gated ion channel, 4
GO zinc ion binding	154	1867	0.0071938	5071 Parkinson disease (autosomal recessive, juvenile) 2, parkin
GO zinc ion binding	154	1867	0.0071938	51274 Kruppel-like factor 3 (basic)
GO zinc ion binding	154	1867	0.0071938	51523 CXXC finger 5
GO zinc ion binding	154	1867	0.0071938	51621 Kruppel-like factor 13
GO zinc ion binding	154	1867	0.0071938	51710 zinc finger protein 44
GO zinc ion binding	154	1867	0.0071938	5325 pleiomorphic adenoma gene-like 1
GO zinc ion binding	154	1867	0.0071938	5371 promyelocytic leukemia
GO zinc ion binding	154	1867	0.0071938	5465 peroxisome proliferator-activated receptor alpha
GO zinc ion binding	154	1867	0.0071938	54739 XIAP associated factor 1
GO zinc ion binding	154	1867	0.0071938	54877 zinc finger, CCHC domain containing 2
GO zinc ion binding	154	1867	0.0071938	54894 ring finger protein 43
GO zinc ion binding	154	1867	0.0071938	54904 Wolf-Hirschhorn syndrome candidate 1-like 1
GO zinc ion binding	154	1867	0.0071938	55184 chromosome 20 open reading frame 12
GO zinc ion binding	154	1867	0.0071938	55432 YOD1 OTU deubiquinating enzyme 1 homolog ( <i>S. cerevisiae</i> )
GO zinc ion binding	154	1867	0.0071938	55616 ArfGAP with SH3 domain, ankyrin repeat and PH domain 3
GO zinc ion binding	154	1867	0.0071938	55657 zinc finger protein 692
GO zinc ion binding	154	1867	0.0071938	55762 zinc finger protein 701
GO zinc ion binding	154	1867	0.0071938	55769 zinc finger protein 83
GO zinc ion binding	154	1867	0.0071938	55870 ash1 (absent, small, or homeotic)-like ( <i>Drosophila</i> )
GO zinc ion binding	154	1867	0.0071938	55893 zinc finger protein 395
GO zinc ion binding	154	1867	0.0071938	56547 matrix metallopeptidase 26
GO zinc ion binding	154	1867	0.0071938	56978 PR domain containing 8
GO zinc ion binding	154	1867	0.0071938	57094 carboxypeptidase A6
GO zinc ion binding	154	1867	0.0071938	57379 activation-induced cytidine deaminase
GO zinc ion binding	154	1867	0.0071938	57459 GATA zinc finger domain containing 2B
GO zinc ion binding	154	1867	0.0071938	57643 zinc finger, SWIM-type containing 5
GO zinc ion binding	154	1867	0.0071938	604 B-cell CLL/lymphoma 6
GO zinc ion binding	154	1867	0.0071938	6096 RAR-related orphan receptor B
GO zinc ion binding	154	1867	0.0071938	6097 RAR-related orphan receptor C
GO zinc ion binding	154	1867	0.0071938	6239 ras responsive element binding protein 1
GO zinc ion binding	154	1867	0.0071938	6256 retinoid X receptor, alpha
GO zinc ion binding	154	1867	0.0071938	64135 interferon induced with helicase C domain 1
GO zinc ion binding	154	1867	0.0071938	6622 synuclein, alpha (non A4 component of amyloid precursor)

GO zinc ion binding	154	1867	0.0071938	687 Kruppel-like factor 9
GO zinc ion binding	154	1867	0.0071938	6941 transcription factor 19
GO zinc ion binding	154	1867	0.0071938	7026 nuclear receptor subfamily 2, group F, member 2
GO zinc ion binding	154	1867	0.0071938	7071 Kruppel-like factor 10
GO zinc ion binding	154	1867	0.0071938	7092 tolloid-like 1
GO zinc ion binding	154	1867	0.0071938	7227 trichorhinophalangeal syndrome I
GO zinc ion binding	154	1867	0.0071938	7538 zinc finger protein 36, C3H type, homolog (mouse)
GO zinc ion binding	154	1867	0.0071938	7546 Zic family member 2 (odd-paired homolog, Drosophila)
GO zinc ion binding	154	1867	0.0071938	7565 zinc finger protein 17
GO zinc ion binding	154	1867	0.0071938	7597 zinc finger and BTB domain containing 25
GO zinc ion binding	154	1867	0.0071938	760 carbonic anhydrase II
GO zinc ion binding	154	1867	0.0071938	7678 zinc finger protein 124
GO zinc ion binding	154	1867	0.0071938	7706 tripartite motif-containing 25
GO zinc ion binding	154	1867	0.0071938	771 carbonic anhydrase XII
GO zinc ion binding	154	1867	0.0071938	79132 DEXH (Asp-Glu-X-His) box polypeptide 58
GO zinc ion binding	154	1867	0.0071938	79444 baculoviral IAP repeat-containing 7
GO zinc ion binding	154	1867	0.0071938	79661 nei endonuclease VIII-like 1 (E. coli)
GO zinc ion binding	154	1867	0.0071938	79673 zinc finger protein 329
GO zinc ion binding	154	1867	0.0071938	79872 Cas-Br-M (murine) ecotropic retroviral transforming sequence-like 1
GO zinc ion binding	154	1867	0.0071938	79894 zinc finger protein 672
GO zinc ion binding	154	1867	0.0071938	8013 nuclear receptor subfamily 4, group A, member 3
GO zinc ion binding	154	1867	0.0071938	81603 tripartite motif-containing 8
GO zinc ion binding	154	1867	0.0071938	81844 tripartite motif-containing 56
GO zinc ion binding	154	1867	0.0071938	84124 zinc finger protein 394
GO zinc ion binding	154	1867	0.0071938	8462 Kruppel-like factor 11
GO zinc ion binding	154	1867	0.0071938	84858 zinc finger protein 503
GO zinc ion binding	154	1867	0.0071938	84911 zinc finger protein 382
GO zinc ion binding	154	1867	0.0071938	85416 Zic family member 5 (odd-paired homolog, Drosophila)
GO zinc ion binding	154	1867	0.0071938	8543 LIM domain only 4
GO zinc ion binding	154	1867	0.0071938	85441 peroxisomal proliferator-activated receptor A interacting complex 285
GO zinc ion binding	154	1867	0.0071938	862 runt-related transcription factor 1; translocated to, 1 (cyclin D-related)
GO zinc ion binding	154	1867	0.0071938	8751 ADAM metallopeptidase domain 15
GO zinc ion binding	154	1867	0.0071938	8796 sciellin
GO zinc ion binding	154	1867	0.0071938	89870 tripartite motif-containing 15
GO zinc ion binding	154	1867	0.0071938	90592 zinc finger protein 700
GO zinc ion binding	154	1867	0.0071938	92283 zinc finger protein 461

GO zinc ion binding	154	1867	0.0071938	92822 zinc finger protein 276
GO zinc ion binding	154	1867	0.0071938	9314 Kruppel-like factor 4 (gut)
GO zinc ion binding	154	1867	0.0071938	93349 SP140 nuclear body protein-like
GO zinc ion binding	154	1867	0.0071938	94059 leukocyte receptor cluster (LRC) member 9
GO zinc ion binding	154	1867	0.0071938	9422 zinc finger protein 264
GO zinc ion binding	154	1867	0.0071938	9510 ADAM metallopeptidase with thrombospondin type 1 motif, 1
GO zinc ion binding	154	1867	0.0071938	9572 nuclear receptor subfamily 1, group D, member 1
GO zinc ion binding	154	1867	0.0071938	9615 guanine deaminase
GO zinc ion binding	154	1867	0.0071938	9971 nuclear receptor subfamily 1, group H, member 4
GO B cell differentiation	7	34	0.0072127	10014 histone deacetylase 5
GO B cell differentiation	7	34	0.0072127	23529 cardiotrophin-like cytokine factor 1
GO B cell differentiation	7	34	0.0072127	29760 B-cell linker
GO B cell differentiation	7	34	0.0072127	3175 one cut homeobox 1
GO B cell differentiation	7	34	0.0072127	57379 activation-induced cytidine deaminase
GO B cell differentiation	7	34	0.0072127	604 B-cell CLL/lymphoma 6
GO B cell differentiation	7	34	0.0072127	9734 histone deacetylase 9
GO palate development	7	34	0.0072127	4087 SMAD family member 2
GO palate development	7	34	0.0072127	4223 mesenchyme homeobox 2
GO palate development	7	34	0.0072127	5396 paired related homeobox 1
GO palate development	7	34	0.0072127	64651 cysteine-serine-rich nuclear protein 1
GO palate development	7	34	0.0072127	7049 transforming growth factor, beta receptor III
GO palate development	7	34	0.0072127	84159 AT rich interactive domain 5B (MRF1-like)
GO palate development	7	34	0.0072127	91461 protein kinase domain containing, cytoplasmic homolog (mouse)
GO protein amino acid dephosphorylatio	16	120	0.0076423	10076 protein tyrosine phosphatase, receptor type, U
GO protein amino acid dephosphorylatio	16	120	0.0076423	10106 CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) sma
GO protein amino acid dephosphorylatio	16	120	0.0076423	11156 protein tyrosine phosphatase type IVA, member 3
GO protein amino acid dephosphorylatio	16	120	0.0076423	1843 dual specificity phosphatase 1
GO protein amino acid dephosphorylatio	16	120	0.0076423	1844 dual specificity phosphatase 2
GO protein amino acid dephosphorylatio	16	120	0.0076423	1847 dual specificity phosphatase 5
GO protein amino acid dephosphorylatio	16	120	0.0076423	26191 protein tyrosine phosphatase, non-receptor type 22 (lymphoid)
GO protein amino acid dephosphorylatio	16	120	0.0076423	54961 slingshot homolog 3 (Drosophila)
GO protein amino acid dephosphorylatio	16	120	0.0076423	5774 protein tyrosine phosphatase, non-receptor type 3
GO protein amino acid dephosphorylatio	16	120	0.0076423	5787 protein tyrosine phosphatase, receptor type, B
GO protein amino acid dephosphorylatio	16	120	0.0076423	5789 protein tyrosine phosphatase, receptor type, D
GO protein amino acid dephosphorylatio	16	120	0.0076423	5791 protein tyrosine phosphatase, receptor type, E
GO protein amino acid dephosphorylatio	16	120	0.0076423	5794 protein tyrosine phosphatase, receptor type, H

GO protein amino acid dephosphorylation	16	120	0.0076423	5799 protein tyrosine phosphatase, receptor type, N polypeptide 2
GO protein amino acid dephosphorylation	16	120	0.0076423	5801 protein tyrosine phosphatase, receptor type, R
GO protein amino acid dephosphorylation	16	120	0.0076423	8556 CDC14 cell division cycle 14 homolog A ( <i>S. cerevisiae</i> )
GO leukotriene biosynthetic process	5	19	0.0076729	2205 Fc fragment of IgE, high affinity I, receptor for; alpha polypeptide
GO leukotriene biosynthetic process	5	19	0.0076729	240 arachidonate 5-lipoxygenase
GO leukotriene biosynthetic process	5	19	0.0076729	4056 leukotriene C4 synthase
GO leukotriene biosynthetic process	5	19	0.0076729	59344 arachidonate lipoxygenase 3
GO leukotriene biosynthetic process	5	19	0.0076729	6850 spleen tyrosine kinase
GO insulin-like growth factor binding	5	19	0.0076729	3484 insulin-like growth factor binding protein 1
GO insulin-like growth factor binding	5	19	0.0076729	3486 insulin-like growth factor binding protein 3
GO insulin-like growth factor binding	5	19	0.0076729	3491 cysteine-rich, angiogenic inducer, 61
GO insulin-like growth factor binding	5	19	0.0076729	4856 nephroblastoma overexpressed gene
GO insulin-like growth factor binding	5	19	0.0076729	8839 WNT1 inducible signaling pathway protein 2
GO response to estradiol stimulus	10	61	0.0079369	10568 solute carrier family 34 (sodium phosphate), member 2
GO response to estradiol stimulus	10	61	0.0079369	10628 thioredoxin interacting protein
GO response to estradiol stimulus	10	61	0.0079369	1843 dual specificity phosphatase 1
GO response to estradiol stimulus	10	61	0.0079369	2026 enolase 2 (gamma, neuronal)
GO response to estradiol stimulus	10	61	0.0079369	3169 forkhead box A1
GO response to estradiol stimulus	10	61	0.0079369	3643 insulin receptor
GO response to estradiol stimulus	10	61	0.0079369	4886 neuropeptide Y receptor Y1
GO response to estradiol stimulus	10	61	0.0079369	652 bone morphogenetic protein 4
GO response to estradiol stimulus	10	61	0.0079369	9021 suppressor of cytokine signaling 3
GO response to estradiol stimulus	10	61	0.0079369	952 CD38 molecule
GO basement membrane	10	61	0.0079369	1295 collagen, type VIII, alpha 1
GO basement membrane	10	61	0.0079369	2200 fibrillin 1
GO basement membrane	10	61	0.0079369	22795 nidogen 2 (osteonidogen)
GO basement membrane	10	61	0.0079369	30008 EGF-containing fibulin-like extracellular matrix protein 2
GO basement membrane	10	61	0.0079369	3911 laminin, alpha 5
GO basement membrane	10	61	0.0079369	3913 laminin, beta 2 (laminin S)
GO basement membrane	10	61	0.0079369	3914 laminin, beta 3
GO basement membrane	10	61	0.0079369	64093 SPARC related modular calcium binding 1
GO basement membrane	10	61	0.0079369	83872 hemicentin 1
GO basement membrane	10	61	0.0079369	9510 ADAM metallopeptidase with thrombospondin type 1 motif, 1
GO kidney development	10	61	0.0079369	183 angiotensinogen (serpin peptidase inhibitor, clade A, member 8)
GO kidney development	10	61	0.0079369	2200 fibrillin 1
GO kidney development	10	61	0.0079369	2296 forkhead box C1

GO kidney development	10	61	0.0079369	255738 proprotein convertase subtilisin/kexin type 9
GO kidney development	10	61	0.0079369	56913 core 1 synthase, glycoprotein-N-acetylgalactosamine 3-beta-galactosyl
GO kidney development	10	61	0.0079369	5972 renin
GO kidney development	10	61	0.0079369	652 bone morphogenetic protein 4
GO kidney development	10	61	0.0079369	760 carbonic anhydrase II
GO kidney development	10	61	0.0079369	84159 AT rich interactive domain 5B (MRF1-like)
GO kidney development	10	61	0.0079369	9510 ADAM metalloproteinase with thrombospondin type 1 motif, 1
GO positive regulation of cell proliferatio	31	290	0.0089975	10312 T-cell, immune regulator 1, ATPase, H+ transporting, lysosomal V0 subu
GO positive regulation of cell proliferatio	31	290	0.0089975	1139 cholinergic receptor, nicotinic, alpha 7
GO positive regulation of cell proliferatio	31	290	0.0089975	1435 colony stimulating factor 1 (macrophage)
GO positive regulation of cell proliferatio	31	290	0.0089975	154 adrenergic, beta-2-, receptor, surface
GO positive regulation of cell proliferatio	31	290	0.0089975	1803 dipeptidyl-peptidase 4
GO positive regulation of cell proliferatio	31	290	0.0089975	1906 endothelin 1
GO positive regulation of cell proliferatio	31	290	0.0089975	2263 fibroblast growth factor receptor 2
GO positive regulation of cell proliferatio	31	290	0.0089975	26281 fibroblast growth factor 20
GO positive regulation of cell proliferatio	31	290	0.0089975	27035 NADPH oxidase 1
GO positive regulation of cell proliferatio	31	290	0.0089975	28996 homeodomain interacting protein kinase 2
GO positive regulation of cell proliferatio	31	290	0.0089975	3142 H2.0-like homeobox
GO positive regulation of cell proliferatio	31	290	0.0089975	3400 inhibitor of DNA binding 4, dominant negative helix-loop-helix protein
GO positive regulation of cell proliferatio	31	290	0.0089975	3479 insulin-like growth factor 1 (somatomedin C)
GO positive regulation of cell proliferatio	31	290	0.0089975	3569 interleukin 6 (interferon, beta 2)
GO positive regulation of cell proliferatio	31	290	0.0089975	3570 interleukin 6 receptor
GO positive regulation of cell proliferatio	31	290	0.0089975	3643 insulin receptor
GO positive regulation of cell proliferatio	31	290	0.0089975	3815 v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog
GO positive regulation of cell proliferatio	31	290	0.0089975	3845 v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog
GO positive regulation of cell proliferatio	31	290	0.0089975	412 steroid sulfatase (microsomal), isozyme S
GO positive regulation of cell proliferatio	31	290	0.0089975	4194 Mdm4 p53 binding protein homolog (mouse)
GO positive regulation of cell proliferatio	31	290	0.0089975	4254 KIT ligand
GO positive regulation of cell proliferatio	31	290	0.0089975	4486 macrophage stimulating 1 receptor (c-met-related tyrosine kinase)
GO positive regulation of cell proliferatio	31	290	0.0089975	467 activating transcription factor 3
GO positive regulation of cell proliferatio	31	290	0.0089975	4851 Notch homolog 1, translocation-associated (Drosophila)
GO positive regulation of cell proliferatio	31	290	0.0089975	51085 MLX interacting protein-like
GO positive regulation of cell proliferatio	31	290	0.0089975	6374 chemokine (C-X-C motif) ligand 5
GO positive regulation of cell proliferatio	31	290	0.0089975	6489 ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 1
GO positive regulation of cell proliferatio	31	290	0.0089975	7076 TIMP metalloproteinase inhibitor 1
GO positive regulation of cell proliferatio	31	290	0.0089975	8660 insulin receptor substrate 2



GO	positive regulation of cell proliferatio	31	290	0.0089975	885 cholecystokinin
GO	positive regulation of cell proliferatio	31	290	0.0089975	961 CD47 molecule
GO	transmembrane receptor protein tyrosi	3	7	0.0090491	10076 protein tyrosine phosphatase, receptor type, U
GO	transmembrane receptor protein tyrosi	3	7	0.0090491	5789 protein tyrosine phosphatase, receptor type, D
GO	transmembrane receptor protein tyrosi	3	7	0.0090491	5791 protein tyrosine phosphatase, receptor type, E
GO	negative regulation of smooth muscle	3	7	0.0090491	10221 tribbles homolog 1 (Drosophila)
GO	negative regulation of smooth muscle	3	7	0.0090491	3486 insulin-like growth factor binding protein 3
GO	negative regulation of smooth muscle	3	7	0.0090491	3488 insulin-like growth factor binding protein 5
GO	GTP-Rho binding	3	7	0.0090491	10435 CDC42 effector protein (Rho GTPase binding) 2
GO	GTP-Rho binding	3	7	0.0090491	11078 TRIO and F-actin binding protein
GO	GTP-Rho binding	3	7	0.0090491	148170 CDC42 effector protein (Rho GTPase binding) 5
GO	positive regulation of pseudopodium	3	7	0.0090491	10435 CDC42 effector protein (Rho GTPase binding) 2
GO	positive regulation of pseudopodium	3	7	0.0090491	148170 CDC42 effector protein (Rho GTPase binding) 5
GO	positive regulation of pseudopodium	3	7	0.0090491	3815 v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog
GO	P granule	3	7	0.0090491	143689 piwi-like 4 (Drosophila)
GO	P granule	3	7	0.0090491	55124 piwi-like 2 (Drosophila)
GO	P granule	3	7	0.0090491	9271 piwi-like 1 (Drosophila)
GO	piRNA metabolic process	3	7	0.0090491	143689 piwi-like 4 (Drosophila)
GO	piRNA metabolic process	3	7	0.0090491	55124 piwi-like 2 (Drosophila)
GO	piRNA metabolic process	3	7	0.0090491	9271 piwi-like 1 (Drosophila)
GO	natriuresis	3	7	0.0090491	1813 dopamine receptor D2
GO	natriuresis	3	7	0.0090491	1906 endothelin 1
GO	natriuresis	3	7	0.0090491	3827 kininogen 1
GO	drinking behavior	3	7	0.0090491	183 angiotensinogen (serpin peptidase inhibitor, clade A, member 8)
GO	drinking behavior	3	7	0.0090491	5367 pro-melanin-concentrating hormone
GO	drinking behavior	3	7	0.0090491	5972 renin
GO	regulation of organ growth	3	7	0.0090491	2296 forkhead box C1
GO	regulation of organ growth	3	7	0.0090491	2303 forkhead box C2 (MFH-1, mesenchyme forkhead 1)
GO	regulation of organ growth	3	7	0.0090491	28982 feline leukemia virus subgroup C cellular receptor 1
GO	neurotransmitter biosynthetic proces	3	7	0.0090491	2571 glutamate decarboxylase 1 (brain, 67kDa)
GO	neurotransmitter biosynthetic proces	3	7	0.0090491	4842 nitric oxide synthase 1 (neuronal)
GO	neurotransmitter biosynthetic proces	3	7	0.0090491	5053 phenylalanine hydroxylase
GO	positive regulation of glycolysis	3	7	0.0090491	3479 insulin-like growth factor 1 (somatomedin C)
GO	positive regulation of glycolysis	3	7	0.0090491	3643 insulin receptor
GO	positive regulation of glycolysis	3	7	0.0090491	51085 MLX interacting protein-like
GO	osteoclast differentiation	3	7	0.0090491	3726 jun B proto-oncogene

GO osteoclast differentiation	3	7	0.0090491	799 calcitonin receptor
GO osteoclast differentiation	3	7	0.0090491	8600 tumor necrosis factor (ligand) superfamily, member 11
GO positive regulation of fatty acid beta-	3	7	0.0090491	51703 acyl-CoA synthetase long-chain family member 5
GO positive regulation of fatty acid beta-	3	7	0.0090491	5465 peroxisome proliferator-activated receptor alpha
GO positive regulation of fatty acid beta-	3	7	0.0090491	8660 insulin receptor substrate 2
GO calcium-activated potassium channel	4	13	0.0094275	157855 potassium channel, subfamily U, member 1
GO calcium-activated potassium channel	4	13	0.0094275	27345 potassium large conductance calcium-activated channel, subfamily M,
GO calcium-activated potassium channel	4	13	0.0094275	343450 potassium channel, subfamily T, member 2
GO calcium-activated potassium channel	4	13	0.0094275	3783 potassium intermediate/small conductance calcium-activated channel,
GO insulin-like growth factor receptor bi	4	13	0.0094275	3479 insulin-like growth factor 1 (somatomedin C)
GO insulin-like growth factor receptor bi	4	13	0.0094275	3643 insulin receptor
GO insulin-like growth factor receptor bi	4	13	0.0094275	5295 phosphoinositide-3-kinase, regulatory subunit 1 (alpha)
GO insulin-like growth factor receptor bi	4	13	0.0094275	5972 renin
GO inflammatory response	25	222	0.0096029	10014 histone deacetylase 5
GO inflammatory response	25	222	0.0096029	11343 monoglyceride lipase
GO inflammatory response	25	222	0.0096029	1999 E74-like factor 3 (ets domain transcription factor, epithelial-specific )
GO inflammatory response	25	222	0.0096029	2353 FBJ murine osteosarcoma viral oncogene homolog
GO inflammatory response	25	222	0.0096029	240 arachidonate 5-lipoxygenase
GO inflammatory response	25	222	0.0096029	27035 NADPH oxidase 1
GO inflammatory response	25	222	0.0096029	2921 chemokine (C-X-C motif) ligand 3
GO inflammatory response	25	222	0.0096029	29760 B-cell linker
GO inflammatory response	25	222	0.0096029	316 aldehyde oxidase 1
GO inflammatory response	25	222	0.0096029	3569 interleukin 6 (interferon, beta 2)
GO inflammatory response	25	222	0.0096029	3689 integrin, beta 2 (complement component 3 receptor 3 and 4 subunit)
GO inflammatory response	25	222	0.0096029	3827 kininogen 1
GO inflammatory response	25	222	0.0096029	4065 lymphocyte antigen 75
GO inflammatory response	25	222	0.0096029	5724 platelet-activating factor receptor
GO inflammatory response	25	222	0.0096029	6256 retinoid X receptor, alpha
GO inflammatory response	25	222	0.0096029	6372 chemokine (C-X-C motif) ligand 6 (granulocyte chemotactic protein 2)
GO inflammatory response	25	222	0.0096029	64332 nuclear factor of kappa light polypeptide gene enhancer in B-cells inhib
GO inflammatory response	25	222	0.0096029	7100 toll-like receptor 5
GO inflammatory response	25	222	0.0096029	718 complement component 3
GO inflammatory response	25	222	0.0096029	7852 chemokine (C-X-C motif) receptor 4
GO inflammatory response	25	222	0.0096029	7941 phospholipase A2, group VII (platelet-activating factor acetylhydrolase,
GO inflammatory response	25	222	0.0096029	80833 apolipoprotein L, 3
GO inflammatory response	25	222	0.0096029	929 CD14 molecule

GO inflammatory response	25	222	0.0096029	9435 carbohydrate (N-acetylglucosamine-6-O) sulfotransferase 2
GO inflammatory response	25	222	0.0096029	9734 histone deacetylase 9
GO integral to Golgi membrane	8	45	0.0104108	166929 sphingomyelin synthase 2
GO integral to Golgi membrane	8	45	0.0104108	27090 ST6 (alpha-N-acetyl-neuraminy-2,3-beta-galactosyl-1,3)-N-acetylgalact
GO integral to Golgi membrane	8	45	0.0104108	53947 alpha 1,4-galactosyltransferase
GO integral to Golgi membrane	8	45	0.0104108	55808 ST6 (alpha-N-acetyl-neuraminy-2,3-beta-galactosyl-1,3)-N-acetylgalact
GO integral to Golgi membrane	8	45	0.0104108	57134 mannosidase, alpha, class 1C, member 1
GO integral to Golgi membrane	8	45	0.0104108	5768 quiescin Q6 sulfhydryl oxidase 1
GO integral to Golgi membrane	8	45	0.0104108	6484 ST3 beta-galactoside alpha-2,3-sialyltransferase 4
GO integral to Golgi membrane	8	45	0.0104108	6489 ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 1
GO protein dimerization activity	12	84	0.0115402	116071 basic leucine zipper transcription factor, ATF-like 2
GO protein dimerization activity	12	84	0.0115402	1628 D site of albumin promoter (albumin D-box) binding protein
GO protein dimerization activity	12	84	0.0115402	2354 FBJ murine osteosarcoma viral oncogene homolog B
GO protein dimerization activity	12	84	0.0115402	3131 hepatic leukemia factor
GO protein dimerization activity	12	84	0.0115402	3726 jun B proto-oncogene
GO protein dimerization activity	12	84	0.0115402	467 activating transcription factor 3
GO protein dimerization activity	12	84	0.0115402	4778 nuclear factor (erythroid-derived 2), 45kDa
GO protein dimerization activity	12	84	0.0115402	4783 nuclear factor, interleukin 3 regulated
GO protein dimerization activity	12	84	0.0115402	7008 thyrotrophic embryonic factor
GO protein dimerization activity	12	84	0.0115402	7022 transcription factor AP-2 gamma (activating enhancer binding protein 2)
GO protein dimerization activity	12	84	0.0115402	90993 cAMP responsive element binding protein 3-like 1
GO protein dimerization activity	12	84	0.0115402	9619 ATP-binding cassette, sub-family G (WHITE), member 1
GO branching morphogenesis of a tube	5	21	0.0119847	10253 sprouty homolog 2 (Drosophila)
GO branching morphogenesis of a tube	5	21	0.0119847	3169 forkhead box A1
GO branching morphogenesis of a tube	5	21	0.0119847	3479 insulin-like growth factor 1 (somatomedin C)
GO branching morphogenesis of a tube	5	21	0.0119847	4851 Notch homolog 1, translocation-associated (Drosophila)
GO branching morphogenesis of a tube	5	21	0.0119847	652 bone morphogenetic protein 4
GO negative regulation of BMP signaling	5	21	0.0119847	168667 BMP binding endothelial regulator
GO negative regulation of BMP signaling	5	21	0.0119847	28996 homeodomain interacting protein kinase 2
GO negative regulation of BMP signaling	5	21	0.0119847	4851 Notch homolog 1, translocation-associated (Drosophila)
GO negative regulation of BMP signaling	5	21	0.0119847	7474 wingless-type MMTV integration site family, member 5A
GO negative regulation of BMP signaling	5	21	0.0119847	8646 chordin
GO induction of apoptosis	20	170	0.01228	10081 programmed cell death 7
GO induction of apoptosis	20	170	0.01228	10116 fem-1 homolog b (C. elegans)
GO induction of apoptosis	20	170	0.01228	1612 death-associated protein kinase 1
GO induction of apoptosis	20	170	0.01228	23368 protein phosphatase 1, regulatory (inhibitor) subunit 13B

GO induction of apoptosis	20	170	0.01228	23604 death-associated protein kinase 2
GO induction of apoptosis	20	170	0.01228	255738 proprotein convertase subtilisin/kexin type 9
GO induction of apoptosis	20	170	0.01228	29108 PYD and CARD domain containing
GO induction of apoptosis	20	170	0.01228	3164 nuclear receptor subfamily 4, group A, member 1
GO induction of apoptosis	20	170	0.01228	3604 tumor necrosis factor receptor superfamily, member 9
GO induction of apoptosis	20	170	0.01228	4599 myxovirus (influenza virus) resistance 1, interferon-inducible protein p
GO induction of apoptosis	20	170	0.01228	4853 Notch homolog 2 (Drosophila)
GO induction of apoptosis	20	170	0.01228	5325 pleiomorphic adenoma gene-like 1
GO induction of apoptosis	20	170	0.01228	5371 promyelocytic leukemia
GO induction of apoptosis	20	170	0.01228	7097 toll-like receptor 2
GO induction of apoptosis	20	170	0.01228	834 caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, co
GO induction of apoptosis	20	170	0.01228	837 caspase 4, apoptosis-related cysteine peptidase
GO induction of apoptosis	20	170	0.01228	8740 tumor necrosis factor (ligand) superfamily, member 14
GO induction of apoptosis	20	170	0.01228	91 activin A receptor, type IB
GO induction of apoptosis	20	170	0.01228	9263 serine/threonine kinase 17a
GO induction of apoptosis	20	170	0.01228	9445 integral membrane protein 2B
GO cell fate commitment	6	29	0.0122817	10253 sprouty homolog 2 (Drosophila)
GO cell fate commitment	6	29	0.0122817	3175 one cut homeobox 1
GO cell fate commitment	6	29	0.0122817	4087 SMAD family member 2
GO cell fate commitment	6	29	0.0122817	4286 microphthalmia-associated transcription factor
GO cell fate commitment	6	29	0.0122817	5371 promyelocytic leukemia
GO cell fate commitment	6	29	0.0122817	54361 wingless-type MMTV integration site family, member 4
GO positive regulation of vasodilation	4	14	0.0124949	1080 cystic fibrosis transmembrane conductance regulator (ATP-binding cas
GO positive regulation of vasodilation	4	14	0.0124949	1373 carbamoyl-phosphate synthetase 1, mitochondrial
GO positive regulation of vasodilation	4	14	0.0124949	154 adrenergic, beta-2-, receptor, surface
GO positive regulation of vasodilation	4	14	0.0124949	4842 nitric oxide synthase 1 (neuronal)
GO negative regulation of tumor necrosi	4	14	0.0124949	11213 interleukin-1 receptor-associated kinase 3
GO negative regulation of tumor necrosi	4	14	0.0124949	1139 cholinergic receptor, nicotinic, alpha 7
GO negative regulation of tumor necrosi	4	14	0.0124949	64127 nucleotide-binding oligomerization domain containing 2
GO negative regulation of tumor necrosi	4	14	0.0124949	7099 toll-like receptor 4
GO cytoskeletal adaptor activity	4	14	0.0124949	23092 Rho GTPase activating protein 26
GO cytoskeletal adaptor activity	4	14	0.0124949	55909 bridging integrator 3
GO cytoskeletal adaptor activity	4	14	0.0124949	80115 BAI1-associated protein 2-like 2
GO cytoskeletal adaptor activity	4	14	0.0124949	9788 metastasis suppressor 1
GO complement activation, alternative p	4	14	0.0124949	629 complement factor B
GO complement activation, alternative p	4	14	0.0124949	717 complement component 2

GO complement activation, alternative p	4	14	0.0124949	718 complement component 3
GO complement activation, alternative p	4	14	0.0124949	731 complement component 8, alpha polypeptide
GO negative regulation of transcription fi	25	227	0.0125139	10014 histone deacetylase 5
GO negative regulation of transcription fi	25	227	0.0125139	10628 thioredoxin interacting protein
GO negative regulation of transcription fi	25	227	0.0125139	116113 forkhead box P4
GO negative regulation of transcription fi	25	227	0.0125139	127343 diencephalon/mesencephalon homeobox 1
GO negative regulation of transcription fi	25	227	0.0125139	150094 salt-inducible kinase 1
GO negative regulation of transcription fi	25	227	0.0125139	1822 atrophin 1
GO negative regulation of transcription fi	25	227	0.0125139	1958 early growth response 1
GO negative regulation of transcription fi	25	227	0.0125139	2117 ets variant 3
GO negative regulation of transcription fi	25	227	0.0125139	2354 FBJ murine osteosarcoma viral oncogene homolog B
GO negative regulation of transcription fi	25	227	0.0125139	2737 GLI family zinc finger 3
GO negative regulation of transcription fi	25	227	0.0125139	28996 homeodomain interacting protein kinase 2
GO negative regulation of transcription fi	25	227	0.0125139	3169 forkhead box A1
GO negative regulation of transcription fi	25	227	0.0125139	3665 interferon regulatory factor 7
GO negative regulation of transcription fi	25	227	0.0125139	4194 Mdm4 p53 binding protein homolog (mouse)
GO negative regulation of transcription fi	25	227	0.0125139	4204 methyl CpG binding protein 2 (Rett syndrome)
GO negative regulation of transcription fi	25	227	0.0125139	4212 Meis homeobox 2
GO negative regulation of transcription fi	25	227	0.0125139	51085 MLX interacting protein-like
GO negative regulation of transcription fi	25	227	0.0125139	5396 paired related homeobox 1
GO negative regulation of transcription fi	25	227	0.0125139	604 B-cell CLL/lymphoma 6
GO negative regulation of transcription fi	25	227	0.0125139	7026 nuclear receptor subfamily 2, group F, member 2
GO negative regulation of transcription fi	25	227	0.0125139	7071 Kruppel-like factor 10
GO negative regulation of transcription fi	25	227	0.0125139	8462 Kruppel-like factor 11
GO negative regulation of transcription fi	25	227	0.0125139	8531 cold shock domain protein A
GO negative regulation of transcription fi	25	227	0.0125139	9734 histone deacetylase 9
GO negative regulation of transcription fi	25	227	0.0125139	9971 nuclear receptor subfamily 1, group H, member 4
GO transcription activator activity	25	227	0.0125139	1785 dynamin 2
GO transcription activator activity	25	227	0.0125139	1958 early growth response 1
GO transcription activator activity	25	227	0.0125139	1999 E74-like factor 3 (ets domain transcription factor, epithelial-specific )
GO transcription activator activity	25	227	0.0125139	222546 regulatory factor X, 6
GO transcription activator activity	25	227	0.0125139	22807 IKAROS family zinc finger 2 (Helios)
GO transcription activator activity	25	227	0.0125139	2296 forkhead box C1
GO transcription activator activity	25	227	0.0125139	2303 forkhead box C2 (MFH-1, mesenchyme forkhead 1)
GO transcription activator activity	25	227	0.0125139	3164 nuclear receptor subfamily 4, group A, member 1
GO transcription activator activity	25	227	0.0125139	3175 one cut homeobox 1

GO transcription activator activity	25	227	0.0125139	3725 jun oncogene
GO transcription activator activity	25	227	0.0125139	4087 SMAD family member 2
GO transcription activator activity	25	227	0.0125139	4209 myocyte enhancer factor 2D
GO transcription activator activity	25	227	0.0125139	4286 microphthalmia-associated transcription factor
GO transcription activator activity	25	227	0.0125139	4851 Notch homolog 1, translocation-associated (Drosophila)
GO transcription activator activity	25	227	0.0125139	4929 nuclear receptor subfamily 4, group A, member 2
GO transcription activator activity	25	227	0.0125139	51085 MLX interacting protein-like
GO transcription activator activity	25	227	0.0125139	5465 peroxisome proliferator-activated receptor alpha
GO transcription activator activity	25	227	0.0125139	55810 forkhead box J2
GO transcription activator activity	25	227	0.0125139	6239 ras responsive element binding protein 1
GO transcription activator activity	25	227	0.0125139	652 bone morphogenetic protein 4
GO transcription activator activity	25	227	0.0125139	7026 nuclear receptor subfamily 2, group F, member 2
GO transcription activator activity	25	227	0.0125139	8013 nuclear receptor subfamily 4, group A, member 3
GO transcription activator activity	25	227	0.0125139	80714 pre-B-cell leukemia homeobox 4
GO transcription activator activity	25	227	0.0125139	8631 src kinase associated phosphoprotein 1
GO transcription activator activity	25	227	0.0125139	9314 Kruppel-like factor 4 (gut)
GO epidermis development	11	75	0.0126188	10481 homeobox B13
GO epidermis development	11	75	0.0126188	10913 ectodysplasin A receptor
GO epidermis development	11	75	0.0126188	1382 cellular retinoic acid binding protein 2
GO epidermis development	11	75	0.0126188	1999 E74-like factor 3 (ets domain transcription factor, epithelial-specific )
GO epidermis development	11	75	0.0126188	3914 laminin, beta 3
GO epidermis development	11	75	0.0126188	412 steroid sulfatase (microsomal), isozyme S
GO epidermis development	11	75	0.0126188	4851 Notch homolog 1, translocation-associated (Drosophila)
GO epidermis development	11	75	0.0126188	5351 procollagen-lysine 1, 2-oxoglutarate 5-dioxygenase 1
GO epidermis development	11	75	0.0126188	5465 peroxisome proliferator-activated receptor alpha
GO epidermis development	11	75	0.0126188	6706 small proline-rich protein 2G
GO epidermis development	11	75	0.0126188	8796 sciellin
GO double-stranded DNA binding	11	75	0.0126188	1958 early growth response 1
GO double-stranded DNA binding	11	75	0.0126188	2353 FBJ murine osteosarcoma viral oncogene homolog
GO double-stranded DNA binding	11	75	0.0126188	3131 hepatic leukemia factor
GO double-stranded DNA binding	11	75	0.0126188	3428 interferon, gamma-inducible protein 16
GO double-stranded DNA binding	11	75	0.0126188	3725 jun oncogene
GO double-stranded DNA binding	11	75	0.0126188	3726 jun B proto-oncogene
GO double-stranded DNA binding	11	75	0.0126188	4087 SMAD family member 2
GO double-stranded DNA binding	11	75	0.0126188	429 achaete-scute complex homolog 1 (Drosophila)
GO double-stranded DNA binding	11	75	0.0126188	6256 retinoid X receptor, alpha

GO double-stranded DNA binding	11	75	0.0126188	8531 cold shock domain protein A
GO double-stranded DNA binding	11	75	0.0126188	9971 nuclear receptor subfamily 1, group H, member 4
GO axon	16	127	0.0128948	127933 U2AF homology motif (UHM) kinase 1
GO axon	16	127	0.0128948	154 adrenergic, beta-2-, receptor, surface
GO axon	16	127	0.0128948	1813 dopamine receptor D2
GO axon	16	127	0.0128948	2571 glutamate decarboxylase 1 (brain, 67kDa)
GO axon	16	127	0.0128948	27242 tumor necrosis factor receptor superfamily, member 21
GO axon	16	127	0.0128948	2911 glutamate receptor, metabotropic 1
GO axon	16	127	0.0128948	3709 inositol 1,4,5-triphosphate receptor, type 2
GO axon	16	127	0.0128948	4684 neural cell adhesion molecule 1
GO axon	16	127	0.0128948	4856 neuroblastoma overexpressed gene
GO axon	16	127	0.0128948	4886 neuropeptide Y receptor Y1
GO axon	16	127	0.0128948	5025 purinergic receptor P2X, ligand-gated ion channel, 4
GO axon	16	127	0.0128948	6256 retinoid X receptor, alpha
GO axon	16	127	0.0128948	6622 synuclein, alpha (non A4 component of amyloid precursor)
GO axon	16	127	0.0128948	760 carbonic anhydrase II
GO axon	16	127	0.0128948	799 calcitonin receptor
GO axon	16	127	0.0128948	885 cholecystokinin
GO endoplasmic reticulum membrane	49	518	0.013107	10162 lysophosphatidylcholine acyltransferase 3
GO endoplasmic reticulum membrane	49	518	0.013107	10170 dehydrogenase/reductase (SDR family) member 9
GO endoplasmic reticulum membrane	49	518	0.013107	10282 blocked early in transport 1 homolog ( <i>S. cerevisiae</i> )
GO endoplasmic reticulum membrane	49	518	0.013107	10335 murine retrovirus integration site 1 homolog
GO endoplasmic reticulum membrane	49	518	0.013107	11322 transmembrane channel-like 6
GO endoplasmic reticulum membrane	49	518	0.013107	118429 anthrax toxin receptor 2
GO endoplasmic reticulum membrane	49	518	0.013107	123099 degenerative spermatocyte homolog 2, lipid desaturase ( <i>Drosophila</i> )
GO endoplasmic reticulum membrane	49	518	0.013107	130367 sphingosine-1-phosphate phosphatase 2
GO endoplasmic reticulum membrane	49	518	0.013107	147138 transmembrane channel-like 8
GO endoplasmic reticulum membrane	49	518	0.013107	1558 cytochrome P450, family 2, subfamily C, polypeptide 8
GO endoplasmic reticulum membrane	49	518	0.013107	1559 cytochrome P450, family 2, subfamily C, polypeptide 9
GO endoplasmic reticulum membrane	49	518	0.013107	1571 cytochrome P450, family 2, subfamily E, polypeptide 1
GO endoplasmic reticulum membrane	49	518	0.013107	157506 retinol dehydrogenase 10 (all-trans)
GO endoplasmic reticulum membrane	49	518	0.013107	1577 cytochrome P450, family 3, subfamily A, polypeptide 5
GO endoplasmic reticulum membrane	49	518	0.013107	163590 torsin A interacting protein 2
GO endoplasmic reticulum membrane	49	518	0.013107	165679 chromosome 3 open reading frame 57
GO endoplasmic reticulum membrane	49	518	0.013107	195814 short chain dehydrogenase/reductase family 16C, member 5
GO endoplasmic reticulum membrane	49	518	0.013107	2055 ceroid-lipofuscinosis, neuronal 8 (epilepsy, progressive with mental ret

GO	endoplasmic reticulum membrane	49	518	0.013107	2182 acyl-CoA synthetase long-chain family member 4
GO	endoplasmic reticulum membrane	49	518	0.013107	23780 apolipoprotein L, 2
GO	endoplasmic reticulum membrane	49	518	0.013107	256987 serine incorporator 5
GO	endoplasmic reticulum membrane	49	518	0.013107	25956 SEC31 homolog B ( <i>S. cerevisiae</i> )
GO	endoplasmic reticulum membrane	49	518	0.013107	2861 G protein-coupled receptor 37 (endothelin receptor type B-like)
GO	endoplasmic reticulum membrane	49	518	0.013107	3294 hydroxysteroid (17-beta) dehydrogenase 2
GO	endoplasmic reticulum membrane	49	518	0.013107	3601 interleukin 15 receptor, alpha
GO	endoplasmic reticulum membrane	49	518	0.013107	375056 melanoma inhibitory activity family, member 3
GO	endoplasmic reticulum membrane	49	518	0.013107	387923 stress-associated endoplasmic reticulum protein family member 2
GO	endoplasmic reticulum membrane	49	518	0.013107	4056 leukotriene C4 synthase
GO	endoplasmic reticulum membrane	49	518	0.013107	405753 dual oxidase maturation factor 2
GO	endoplasmic reticulum membrane	49	518	0.013107	412 steroid sulfatase (microsomal), isozyme S
GO	endoplasmic reticulum membrane	49	518	0.013107	4306 nuclear receptor subfamily 3, group C, member 2
GO	endoplasmic reticulum membrane	49	518	0.013107	51703 acyl-CoA synthetase long-chain family member 5
GO	endoplasmic reticulum membrane	49	518	0.013107	54681 prolyl 4-hydroxylase, transmembrane (endoplasmic reticulum)
GO	endoplasmic reticulum membrane	49	518	0.013107	54894 ring finger protein 43
GO	endoplasmic reticulum membrane	49	518	0.013107	54947 lysophosphatidylcholine acyltransferase 2
GO	endoplasmic reticulum membrane	49	518	0.013107	55080 TAP binding protein-like
GO	endoplasmic reticulum membrane	49	518	0.013107	55304 serine palmitoyltransferase, long chain base subunit 3
GO	endoplasmic reticulum membrane	49	518	0.013107	56605 ERO1-like beta ( <i>S. cerevisiae</i> )
GO	endoplasmic reticulum membrane	49	518	0.013107	5742 prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase a)
GO	endoplasmic reticulum membrane	49	518	0.013107	57620 stromal interaction molecule 2
GO	endoplasmic reticulum membrane	49	518	0.013107	6238 ribosome binding protein 1 homolog 180kDa (dog)
GO	endoplasmic reticulum membrane	49	518	0.013107	64699 transmembrane protease, serine 3
GO	endoplasmic reticulum membrane	49	518	0.013107	7098 toll-like receptor 3
GO	endoplasmic reticulum membrane	49	518	0.013107	79152 fatty acid 2-hydroxylase
GO	endoplasmic reticulum membrane	49	518	0.013107	79956 endoplasmic reticulum metalloproteinase 1
GO	endoplasmic reticulum membrane	49	518	0.013107	84879 major facilitator superfamily domain containing 2A
GO	endoplasmic reticulum membrane	49	518	0.013107	89866 SEC16 homolog B ( <i>S. cerevisiae</i> )
GO	endoplasmic reticulum membrane	49	518	0.013107	90993 cAMP responsive element binding protein 3-like 1
GO	endoplasmic reticulum membrane	49	518	0.013107	9619 ATP-binding cassette, sub-family G (WHITE), member 1
GO	regulation of potassium ion transport	2	3	0.0133672	10008 potassium voltage-gated channel, Isk-related family, member 3
GO	regulation of potassium ion transport	2	3	0.0133672	1813 dopamine receptor D2
GO	homotypic cell-cell adhesion	2	3	0.0133672	10076 protein tyrosine phosphatase, receptor type, U
GO	homotypic cell-cell adhesion	2	3	0.0133672	4684 neural cell adhesion molecule 1
GO	negative regulation of lipopolysaccha	2	3	0.0133672	10221 tribbles homolog 1 ( <i>Drosophila</i> )



GO	negative regulation of lipopolysaccha	2	3	0.0133672	7001 peroxiredoxin 2
GO	regulation of MAP kinase activity	2	3	0.0133672	10221 tribbles homolog 1 (Drosophila)
GO	regulation of MAP kinase activity	2	3	0.0133672	28951 tribbles homolog 2 (Drosophila)
GO	ubiquitin-protein ligase regulator acti	2	3	0.0133672	10221 tribbles homolog 1 (Drosophila)
GO	ubiquitin-protein ligase regulator acti	2	3	0.0133672	28951 tribbles homolog 2 (Drosophila)
GO	activin receptor complex	2	3	0.0133672	130399 activin A receptor, type IC
GO	activin receptor complex	2	3	0.0133672	91 activin A receptor, type IB
GO	dense core granule	2	3	0.0133672	143425 synaptotagmin IX
GO	dense core granule	2	3	0.0133672	6857 synaptotagmin I
GO	positive regulation of monocyte diffe	2	3	0.0133672	1435 colony stimulating factor 1 (macrophage)
GO	positive regulation of monocyte diffe	2	3	0.0133672	3725 jun oncogene
GO	negative regulation of extracellular m	2	3	0.0133672	1471 cystatin C
GO	negative regulation of extracellular m	2	3	0.0133672	1803 dipeptidyl-peptidase 4
GO	endothelial cell activation	2	3	0.0133672	168667 BMP binding endothelial regulator
GO	endothelial cell activation	2	3	0.0133672	5025 purinergic receptor P2X, ligand-gated ion channel, 4
GO	regulation of pathway-restricted SMA	2	3	0.0133672	168667 BMP binding endothelial regulator
GO	regulation of pathway-restricted SMA	2	3	0.0133672	652 bone morphogenetic protein 4
GO	dopamine receptor activity, coupled w	2	3	0.0133672	1813 dopamine receptor D2
GO	dopamine receptor activity, coupled w	2	3	0.0133672	1815 dopamine receptor D4
GO	response to histamine	2	3	0.0133672	1813 dopamine receptor D2
GO	response to histamine	2	3	0.0133672	1815 dopamine receptor D4
GO	nitric oxide transport	2	3	0.0133672	1906 endothelin 1
GO	nitric oxide transport	2	3	0.0133672	358 aquaporin 1 (Colton blood group)
GO	positive regulation of sarcomere orga	2	3	0.0133672	1906 endothelin 1
GO	positive regulation of sarcomere orga	2	3	0.0133672	2033 E1A binding protein p300
GO	brain segmentation	2	3	0.0133672	1959 early growth response 2
GO	brain segmentation	2	3	0.0133672	9935 v-maf musculoaponeurotic fibrosarcoma oncogene homolog B (avian)
GO	positive regulation of granulocyte ma	2	3	0.0133672	2205 Fc fragment of IgE, high affinity I, receptor for; alpha polypeptide
GO	positive regulation of granulocyte ma	2	3	0.0133672	6850 spleen tyrosine kinase
GO	negative regulation of low-density lip	2	3	0.0133672	255738 proprotein convertase subtilisin/kexin type 9
GO	negative regulation of low-density lip	2	3	0.0133672	29116 myosin regulatory light chain interacting protein
GO	glutamate decarboxylase activity	2	3	0.0133672	2571 glutamate decarboxylase 1 (brain, 67kDa)
GO	glutamate decarboxylase activity	2	3	0.0133672	2752 glutamate-ammonia ligase (glutamine synthetase)
GO	cerebral cortex neuron differentiatio	2	3	0.0133672	26468 LIM homeobox 6
GO	cerebral cortex neuron differentiatio	2	3	0.0133672	3400 inhibitor of DNA binding 4, dominant negative helix-loop-helix protein
GO	negative regulation of T-helper 2 cell	2	3	0.0133672	3142 H2.0-like homeobox

GO	negative regulation of T-helper 2 cell	2	3	0.0133672	604 B-cell CLL/lymphoma 6
GO	interleukin-6 receptor complex	2	3	0.0133672	3569 interleukin 6 (interferon, beta 2)
GO	interleukin-6 receptor complex	2	3	0.0133672	3570 interleukin 6 receptor
GO	interleukin-6-mediated signaling path	2	3	0.0133672	3569 interleukin 6 (interferon, beta 2)
GO	interleukin-6-mediated signaling path	2	3	0.0133672	3570 interleukin 6 receptor
GO	germ cell programmed cell death	2	3	0.0133672	3815 v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog
GO	germ cell programmed cell death	2	3	0.0133672	4254 KIT ligand
GO	laminin-11 complex	2	3	0.0133672	3911 laminin, alpha 5
GO	laminin-11 complex	2	3	0.0133672	3913 laminin, beta 2 (laminin 5)
GO	protein-lysine 6-oxidase activity	2	3	0.0133672	4015 lysyl oxidase
GO	protein-lysine 6-oxidase activity	2	3	0.0133672	84171 lysyl oxidase-like 4
GO	common-partner SMAD protein phos	2	3	0.0133672	4087 SMAD family member 2
GO	common-partner SMAD protein phos	2	3	0.0133672	5371 promyelocytic leukemia
GO	positive regulation of keratinocyte di	2	3	0.0133672	4851 Notch homolog 1, translocation-associated (Drosophila)
GO	positive regulation of keratinocyte di	2	3	0.0133672	50604 interleukin 20
GO	pancreatic polypeptide receptor activ	2	3	0.0133672	4886 neuropeptide Y receptor Y1
GO	pancreatic polypeptide receptor activ	2	3	0.0133672	4889 neuropeptide Y receptor Y5
GO	xenobiotic-transporting ATPase activi	2	3	0.0133672	5243 ATP-binding cassette, sub-family B (MDR/TAP), member 1
GO	xenobiotic-transporting ATPase activi	2	3	0.0133672	5244 ATP-binding cassette, sub-family B (MDR/TAP), member 4
GO	negative regulation of B cell apoptosi	2	3	0.0133672	604 B-cell CLL/lymphoma 6
GO	negative regulation of B cell apoptosi	2	3	0.0133672	8660 insulin receptor substrate 2
GO	negative regulation of T-helper 2 type	2	3	0.0133672	604 B-cell CLL/lymphoma 6
GO	negative regulation of T-helper 2 type	2	3	0.0133672	6778 signal transducer and activator of transcription 6, interleukin-4 inducec
GO	negative regulation of prostatic bud f	2	3	0.0133672	652 bone morphogenetic protein 4
GO	negative regulation of prostatic bud f	2	3	0.0133672	7474 wingless-type MMTV integration site family, member 5A
GO	microglial cell activation	2	3	0.0133672	6622 synuclein, alpha (non A4 component of amyloid precursor)
GO	microglial cell activation	2	3	0.0133672	834 caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, co
GO	cellular response to lipoteichoic acid	2	3	0.0133672	7097 toll-like receptor 2
GO	cellular response to lipoteichoic acid	2	3	0.0133672	929 CD14 molecule
GO	low voltage-gated calcium channel ac	2	3	0.0133672	8911 calcium channel, voltage-dependent, T type, alpha 1I subunit
GO	low voltage-gated calcium channel ac	2	3	0.0133672	8912 calcium channel, voltage-dependent, T type, alpha 1H subunit
GO	regulation of protein binding	3	8	0.0137487	10014 histone deacetylase 5
GO	regulation of protein binding	3	8	0.0137487	26119 low density lipoprotein receptor adaptor protein 1
GO	regulation of protein binding	3	8	0.0137487	6604 SWI/SNF related, matrix associated, actin dependent regulator of chrom
GO	positive regulation of SMAD protein r	3	8	0.0137487	11030 RNA binding protein with multiple splicing
GO	positive regulation of SMAD protein r	3	8	0.0137487	5460 POU class 5 homeobox 1

GO positive regulation of SMAD protein r	3	8	0.0137487	652 bone morphogenetic protein 4
GO regulation of ossification	3	8	0.0137487	1435 colony stimulating factor 1 (macrophage)
GO regulation of ossification	3	8	0.0137487	1959 early growth response 2
GO regulation of ossification	3	8	0.0137487	5734 prostaglandin E receptor 4 (subtype EP4)
GO negative regulation of calcium ion tra	3	8	0.0137487	154 adrenergic, beta-2-, receptor, surface
GO negative regulation of calcium ion tra	3	8	0.0137487	1813 dopamine receptor D2
GO negative regulation of calcium ion tra	3	8	0.0137487	1815 dopamine receptor D4
GO oxidative demethylation	3	8	0.0137487	1558 cytochrome P450, family 2, subfamily C, polypeptide 8
GO oxidative demethylation	3	8	0.0137487	1559 cytochrome P450, family 2, subfamily C, polypeptide 9
GO oxidative demethylation	3	8	0.0137487	1577 cytochrome P450, family 3, subfamily A, polypeptide 5
GO retinal metabolic process	3	8	0.0137487	157506 retinol dehydrogenase 10 (all-trans)
GO retinal metabolic process	3	8	0.0137487	195814 short chain dehydrogenase/reductase family 16C, member 5
GO retinal metabolic process	3	8	0.0137487	5950 retinol binding protein 4, plasma
GO diuresis	3	8	0.0137487	1813 dopamine receptor D2
GO diuresis	3	8	0.0137487	1906 endothelin 1
GO diuresis	3	8	0.0137487	3827 kininogen 1
GO heart trabecula formation	3	8	0.0137487	5950 retinol binding protein 4, plasma
GO heart trabecula formation	3	8	0.0137487	7049 transforming growth factor, beta receptor III
GO heart trabecula formation	3	8	0.0137487	9510 ADAM metalloproteinase with thrombospondin type 1 motif, 1
GO positive regulation of NF-kappaB imp	3	8	0.0137487	7097 toll-like receptor 2
GO positive regulation of NF-kappaB imp	3	8	0.0137487	7098 toll-like receptor 3
GO positive regulation of NF-kappaB imp	3	8	0.0137487	7099 toll-like receptor 4
GO integrin-mediated signaling pathway	9	57	0.0145803	3678 integrin, alpha 5 (fibronectin receptor, alpha polypeptide)
GO integrin-mediated signaling pathway	9	57	0.0145803	3687 integrin, alpha X (complement component 3 receptor 4 subunit)
GO integrin-mediated signaling pathway	9	57	0.0145803	3689 integrin, beta 2 (complement component 3 receptor 3 and 4 subunit)
GO integrin-mediated signaling pathway	9	57	0.0145803	3691 integrin, beta 4
GO integrin-mediated signaling pathway	9	57	0.0145803	3696 integrin, beta 8
GO integrin-mediated signaling pathway	9	57	0.0145803	3911 laminin, alpha 5
GO integrin-mediated signaling pathway	9	57	0.0145803	6850 spleen tyrosine kinase
GO integrin-mediated signaling pathway	9	57	0.0145803	9510 ADAM metalloproteinase with thrombospondin type 1 motif, 1
GO integrin-mediated signaling pathway	9	57	0.0145803	961 CD47 molecule
GO lyase activity	13	97	0.0146538	11238 carbonic anhydrase VB, mitochondrial
GO lyase activity	13	97	0.0146538	2026 enolase 2 (gamma, neuronal)
GO lyase activity	13	97	0.0146538	2571 glutamate decarboxylase 1 (brain, 67kDa)
GO lyase activity	13	97	0.0146538	2752 glutamate-ammonia ligase (glutamine synthetase)
GO lyase activity	13	97	0.0146538	3034 histidine ammonia-lyase

GO	lyase activity	13	97	0.0146538	4056 leukotriene C4 synthase
GO	lyase activity	13	97	0.0146538	48 aconitase 1, soluble
GO	lyase activity	13	97	0.0146538	5066 peptidylglycine alpha-amidating monooxygenase
GO	lyase activity	13	97	0.0146538	54511 3-hydroxymethyl-3-methylglutaryl-Coenzyme A lyase-like 1
GO	lyase activity	13	97	0.0146538	55268 enoyl Coenzyme A hydratase domain containing 2
GO	lyase activity	13	97	0.0146538	760 carbonic anhydrase II
GO	lyase activity	13	97	0.0146538	771 carbonic anhydrase XII
GO	lyase activity	13	97	0.0146538	79661 nei endonuclease VIII-like 1 (E. coli)
GO	endomembrane system	11	77	0.0152149	10435 CDC42 effector protein (Rho GTPase binding) 2
GO	endomembrane system	11	77	0.0152149	112574 sorting nexin 18
GO	endomembrane system	11	77	0.0152149	114569 mal, T-cell differentiation protein 2
GO	endomembrane system	11	77	0.0152149	148170 CDC42 effector protein (Rho GTPase binding) 5
GO	endomembrane system	11	77	0.0152149	23348 dedicator of cytokinesis 9
GO	endomembrane system	11	77	0.0152149	29126 CD274 molecule
GO	endomembrane system	11	77	0.0152149	5046 proprotein convertase subtilisin/kexin type 6
GO	endomembrane system	11	77	0.0152149	56288 par-3 partitioning defective 3 homolog (C. elegans)
GO	endomembrane system	11	77	0.0152149	6494 signal-induced proliferation-associated 1
GO	endomembrane system	11	77	0.0152149	81544 glycerophosphodiester phosphodiesterase domain containing 5
GO	endomembrane system	11	77	0.0152149	83394 PTPNM family member 3
GO	ureteric bud development	7	39	0.0153323	10252 sprouty homolog 1, antagonist of FGF signaling (Drosophila)
GO	ureteric bud development	7	39	0.0153323	168667 BMP binding endothelial regulator
GO	ureteric bud development	7	39	0.0153323	2296 forkhead box C1
GO	ureteric bud development	7	39	0.0153323	2303 forkhead box C2 (MFH-1, mesenchyme forkhead 1)
GO	ureteric bud development	7	39	0.0153323	4087 SMAD family member 2
GO	ureteric bud development	7	39	0.0153323	627 brain-derived neurotrophic factor
GO	ureteric bud development	7	39	0.0153323	652 bone morphogenetic protein 4
GO	positive regulation of gene-specific tr	7	39	0.0153323	10891 peroxisome proliferator-activated receptor gamma, coactivator 1 alpha
GO	positive regulation of gene-specific tr	7	39	0.0153323	3479 insulin-like growth factor 1 (somatomedin C)
GO	positive regulation of gene-specific tr	7	39	0.0153323	3569 interleukin 6 (interferon, beta 2)
GO	positive regulation of gene-specific tr	7	39	0.0153323	4087 SMAD family member 2
GO	positive regulation of gene-specific tr	7	39	0.0153323	6096 RAR-related orphan receptor B
GO	positive regulation of gene-specific tr	7	39	0.0153323	652 bone morphogenetic protein 4
GO	positive regulation of gene-specific tr	7	39	0.0153323	7026 nuclear receptor subfamily 2, group F, member 2
GO	regulation of mitotic cell cycle	4	15	0.0161327	150094 salt-inducible kinase 1
GO	regulation of mitotic cell cycle	4	15	0.0161327	2290 forkhead box G1
GO	regulation of mitotic cell cycle	4	15	0.0161327	415116 pim-3 oncogene

GO regulation of mitotic cell cycle	4	15	0.0161327	51754 transmembrane protein 8B
GO neural tube development	4	15	0.0161327	1969 EPH receptor A2
GO neural tube development	4	15	0.0161327	2737 GLI family zinc finger 3
GO neural tube development	4	15	0.0161327	4851 Notch homolog 1, translocation-associated (Drosophila)
GO neural tube development	4	15	0.0161327	5362 plexin A2
GO cholesterol metabolic process	9	58	0.0162435	2055 ceroid-lipofuscinosis, neuronal 8 (epilepsy, progressive with mental ret
GO cholesterol metabolic process	9	58	0.0162435	23780 apolipoprotein L, 2
GO cholesterol metabolic process	9	58	0.0162435	255738 proprotein convertase subtilisin/kexin type 9
GO cholesterol metabolic process	9	58	0.0162435	26119 low density lipoprotein receptor adaptor protein 1
GO cholesterol metabolic process	9	58	0.0162435	3949 low density lipoprotein receptor
GO cholesterol metabolic process	9	58	0.0162435	6256 retinoid X receptor, alpha
GO cholesterol metabolic process	9	58	0.0162435	6653 sortilin-related receptor, L(DLR class) A repeats-containing
GO cholesterol metabolic process	9	58	0.0162435	8542 apolipoprotein L, 1
GO cholesterol metabolic process	9	58	0.0162435	9619 ATP-binding cassette, sub-family G (WHITE), member 1
GO SMAD binding	6	31	0.0169507	2033 E1A binding protein p300
GO SMAD binding	6	31	0.0169507	28996 homeodomain interacting protein kinase 2
GO SMAD binding	6	31	0.0169507	5371 promyelocytic leukemia
GO SMAD binding	6	31	0.0169507	7049 transforming growth factor, beta receptor III
GO SMAD binding	6	31	0.0169507	91 activin A receptor, type IB
GO SMAD binding	6	31	0.0169507	94 activin A receptor type II-like 1
GO intracellular	145	1794	0.0172868	10156 RAS p21 protein activator 4
GO intracellular	145	1794	0.0172868	10346 tripartite motif-containing 22
GO intracellular	145	1794	0.0172868	104 adenosine deaminase, RNA-specific, B1 (RED1 homolog rat)
GO intracellular	145	1794	0.0172868	10838 zinc finger protein 275
GO intracellular	145	1794	0.0172868	10906 TRAF-type zinc finger domain containing 1
GO intracellular	145	1794	0.0172868	11043 midline 2
GO intracellular	145	1794	0.0172868	11074 tripartite motif-containing 31
GO intracellular	145	1794	0.0172868	1124 chimerin (chimaerin) 2
GO intracellular	145	1794	0.0172868	11279 Kruppel-like factor 8
GO intracellular	145	1794	0.0172868	115196 zinc finger protein 554
GO intracellular	145	1794	0.0172868	116113 forkhead box P4
GO intracellular	145	1794	0.0172868	116984 ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 2
GO intracellular	145	1794	0.0172868	1193 chloride intracellular channel 2
GO intracellular	145	1794	0.0172868	129049 small G protein signaling modulator 1
GO intracellular	145	1794	0.0172868	134218 DnaJ (Hsp40) homolog, subfamily C, member 21
GO intracellular	145	1794	0.0172868	135112 nuclear receptor coactivator 7

GO intracellular	145	1794	0.0172868	135644 tripartite motif-containing 40
GO intracellular	145	1794	0.0172868	147694 zinc finger protein 548
GO intracellular	145	1794	0.0172868	147923 zinc finger protein 420
GO intracellular	145	1794	0.0172868	1508 cathepsin B
GO intracellular	145	1794	0.0172868	152273 FYVE, RhoGEF and PH domain containing 5
GO intracellular	145	1794	0.0172868	1540 cylindromatosis (turban tumor syndrome)
GO intracellular	145	1794	0.0172868	162962 zinc finger protein 836
GO intracellular	145	1794	0.0172868	163050 zinc finger protein 564
GO intracellular	145	1794	0.0172868	163115 zinc finger protein 781
GO intracellular	145	1794	0.0172868	1820 AT rich interactive domain 3A (BRIGHT-like)
GO intracellular	145	1794	0.0172868	1958 early growth response 1
GO intracellular	145	1794	0.0172868	1959 early growth response 2
GO intracellular	145	1794	0.0172868	1960 early growth response 3
GO intracellular	145	1794	0.0172868	201501 zinc finger and BTB domain containing 7C
GO intracellular	145	1794	0.0172868	2026 enolase 2 (gamma, neuronal)
GO intracellular	145	1794	0.0172868	2122 MDS1 and EVI1 complex locus
GO intracellular	145	1794	0.0172868	221178 spermatogenesis associated 13
GO intracellular	145	1794	0.0172868	22807 IKAROS family zinc finger 2 (Helios)
GO intracellular	145	1794	0.0172868	23092 Rho GTPase activating protein 26
GO intracellular	145	1794	0.0172868	23099 zinc finger and BTB domain containing 43
GO intracellular	145	1794	0.0172868	23119 hypermethylated in cancer 2
GO intracellular	145	1794	0.0172868	23179 ral guanine nucleotide dissociation stimulator-like 1
GO intracellular	145	1794	0.0172868	23263 MCF.2 cell line derived transforming sequence-like
GO intracellular	145	1794	0.0172868	2331 fibromodulin
GO intracellular	145	1794	0.0172868	23365 Rho guanine nucleotide exchange factor (GEF) 12
GO intracellular	145	1794	0.0172868	23650 tripartite motif-containing 29
GO intracellular	145	1794	0.0172868	23654 plexin B2
GO intracellular	145	1794	0.0172868	2521 fused in sarcoma
GO intracellular	145	1794	0.0172868	256051 zinc finger protein 549
GO intracellular	145	1794	0.0172868	2571 glutamate decarboxylase 1 (brain, 67kDa)
GO intracellular	145	1794	0.0172868	25946 zinc finger protein 385A
GO intracellular	145	1794	0.0172868	26030 pleckstrin homology domain containing, family G (with RhoGef domain)
GO intracellular	145	1794	0.0172868	2737 GLI family zinc finger 3
GO intracellular	145	1794	0.0172868	27434 polymerase (DNA directed), mu
GO intracellular	145	1794	0.0172868	2752 glutamate-ammonia ligase (glutamine synthetase)
GO intracellular	145	1794	0.0172868	284346 zinc finger protein 575

GO intracellular	145	1794	0.0172868	29108 PYD and CARD domain containing
GO intracellular	145	1794	0.0172868	29116 myosin regulatory light chain interacting protein
GO intracellular	145	1794	0.0172868	29760 B-cell linker
GO intracellular	145	1794	0.0172868	342908 zinc finger protein 404
GO intracellular	145	1794	0.0172868	345462 zinc finger protein 879
GO intracellular	145	1794	0.0172868	379 ADP-ribosylation factor-like 4D
GO intracellular	145	1794	0.0172868	3845 v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog
GO intracellular	145	1794	0.0172868	388536 zinc finger protein 790
GO intracellular	145	1794	0.0172868	388558 zinc finger protein 808
GO intracellular	145	1794	0.0172868	388567 zinc finger protein 749
GO intracellular	145	1794	0.0172868	388591 ring finger protein 207
GO intracellular	145	1794	0.0172868	388743 calpain 8
GO intracellular	145	1794	0.0172868	389058 Sp5 transcription factor
GO intracellular	145	1794	0.0172868	389337 Rho guanine nucleotide exchange factor (GEF) 37
GO intracellular	145	1794	0.0172868	395 Rho GTPase activating protein 6
GO intracellular	145	1794	0.0172868	400713 zinc finger protein 880
GO intracellular	145	1794	0.0172868	4087 SMAD family member 2
GO intracellular	145	1794	0.0172868	4194 Mdm4 p53 binding protein homolog (mouse)
GO intracellular	145	1794	0.0172868	440107 pleckstrin homology domain containing, family G (with RhoGef domain)
GO intracellular	145	1794	0.0172868	4784 nuclear factor I/X (CCAAT-binding transcription factor)
GO intracellular	145	1794	0.0172868	4802 nuclear transcription factor Y, gamma
GO intracellular	145	1794	0.0172868	51274 Kruppel-like factor 3 (basic)
GO intracellular	145	1794	0.0172868	51621 Kruppel-like factor 13
GO intracellular	145	1794	0.0172868	51655 RAS, dexamethasone-induced 1
GO intracellular	145	1794	0.0172868	51710 zinc finger protein 44
GO intracellular	145	1794	0.0172868	5295 phosphoinositide-3-kinase, regulatory subunit 1 (alpha)
GO intracellular	145	1794	0.0172868	5325 pleiomorphic adenoma gene-like 1
GO intracellular	145	1794	0.0172868	5362 plexin A2
GO intracellular	145	1794	0.0172868	5371 promyelocytic leukemia
GO intracellular	145	1794	0.0172868	54769 DIRAS family, GTP-binding RAS-like 2
GO intracellular	145	1794	0.0172868	54848 Rho guanine nucleotide exchange factor (GEF) 38
GO intracellular	145	1794	0.0172868	54932 exonuclease 3'-5' domain containing 3
GO intracellular	145	1794	0.0172868	55160 Rho guanine nucleotide exchange factor (GEF) 10-like
GO intracellular	145	1794	0.0172868	55184 chromosome 20 open reading frame 12
GO intracellular	145	1794	0.0172868	55200 pleckstrin homology domain containing, family G (with RhoGef domain)
GO intracellular	145	1794	0.0172868	55357 TBC1 domain family, member 2

GO intracellular	145	1794	0.0172868	55432 YOD1 OTU deubiquinating enzyme 1 homolog ( <i>S. cerevisiae</i> )
GO intracellular	145	1794	0.0172868	55657 zinc finger protein 692
GO intracellular	145	1794	0.0172868	55762 zinc finger protein 701
GO intracellular	145	1794	0.0172868	55769 zinc finger protein 83
GO intracellular	145	1794	0.0172868	55893 zinc finger protein 395
GO intracellular	145	1794	0.0172868	56978 PR domain containing 8
GO intracellular	145	1794	0.0172868	57139 ral guanine nucleotide dissociation stimulator-like 3
GO intracellular	145	1794	0.0172868	57186 Ral GTPase activating protein, alpha subunit 2 (catalytic)
GO intracellular	145	1794	0.0172868	57221 KIAA1244
GO intracellular	145	1794	0.0172868	57636 Rho GTPase activating protein 23
GO intracellular	145	1794	0.0172868	5900 ral guanine nucleotide dissociation stimulator
GO intracellular	145	1794	0.0172868	604 B-cell CLL/lymphoma 6
GO intracellular	145	1794	0.0172868	6239 ras responsive element binding protein 1
GO intracellular	145	1794	0.0172868	64127 nucleotide-binding oligomerization domain containing 2
GO intracellular	145	1794	0.0172868	64135 interferon induced with helicase C domain 1
GO intracellular	145	1794	0.0172868	64798 DEP domain containing 6
GO intracellular	145	1794	0.0172868	6494 signal-induced proliferation-associated 1
GO intracellular	145	1794	0.0172868	687 Kruppel-like factor 9
GO intracellular	145	1794	0.0172868	7071 Kruppel-like factor 10
GO intracellular	145	1794	0.0172868	7227 trichorhinophalangeal syndrome I
GO intracellular	145	1794	0.0172868	726 calpain 5
GO intracellular	145	1794	0.0172868	7546 Zic family member 2 (odd-paired homolog, <i>Drosophila</i> )
GO intracellular	145	1794	0.0172868	7565 zinc finger protein 17
GO intracellular	145	1794	0.0172868	7597 zinc finger and BTB domain containing 25
GO intracellular	145	1794	0.0172868	7678 zinc finger protein 124
GO intracellular	145	1794	0.0172868	79092 caspase recruitment domain family, member 14
GO intracellular	145	1794	0.0172868	79444 baculoviral IAP repeat-containing 7
GO intracellular	145	1794	0.0172868	79668 poly (ADP-ribose) polymerase family, member 8
GO intracellular	145	1794	0.0172868	79673 zinc finger protein 329
GO intracellular	145	1794	0.0172868	7984 Rho guanine nucleotide exchange factor (GEF) 5
GO intracellular	145	1794	0.0172868	79872 Cas-Br-M (murine) ecotropic retroviral transforming sequence-like 1
GO intracellular	145	1794	0.0172868	79894 zinc finger protein 672
GO intracellular	145	1794	0.0172868	81844 tripartite motif-containing 56
GO intracellular	145	1794	0.0172868	8313 axin 2
GO intracellular	145	1794	0.0172868	83394 PITPNM family member 3
GO intracellular	145	1794	0.0172868	834 caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, co



GO intracellular	145	1794	0.0172868	837 caspase 4, apoptosis-related cysteine peptidase
GO intracellular	145	1794	0.0172868	84033 obscurin, cytoskeletal calmodulin and titin-interacting RhoGEF
GO intracellular	145	1794	0.0172868	84124 zinc finger protein 394
GO intracellular	145	1794	0.0172868	84159 AT rich interactive domain 5B (MRF1-like)
GO intracellular	145	1794	0.0172868	8462 Kruppel-like factor 11
GO intracellular	145	1794	0.0172868	84674 caspase recruitment domain family, member 6
GO intracellular	145	1794	0.0172868	84858 zinc finger protein 503
GO intracellular	145	1794	0.0172868	84911 zinc finger protein 382
GO intracellular	145	1794	0.0172868	85004 RAS-like, estrogen-regulated, growth inhibitor
GO intracellular	145	1794	0.0172868	85416 Zic family member 5 (odd-paired homolog, Drosophila)
GO intracellular	145	1794	0.0172868	85441 peroxisomal proliferator-activated receptor A interacting complex 285
GO intracellular	145	1794	0.0172868	89870 tripartite motif-containing 15
GO intracellular	145	1794	0.0172868	8996 nucleolar protein 3 (apoptosis repressor with CARD domain)
GO intracellular	145	1794	0.0172868	90592 zinc finger protein 700
GO intracellular	145	1794	0.0172868	92283 zinc finger protein 461
GO intracellular	145	1794	0.0172868	92822 zinc finger protein 276
GO intracellular	145	1794	0.0172868	9314 Kruppel-like factor 4 (gut)
GO intracellular	145	1794	0.0172868	94059 leukocyte receptor cluster (LRC) member 9
GO intracellular	145	1794	0.0172868	9422 zinc finger protein 264
GO intracellular	145	1794	0.0172868	9459 Rac/Cdc42 guanine nucleotide exchange factor (GEF) 6
GO intracellular	145	1794	0.0172868	9615 guanine deaminase
GO blood vessel development	7	40	0.0175194	183 angiotensinogen (serpin peptidase inhibitor, clade A, member 8)
GO blood vessel development	7	40	0.0175194	1969 EPH receptor A2
GO blood vessel development	7	40	0.0175194	2296 forkhead box C1
GO blood vessel development	7	40	0.0175194	2303 forkhead box C2 (MFH-1, mesenchyme forkhead 1)
GO blood vessel development	7	40	0.0175194	4005 LIM domain only 2 (rhombotin-like 1)
GO blood vessel development	7	40	0.0175194	4015 lysyl oxidase
GO blood vessel development	7	40	0.0175194	652 bone morphogenetic protein 4
GO positive regulation of glucose import	5	23	0.0176969	2066 v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian)
GO positive regulation of glucose import	5	23	0.0176969	3643 insulin receptor
GO positive regulation of glucose import	5	23	0.0176969	5295 phosphoinositide-3-kinase, regulatory subunit 1 (alpha)
GO positive regulation of glucose import	5	23	0.0176969	55600 intelectin 1 (galactofuranose binding)
GO positive regulation of glucose import	5	23	0.0176969	8660 insulin receptor substrate 2
GO negative regulation of cell adhesion	5	23	0.0176969	375056 melanoma inhibitory activity family, member 3
GO negative regulation of cell adhesion	5	23	0.0176969	3827 kininogen 1
GO negative regulation of cell adhesion	5	23	0.0176969	6494 signal-induced proliferation-associated 1

GO	negative regulation of cell adhesion	5	23	0.0176969	79872	Cas-Br-M (murine) ecotropic retroviral transforming sequence-like 1
GO	negative regulation of cell adhesion	5	23	0.0176969	94	activin A receptor type II-like 1
GO	SH3/SH2 adaptor activity	8	50	0.0192139	10140	transducer of ERBB2, 1
GO	SH3/SH2 adaptor activity	8	50	0.0192139	1124	chimerin (chimaerin) 2
GO	SH3/SH2 adaptor activity	8	50	0.0192139	29760	B-cell linker
GO	SH3/SH2 adaptor activity	8	50	0.0192139	395	Rho GTPase activating protein 6
GO	SH3/SH2 adaptor activity	8	50	0.0192139	55824	phosphoprotein associated with glycosphingolipid microdomains 1
GO	SH3/SH2 adaptor activity	8	50	0.0192139	6452	SH3-domain binding protein 2
GO	SH3/SH2 adaptor activity	8	50	0.0192139	84941	hematopoietic SH2 domain containing
GO	SH3/SH2 adaptor activity	8	50	0.0192139	8631	src kinase associated phosphoprotein 1
GO	response to estrogen stimulus	8	50	0.0192139	10568	solute carrier family 34 (sodium phosphate), member 2
GO	response to estrogen stimulus	8	50	0.0192139	1080	cystic fibrosis transmembrane conductance regulator (ATP-binding cas-
GO	response to estrogen stimulus	8	50	0.0192139	2033	E1A binding protein p300
GO	response to estrogen stimulus	8	50	0.0192139	2947	glutathione S-transferase mu 3 (brain)
GO	response to estrogen stimulus	8	50	0.0192139	3949	low density lipoprotein receptor
GO	response to estrogen stimulus	8	50	0.0192139	412	steroid sulfatase (microsomal), isozyme S
GO	response to estrogen stimulus	8	50	0.0192139	760	carbonic anhydrase II
GO	response to estrogen stimulus	8	50	0.0192139	7706	tripartite motif-containing 25
GO	blood vessel morphogenesis	3	9	0.0195873	1906	endothelin 1
GO	blood vessel morphogenesis	3	9	0.0195873	5327	plasminogen activator, tissue
GO	blood vessel morphogenesis	3	9	0.0195873	7026	nuclear receptor subfamily 2, group F, member 2
GO	cytoplasmic sequestering of transcrip	3	9	0.0195873	4792	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhib
GO	cytoplasmic sequestering of transcrip	3	9	0.0195873	4794	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhib
GO	cytoplasmic sequestering of transcrip	3	9	0.0195873	4795	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhib
GO	oxidoreductase activity	40	418	0.0196684	10170	dehydrogenase/reductase (SDR family) member 9
GO	oxidoreductase activity	40	418	0.0196684	10826	chromosome 5 open reading frame 4
GO	oxidoreductase activity	40	418	0.0196684	112724	retinol dehydrogenase 13 (all-trans/9-cis)
GO	oxidoreductase activity	40	418	0.0196684	124	alcohol dehydrogenase 1A (class I), alpha polypeptide
GO	oxidoreductase activity	40	418	0.0196684	125	alcohol dehydrogenase 1B (class I), beta polypeptide
GO	oxidoreductase activity	40	418	0.0196684	1559	cytochrome P450, family 2, subfamily C, polypeptide 9
GO	oxidoreductase activity	40	418	0.0196684	1571	cytochrome P450, family 2, subfamily E, polypeptide 1
GO	oxidoreductase activity	40	418	0.0196684	157506	retinol dehydrogenase 10 (all-trans)
GO	oxidoreductase activity	40	418	0.0196684	1577	cytochrome P450, family 3, subfamily A, polypeptide 5
GO	oxidoreductase activity	40	418	0.0196684	195814	short chain dehydrogenase/reductase family 16C, member 5
GO	oxidoreductase activity	40	418	0.0196684	2153	coagulation factor V (proaccelerin, labile factor)
GO	oxidoreductase activity	40	418	0.0196684	23081	lysine (K)-specific demethylase 4C

GO oxidoreductase activity	40	418	0.0196684	240 arachidonate 5-lipoxygenase
GO oxidoreductase activity	40	418	0.0196684	254295 phytanoyl-CoA dioxygenase domain containing 1
GO oxidoreductase activity	40	418	0.0196684	27035 NADPH oxidase 1
GO oxidoreductase activity	40	418	0.0196684	316 aldehyde oxidase 1
GO oxidoreductase activity	40	418	0.0196684	3294 hydroxysteroid (17-beta) dehydrogenase 2
GO oxidoreductase activity	40	418	0.0196684	345275 hydroxysteroid (17-beta) dehydrogenase 13
GO oxidoreductase activity	40	418	0.0196684	4015 lysyl oxidase
GO oxidoreductase activity	40	418	0.0196684	4128 monoamine oxidase A
GO oxidoreductase activity	40	418	0.0196684	4129 monoamine oxidase B
GO oxidoreductase activity	40	418	0.0196684	4524 5,10-methylenetetrahydrofolate reductase (NADPH)
GO oxidoreductase activity	40	418	0.0196684	4842 nitric oxide synthase 1 (neuronal)
GO oxidoreductase activity	40	418	0.0196684	55068 ecto-NOX disulfide-thiol exchanger 1
GO oxidoreductase activity	40	418	0.0196684	55693 lysine (K)-specific demethylase 4D
GO oxidoreductase activity	40	418	0.0196684	56605 ERO1-like beta ( <i>S. cerevisiae</i> )
GO oxidoreductase activity	40	418	0.0196684	5742 prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and
GO oxidoreductase activity	40	418	0.0196684	5768 quiescin Q6 sulfhydryl oxidase 1
GO oxidoreductase activity	40	418	0.0196684	59344 arachidonate lipoxygenase 3
GO oxidoreductase activity	40	418	0.0196684	622 3-hydroxybutyrate dehydrogenase, type 1
GO oxidoreductase activity	40	418	0.0196684	64359 nucleoredoxin
GO oxidoreductase activity	40	418	0.0196684	7001 peroxiredoxin 2
GO oxidoreductase activity	40	418	0.0196684	7404 ubiquitously transcribed tetratricopeptide repeat gene, Y-linked
GO oxidoreductase activity	40	418	0.0196684	79152 fatty acid 2-hydroxylase
GO oxidoreductase activity	40	418	0.0196684	79689 STEAP family member 4
GO oxidoreductase activity	40	418	0.0196684	84171 lysyl oxidase-like 4
GO oxidoreductase activity	40	418	0.0196684	8418 cytidine monophosphate-N-acetylneuraminic acid hydroxylase (CMP-N
GO oxidoreductase activity	40	418	0.0196684	84795 pyridine nucleotide-disulphide oxidoreductase domain 2
GO oxidoreductase activity	40	418	0.0196684	8514 potassium voltage-gated channel, shaker-related subfamily, beta mem
GO oxidoreductase activity	40	418	0.0196684	9563 hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase)
GO negative regulation of MAP kinase ac	4	16	0.0203699	10252 sprouty homolog 1, antagonist of FGF signaling ( <i>Drosophila</i> )
GO negative regulation of MAP kinase ac	4	16	0.0203699	10253 sprouty homolog 2 ( <i>Drosophila</i> )
GO negative regulation of MAP kinase ac	4	16	0.0203699	11213 interleukin-1 receptor-associated kinase 3
GO negative regulation of MAP kinase ac	4	16	0.0203699	652 bone morphogenetic protein 4
GO positive regulation of endothelial cell	4	16	0.0203699	183 angiotensinogen (serpin peptidase inhibitor, clade A, member 8)
GO positive regulation of endothelial cell	4	16	0.0203699	1906 endothelin 1
GO positive regulation of endothelial cell	4	16	0.0203699	652 bone morphogenetic protein 4
GO positive regulation of endothelial cell	4	16	0.0203699	7474 wntless-type MMTV integration site family, member 5A

GO	membrane depolarization	4	16	0.0203699	1906 endothelin 1
GO	membrane depolarization	4	16	0.0203699	3725 jun oncogene
GO	membrane depolarization	4	16	0.0203699	5025 purinergic receptor P2X, ligand-gated ion channel, 4
GO	membrane depolarization	4	16	0.0203699	8973 cholinergic receptor, nicotinic, alpha 6
GO	SMAD protein signal transduction	4	16	0.0203699	2353 FBJ murine osteosarcoma viral oncogene homolog
GO	SMAD protein signal transduction	4	16	0.0203699	28996 homeodomain interacting protein kinase 2
GO	SMAD protein signal transduction	4	16	0.0203699	3725 jun oncogene
GO	SMAD protein signal transduction	4	16	0.0203699	652 bone morphogenetic protein 4
GO	positive regulation of vasoconstrictio	4	16	0.0203699	240 arachidonate 5-lipoxygenase
GO	positive regulation of vasoconstrictio	4	16	0.0203699	4886 neuropeptide Y receptor Y1
GO	positive regulation of vasoconstrictio	4	16	0.0203699	5742 prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase a
GO	positive regulation of vasoconstrictio	4	16	0.0203699	952 CD38 molecule
GO	negative regulation of transcription, l	12	91	0.0208708	2122 MDS1 and EVI1 complex locus
GO	negative regulation of transcription, l	12	91	0.0208708	2290 forkhead box G1
GO	negative regulation of transcription, l	12	91	0.0208708	22904 strawberry notch homolog 2 (Drosophila)
GO	negative regulation of transcription, l	12	91	0.0208708	23119 hypermethylated in cancer 2
GO	negative regulation of transcription, l	12	91	0.0208708	4087 SMAD family member 2
GO	negative regulation of transcription, l	12	91	0.0208708	5083 paired box 9
GO	negative regulation of transcription, l	12	91	0.0208708	51085 MLX interacting protein-like
GO	negative regulation of transcription, l	12	91	0.0208708	51655 RAS, dexamethasone-induced 1
GO	negative regulation of transcription, l	12	91	0.0208708	7227 trichorhinophalangeal syndrome I
GO	negative regulation of transcription, l	12	91	0.0208708	84159 AT rich interactive domain 5B (MRF1-like)
GO	negative regulation of transcription, l	12	91	0.0208708	8553 basic helix-loop-helix family, member e40
GO	negative regulation of transcription, l	12	91	0.0208708	9314 Kruppel-like factor 4 (gut)
GO	positive regulation of nitric oxide bio:	5	24	0.0211278	1906 endothelin 1
GO	positive regulation of nitric oxide bio:	5	24	0.0211278	3643 insulin receptor
GO	positive regulation of nitric oxide bio:	5	24	0.0211278	5025 purinergic receptor P2X, ligand-gated ion channel, 4
GO	positive regulation of nitric oxide bio:	5	24	0.0211278	7097 toll-like receptor 2
GO	positive regulation of nitric oxide bio:	5	24	0.0211278	7099 toll-like receptor 4
GO	response to insulin stimulus	8	51	0.0214672	130399 activin A receptor, type IC
GO	response to insulin stimulus	8	51	0.0214672	1958 early growth response 1
GO	response to insulin stimulus	8	51	0.0214672	1959 early growth response 2
GO	response to insulin stimulus	8	51	0.0214672	5465 peroxisome proliferator-activated receptor alpha
GO	response to insulin stimulus	8	51	0.0214672	5950 retinol binding protein 4, plasma
GO	response to insulin stimulus	8	51	0.0214672	7097 toll-like receptor 2
GO	response to insulin stimulus	8	51	0.0214672	7099 toll-like receptor 4

GO response to insulin stimulus	8	51	0.0214672	9021 suppressor of cytokine signaling 3
GO cell growth	7	42	0.0225346	2263 fibroblast growth factor receptor 2
GO cell growth	7	42	0.0225346	26281 fibroblast growth factor 20
GO cell growth	7	42	0.0225346	4853 Notch homolog 2 (Drosophila)
GO cell growth	7	42	0.0225346	54904 Wolf-Hirschhorn syndrome candidate 1-like 1
GO cell growth	7	42	0.0225346	7049 transforming growth factor, beta receptor III
GO cell growth	7	42	0.0225346	8527 diacylglycerol kinase, delta 130kDa
GO cell growth	7	42	0.0225346	8992 ATPase, H+ transporting, lysosomal 9kDa, V0 subunit e1
GO heart development	14	114	0.0234467	116113 forkhead box P4
GO heart development	14	114	0.0234467	1906 endothelin 1
GO heart development	14	114	0.0234467	2033 E1A binding protein p300
GO heart development	14	114	0.0234467	2200 fibrillin 1
GO heart development	14	114	0.0234467	2296 forkhead box C1
GO heart development	14	114	0.0234467	27295 PDZ and LIM domain 3
GO heart development	14	114	0.0234467	2737 GLI family zinc finger 3
GO heart development	14	114	0.0234467	4151 myoglobin
GO heart development	14	114	0.0234467	4851 Notch homolog 1, translocation-associated (Drosophila)
GO heart development	14	114	0.0234467	5318 plakophilin 2
GO heart development	14	114	0.0234467	5463 POU class 6 homeobox 1
GO heart development	14	114	0.0234467	5950 retinol binding protein 4, plasma
GO heart development	14	114	0.0234467	6256 retinoid X receptor, alpha
GO heart development	14	114	0.0234467	9734 histone deacetylase 9
GO skeletal system development	15	125	0.0235015	1009 cadherin 11, type 2, OB-cadherin (osteoblast)
GO skeletal system development	15	125	0.0235015	1969 EPH receptor A2
GO skeletal system development	15	125	0.0235015	2114 v-ets erythroblastosis virus E26 oncogene homolog 2 (avian)
GO skeletal system development	15	125	0.0235015	2200 fibrillin 1
GO skeletal system development	15	125	0.0235015	2296 forkhead box C1
GO skeletal system development	15	125	0.0235015	2303 forkhead box C2 (MFH-1, mesenchyme forkhead 1)
GO skeletal system development	15	125	0.0235015	3479 insulin-like growth factor 1 (somatomedin C)
GO skeletal system development	15	125	0.0235015	3958 lectin, galactoside-binding, soluble, 3
GO skeletal system development	15	125	0.0235015	5307 paired-like homeodomain 1
GO skeletal system development	15	125	0.0235015	56172 ankylosis, progressive homolog (mouse)
GO skeletal system development	15	125	0.0235015	7071 Kruppel-like factor 10
GO skeletal system development	15	125	0.0235015	7092 tolloid-like 1
GO skeletal system development	15	125	0.0235015	7227 trichorhinophalangeal syndrome I
GO skeletal system development	15	125	0.0235015	8646 chordin

GO skeletal system development	15	125	0.0235015	9060 3'-phosphoadenosine 5'-phosphosulfate synthase 2
GO response to peptide hormone stimuli	9	62	0.0243001	1080 cystic fibrosis transmembrane conductance regulator (ATP-binding cas:
GO response to peptide hormone stimuli	9	62	0.0243001	1508 cathepsin B
GO response to peptide hormone stimuli	9	62	0.0243001	3570 interleukin 6 receptor
GO response to peptide hormone stimuli	9	62	0.0243001	3726 jun B proto-oncogene
GO response to peptide hormone stimuli	9	62	0.0243001	412 steroid sulfatase (microsomal), isozyme S
GO response to peptide hormone stimuli	9	62	0.0243001	5122 proprotein convertase subtilisin/kexin type 1
GO response to peptide hormone stimuli	9	62	0.0243001	5327 plasminogen activator, tissue
GO response to peptide hormone stimuli	9	62	0.0243001	682 basigin (Ok blood group)
GO response to peptide hormone stimuli	9	62	0.0243001	8013 nuclear receptor subfamily 4, group A, member 3
GO positive regulation of transcription fa	5	25	0.0249642	10014 histone deacetylase 5
GO positive regulation of transcription fa	5	25	0.0249642	10891 peroxisome proliferator-activated receptor gamma, coactivator 1 alpha
GO positive regulation of transcription fa	5	25	0.0249642	2033 E1A binding protein p300
GO positive regulation of transcription fa	5	25	0.0249642	3169 forkhead box A1
GO positive regulation of transcription fa	5	25	0.0249642	3569 interleukin 6 (interferon, beta 2)
GO brown fat cell differentiation	5	25	0.0249642	10891 peroxisome proliferator-activated receptor gamma, coactivator 1 alpha
GO brown fat cell differentiation	5	25	0.0249642	116844 leucine-rich alpha-2-glycoprotein 1
GO brown fat cell differentiation	5	25	0.0249642	154 adrenergic, beta-2-, receptor, surface
GO brown fat cell differentiation	5	25	0.0249642	3914 laminin, beta 3
GO brown fat cell differentiation	5	25	0.0249642	4151 myoglobin
GO activation of JUN kinase activity	5	25	0.0249642	2205 Fc fragment of IgE, high affinity I, receptor for; alpha polypeptide
GO activation of JUN kinase activity	5	25	0.0249642	4293 mitogen-activated protein kinase kinase kinase 9
GO activation of JUN kinase activity	5	25	0.0249642	6850 spleen tyrosine kinase
GO activation of JUN kinase activity	5	25	0.0249642	79444 baculoviral IAP repeat-containing 7
GO activation of JUN kinase activity	5	25	0.0249642	9064 mitogen-activated protein kinase kinase kinase 6
GO organ morphogenesis	14	115	0.0250801	10253 sprouty homolog 2 (Drosophila)
GO organ morphogenesis	14	115	0.0250801	157506 retinol dehydrogenase 10 (all-trans)
GO organ morphogenesis	14	115	0.0250801	1948 ephrin-B2
GO organ morphogenesis	14	115	0.0250801	2033 E1A binding protein p300
GO organ morphogenesis	14	115	0.0250801	28959 transmembrane protein 176B
GO organ morphogenesis	14	115	0.0250801	3687 integrin, alpha X (complement component 3 receptor 4 subunit)
GO organ morphogenesis	14	115	0.0250801	3911 laminin, alpha 5
GO organ morphogenesis	14	115	0.0250801	3983 actin binding LIM protein 1
GO organ morphogenesis	14	115	0.0250801	4853 Notch homolog 2 (Drosophila)
GO organ morphogenesis	14	115	0.0250801	5308 paired-like homeodomain 2
GO organ morphogenesis	14	115	0.0250801	6850 spleen tyrosine kinase

GO organ morphogenesis	14	115	0.0250801	7089 transducin-like enhancer of split 2 (E(sp1) homolog, Drosophila)
GO organ morphogenesis	14	115	0.0250801	7090 transducin-like enhancer of split 3 (E(sp1) homolog, Drosophila)
GO organ morphogenesis	14	115	0.0250801	8600 tumor necrosis factor (ligand) superfamily, member 11
GO positive regulation of calcium-mediated signaling	4	17	0.0252293	2205 Fc fragment of IgE, high affinity I, receptor for; alpha polypeptide
GO positive regulation of calcium-mediated signaling	4	17	0.0252293	4684 neural cell adhesion molecule 1
GO positive regulation of calcium-mediated signaling	4	17	0.0252293	5025 purinergic receptor P2X, ligand-gated ion channel, 4
GO positive regulation of calcium-mediated signaling	4	17	0.0252293	6850 spleen tyrosine kinase
GO nitrogen compound metabolic process	4	17	0.0252293	2752 glutamate-ammonia ligase (glutamine synthetase)
GO nitrogen compound metabolic process	4	17	0.0252293	4817 nitrilase 1
GO nitrogen compound metabolic process	4	17	0.0252293	84159 AT rich interactive domain 5B (MRF1-like)
GO nitrogen compound metabolic process	4	17	0.0252293	8875 vanin 2
GO endoderm development	4	17	0.0252293	3175 one cut homeobox 1
GO endoderm development	4	17	0.0252293	4087 SMAD family member 2
GO endoderm development	4	17	0.0252293	4851 Notch homolog 1, translocation-associated (Drosophila)
GO endoderm development	4	17	0.0252293	5083 paired box 9
GO 1-acylglycerophosphocholine O-acyltransferase activity	2	4	0.0255251	10162 lysophosphatidylcholine acyltransferase 3
GO 1-acylglycerophosphocholine O-acyltransferase activity	2	4	0.0255251	54947 lysophosphatidylcholine acyltransferase 2
GO proton-transporting two-sector ATPase activity	2	4	0.0255251	10312 T-cell, immune regulator 1, ATPase, H+ transporting, lysosomal V0 subunit
GO proton-transporting two-sector ATPase activity	2	4	0.0255251	50617 ATPase, H+ transporting, lysosomal V0 subunit a4
GO positive regulation of fatty acid oxidation	2	4	0.0255251	10891 peroxisome proliferator-activated receptor gamma, coactivator 1 alpha
GO positive regulation of fatty acid oxidation	2	4	0.0255251	5465 peroxisome proliferator-activated receptor alpha
GO MyD88-dependent toll-like receptor signaling pathway	2	4	0.0255251	11213 interleukin-1 receptor-associated kinase 3
GO MyD88-dependent toll-like receptor signaling pathway	2	4	0.0255251	7097 toll-like receptor 2
GO alcohol dehydrogenase activity, zinc-dependent	2	4	0.0255251	124 alcohol dehydrogenase 1A (class I), alpha polypeptide
GO alcohol dehydrogenase activity, zinc-dependent	2	4	0.0255251	125 alcohol dehydrogenase 1B (class I), beta polypeptide
GO glial cell migration	2	4	0.0255251	1462 versican
GO glial cell migration	2	4	0.0255251	4692 necdin homolog (mouse)
GO phospholipid translocation	2	4	0.0255251	148229 ATPase, class I, type 8B, member 3
GO phospholipid translocation	2	4	0.0255251	3783 potassium intermediate/small conductance calcium-activated channel, subfamily A, member 1
GO caffeine oxidase activity	2	4	0.0255251	1558 cytochrome P450, family 2, subfamily C, polypeptide 8
GO caffeine oxidase activity	2	4	0.0255251	1559 cytochrome P450, family 2, subfamily C, polypeptide 9
GO drug catabolic process	2	4	0.0255251	1559 cytochrome P450, family 2, subfamily C, polypeptide 9
GO drug catabolic process	2	4	0.0255251	1577 cytochrome P450, family 3, subfamily A, polypeptide 5
GO Gram-positive bacterial cell surface biogenesis	2	4	0.0255251	1755 deleted in malignant brain tumors 1
GO Gram-positive bacterial cell surface biogenesis	2	4	0.0255251	7097 toll-like receptor 2
GO intercellular canaliculus	2	4	0.0255251	1803 dipeptidyl-peptidase 4

GO	intercellular canaliculus	2	4	0.0255251	5244 ATP-binding cassette, sub-family B (MDR/TAP), member 4
GO	behavioral response to ethanol	2	4	0.0255251	1813 dopamine receptor D2
GO	behavioral response to ethanol	2	4	0.0255251	1815 dopamine receptor D4
GO	cerebral cortex GABAergic interneurc	2	4	0.0255251	1813 dopamine receptor D2
GO	cerebral cortex GABAergic interneurc	2	4	0.0255251	26468 LIM homeobox 6
GO	dopamine receptor activity	2	4	0.0255251	1813 dopamine receptor D2
GO	dopamine receptor activity	2	4	0.0255251	1815 dopamine receptor D4
GO	cellular sodium ion homeostasis	2	4	0.0255251	183 angiotensinogen (serpin peptidase inhibitor, clade A, member 8)
GO	cellular sodium ion homeostasis	2	4	0.0255251	64699 transmembrane protease, serine 3
GO	positive regulation of cardiac muscle	2	4	0.0255251	183 angiotensinogen (serpin peptidase inhibitor, clade A, member 8)
GO	positive regulation of cardiac muscle	2	4	0.0255251	1906 endothelin 1
GO	regulation of blood volume by renin-i	2	4	0.0255251	183 angiotensinogen (serpin peptidase inhibitor, clade A, member 8)
GO	regulation of blood volume by renin-i	2	4	0.0255251	5972 renin
GO	bioluminescence	2	4	0.0255251	22795 nidogen 2 (osteonidogen)
GO	bioluminescence	2	4	0.0255251	83872 hemicentin 1
GO	hindgut morphogenesis	2	4	0.0255251	2737 GLI family zinc finger 3
GO	hindgut morphogenesis	2	4	0.0255251	7474 wingless-type MMTV integration site family, member 5A
GO	head morphogenesis	2	4	0.0255251	28982 feline leukemia virus subgroup C cellular receptor 1
GO	head morphogenesis	2	4	0.0255251	29123 ankyrin repeat domain 11
GO	monocyte chemotaxis	2	4	0.0255251	3569 interleukin 6 (interferon, beta 2)
GO	monocyte chemotaxis	2	4	0.0255251	3570 interleukin 6 receptor
GO	negative regulation of collagen biosyn	2	4	0.0255251	3569 interleukin 6 (interferon, beta 2)
GO	negative regulation of collagen biosyn	2	4	0.0255251	3570 interleukin 6 receptor
GO	carbon dioxide transport	2	4	0.0255251	358 aquaporin 1 (Colton blood group)
GO	carbon dioxide transport	2	4	0.0255251	760 carbonic anhydrase II
GO	cellular response to dexamethasone :	2	4	0.0255251	358 aquaporin 1 (Colton blood group)
GO	cellular response to dexamethasone :	2	4	0.0255251	652 bone morphogenetic protein 4
GO	plasma membrane organization	2	4	0.0255251	375790 agrin
GO	plasma membrane organization	2	4	0.0255251	53947 alpha 1,4-galactosyltransferase
GO	fibril	2	4	0.0255251	4586 mucin 5AC, oligomeric mucus/gel-forming
GO	fibril	2	4	0.0255251	6622 synuclein, alpha (non A4 component of amyloid precursor)
GO	negative regulation of myeloid cell di	2	4	0.0255251	4792 nuclear factor of kappa light polypeptide gene enhancer in B-cells inhib
GO	negative regulation of myeloid cell di	2	4	0.0255251	7538 zinc finger protein 36, C3H type, homolog (mouse)
GO	nucleotide-binding oligomerization d	2	4	0.0255251	4792 nuclear factor of kappa light polypeptide gene enhancer in B-cells inhib
GO	nucleotide-binding oligomerization d	2	4	0.0255251	64127 nucleotide-binding oligomerization domain containing 2
GO	response to muramyl dipeptide	2	4	0.0255251	4792 nuclear factor of kappa light polypeptide gene enhancer in B-cells inhib



GO response to muramyl dipeptide	2	4	0.0255251	64127 nucleotide-binding oligomerization domain containing 2
GO peptide YY receptor activity	2	4	0.0255251	4886 neuropeptide Y receptor Y1
GO peptide YY receptor activity	2	4	0.0255251	4889 neuropeptide Y receptor Y5
GO regulation of Wnt receptor signaling	2	4	0.0255251	5218 cyclin-dependent kinase 14
GO regulation of Wnt receptor signaling	2	4	0.0255251	83595 SRY (sex determining region Y)-box 7
GO negative regulation of appetite	2	4	0.0255251	5465 peroxisome proliferator-activated receptor alpha
GO negative regulation of appetite	2	4	0.0255251	885 cholecystokinin
GO negative regulation of sequestering c	2	4	0.0255251	5465 peroxisome proliferator-activated receptor alpha
GO negative regulation of sequestering c	2	4	0.0255251	57104 patatin-like phospholipase domain containing 2
GO negative regulation of membrane pro	2	4	0.0255251	5774 protein tyrosine phosphatase, non-receptor type 3
GO negative regulation of membrane pro	2	4	0.0255251	7076 TIMP metalloproteinase inhibitor 1
GO urinary bladder development	2	4	0.0255251	5950 retinol binding protein 4, plasma
GO urinary bladder development	2	4	0.0255251	7474 wingless-type MMTV integration site family, member 5A
GO peptide:hydrogen symporter activity	2	4	0.0255251	6564 solute carrier family 15 (oligopeptide transporter), member 1
GO peptide:hydrogen symporter activity	2	4	0.0255251	6565 solute carrier family 15 (H+/peptide transporter), member 2
GO cobalamin transport	2	4	0.0255251	6947 transcobalamin I (vitamin B12 binding protein, R binder family)
GO cobalamin transport	2	4	0.0255251	6948 transcobalamin II; macrocytic anemia
GO positive regulation of nitric-oxide syn	2	4	0.0255251	7097 toll-like receptor 2
GO positive regulation of nitric-oxide syn	2	4	0.0255251	7099 toll-like receptor 4
GO lipopolysaccharide receptor complex	2	4	0.0255251	7099 toll-like receptor 4
GO lipopolysaccharide receptor complex	2	4	0.0255251	929 CD14 molecule
GO positive regulation of bone resorptio	2	4	0.0255251	760 carbonic anhydrase II
GO positive regulation of bone resorptio	2	4	0.0255251	8600 tumor necrosis factor (ligand) superfamily, member 11
GO activation of MAPK activity	8	53	0.0265222	1139 cholinergic receptor, nicotinic, alpha 7
GO activation of MAPK activity	8	53	0.0265222	1815 dopamine receptor D4
GO activation of MAPK activity	8	53	0.0265222	2911 glutamate receptor, metabotropic 1
GO activation of MAPK activity	8	53	0.0265222	3643 insulin receptor
GO activation of MAPK activity	8	53	0.0265222	5608 mitogen-activated protein kinase kinase 6
GO activation of MAPK activity	8	53	0.0265222	7001 peroxiredoxin 2
GO activation of MAPK activity	8	53	0.0265222	7099 toll-like receptor 4
GO activation of MAPK activity	8	53	0.0265222	7852 chemokine (C-X-C motif) receptor 4
GO dopamine metabolic process	3	10	0.026582	1813 dopamine receptor D2
GO dopamine metabolic process	3	10	0.026582	1815 dopamine receptor D4
GO dopamine metabolic process	3	10	0.026582	5071 Parkinson disease (autosomal recessive, juvenile) 2, parkin
GO prostaglandin biosynthetic process	3	10	0.026582	1906 endothelin 1
GO prostaglandin biosynthetic process	3	10	0.026582	5742 prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase a)

GO prostaglandin biosynthetic process	3	10	0.026582	6916 thromboxane A synthase 1 (platelet)
GO fatty acid transport	3	10	0.026582	2182 acyl-CoA synthetase long-chain family member 4
GO fatty acid transport	3	10	0.026582	51703 acyl-CoA synthetase long-chain family member 5
GO fatty acid transport	3	10	0.026582	5465 peroxisome proliferator-activated receptor alpha
GO R-SMAD binding	3	10	0.026582	2353 FBJ murine osteosarcoma viral oncogene homolog
GO R-SMAD binding	3	10	0.026582	3725 jun oncogene
GO R-SMAD binding	3	10	0.026582	4087 SMAD family member 2
GO prostate gland epithelium morphoge	3	10	0.026582	3169 forkhead box A1
GO prostate gland epithelium morphoge	3	10	0.026582	3479 insulin-like growth factor 1 (somatomedin C)
GO prostate gland epithelium morphoge	3	10	0.026582	4851 Notch homolog 1, translocation-associated (Drosophila)
GO defense response to Gram-negative b	3	10	0.026582	3569 interleukin 6 (interferon, beta 2)
GO defense response to Gram-negative b	3	10	0.026582	3570 interleukin 6 receptor
GO defense response to Gram-negative b	3	10	0.026582	7099 toll-like receptor 4
GO phosphoinositide 3-kinase binding	3	10	0.026582	3643 insulin receptor
GO phosphoinositide 3-kinase binding	3	10	0.026582	7099 toll-like receptor 4
GO phosphoinositide 3-kinase binding	3	10	0.026582	8660 insulin receptor substrate 2
GO metalloendopeptidase inhibitor activ	3	10	0.026582	50859 sparco/osteonectin, cwcv and kazal-like domains proteoglycan (testican)
GO metalloendopeptidase inhibitor activ	3	10	0.026582	7076 TIMP metallopeptidase inhibitor 1
GO metalloendopeptidase inhibitor activ	3	10	0.026582	8434 reversion-inducing-cysteine-rich protein with kazal motifs
GO response to virus	13	105	0.0266736	10346 tripartite motif-containing 22
GO response to virus	13	105	0.0266736	10561 interferon-induced protein 44
GO response to virus	13	105	0.0266736	11213 interleukin-1 receptor-associated kinase 3
GO response to virus	13	105	0.0266736	1755 deleted in malignant brain tumors 1
GO response to virus	13	105	0.0266736	3428 interferon, gamma-inducible protein 16
GO response to virus	13	105	0.0266736	3665 interferon regulatory factor 7
GO response to virus	13	105	0.0266736	4486 macrophage stimulating 1 receptor (c-met-related tyrosine kinase)
GO response to virus	13	105	0.0266736	4599 myxovirus (influenza virus) resistance 1, interferon-inducible protein p1
GO response to virus	13	105	0.0266736	4600 myxovirus (influenza virus) resistance 2 (mouse)
GO response to virus	13	105	0.0266736	64135 interferon induced with helicase C domain 1
GO response to virus	13	105	0.0266736	684 bone marrow stromal cell antigen 2
GO response to virus	13	105	0.0266736	7706 tripartite motif-containing 25
GO response to virus	13	105	0.0266736	7852 chemokine (C-X-C motif) receptor 4
GO peptidase activity	43	465	0.0268423	10942 protease, serine, 21 (testisin)
GO peptidase activity	43	465	0.0268423	11202 kallikrein-related peptidase 8
GO peptidase activity	43	465	0.0268423	121665 signal peptide peptidase 3
GO peptidase activity	43	465	0.0268423	1363 carboxypeptidase E

GO	peptidase activity	43	465	0.0268423	1368	carboxypeptidase M
GO	peptidase activity	43	465	0.0268423	1508	cathepsin B
GO	peptidase activity	43	465	0.0268423	1519	cathepsin O
GO	peptidase activity	43	465	0.0268423	1540	cylindromatosis (turban tumor syndrome)
GO	peptidase activity	43	465	0.0268423	170692	ADAM metallopeptidase with thrombospondin type 1 motif, 18
GO	peptidase activity	43	465	0.0268423	1803	dipeptidyl-peptidase 4
GO	peptidase activity	43	465	0.0268423	255738	proprotein convertase subtilisin/kexin type 9
GO	peptidase activity	43	465	0.0268423	25825	beta-site APP-cleaving enzyme 2
GO	peptidase activity	43	465	0.0268423	25862	ubiquitin specific peptidase 49
GO	peptidase activity	43	465	0.0268423	388743	calpain 8
GO	peptidase activity	43	465	0.0268423	4316	matrix metallopeptidase 7 (matrilysin, uterine)
GO	peptidase activity	43	465	0.0268423	5046	proprotein convertase subtilisin/kexin type 6
GO	peptidase activity	43	465	0.0268423	5122	proprotein convertase subtilisin/kexin type 1
GO	peptidase activity	43	465	0.0268423	51279	complement component 1, r subcomponent-like
GO	peptidase activity	43	465	0.0268423	5327	plasminogen activator, tissue
GO	peptidase activity	43	465	0.0268423	54504	carboxypeptidase, vitellogenic-like
GO	peptidase activity	43	465	0.0268423	54933	rhomboid, veinlet-like 2 ( <i>Drosophila</i> )
GO	peptidase activity	43	465	0.0268423	55432	YOD1 OTU deubiquinating enzyme 1 homolog ( <i>S. cerevisiae</i> )
GO	peptidase activity	43	465	0.0268423	5648	mannan-binding lectin serine peptidase 1 (C4/C2 activating component)
GO	peptidase activity	43	465	0.0268423	56547	matrix metallopeptidase 26
GO	peptidase activity	43	465	0.0268423	5655	kallikrein-related peptidase 10
GO	peptidase activity	43	465	0.0268423	56649	transmembrane protease, serine 4
GO	peptidase activity	43	465	0.0268423	5696	proteasome (prosome, macropain) subunit, beta type, 8 (large multifur)
GO	peptidase activity	43	465	0.0268423	5698	proteasome (prosome, macropain) subunit, beta type, 9 (large multifur)
GO	peptidase activity	43	465	0.0268423	5699	proteasome (prosome, macropain) subunit, beta type, 10
GO	peptidase activity	43	465	0.0268423	57094	carboxypeptidase A6
GO	peptidase activity	43	465	0.0268423	5972	renin
GO	peptidase activity	43	465	0.0268423	629	complement factor B
GO	peptidase activity	43	465	0.0268423	64699	transmembrane protease, serine 3
GO	peptidase activity	43	465	0.0268423	7092	tolloid-like 1
GO	peptidase activity	43	465	0.0268423	715	complement component 1, r subcomponent
GO	peptidase activity	43	465	0.0268423	717	complement component 2
GO	peptidase activity	43	465	0.0268423	726	calpain 5
GO	peptidase activity	43	465	0.0268423	79956	endoplasmic reticulum metallopeptidase 1
GO	peptidase activity	43	465	0.0268423	834	caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, co)
GO	peptidase activity	43	465	0.0268423	837	caspase 4, apoptosis-related cysteine peptidase

GO	peptidase activity	43	465	0.0268423	8722	cathepsin F
GO	peptidase activity	43	465	0.0268423	8751	ADAM metallopeptidase domain 15
GO	peptidase activity	43	465	0.0268423	9510	ADAM metallopeptidase with thrombospondin type 1 motif, 1
GO	sugar binding	18	161	0.0268651	124220	zymogen granule protein 16 homolog B (rat)
GO	sugar binding	18	161	0.0268651	1462	versican
GO	sugar binding	18	161	0.0268651	202	absent in melanoma 1
GO	sugar binding	18	161	0.0268651	22859	latrophilin 1
GO	sugar binding	18	161	0.0268651	22925	phospholipase A2 receptor 1, 180kDa
GO	sugar binding	18	161	0.0268651	23266	latrophilin 2
GO	sugar binding	18	161	0.0268651	23284	latrophilin 3
GO	sugar binding	18	161	0.0268651	2517	fucosidase, alpha-L- 1, tissue
GO	sugar binding	18	161	0.0268651	2589	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosami
GO	sugar binding	18	161	0.0268651	374378	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosami
GO	sugar binding	18	161	0.0268651	3823	killer cell lectin-like receptor subfamily C, member 3
GO	sugar binding	18	161	0.0268651	3958	lectin, galactoside-binding, soluble, 3
GO	sugar binding	18	161	0.0268651	4065	lymphocyte antigen 75
GO	sugar binding	18	161	0.0268651	55600	intelectin 1 (galactofuranose binding)
GO	sugar binding	18	161	0.0268651	59271	chromosome 21 open reading frame 63
GO	sugar binding	18	161	0.0268651	6402	selectin L
GO	sugar binding	18	161	0.0268651	682	basigin (Ok blood group)
GO	sugar binding	18	161	0.0268651	79695	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosami
GO	protein binding	459	6249	0.0278374	10014	histone deacetylase 5
GO	protein binding	459	6249	0.0278374	10076	protein tyrosine phosphatase, receptor type, U
GO	protein binding	459	6249	0.0278374	1009	cadherin 11, type 2, OB-cadherin (osteoblast)
GO	protein binding	459	6249	0.0278374	10116	fem-1 homolog b (C. elegans)
GO	protein binding	459	6249	0.0278374	10140	transducer of ERBB2, 1
GO	protein binding	459	6249	0.0278374	10216	proteoglycan 4
GO	protein binding	459	6249	0.0278374	10221	tribbles homolog 1 (Drosophila)
GO	protein binding	459	6249	0.0278374	10252	sprouty homolog 1, antagonist of FGF signaling (Drosophila)
GO	protein binding	459	6249	0.0278374	10253	sprouty homolog 2 (Drosophila)
GO	protein binding	459	6249	0.0278374	10282	blocked early in transport 1 homolog (S. cerevisiae)
GO	protein binding	459	6249	0.0278374	10346	tripartite motif-containing 22
GO	protein binding	459	6249	0.0278374	10397	N-myc downstream regulated 1
GO	protein binding	459	6249	0.0278374	10418	spondin 1, extracellular matrix protein
GO	protein binding	459	6249	0.0278374	10435	CDC42 effector protein (Rho GTPase binding) 2
GO	protein binding	459	6249	0.0278374	10439	olfactomedin 1

GO protein binding	459	6249	0.0278374	10481 homeobox B13
GO protein binding	459	6249	0.0278374	10628 thioredoxin interacting protein
GO protein binding	459	6249	0.0278374	10769 polo-like kinase 2 (Drosophila)
GO protein binding	459	6249	0.0278374	1080 cystic fibrosis transmembrane conductance regulator (ATP-binding cas
GO protein binding	459	6249	0.0278374	10811 NADPH oxidase activator 1
GO protein binding	459	6249	0.0278374	10891 peroxisome proliferator-activated receptor gamma, coactivator 1 alpha
GO protein binding	459	6249	0.0278374	10906 TRAF-type zinc finger domain containing 1
GO protein binding	459	6249	0.0278374	10912 growth arrest and DNA-damage-inducible, gamma
GO protein binding	459	6249	0.0278374	10913 ectodysplasin A receptor
GO protein binding	459	6249	0.0278374	11030 RNA binding protein with multiple splicing
GO protein binding	459	6249	0.0278374	11043 midline 2
GO protein binding	459	6249	0.0278374	11074 tripartite motif-containing 31
GO protein binding	459	6249	0.0278374	11078 TRIO and F-actin binding protein
GO protein binding	459	6249	0.0278374	1114 chromogranin B (secretogranin 1)
GO protein binding	459	6249	0.0278374	11147 HERV-H LTR-associating 3
GO protein binding	459	6249	0.0278374	11155 LIM domain binding 3
GO protein binding	459	6249	0.0278374	11156 protein tyrosine phosphatase type IVA, member 3
GO protein binding	459	6249	0.0278374	112 adenylate cyclase 6
GO protein binding	459	6249	0.0278374	11200 CHK2 checkpoint homolog (S. pombe)
GO protein binding	459	6249	0.0278374	11202 kallikrein-related peptidase 8
GO protein binding	459	6249	0.0278374	11213 interleukin-1 receptor-associated kinase 3
GO protein binding	459	6249	0.0278374	1124 chimerin (chimaerin) 2
GO protein binding	459	6249	0.0278374	112574 sorting nexin 18
GO protein binding	459	6249	0.0278374	113263 glucocorticoid induced transcript 1
GO protein binding	459	6249	0.0278374	113278 chromosome 20 open reading frame 54
GO protein binding	459	6249	0.0278374	1139 cholinergic receptor, nicotinic, alpha 7
GO protein binding	459	6249	0.0278374	114569 mal, T-cell differentiation protein 2
GO protein binding	459	6249	0.0278374	1152 creatine kinase, brain
GO protein binding	459	6249	0.0278374	1154 cytokine inducible SH2-containing protein
GO protein binding	459	6249	0.0278374	116071 basic leucine zipper transcription factor, ATF-like 2
GO protein binding	459	6249	0.0278374	116844 leucine-rich alpha-2-glycoprotein 1
GO protein binding	459	6249	0.0278374	117157 SH2 domain containing 1B
GO protein binding	459	6249	0.0278374	118429 anthrax toxin receptor 2
GO protein binding	459	6249	0.0278374	118987 PDZ domain containing 8
GO protein binding	459	6249	0.0278374	121227 leucine-rich repeats and immunoglobulin-like domains 3
GO protein binding	459	6249	0.0278374	123 perilipin 2

GO protein binding	459	6249	0.0278374	124 alcohol dehydrogenase 1A (class I), alpha polypeptide
GO protein binding	459	6249	0.0278374	126147 netrin 5
GO protein binding	459	6249	0.0278374	127933 U2AF homology motif (UHM) kinase 1
GO protein binding	459	6249	0.0278374	135112 nuclear receptor coactivator 7
GO protein binding	459	6249	0.0278374	135644 tripartite motif-containing 40
GO protein binding	459	6249	0.0278374	1363 carboxypeptidase E
GO protein binding	459	6249	0.0278374	1373 carbamoyl-phosphate synthetase 1, mitochondrial
GO protein binding	459	6249	0.0278374	143098 membrane protein, palmitoylated 7 (MAGUK p55 subfamily member 7)
GO protein binding	459	6249	0.0278374	143425 synaptotagmin IX
GO protein binding	459	6249	0.0278374	1435 colony stimulating factor 1 (macrophage)
GO protein binding	459	6249	0.0278374	144699 F-box and leucine-rich repeat protein 14
GO protein binding	459	6249	0.0278374	145581 leucine rich repeat and fibronectin type III domain containing 5
GO protein binding	459	6249	0.0278374	147945 NLR family, pyrin domain containing 4
GO protein binding	459	6249	0.0278374	148170 CDC42 effector protein (Rho GTPase binding) 5
GO protein binding	459	6249	0.0278374	150094 salt-inducible kinase 1
GO protein binding	459	6249	0.0278374	1508 cathepsin B
GO protein binding	459	6249	0.0278374	151636 deltex 3-like (Drosophila)
GO protein binding	459	6249	0.0278374	151827 leucine rich repeat containing 34
GO protein binding	459	6249	0.0278374	154 adrenergic, beta-2-, receptor, surface
GO protein binding	459	6249	0.0278374	1540 cylindromatosis (turban tumor syndrome)
GO protein binding	459	6249	0.0278374	154043 CNKSR family member 3
GO protein binding	459	6249	0.0278374	154810 angiomin like 1
GO protein binding	459	6249	0.0278374	157638 family with sequence similarity 84, member B
GO protein binding	459	6249	0.0278374	158038 leucine rich repeat and Ig domain containing 2
GO protein binding	459	6249	0.0278374	159195 ubiquitin specific peptidase 54
GO protein binding	459	6249	0.0278374	1612 death-associated protein kinase 1
GO protein binding	459	6249	0.0278374	163590 torsin A interacting protein 2
GO protein binding	459	6249	0.0278374	165679 chromosome 3 open reading frame 57
GO protein binding	459	6249	0.0278374	168667 BMP binding endothelial regulator
GO protein binding	459	6249	0.0278374	1741 discs, large homolog 3 (Drosophila)
GO protein binding	459	6249	0.0278374	1785 dynamin 2
GO protein binding	459	6249	0.0278374	1803 dipeptidyl-peptidase 4
GO protein binding	459	6249	0.0278374	1813 dopamine receptor D2
GO protein binding	459	6249	0.0278374	1815 dopamine receptor D4
GO protein binding	459	6249	0.0278374	1820 AT rich interactive domain 3A (BRIGHT-like)
GO protein binding	459	6249	0.0278374	1821 dystrophin related protein 2

GO protein binding	459	6249	0.0278374	1822 atrophin 1
GO protein binding	459	6249	0.0278374	1843 dual specificity phosphatase 1
GO protein binding	459	6249	0.0278374	1902 lysophosphatidic acid receptor 1
GO protein binding	459	6249	0.0278374	1915 eukaryotic translation elongation factor 1 alpha 1
GO protein binding	459	6249	0.0278374	1958 early growth response 1
GO protein binding	459	6249	0.0278374	1959 early growth response 2
GO protein binding	459	6249	0.0278374	1969 EPH receptor A2
GO protein binding	459	6249	0.0278374	197259 mixed lineage kinase domain-like
GO protein binding	459	6249	0.0278374	1999 E74-like factor 3 (ets domain transcription factor, epithelial-specific )
GO protein binding	459	6249	0.0278374	201501 zinc finger and BTB domain containing 7C
GO protein binding	459	6249	0.0278374	201895 chromosome 4 open reading frame 34
GO protein binding	459	6249	0.0278374	2033 E1A binding protein p300
GO protein binding	459	6249	0.0278374	2040 stomatin
GO protein binding	459	6249	0.0278374	2044 EPH receptor A5
GO protein binding	459	6249	0.0278374	2066 v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian)
GO protein binding	459	6249	0.0278374	2114 v-ets erythroblastosis virus E26 oncogene homolog 2 (avian)
GO protein binding	459	6249	0.0278374	2117 ets variant 3
GO protein binding	459	6249	0.0278374	2122 MDS1 and EVI1 complex locus
GO protein binding	459	6249	0.0278374	2200 fibrillin 1
GO protein binding	459	6249	0.0278374	220441 ring finger protein 152
GO protein binding	459	6249	0.0278374	222223 KIAA1324-like
GO protein binding	459	6249	0.0278374	222546 regulatory factor X, 6
GO protein binding	459	6249	0.0278374	2263 fibroblast growth factor receptor 2
GO protein binding	459	6249	0.0278374	22795 nidogen 2 (osteonidogen)
GO protein binding	459	6249	0.0278374	22859 latrophilin 1
GO protein binding	459	6249	0.0278374	2290 forkhead box G1
GO protein binding	459	6249	0.0278374	22906 trafficking protein, kinesin binding 1
GO protein binding	459	6249	0.0278374	2296 forkhead box C1
GO protein binding	459	6249	0.0278374	23035 PH domain and leucine rich repeat protein phosphatase 2
GO protein binding	459	6249	0.0278374	23043 TRAF2 and NCK interacting kinase
GO protein binding	459	6249	0.0278374	23048 formin binding protein 1
GO protein binding	459	6249	0.0278374	23081 lysine (K)-specific demethylase 4C
GO protein binding	459	6249	0.0278374	23092 Rho GTPase activating protein 26
GO protein binding	459	6249	0.0278374	23095 kinesin family member 1B
GO protein binding	459	6249	0.0278374	23099 zinc finger and BTB domain containing 43
GO protein binding	459	6249	0.0278374	23179 ral guanine nucleotide dissociation stimulator-like 1

GO protein binding	459	6249	0.0278374	23199 KIAA0182
GO protein binding	459	6249	0.0278374	23208 synaptotagmin XI
GO protein binding	459	6249	0.0278374	23248 regulation of nuclear pre-mRNA domain containing 2
GO protein binding	459	6249	0.0278374	23303 kinesin family member 13B
GO protein binding	459	6249	0.0278374	2331 fibromodulin
GO protein binding	459	6249	0.0278374	23338 PHD finger protein 15
GO protein binding	459	6249	0.0278374	23365 Rho guanine nucleotide exchange factor (GEF) 12
GO protein binding	459	6249	0.0278374	23368 protein phosphatase 1, regulatory (inhibitor) subunit 13B
GO protein binding	459	6249	0.0278374	23371 tensin like C1 domain containing phosphatase (tensin 2)
GO protein binding	459	6249	0.0278374	23373 CREB regulated transcription coactivator 1
GO protein binding	459	6249	0.0278374	23387 SIK family kinase 3
GO protein binding	459	6249	0.0278374	23476 bromodomain containing 4
GO protein binding	459	6249	0.0278374	23492 chromobox homolog 7
GO protein binding	459	6249	0.0278374	2353 FBJ murine osteosarcoma viral oncogene homolog
GO protein binding	459	6249	0.0278374	23650 tripartite motif-containing 29
GO protein binding	459	6249	0.0278374	23654 plexin B2
GO protein binding	459	6249	0.0278374	23774 bromodomain containing 1
GO protein binding	459	6249	0.0278374	240 arachidonate 5-lipoxygenase
GO protein binding	459	6249	0.0278374	2521 fused in sarcoma
GO protein binding	459	6249	0.0278374	255488 ring finger protein 144B
GO protein binding	459	6249	0.0278374	2571 glutamate decarboxylase 1 (brain, 67kDa)
GO protein binding	459	6249	0.0278374	25837 RAB26, member RAS oncogene family
GO protein binding	459	6249	0.0278374	25946 zinc finger protein 385A
GO protein binding	459	6249	0.0278374	26050 SLIT and NTRK-like family, member 5
GO protein binding	459	6249	0.0278374	26119 low density lipoprotein receptor adaptor protein 1
GO protein binding	459	6249	0.0278374	2615 leucine rich repeat containing 32
GO protein binding	459	6249	0.0278374	26191 protein tyrosine phosphatase, non-receptor type 22 (lymphoid)
GO protein binding	459	6249	0.0278374	26232 F-box protein 2
GO protein binding	459	6249	0.0278374	2624 GATA binding protein 2
GO protein binding	459	6249	0.0278374	26270 F-box protein 6
GO protein binding	459	6249	0.0278374	26468 LIM homeobox 6
GO protein binding	459	6249	0.0278374	27035 NADPH oxidase 1
GO protein binding	459	6249	0.0278374	2706 gap junction protein, beta 2, 26kDa
GO protein binding	459	6249	0.0278374	2707 gap junction protein, beta 3, 31kDa
GO protein binding	459	6249	0.0278374	27134 tight junction protein 3 (zona occludens 3)
GO protein binding	459	6249	0.0278374	27165 glutaminase 2 (liver, mitochondrial)



GO protein binding	459	6249	0.0278374	27242 tumor necrosis factor receptor superfamily, member 21
GO protein binding	459	6249	0.0278374	27246 ring finger protein 115
GO protein binding	459	6249	0.0278374	27345 potassium large conductance calcium-activated channel, subfamily M,
GO protein binding	459	6249	0.0278374	2737 GLI family zinc finger 3
GO protein binding	459	6249	0.0278374	2801 golgin A2
GO protein binding	459	6249	0.0278374	286133 scavenger receptor class A, member 5 (putative)
GO protein binding	459	6249	0.0278374	28996 homeodomain interacting protein kinase 2
GO protein binding	459	6249	0.0278374	29108 PYD and CARD domain containing
GO protein binding	459	6249	0.0278374	2911 glutamate receptor, metabotropic 1
GO protein binding	459	6249	0.0278374	29116 myosin regulatory light chain interacting protein
GO protein binding	459	6249	0.0278374	29126 CD274 molecule
GO protein binding	459	6249	0.0278374	2947 glutathione S-transferase mu 3 (brain)
GO protein binding	459	6249	0.0278374	29760 B-cell linker
GO protein binding	459	6249	0.0278374	30008 EGF-containing fibulin-like extracellular matrix protein 2
GO protein binding	459	6249	0.0278374	311 annexin A11
GO protein binding	459	6249	0.0278374	3164 nuclear receptor subfamily 4, group A, member 1
GO protein binding	459	6249	0.0278374	3192 heterogeneous nuclear ribonucleoprotein U (scaffold attachment facto
GO protein binding	459	6249	0.0278374	3400 inhibitor of DNA binding 4, dominant negative helix-loop-helix protein
GO protein binding	459	6249	0.0278374	3428 interferon, gamma-inducible protein 16
GO protein binding	459	6249	0.0278374	3479 insulin-like growth factor 1 (somatomedin C)
GO protein binding	459	6249	0.0278374	3486 insulin-like growth factor binding protein 3
GO protein binding	459	6249	0.0278374	3488 insulin-like growth factor binding protein 5
GO protein binding	459	6249	0.0278374	3561 interleukin 2 receptor, gamma (severe combined immunodeficiency)
GO protein binding	459	6249	0.0278374	3570 interleukin 6 receptor
GO protein binding	459	6249	0.0278374	358 aquaporin 1 (Colton blood group)
GO protein binding	459	6249	0.0278374	3587 interleukin 10 receptor, alpha
GO protein binding	459	6249	0.0278374	3601 interleukin 15 receptor, alpha
GO protein binding	459	6249	0.0278374	3604 tumor necrosis factor receptor superfamily, member 9
GO protein binding	459	6249	0.0278374	3643 insulin receptor
GO protein binding	459	6249	0.0278374	3678 integrin, alpha 5 (fibronectin receptor, alpha polypeptide)
GO protein binding	459	6249	0.0278374	3687 integrin, alpha X (complement component 3 receptor 4 subunit)
GO protein binding	459	6249	0.0278374	3689 integrin, beta 2 (complement component 3 receptor 3 and 4 subunit)
GO protein binding	459	6249	0.0278374	3691 integrin, beta 4
GO protein binding	459	6249	0.0278374	3696 integrin, beta 8
GO protein binding	459	6249	0.0278374	3725 jun oncogene
GO protein binding	459	6249	0.0278374	3732 CD82 molecule

GO protein binding	459	6249	0.0278374	375056 melanoma inhibitory activity family, member 3
GO protein binding	459	6249	0.0278374	375449 microtubule associated serine/threonine kinase family member 4
GO protein binding	459	6249	0.0278374	375790 agrin
GO protein binding	459	6249	0.0278374	3759 potassium inwardly-rectifying channel, subfamily J, member 2
GO protein binding	459	6249	0.0278374	378925 ring finger protein 148
GO protein binding	459	6249	0.0278374	3790 potassium voltage-gated channel, delayed-rectifier, subfamily S, memb
GO protein binding	459	6249	0.0278374	3814 KiSS-1 metastasis-suppressor
GO protein binding	459	6249	0.0278374	3815 v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog
GO protein binding	459	6249	0.0278374	3845 v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog
GO protein binding	459	6249	0.0278374	387496 RAS-like, family 11, member A
GO protein binding	459	6249	0.0278374	388591 ring finger protein 207
GO protein binding	459	6249	0.0278374	389337 Rho guanine nucleotide exchange factor (GEF) 37
GO protein binding	459	6249	0.0278374	3914 laminin, beta 3
GO protein binding	459	6249	0.0278374	3949 low density lipoprotein receptor
GO protein binding	459	6249	0.0278374	3958 lectin, galactoside-binding, soluble, 3
GO protein binding	459	6249	0.0278374	3959 lectin, galactoside-binding, soluble, 3 binding protein
GO protein binding	459	6249	0.0278374	3983 actin binding LIM protein 1
GO protein binding	459	6249	0.0278374	4005 LIM domain only 2 (rhombotin-like 1)
GO protein binding	459	6249	0.0278374	4007 prickle homolog 3 (Drosophila)
GO protein binding	459	6249	0.0278374	4008 LIM domain 7
GO protein binding	459	6249	0.0278374	4015 lysyl oxidase
GO protein binding	459	6249	0.0278374	4056 leukotriene C4 synthase
GO protein binding	459	6249	0.0278374	4087 SMAD family member 2
GO protein binding	459	6249	0.0278374	4128 monoamine oxidase A
GO protein binding	459	6249	0.0278374	415116 pim-3 oncogene
GO protein binding	459	6249	0.0278374	4163 mutated in colorectal cancers
GO protein binding	459	6249	0.0278374	4170 myeloid cell leukemia sequence 1 (BCL2-related)
GO protein binding	459	6249	0.0278374	4194 Mdm4 p53 binding protein homolog (mouse)
GO protein binding	459	6249	0.0278374	4204 methyl CpG binding protein 2 (Rett syndrome)
GO protein binding	459	6249	0.0278374	4209 myocyte enhancer factor 2D
GO protein binding	459	6249	0.0278374	4223 mesenchyme homeobox 2
GO protein binding	459	6249	0.0278374	4254 KIT ligand
GO protein binding	459	6249	0.0278374	429 achaete-scute complex homolog 1 (Drosophila)
GO protein binding	459	6249	0.0278374	4306 nuclear receptor subfamily 3, group C, member 2
GO protein binding	459	6249	0.0278374	4359 myelin protein zero
GO protein binding	459	6249	0.0278374	4486 macrophage stimulating 1 receptor (c-met-related tyrosine kinase)

GO protein binding	459	6249	0.0278374	4524 5,10-methylenetetrahydrofolate reductase (NADPH)
GO protein binding	459	6249	0.0278374	4599 myxovirus (influenza virus) resistance 1, interferon-inducible protein p1
GO protein binding	459	6249	0.0278374	4613 v-myc myelocytomatosis viral related oncogene, neuroblastoma derive
GO protein binding	459	6249	0.0278374	4616 growth arrest and DNA-damage-inducible, beta
GO protein binding	459	6249	0.0278374	4638 myosin light chain kinase
GO protein binding	459	6249	0.0278374	467 activating transcription factor 3
GO protein binding	459	6249	0.0278374	4692 necdin homolog (mouse)
GO protein binding	459	6249	0.0278374	4791 nuclear factor of kappa light polypeptide gene enhancer in B-cells 2 (p4
GO protein binding	459	6249	0.0278374	4792 nuclear factor of kappa light polypeptide gene enhancer in B-cells inhib
GO protein binding	459	6249	0.0278374	4794 nuclear factor of kappa light polypeptide gene enhancer in B-cells inhib
GO protein binding	459	6249	0.0278374	4795 nuclear factor of kappa light polypeptide gene enhancer in B-cells inhib
GO protein binding	459	6249	0.0278374	48 aconitase 1, soluble
GO protein binding	459	6249	0.0278374	4802 nuclear transcription factor Y, gamma
GO protein binding	459	6249	0.0278374	4842 nitric oxide synthase 1 (neuronal)
GO protein binding	459	6249	0.0278374	4849 CCR4-NOT transcription complex, subunit 3
GO protein binding	459	6249	0.0278374	4851 Notch homolog 1, translocation-associated (Drosophila)
GO protein binding	459	6249	0.0278374	4853 Notch homolog 2 (Drosophila)
GO protein binding	459	6249	0.0278374	4886 neuropeptide Y receptor Y1
GO protein binding	459	6249	0.0278374	4915 neurotrophic tyrosine kinase, receptor, type 2
GO protein binding	459	6249	0.0278374	4929 nuclear receptor subfamily 4, group A, member 2
GO protein binding	459	6249	0.0278374	493 ATPase, Ca <sup>++</sup> transporting, plasma membrane 4
GO protein binding	459	6249	0.0278374	498 ATP synthase, H <sup>+</sup> transporting, mitochondrial F1 complex, alpha subun
GO protein binding	459	6249	0.0278374	50617 ATPase, H <sup>+</sup> transporting, lysosomal V0 subunit a4
GO protein binding	459	6249	0.0278374	5066 peptidylglycine alpha-amidating monooxygenase
GO protein binding	459	6249	0.0278374	5071 Parkinson disease (autosomal recessive, juvenile) 2, parkin
GO protein binding	459	6249	0.0278374	5083 paired box 9
GO protein binding	459	6249	0.0278374	50937 Cdon homolog (mouse)
GO protein binding	459	6249	0.0278374	51168 myosin XVA
GO protein binding	459	6249	0.0278374	5129 cyclin-dependent kinase 18
GO protein binding	459	6249	0.0278374	5152 phosphodiesterase 9A
GO protein binding	459	6249	0.0278374	51621 Kruppel-like factor 13
GO protein binding	459	6249	0.0278374	51655 RAS, dexamethasone-induced 1
GO protein binding	459	6249	0.0278374	51710 zinc finger protein 44
GO protein binding	459	6249	0.0278374	51754 transmembrane protein 8B
GO protein binding	459	6249	0.0278374	5187 period homolog 1 (Drosophila)
GO protein binding	459	6249	0.0278374	5218 cyclin-dependent kinase 14

GO protein binding	459	6249	0.0278374	5239 phosphoglucomutase 5
GO protein binding	459	6249	0.0278374	5243 ATP-binding cassette, sub-family B (MDR/TAP), member 1
GO protein binding	459	6249	0.0278374	5244 ATP-binding cassette, sub-family B (MDR/TAP), member 4
GO protein binding	459	6249	0.0278374	5284 polymeric immunoglobulin receptor
GO protein binding	459	6249	0.0278374	5295 phosphoinositide-3-kinase, regulatory subunit 1 (alpha)
GO protein binding	459	6249	0.0278374	5304 prolactin-induced protein
GO protein binding	459	6249	0.0278374	5308 paired-like homeodomain 2
GO protein binding	459	6249	0.0278374	5325 pleiomorphic adenoma gene-like 1
GO protein binding	459	6249	0.0278374	5327 plasminogen activator, tissue
GO protein binding	459	6249	0.0278374	53405 chloride intracellular channel 5
GO protein binding	459	6249	0.0278374	5346 perilipin 1
GO protein binding	459	6249	0.0278374	5371 promyelocytic leukemia
GO protein binding	459	6249	0.0278374	54361 wingless-type MMTV integration site family, member 4
GO protein binding	459	6249	0.0278374	54504 carboxypeptidase, vitellogenic-like
GO protein binding	459	6249	0.0278374	5460 POU class 5 homeobox 1
GO protein binding	459	6249	0.0278374	5465 peroxisome proliferator-activated receptor alpha
GO protein binding	459	6249	0.0278374	54877 zinc finger, CCHC domain containing 2
GO protein binding	459	6249	0.0278374	54894 ring finger protein 43
GO protein binding	459	6249	0.0278374	54904 Wolf-Hirschhorn syndrome candidate 1-like 1
GO protein binding	459	6249	0.0278374	54932 exonuclease 3'-5' domain containing 3
GO protein binding	459	6249	0.0278374	55124 piwi-like 2 (Drosophila)
GO protein binding	459	6249	0.0278374	55140 elongation protein 3 homolog ( <i>S. cerevisiae</i> )
GO protein binding	459	6249	0.0278374	55249 YY1 associated protein 1
GO protein binding	459	6249	0.0278374	55432 YOD1 OTU deubiquinating enzyme 1 homolog ( <i>S. cerevisiae</i> )
GO protein binding	459	6249	0.0278374	55705 importin 9
GO protein binding	459	6249	0.0278374	55824 phosphoprotein associated with glycosphingolipid microdomains 1
GO protein binding	459	6249	0.0278374	55867 solute carrier family 22 (organic anion/urate transporter), member 11
GO protein binding	459	6249	0.0278374	55870 ash1 (absent, small, or homeotic)-like ( <i>Drosophila</i> )
GO protein binding	459	6249	0.0278374	55909 bridging integrator 3
GO protein binding	459	6249	0.0278374	5608 mitogen-activated protein kinase kinase 6
GO protein binding	459	6249	0.0278374	56256 SERTA domain containing 4
GO protein binding	459	6249	0.0278374	56288 par-3 partitioning defective 3 homolog ( <i>C. elegans</i> )
GO protein binding	459	6249	0.0278374	5648 mannan-binding lectin serine peptidase 1 (C4/C2 activating component)
GO protein binding	459	6249	0.0278374	5696 proteasome (prosome, macropain) subunit, beta type, 8 (large multifur)
GO protein binding	459	6249	0.0278374	57132 chromatin modifying protein 1B
GO protein binding	459	6249	0.0278374	57139 ral guanine nucleotide dissociation stimulator-like 3

GO protein binding	459	6249	0.0278374	57147 SCY1-like 3 ( <i>S. cerevisiae</i> )
GO protein binding	459	6249	0.0278374	57161 pellino homolog 2 ( <i>Drosophila</i> )
GO protein binding	459	6249	0.0278374	573 BCL2-associated athanogene
GO protein binding	459	6249	0.0278374	57379 activation-induced cytidine deaminase
GO protein binding	459	6249	0.0278374	57459 GATA zinc finger domain containing 2B
GO protein binding	459	6249	0.0278374	57535 KIAA1324
GO protein binding	459	6249	0.0278374	57619 shroom family member 3
GO protein binding	459	6249	0.0278374	57620 stromal interaction molecule 2
GO protein binding	459	6249	0.0278374	57636 Rho GTPase activating protein 23
GO protein binding	459	6249	0.0278374	5774 protein tyrosine phosphatase, non-receptor type 3
GO protein binding	459	6249	0.0278374	5787 protein tyrosine phosphatase, receptor type, B
GO protein binding	459	6249	0.0278374	5789 protein tyrosine phosphatase, receptor type, D
GO protein binding	459	6249	0.0278374	5791 protein tyrosine phosphatase, receptor type, E
GO protein binding	459	6249	0.0278374	5794 protein tyrosine phosphatase, receptor type, H
GO protein binding	459	6249	0.0278374	5799 protein tyrosine phosphatase, receptor type, N polypeptide 2
GO protein binding	459	6249	0.0278374	5801 protein tyrosine phosphatase, receptor type, R
GO protein binding	459	6249	0.0278374	5873 RAB27A, member RAS oncogene family
GO protein binding	459	6249	0.0278374	5950 retinol binding protein 4, plasma
GO protein binding	459	6249	0.0278374	604 B-cell CLL/lymphoma 6
GO protein binding	459	6249	0.0278374	60485 salvador homolog 1 ( <i>Drosophila</i> )
GO protein binding	459	6249	0.0278374	6096 RAR-related orphan receptor B
GO protein binding	459	6249	0.0278374	6256 retinoid X receptor, alpha
GO protein binding	459	6249	0.0278374	627 brain-derived neurotrophic factor
GO protein binding	459	6249	0.0278374	6402 selectin L
GO protein binding	459	6249	0.0278374	64083 golgi phosphoprotein 3 (coat-protein)
GO protein binding	459	6249	0.0278374	64108 receptor (chemosensory) transporter protein 4
GO protein binding	459	6249	0.0278374	64127 nucleotide-binding oligomerization domain containing 2
GO protein binding	459	6249	0.0278374	64135 interferon induced with helicase C domain 1
GO protein binding	459	6249	0.0278374	6446 serum/glucocorticoid regulated kinase 1
GO protein binding	459	6249	0.0278374	6452 SH3-domain binding protein 2
GO protein binding	459	6249	0.0278374	64798 DEP domain containing 6
GO protein binding	459	6249	0.0278374	6505 solute carrier family 1 (neuronal/epithelial high affinity glutamate transp
GO protein binding	459	6249	0.0278374	652 bone morphogenetic protein 4
GO protein binding	459	6249	0.0278374	6521 solute carrier family 4, anion exchanger, member 1 (erythrocyte memb
GO protein binding	459	6249	0.0278374	6565 solute carrier family 15 (H <sup>+</sup> /peptide transporter), member 2
GO protein binding	459	6249	0.0278374	65999 leucine rich repeat containing 61

GO protein binding	459	6249	0.0278374	6604 SWI/SNF related, matrix associated, actin dependent regulator of chromatin
GO protein binding	459	6249	0.0278374	6622 synuclein, alpha (non A4 component of amyloid precursor)
GO protein binding	459	6249	0.0278374	6690 serine peptidase inhibitor, Kazal type 1
GO protein binding	459	6249	0.0278374	6692 serine peptidase inhibitor, Kunitz type 1
GO protein binding	459	6249	0.0278374	6710 spectrin, beta, erythrocytic
GO protein binding	459	6249	0.0278374	6778 signal transducer and activator of transcription 6, interleukin-4 inducible
GO protein binding	459	6249	0.0278374	682 basigin (Ok blood group)
GO protein binding	459	6249	0.0278374	6850 spleen tyrosine kinase
GO protein binding	459	6249	0.0278374	6857 synaptotagmin I
GO protein binding	459	6249	0.0278374	6921 transcription elongation factor B (SIII), polypeptide 1 (15kDa, elongin C)
GO protein binding	459	6249	0.0278374	6941 transcription factor 19
GO protein binding	459	6249	0.0278374	7001 peroxiredoxin 2
GO protein binding	459	6249	0.0278374	7022 transcription factor AP-2 gamma (activating enhancer binding protein 2)
GO protein binding	459	6249	0.0278374	7026 nuclear receptor subfamily 2, group F, member 2
GO protein binding	459	6249	0.0278374	7049 transforming growth factor, beta receptor III
GO protein binding	459	6249	0.0278374	7069 thyroid hormone responsive (SPOT14 homolog, rat)
GO protein binding	459	6249	0.0278374	7071 Kruppel-like factor 10
GO protein binding	459	6249	0.0278374	7076 TIMP metalloproteinase inhibitor 1
GO protein binding	459	6249	0.0278374	7089 transducin-like enhancer of split 2 (E(sp1) homolog, Drosophila)
GO protein binding	459	6249	0.0278374	7090 transducin-like enhancer of split 3 (E(sp1) homolog, Drosophila)
GO protein binding	459	6249	0.0278374	7097 toll-like receptor 2
GO protein binding	459	6249	0.0278374	7098 toll-like receptor 3
GO protein binding	459	6249	0.0278374	7099 toll-like receptor 4
GO protein binding	459	6249	0.0278374	7100 toll-like receptor 5
GO protein binding	459	6249	0.0278374	7106 tetraspanin 4
GO protein binding	459	6249	0.0278374	7133 tumor necrosis factor receptor superfamily, member 1B
GO protein binding	459	6249	0.0278374	7170 tropomyosin 3
GO protein binding	459	6249	0.0278374	718 complement component 3
GO protein binding	459	6249	0.0278374	722 complement component 4 binding protein, alpha
GO protein binding	459	6249	0.0278374	7223 transient receptor potential cation channel, subfamily C, member 4
GO protein binding	459	6249	0.0278374	7227 trichorhinophalangeal syndrome I
GO protein binding	459	6249	0.0278374	7474 wingless-type MMTV integration site family, member 5A
GO protein binding	459	6249	0.0278374	7538 zinc finger protein 36, C3H type, homolog (mouse)
GO protein binding	459	6249	0.0278374	7546 Zic family member 2 (odd-paired homolog, Drosophila)
GO protein binding	459	6249	0.0278374	7597 zinc finger and BTB domain containing 25
GO protein binding	459	6249	0.0278374	760 carbonic anhydrase II

GO protein binding	459	6249	0.0278374	7706 tripartite motif-containing 25
GO protein binding	459	6249	0.0278374	783 calcium channel, voltage-dependent, beta 2 subunit
GO protein binding	459	6249	0.0278374	7852 chemokine (C-X-C motif) receptor 4
GO protein binding	459	6249	0.0278374	79092 caspase recruitment domain family, member 14
GO protein binding	459	6249	0.0278374	79132 DEXH (Asp-Glu-X-His) box polypeptide 58
GO protein binding	459	6249	0.0278374	79180 EF-hand domain family, member D2
GO protein binding	459	6249	0.0278374	79444 baculoviral IAP repeat-containing 7
GO protein binding	459	6249	0.0278374	79782 leucine rich repeat containing 31
GO protein binding	459	6249	0.0278374	79820 cation channel, sperm-associated, beta
GO protein binding	459	6249	0.0278374	7984 Rho guanine nucleotide exchange factor (GEF) 5
GO protein binding	459	6249	0.0278374	79872 Cas-Br-M (murine) ecotropic retroviral transforming sequence-like 1
GO protein binding	459	6249	0.0278374	799 calcitonin receptor
GO protein binding	459	6249	0.0278374	80125 coiled-coil domain containing 33
GO protein binding	459	6249	0.0278374	80169 chromosome 17 open reading frame 68
GO protein binding	459	6249	0.0278374	80223 RAB11 family interacting protein 1 (class I)
GO protein binding	459	6249	0.0278374	80311 kelch-like 15 (Drosophila)
GO protein binding	459	6249	0.0278374	81603 tripartite motif-containing 8
GO protein binding	459	6249	0.0278374	81844 tripartite motif-containing 56
GO protein binding	459	6249	0.0278374	819 calcium modulating ligand
GO protein binding	459	6249	0.0278374	831 calpastatin
GO protein binding	459	6249	0.0278374	834 caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, co
GO protein binding	459	6249	0.0278374	83593 Ras association (RalGDS/AF-6) domain family member 5
GO protein binding	459	6249	0.0278374	83666 poly (ADP-ribose) polymerase family, member 9
GO protein binding	459	6249	0.0278374	837 caspase 4, apoptosis-related cysteine peptidase
GO protein binding	459	6249	0.0278374	8382 non-metastatic cells 5, protein expressed in (nucleoside-diphosphate k
GO protein binding	459	6249	0.0278374	83937 Ras association (RalGDS/AF-6) domain family member 4
GO protein binding	459	6249	0.0278374	84033 obscurin, cytoskeletal calmodulin and titin-interacting RhoGEF
GO protein binding	459	6249	0.0278374	84171 lysyl oxidase-like 4
GO protein binding	459	6249	0.0278374	84674 caspase recruitment domain family, member 6
GO protein binding	459	6249	0.0278374	84941 hematopoietic SH2 domain containing
GO protein binding	459	6249	0.0278374	8519 interferon induced transmembrane protein 1 (9-27)
GO protein binding	459	6249	0.0278374	8531 cold shock domain protein A
GO protein binding	459	6249	0.0278374	8542 apolipoprotein L, 1
GO protein binding	459	6249	0.0278374	8553 basic helix-loop-helix family, member e40
GO protein binding	459	6249	0.0278374	8556 CDC14 cell division cycle 14 homolog A (S. cerevisiae)
GO protein binding	459	6249	0.0278374	8600 tumor necrosis factor (ligand) superfamily, member 11

GO protein binding	459	6249	0.0278374	862 runt-related transcription factor 1; translocated to, 1 (cyclin D-related)
GO protein binding	459	6249	0.0278374	8631 src kinase associated phosphoprotein 1
GO protein binding	459	6249	0.0278374	8646 chordin
GO protein binding	459	6249	0.0278374	8660 insulin receptor substrate 2
GO protein binding	459	6249	0.0278374	8673 vesicle-associated membrane protein 8 (endobrevin)
GO protein binding	459	6249	0.0278374	8740 tumor necrosis factor (ligand) superfamily, member 14
GO protein binding	459	6249	0.0278374	8751 ADAM metallopeptidase domain 15
GO protein binding	459	6249	0.0278374	8793 tumor necrosis factor receptor superfamily, member 10d, decoy with t
GO protein binding	459	6249	0.0278374	8796 sciellin
GO protein binding	459	6249	0.0278374	8848 TSC22 domain family, member 1
GO protein binding	459	6249	0.0278374	885 cholecystokinin
GO protein binding	459	6249	0.0278374	8857 Fc fragment of IgG binding protein
GO protein binding	459	6249	0.0278374	8864 period homolog 2 (Drosophila)
GO protein binding	459	6249	0.0278374	8900 cyclin A1
GO protein binding	459	6249	0.0278374	8911 calcium channel, voltage-dependent, T type, alpha 1l subunit
GO protein binding	459	6249	0.0278374	8938 BAI1-associated protein 3
GO protein binding	459	6249	0.0278374	8973 cholinergic receptor, nicotinic, alpha 6
GO protein binding	459	6249	0.0278374	89870 tripartite motif-containing 15
GO protein binding	459	6249	0.0278374	8996 nucleolar protein 3 (apoptosis repressor with CARD domain)
GO protein binding	459	6249	0.0278374	9019 myelin protein zero-like 1
GO protein binding	459	6249	0.0278374	9021 suppressor of cytokine signaling 3
GO protein binding	459	6249	0.0278374	9060 3'-phosphoadenosine 5'-phosphosulfate synthase 2
GO protein binding	459	6249	0.0278374	9064 mitogen-activated protein kinase kinase kinase 6
GO protein binding	459	6249	0.0278374	90865 interleukin 33
GO protein binding	459	6249	0.0278374	91 activin A receptor, type IB
GO protein binding	459	6249	0.0278374	91404 SEC14 and spectrin domains 1
GO protein binding	459	6249	0.0278374	91653 Boc homolog (mouse)
GO protein binding	459	6249	0.0278374	9182 Ras association (RalGDS/AF-6) domain family (N-terminal) member 9
GO protein binding	459	6249	0.0278374	9185 RALBP1 associated Eps domain containing 2
GO protein binding	459	6249	0.0278374	9271 piwi-like 1 (Drosophila)
GO protein binding	459	6249	0.0278374	929 CD14 molecule
GO protein binding	459	6249	0.0278374	9324 high mobility group nucleosomal binding domain 3
GO protein binding	459	6249	0.0278374	94 activin A receptor type II-like 1
GO protein binding	459	6249	0.0278374	94025 mucin 16, cell surface associated
GO protein binding	459	6249	0.0278374	9414 tight junction protein 2 (zona occludens 2)
GO protein binding	459	6249	0.0278374	9452 integral membrane protein 2A



GO protein binding	459	6249	0.0278374	9510 ADAM metallopeptidase with thrombospondin type 1 motif, 1
GO protein binding	459	6249	0.0278374	9595 cytohesin 1 interacting protein
GO protein binding	459	6249	0.0278374	961 CD47 molecule
GO protein binding	459	6249	0.0278374	9615 guanine deaminase
GO protein binding	459	6249	0.0278374	9722 nitric oxide synthase 1 (neuronal) adaptor protein
GO protein binding	459	6249	0.0278374	9734 histone deacetylase 9
GO protein binding	459	6249	0.0278374	9749 phosphatase and actin regulator 2
GO protein binding	459	6249	0.0278374	9804 translocase of outer mitochondrial membrane 20 homolog (yeast)
GO protein binding	459	6249	0.0278374	9875 URB1 ribosome biogenesis 1 homolog ( <i>S. cerevisiae</i> )
GO protein binding	459	6249	0.0278374	9935 v-maf musculoaponeurotic fibrosarcoma oncogene homolog B (avian)
GO protein binding	459	6249	0.0278374	9971 nuclear receptor subfamily 1, group H, member 4
GO protein binding	459	6249	0.0278374	9985 REC8 homolog (yeast)
GO brush border membrane	5	26	0.02922	10568 solute carrier family 34 (sodium phosphate), member 2
GO brush border membrane	5	26	0.02922	358 aquaporin 1 (Colton blood group)
GO brush border membrane	5	26	0.02922	3775 potassium channel, subfamily K, member 1
GO brush border membrane	5	26	0.02922	50617 ATPase, H+ transporting, lysosomal V0 subunit a4
GO brush border membrane	5	26	0.02922	55600 intelectin 1 (galactofuranose binding)
GO endopeptidase inhibitor activity	5	26	0.02922	6590 secretory leukocyte peptidase inhibitor
GO endopeptidase inhibitor activity	5	26	0.02922	6690 serine peptidase inhibitor, Kazal type 1
GO endopeptidase inhibitor activity	5	26	0.02922	718 complement component 3
GO endopeptidase inhibitor activity	5	26	0.02922	831 calpastatin
GO endopeptidase inhibitor activity	5	26	0.02922	8434 reversion-inducing-cysteine-rich protein with kazal motifs
GO neuropeptide signaling pathway	11	85	0.0297185	1363 carboxypeptidase E
GO neuropeptide signaling pathway	11	85	0.0297185	2015 egf-like module containing, mucin-like, hormone receptor-like 1
GO neuropeptide signaling pathway	11	85	0.0297185	22859 latrophilin 1
GO neuropeptide signaling pathway	11	85	0.0297185	23266 latrophilin 2
GO neuropeptide signaling pathway	11	85	0.0297185	23284 latrophilin 3
GO neuropeptide signaling pathway	11	85	0.0297185	283383 G protein-coupled receptor 133
GO neuropeptide signaling pathway	11	85	0.0297185	5367 pro-melanin-concentrating hormone
GO neuropeptide signaling pathway	11	85	0.0297185	56923 neuromedin U receptor 2
GO neuropeptide signaling pathway	11	85	0.0297185	57537 sortilin-related VPS10 domain containing receptor 2
GO neuropeptide signaling pathway	11	85	0.0297185	6751 somatostatin receptor 1
GO neuropeptide signaling pathway	11	85	0.0297185	84059 G protein-coupled receptor 98
GO apoptosis	41	444	0.0306553	10081 programmed cell death 7
GO apoptosis	41	444	0.0306553	10912 growth arrest and DNA-damage-inducible, gamma
GO apoptosis	41	444	0.0306553	10913 ectodysplasin A receptor

GO apoptosis	41	444	0.0306553	1969 EPH receptor A2
GO apoptosis	41	444	0.0306553	2033 E1A binding protein p300
GO apoptosis	41	444	0.0306553	2122 MDS1 and EVI1 complex locus
GO apoptosis	41	444	0.0306553	23151 GRAM domain containing 4
GO apoptosis	41	444	0.0306553	23263 MCF.2 cell line derived transforming sequence-like
GO apoptosis	41	444	0.0306553	23365 Rho guanine nucleotide exchange factor (GEF) 12
GO apoptosis	41	444	0.0306553	23368 protein phosphatase 1, regulatory (inhibitor) subunit 13B
GO apoptosis	41	444	0.0306553	23604 death-associated protein kinase 2
GO apoptosis	41	444	0.0306553	255488 ring finger protein 144B
GO apoptosis	41	444	0.0306553	28996 homeodomain interacting protein kinase 2
GO apoptosis	41	444	0.0306553	3689 integrin, beta 2 (complement component 3 receptor 3 and 4 subunit)
GO apoptosis	41	444	0.0306553	4170 myeloid cell leukemia sequence 1 (BCL2-related)
GO apoptosis	41	444	0.0306553	4194 Mdm4 p53 binding protein homolog (mouse)
GO apoptosis	41	444	0.0306553	4209 myocyte enhancer factor 2D
GO apoptosis	41	444	0.0306553	440603 BCL2-like 15
GO apoptosis	41	444	0.0306553	4616 growth arrest and DNA-damage-inducible, beta
GO apoptosis	41	444	0.0306553	4792 nuclear factor of kappa light polypeptide gene enhancer in B-cells inhib
GO apoptosis	41	444	0.0306553	54739 XIAP associated factor 1
GO apoptosis	41	444	0.0306553	55332 DNA-damage regulated autophagy modulator 1
GO apoptosis	41	444	0.0306553	573 BCL2-associated athanogene
GO apoptosis	41	444	0.0306553	5794 protein tyrosine phosphatase, receptor type, H
GO apoptosis	41	444	0.0306553	6446 serum/glucocorticoid regulated kinase 1
GO apoptosis	41	444	0.0306553	64651 cysteine-serine-rich nuclear protein 1
GO apoptosis	41	444	0.0306553	7133 tumor necrosis factor receptor superfamily, member 1B
GO apoptosis	41	444	0.0306553	7852 chemokine (C-X-C motif) receptor 4
GO apoptosis	41	444	0.0306553	79444 baculoviral IAP repeat-containing 7
GO apoptosis	41	444	0.0306553	834 caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, co
GO apoptosis	41	444	0.0306553	83593 Ras association (RalGDS/AF-6) domain family member 5
GO apoptosis	41	444	0.0306553	837 caspase 4, apoptosis-related cysteine peptidase
GO apoptosis	41	444	0.0306553	84033 obscurin, cytoskeletal calmodulin and titin-interacting RhoGEF
GO apoptosis	41	444	0.0306553	8462 Kruppel-like factor 11
GO apoptosis	41	444	0.0306553	8744 tumor necrosis factor (ligand) superfamily, member 9
GO apoptosis	41	444	0.0306553	8793 tumor necrosis factor receptor superfamily, member 10d, decoy with t
GO apoptosis	41	444	0.0306553	8794 tumor necrosis factor receptor superfamily, member 10c, decoy witho
GO apoptosis	41	444	0.0306553	9263 serine/threonine kinase 17a
GO apoptosis	41	444	0.0306553	929 CD14 molecule

GO apoptosis	41	444	0.0306553	9445 integral membrane protein 2B
GO apoptosis	41	444	0.0306553	9459 Rac/Cdc42 guanine nucleotide exchange factor (GEF) 6
GO platelet-derived growth factor recept	4	18	0.0307275	10628 thioredoxin interacting protein
GO platelet-derived growth factor recept	4	18	0.0307275	5327 plasminogen activator, tissue
GO platelet-derived growth factor recept	4	18	0.0307275	64651 cysteine-serine-rich nuclear protein 1
GO platelet-derived growth factor recept	4	18	0.0307275	84159 AT rich interactive domain 5B (MRF1-like)
GO protein ubiquitination involved in ubi	4	18	0.0307275	154214 ring finger protein 217
GO protein ubiquitination involved in ubi	4	18	0.0307275	255488 ring finger protein 144B
GO protein ubiquitination involved in ubi	4	18	0.0307275	29116 myosin regulatory light chain interacting protein
GO protein ubiquitination involved in ubi	4	18	0.0307275	5071 Parkinson disease (autosomal recessive, juvenile) 2, parkin
GO endocrine pancreas development	4	18	0.0307275	222546 regulatory factor X, 6
GO endocrine pancreas development	4	18	0.0307275	3175 one cut homeobox 1
GO endocrine pancreas development	4	18	0.0307275	3569 interleukin 6 (interferon, beta 2)
GO endocrine pancreas development	4	18	0.0307275	3570 interleukin 6 receptor
GO response to corticosterone stimulus	4	18	0.0307275	2353 FBJ murine osteosarcoma viral oncogene homolog
GO response to corticosterone stimulus	4	18	0.0307275	3726 jun B proto-oncogene
GO response to corticosterone stimulus	4	18	0.0307275	4129 monoamine oxidase B
GO response to corticosterone stimulus	4	18	0.0307275	5742 prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase a
GO pituitary gland development	4	18	0.0307275	2624 GATA binding protein 2
GO pituitary gland development	4	18	0.0307275	5122 proprotein convertase subtilisin/kexin type 1
GO pituitary gland development	4	18	0.0307275	5307 paired-like homeodomain 1
GO pituitary gland development	4	18	0.0307275	652 bone morphogenetic protein 4
GO cellular process	4	18	0.0307275	3725 jun oncogene
GO cellular process	4	18	0.0307275	3726 jun B proto-oncogene
GO cellular process	4	18	0.0307275	5066 peptidylglycine alpha-amidating monooxygenase
GO cellular process	4	18	0.0307275	8509 N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 2
GO cortical cytoskeleton	4	18	0.0307275	6521 solute carrier family 4, anion exchanger, member 1 (erythrocyte memb
GO cortical cytoskeleton	4	18	0.0307275	7111 tropomodulin 1
GO cortical cytoskeleton	4	18	0.0307275	7170 tropomyosin 3
GO cortical cytoskeleton	4	18	0.0307275	7223 transient receptor potential cation channel, subfamily C, member 4
GO protein amino acid glycosylation	9	65	0.031965	10317 UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 5
GO protein amino acid glycosylation	9	65	0.031965	192134 UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 6 (core
GO protein amino acid glycosylation	9	65	0.031965	2525 fucosyltransferase 3 (galactoside 3(4)-L-fucosyltransferase, Lewis bloo
GO protein amino acid glycosylation	9	65	0.031965	2526 fucosyltransferase 4 (alpha (1,3) fucosyltransferase, myeloid-specific)
GO protein amino acid glycosylation	9	65	0.031965	27090 ST6 (alpha-N-acetyl-neuraminy-2,3-beta-galactosyl-1,3)-N-acetylgalact
GO protein amino acid glycosylation	9	65	0.031965	55808 ST6 (alpha-N-acetyl-neuraminy-2,3-beta-galactosyl-1,3)-N-acetylgalact

GO protein amino acid glycosylation	9	65	0.031965	6484 ST3 beta-galactoside alpha-2,3-sialyltransferase 4
GO protein amino acid glycosylation	9	65	0.031965	6489 ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 1
GO protein amino acid glycosylation	9	65	0.031965	8706 beta-1,3-N-acetylgalactosaminyltransferase 1 (globoside blood group)
GO iron ion binding	9	65	0.031965	10826 chromosome 5 open reading frame 4
GO iron ion binding	9	65	0.031965	240 arachidonate 5-lipoxygenase
GO iron ion binding	9	65	0.031965	27035 NADPH oxidase 1
GO iron ion binding	9	65	0.031965	316 aldehyde oxidase 1
GO iron ion binding	9	65	0.031965	5053 phenylalanine hydroxylase
GO iron ion binding	9	65	0.031965	5351 procollagen-lysine 1, 2-oxoglutarate 5-dioxygenase 1
GO iron ion binding	9	65	0.031965	54681 prolyl 4-hydroxylase, transmembrane (endoplasmic reticulum)
GO iron ion binding	9	65	0.031965	59344 arachidonate lipoxygenase 3
GO iron ion binding	9	65	0.031965	79689 STEAP family member 4
GO transforming growth factor beta rece	8	55	0.0323494	2353 FBJ murine osteosarcoma viral oncogene homolog
GO transforming growth factor beta rece	8	55	0.0323494	3725 jun oncogene
GO transforming growth factor beta rece	8	55	0.0323494	4087 SMAD family member 2
GO transforming growth factor beta rece	8	55	0.0323494	5371 promyelocytic leukemia
GO transforming growth factor beta rece	8	55	0.0323494	7049 transforming growth factor, beta receptor III
GO transforming growth factor beta rece	8	55	0.0323494	7071 Kruppel-like factor 10
GO transforming growth factor beta rece	8	55	0.0323494	94 activin A receptor type II-like 1
GO transforming growth factor beta rece	8	55	0.0323494	9518 growth differentiation factor 15
GO transmembrane receptor activity	13	108	0.0326637	10913 ectodysplasin A receptor
GO transmembrane receptor activity	13	108	0.0326637	1364 claudin 4
GO transmembrane receptor activity	13	108	0.0326637	1380 complement component (3d/Epstein Barr virus) receptor 2
GO transmembrane receptor activity	13	108	0.0326637	30008 EGF-containing fibulin-like extracellular matrix protein 2
GO transmembrane receptor activity	13	108	0.0326637	3823 killer cell lectin-like receptor subfamily C, member 3
GO transmembrane receptor activity	13	108	0.0326637	3949 low density lipoprotein receptor
GO transmembrane receptor activity	13	108	0.0326637	6653 sortilin-related receptor, L(DLR class) A repeats-containing
GO transmembrane receptor activity	13	108	0.0326637	7097 toll-like receptor 2
GO transmembrane receptor activity	13	108	0.0326637	7098 toll-like receptor 3
GO transmembrane receptor activity	13	108	0.0326637	7099 toll-like receptor 4
GO transmembrane receptor activity	13	108	0.0326637	7100 toll-like receptor 5
GO transmembrane receptor activity	13	108	0.0326637	8793 tumor necrosis factor receptor superfamily, member 10d, decoy with t
GO transmembrane receptor activity	13	108	0.0326637	8794 tumor necrosis factor receptor superfamily, member 10c, decoy witho
GO odontogenesis of dentine-containing	6	36	0.0336095	2296 forkhead box C1
GO odontogenesis of dentine-containing	6	36	0.0336095	2737 GLI family zinc finger 3
GO odontogenesis of dentine-containing	6	36	0.0336095	3911 laminin, alpha 5

GO odontogenesis of dentine-containing	6	36	0.0336095	652 bone morphogenetic protein 4
GO odontogenesis of dentine-containing	6	36	0.0336095	682 basigin (Ok blood group)
GO odontogenesis of dentine-containing	6	36	0.0336095	760 carbonic anhydrase II
GO response to cold	5	27	0.0339066	154 adrenergic, beta-2-, receptor, surface
GO response to cold	5	27	0.0339066	183 angiotensinogen (serpin peptidase inhibitor, clade A, member 8)
GO response to cold	5	27	0.0339066	2353 FBJ murine osteosarcoma viral oncogene homolog
GO response to cold	5	27	0.0339066	5367 pro-melanin-concentrating hormone
GO response to cold	5	27	0.0339066	8531 cold shock domain protein A
GO retinol dehydrogenase activity	3	11	0.0347288	10170 dehydrogenase/reductase (SDR family) member 9
GO retinol dehydrogenase activity	3	11	0.0347288	157506 retinol dehydrogenase 10 (all-trans)
GO retinol dehydrogenase activity	3	11	0.0347288	195814 short chain dehydrogenase/reductase family 16C, member 5
GO negative regulation of osteoclast diffi	3	11	0.0347288	10766 transducer of ERBB2, 2
GO negative regulation of osteoclast diffi	3	11	0.0347288	7098 toll-like receptor 3
GO negative regulation of osteoclast diffi	3	11	0.0347288	7099 toll-like receptor 4
GO sphingolipid biosynthetic process	3	11	0.0347288	123099 degenerative spermatocyte homolog 2, lipid desaturase (Drosophila)
GO sphingolipid biosynthetic process	3	11	0.0347288	165679 chromosome 3 open reading frame 57
GO sphingolipid biosynthetic process	3	11	0.0347288	55304 serine palmitoyltransferase, long chain base subunit 3
GO transforming growth factor beta rece	3	11	0.0347288	130399 activin A receptor, type IC
GO transforming growth factor beta rece	3	11	0.0347288	7049 transforming growth factor, beta receptor III
GO transforming growth factor beta rece	3	11	0.0347288	94 activin A receptor type II-like 1
GO positive regulation of cellular protein	3	11	0.0347288	1435 colony stimulating factor 1 (macrophage)
GO positive regulation of cellular protein	3	11	0.0347288	183 angiotensinogen (serpin peptidase inhibitor, clade A, member 8)
GO positive regulation of cellular protein	3	11	0.0347288	4792 nuclear factor of kappa light polypeptide gene enhancer in B-cells inhib
GO arachidonic acid secretion	3	11	0.0347288	1813 dopamine receptor D2
GO arachidonic acid secretion	3	11	0.0347288	1815 dopamine receptor D4
GO arachidonic acid secretion	3	11	0.0347288	56923 neuromedin U receptor 2
GO peptide hormone processing	3	11	0.0347288	25825 beta-site APP-cleaving enzyme 2
GO peptide hormone processing	3	11	0.0347288	5046 proprotein convertase subtilisin/kexin type 6
GO peptide hormone processing	3	11	0.0347288	5122 proprotein convertase subtilisin/kexin type 1
GO positive regulation of interleukin-1 be	3	11	0.0347288	29108 PYD and CARD domain containing
GO positive regulation of interleukin-1 be	3	11	0.0347288	64127 nucleotide-binding oligomerization domain containing 2
GO positive regulation of interleukin-1 be	3	11	0.0347288	834 caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, co
GO basal lamina	3	11	0.0347288	375790 agrin
GO basal lamina	3	11	0.0347288	3911 laminin, alpha 5
GO basal lamina	3	11	0.0347288	3913 laminin, beta 2 (laminin S)
GO I-kappaB phosphorylation	3	11	0.0347288	7097 toll-like receptor 2

GO	I-kappaB phosphorylation	3	11	0.0347288	7098	toll-like receptor 3
GO	I-kappaB phosphorylation	3	11	0.0347288	7099	toll-like receptor 4
GO	cellular response to insulin stimulus	7	46	0.0353627	10014	histone deacetylase 5
GO	cellular response to insulin stimulus	7	46	0.0353627	255738	proprotein convertase subtilisin/kexin type 9
GO	cellular response to insulin stimulus	7	46	0.0353627	3643	insulin receptor
GO	cellular response to insulin stimulus	7	46	0.0353627	51703	acyl-CoA synthetase long-chain family member 5
GO	cellular response to insulin stimulus	7	46	0.0353627	6256	retinoid X receptor, alpha
GO	cellular response to insulin stimulus	7	46	0.0353627	8660	insulin receptor substrate 2
GO	cellular response to insulin stimulus	7	46	0.0353627	9734	histone deacetylase 9
GO	external side of plasma membrane	14	121	0.0366976	1508	cathepsin B
GO	external side of plasma membrane	14	121	0.0366976	2205	Fc fragment of IgE, high affinity I, receptor for; alpha polypeptide
GO	external side of plasma membrane	14	121	0.0366976	29126	CD274 molecule
GO	external side of plasma membrane	14	121	0.0366976	3561	interleukin 2 receptor, gamma (severe combined immunodeficiency)
GO	external side of plasma membrane	14	121	0.0366976	3678	integrin, alpha 5 (fibronectin receptor, alpha polypeptide)
GO	external side of plasma membrane	14	121	0.0366976	3687	integrin, alpha X (complement component 3 receptor 4 subunit)
GO	external side of plasma membrane	14	121	0.0366976	3815	v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog
GO	external side of plasma membrane	14	121	0.0366976	4684	neural cell adhesion molecule 1
GO	external side of plasma membrane	14	121	0.0366976	55867	solute carrier family 22 (organic anion/urate transporter), member 11
GO	external side of plasma membrane	14	121	0.0366976	6402	selectin L
GO	external side of plasma membrane	14	121	0.0366976	7049	transforming growth factor, beta receptor III
GO	external side of plasma membrane	14	121	0.0366976	7097	toll-like receptor 2
GO	external side of plasma membrane	14	121	0.0366976	7099	toll-like receptor 4
GO	external side of plasma membrane	14	121	0.0366976	9619	ATP-binding cassette, sub-family G (WHITE), member 1
GO	neutrophil chemotaxis	4	19	0.0368754	1906	endothelin 1
GO	neutrophil chemotaxis	4	19	0.0368754	2921	chemokine (C-X-C motif) ligand 3
GO	neutrophil chemotaxis	4	19	0.0368754	3689	integrin, beta 2 (complement component 3 receptor 3 and 4 subunit)
GO	neutrophil chemotaxis	4	19	0.0368754	6850	spleen tyrosine kinase
GO	positive regulation of MAP kinase act	4	19	0.0368754	1906	endothelin 1
GO	positive regulation of MAP kinase act	4	19	0.0368754	3815	v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog
GO	positive regulation of MAP kinase act	4	19	0.0368754	3845	v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog
GO	positive regulation of MAP kinase act	4	19	0.0368754	4254	KIT ligand
GO	positive regulation of JNK cascade	4	19	0.0368754	28996	homeodomain interacting protein kinase 2
GO	positive regulation of JNK cascade	4	19	0.0368754	64127	nucleotide-binding oligomerization domain containing 2
GO	positive regulation of JNK cascade	4	19	0.0368754	7098	toll-like receptor 3
GO	positive regulation of JNK cascade	4	19	0.0368754	7099	toll-like receptor 4
GO	serine-type endopeptidase activity	16	144	0.0371879	10942	protease, serine, 21 (testisin)

GO	serine-type endopeptidase activity	16	144	0.0371879	11202 kallikrein-related peptidase 8
GO	serine-type endopeptidase activity	16	144	0.0371879	1803 dipeptidyl-peptidase 4
GO	serine-type endopeptidase activity	16	144	0.0371879	255738 proprotein convertase subtilisin/kexin type 9
GO	serine-type endopeptidase activity	16	144	0.0371879	5046 proprotein convertase subtilisin/kexin type 6
GO	serine-type endopeptidase activity	16	144	0.0371879	5122 proprotein convertase subtilisin/kexin type 1
GO	serine-type endopeptidase activity	16	144	0.0371879	51279 complement component 1, r subcomponent-like
GO	serine-type endopeptidase activity	16	144	0.0371879	5327 plasminogen activator, tissue
GO	serine-type endopeptidase activity	16	144	0.0371879	54933 rhomboid, veinlet-like 2 (Drosophila)
GO	serine-type endopeptidase activity	16	144	0.0371879	5648 mannan-binding lectin serine peptidase 1 (C4/C2 activating component
GO	serine-type endopeptidase activity	16	144	0.0371879	5655 kallikrein-related peptidase 10
GO	serine-type endopeptidase activity	16	144	0.0371879	56649 transmembrane protease, serine 4
GO	serine-type endopeptidase activity	16	144	0.0371879	629 complement factor B
GO	serine-type endopeptidase activity	16	144	0.0371879	64699 transmembrane protease, serine 3
GO	serine-type endopeptidase activity	16	144	0.0371879	715 complement component 1, r subcomponent
GO	serine-type endopeptidase activity	16	144	0.0371879	717 complement component 2
GO	integrin complex	5	28	0.0390333	3678 integrin, alpha 5 (fibronectin receptor, alpha polypeptide)
GO	integrin complex	5	28	0.0390333	3687 integrin, alpha X (complement component 3 receptor 4 subunit)
GO	integrin complex	5	28	0.0390333	3689 integrin, beta 2 (complement component 3 receptor 3 and 4 subunit)
GO	integrin complex	5	28	0.0390333	3691 integrin, beta 4
GO	integrin complex	5	28	0.0390333	3696 integrin, beta 8
GO	lung morphogenesis	2	5	0.0406292	10253 sprouty homolog 2 (Drosophila)
GO	lung morphogenesis	2	5	0.0406292	652 bone morphogenetic protein 4
GO	activation of MAPKKK activity	2	5	0.0406292	10912 growth arrest and DNA-damage-inducible, gamma
GO	activation of MAPKKK activity	2	5	0.0406292	4616 growth arrest and DNA-damage-inducible, beta
GO	branching involved in mammary gland morphogenesis	2	5	0.0406292	1435 colony stimulating factor 1 (macrophage)
GO	branching involved in mammary gland morphogenesis	2	5	0.0406292	5371 promyelocytic leukemia
GO	positive regulation of sodium ion transport	2	5	0.0406292	154 adrenergic, beta-2-, receptor, surface
GO	positive regulation of sodium ion transport	2	5	0.0406292	154043 CNKSR family member 3
GO	monoterpenoid metabolic process	2	5	0.0406292	1559 cytochrome P450, family 2, subfamily C, polypeptide 9
GO	monoterpenoid metabolic process	2	5	0.0406292	1571 cytochrome P450, family 2, subfamily E, polypeptide 1
GO	serine C-palmitoyltransferase activity	2	5	0.0406292	165679 chromosome 3 open reading frame 57
GO	serine C-palmitoyltransferase activity	2	5	0.0406292	55304 serine palmitoyltransferase, long chain base subunit 3
GO	serine C-palmitoyltransferase complex	2	5	0.0406292	165679 chromosome 3 open reading frame 57
GO	serine C-palmitoyltransferase complex	2	5	0.0406292	55304 serine palmitoyltransferase, long chain base subunit 3
GO	pattern recognition receptor activity	2	5	0.0406292	1755 deleted in malignant brain tumors 1
GO	pattern recognition receptor activity	2	5	0.0406292	7097 toll-like receptor 2

GO inhibition of adenylate cyclase activit	2	5	0.0406292	1813 dopamine receptor D2
GO inhibition of adenylate cyclase activit	2	5	0.0406292	1815 dopamine receptor D4
GO nerve-nerve synaptic transmission	2	5	0.0406292	1813 dopamine receptor D2
GO nerve-nerve synaptic transmission	2	5	0.0406292	23095 kinesin family member 1B
GO fear response	2	5	0.0406292	1815 dopamine receptor D4
GO fear response	2	5	0.0406292	627 brain-derived neurotrophic factor
GO protein tyrosine/threonine phosphat	2	5	0.0406292	1843 dual specificity phosphatase 1
GO protein tyrosine/threonine phosphat	2	5	0.0406292	1844 dual specificity phosphatase 2
GO mitogen-activated protein kinase bin	2	5	0.0406292	1844 dual specificity phosphatase 2
GO mitogen-activated protein kinase bin	2	5	0.0406292	2033 E1A binding protein p300
GO microfibril	2	5	0.0406292	2200 fibrillin 1
GO microfibril	2	5	0.0406292	8076 microfibrillar associated protein 5
GO paraxial mesoderm formation	2	5	0.0406292	2296 forkhead box C1
GO paraxial mesoderm formation	2	5	0.0406292	2303 forkhead box C2 (MFH-1, mesenchyme forkhead 1)
GO neutrophil mediated immunity	2	5	0.0406292	3569 interleukin 6 (interferon, beta 2)
GO neutrophil mediated immunity	2	5	0.0406292	3570 interleukin 6 receptor
GO positive regulation of immunoglobuli	2	5	0.0406292	3569 interleukin 6 (interferon, beta 2)
GO positive regulation of immunoglobuli	2	5	0.0406292	5950 retinol binding protein 4, plasma
GO negative regulation of transporter ac	2	5	0.0406292	3643 insulin receptor
GO negative regulation of transporter ac	2	5	0.0406292	6622 synuclein, alpha (non A4 component of amyloid precursor)
GO negative regulation of focal adhesion	2	5	0.0406292	395 Rho GTPase activating protein 6
GO negative regulation of focal adhesion	2	5	0.0406292	94 activin A receptor type II-like 1
GO response to cholesterol	2	5	0.0406292	4087 SMAD family member 2
GO response to cholesterol	2	5	0.0406292	51703 acyl-CoA synthetase long-chain family member 5
GO amine oxidase activity	2	5	0.0406292	4128 monoamine oxidase A
GO amine oxidase activity	2	5	0.0406292	4129 monoamine oxidase B
GO regulation of cardiac muscle contract	2	5	0.0406292	4842 nitric oxide synthase 1 (neuronal)
GO regulation of cardiac muscle contract	2	5	0.0406292	5025 purinergic receptor P2X, ligand-gated ion channel, 4
GO entrainment of circadian clock	2	5	0.0406292	5187 period homolog 1 (Drosophila)
GO entrainment of circadian clock	2	5	0.0406292	8553 basic helix-loop-helix family, member e40
GO prostaglandin E receptor activity	2	5	0.0406292	5732 prostaglandin E receptor 2 (subtype EP2), 53kDa
GO prostaglandin E receptor activity	2	5	0.0406292	5734 prostaglandin E receptor 4 (subtype EP4)
GO negative regulation of growth of sym	2	5	0.0406292	64127 nucleotide-binding oligomerization domain containing 2
GO negative regulation of growth of sym	2	5	0.0406292	7097 toll-like receptor 2
GO cell-matrix adhesion	9	68	0.0411625	10516 fibulin 5
GO cell-matrix adhesion	9	68	0.0411625	183 angiotensinogen (serpin peptidase inhibitor, clade A, member 8)



GO cell-matrix adhesion	9	68	0.0411625	22795 nidogen 2 (osteonidogen)
GO cell-matrix adhesion	9	68	0.0411625	27076 LY6/PLAUR domain containing 3
GO cell-matrix adhesion	9	68	0.0411625	3689 integrin, beta 2 (complement component 3 receptor 3 and 4 subunit)
GO cell-matrix adhesion	9	68	0.0411625	3691 integrin, beta 4
GO cell-matrix adhesion	9	68	0.0411625	3696 integrin, beta 8
GO cell-matrix adhesion	9	68	0.0411625	51754 transmembrane protein 8B
GO cell-matrix adhesion	9	68	0.0411625	8751 ADAM metallopeptidase domain 15
GO protein homodimerization activity	34	365	0.0411734	11213 interleukin-1 receptor-associated kinase 3
GO protein homodimerization activity	34	365	0.0411734	1139 cholinergic receptor, nicotinic, alpha 7
GO protein homodimerization activity	34	365	0.0411734	116113 forkhead box P4
GO protein homodimerization activity	34	365	0.0411734	127343 diencephalon/mesencephalon homeobox 1
GO protein homodimerization activity	34	365	0.0411734	1380 complement component (3d/Epstein Barr virus) receptor 2
GO protein homodimerization activity	34	365	0.0411734	1435 colony stimulating factor 1 (macrophage)
GO protein homodimerization activity	34	365	0.0411734	154 adrenergic, beta-2-, receptor, surface
GO protein homodimerization activity	34	365	0.0411734	1803 dipeptidyl-peptidase 4
GO protein homodimerization activity	34	365	0.0411734	1820 AT rich interactive domain 3A (BRIGHT-like)
GO protein homodimerization activity	34	365	0.0411734	2026 enolase 2 (gamma, neuronal)
GO protein homodimerization activity	34	365	0.0411734	2122 MDS1 and EVI1 complex locus
GO protein homodimerization activity	34	365	0.0411734	22807 IKAROS family zinc finger 2 (Helios)
GO protein homodimerization activity	34	365	0.0411734	29108 PYD and CARD domain containing
GO protein homodimerization activity	34	365	0.0411734	3164 nuclear receptor subfamily 4, group A, member 1
GO protein homodimerization activity	34	365	0.0411734	3570 interleukin 6 receptor
GO protein homodimerization activity	34	365	0.0411734	4129 monoamine oxidase B
GO protein homodimerization activity	34	365	0.0411734	429 achaete-scute complex homolog 1 (Drosophila)
GO protein homodimerization activity	34	365	0.0411734	4293 mitogen-activated protein kinase kinase kinase 9
GO protein homodimerization activity	34	365	0.0411734	4692 necdin homolog (mouse)
GO protein homodimerization activity	34	365	0.0411734	5025 purinergic receptor P2X, ligand-gated ion channel, 4
GO protein homodimerization activity	34	365	0.0411734	5053 phenylalanine hydroxylase
GO protein homodimerization activity	34	365	0.0411734	51085 MLX interacting protein-like
GO protein homodimerization activity	34	365	0.0411734	5351 procollagen-lysine 1, 2-oxoglutarate 5-dioxygenase 1
GO protein homodimerization activity	34	365	0.0411734	5371 promyelocytic leukemia
GO protein homodimerization activity	34	365	0.0411734	5648 mannan-binding lectin serine peptidase 1 (C4/C2 activating component)
GO protein homodimerization activity	34	365	0.0411734	57453 Down syndrome cell adhesion molecule like 1
GO protein homodimerization activity	34	365	0.0411734	57863 cell adhesion molecule 3
GO protein homodimerization activity	34	365	0.0411734	5791 protein tyrosine phosphatase, receptor type, E
GO protein homodimerization activity	34	365	0.0411734	652 bone morphogenetic protein 4

GO protein homodimerization activity	34	365	0.0411734	6521 solute carrier family 4, anion exchanger, member 1 (erythrocyte memb
GO protein homodimerization activity	34	365	0.0411734	7026 nuclear receptor subfamily 2, group F, member 2
GO protein homodimerization activity	34	365	0.0411734	81603 tripartite motif-containing 8
GO protein homodimerization activity	34	365	0.0411734	8527 diacylglycerol kinase, delta 130kDa
GO protein homodimerization activity	34	365	0.0411734	9619 ATP-binding cassette, sub-family G (WHITE), member 1
GO negative regulation of cell migration	6	38	0.0424786	10076 protein tyrosine phosphatase, receptor type, U
GO negative regulation of cell migration	6	38	0.0424786	1813 dopamine receptor D2
GO negative regulation of cell migration	6	38	0.0424786	3488 insulin-like growth factor binding protein 5
GO negative regulation of cell migration	6	38	0.0424786	375056 melanoma inhibitory activity family, member 3
GO negative regulation of cell migration	6	38	0.0424786	8646 chordin
GO negative regulation of cell migration	6	38	0.0424786	94 activin A receptor type II-like 1
GO response to mechanical stimulus	6	38	0.0424786	10628 thioredoxin interacting protein
GO response to mechanical stimulus	6	38	0.0424786	1508 cathepsin B
GO response to mechanical stimulus	6	38	0.0424786	2353 FBJ murine osteosarcoma viral oncogene homolog
GO response to mechanical stimulus	6	38	0.0424786	3725 jun oncogene
GO response to mechanical stimulus	6	38	0.0424786	3726 jun B proto-oncogene
GO response to mechanical stimulus	6	38	0.0424786	652 bone morphogenetic protein 4
GO transcription factor binding	18	170	0.0427318	10014 histone deacetylase 5
GO transcription factor binding	18	170	0.0427318	10221 tribbles homolog 1 (Drosophila)
GO transcription factor binding	18	170	0.0427318	10891 peroxisome proliferator-activated receptor gamma, coactivator 1 alpha
GO transcription factor binding	18	170	0.0427318	2033 E1A binding protein p300
GO transcription factor binding	18	170	0.0427318	2296 forkhead box C1
GO transcription factor binding	18	170	0.0427318	2354 FBJ murine osteosarcoma viral oncogene homolog B
GO transcription factor binding	18	170	0.0427318	2624 GATA binding protein 2
GO transcription factor binding	18	170	0.0427318	28951 tribbles homolog 2 (Drosophila)
GO transcription factor binding	18	170	0.0427318	3725 jun oncogene
GO transcription factor binding	18	170	0.0427318	4087 SMAD family member 2
GO transcription factor binding	18	170	0.0427318	4792 nuclear factor of kappa light polypeptide gene enhancer in B-cells inhib
GO transcription factor binding	18	170	0.0427318	51085 MLX interacting protein-like
GO transcription factor binding	18	170	0.0427318	5308 paired-like homeodomain 2
GO transcription factor binding	18	170	0.0427318	5460 POU class 5 homeobox 1
GO transcription factor binding	18	170	0.0427318	6604 SWI/SNF related, matrix associated, actin dependent regulator of chrom
GO transcription factor binding	18	170	0.0427318	8543 LIM domain only 4
GO transcription factor binding	18	170	0.0427318	9734 histone deacetylase 9
GO transcription factor binding	18	170	0.0427318	9935 v-maf musculoaponeurotic fibrosarcoma oncogene homolog B (avian)
GO cytokine-mediated signaling pathway	7	48	0.0432871	11213 interleukin-1 receptor-associated kinase 3

GO cytokine-mediated signaling pathway	7	48	0.0432871	23529 cardiotrophin-like cytokine factor 1
GO cytokine-mediated signaling pathway	7	48	0.0432871	3569 interleukin 6 (interferon, beta 2)
GO cytokine-mediated signaling pathway	7	48	0.0432871	3570 interleukin 6 receptor
GO cytokine-mediated signaling pathway	7	48	0.0432871	3815 v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog
GO cytokine-mediated signaling pathway	7	48	0.0432871	3845 v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog
GO cytokine-mediated signaling pathway	7	48	0.0432871	6778 signal transducer and activator of transcription 6, interleukin-4 inducer
GO retina development in camera-type e	4	20	0.0436781	2055 ceroid-lipofuscinosis, neuronal 8 (epilepsy, progressive with mental ret
GO retina development in camera-type e	4	20	0.0436781	4802 nuclear transcription factor Y, gamma
GO retina development in camera-type e	4	20	0.0436781	5950 retinol binding protein 4, plasma
GO retina development in camera-type e	4	20	0.0436781	652 bone morphogenetic protein 4
GO tumor necrosis factor receptor binding	4	20	0.0436781	8600 tumor necrosis factor (ligand) superfamily, member 11
GO tumor necrosis factor receptor binding	4	20	0.0436781	8740 tumor necrosis factor (ligand) superfamily, member 14
GO tumor necrosis factor receptor binding	4	20	0.0436781	8744 tumor necrosis factor (ligand) superfamily, member 9
GO tumor necrosis factor receptor binding	4	20	0.0436781	9966 tumor necrosis factor (ligand) superfamily, member 15
GO drug metabolic process	3	12	0.0440067	1558 cytochrome P450, family 2, subfamily C, polypeptide 8
GO drug metabolic process	3	12	0.0440067	1559 cytochrome P450, family 2, subfamily C, polypeptide 9
GO drug metabolic process	3	12	0.0440067	1571 cytochrome P450, family 2, subfamily E, polypeptide 1
GO photoreceptor inner segment	3	12	0.0440067	2026 enolase 2 (gamma, neuronal)
GO photoreceptor inner segment	3	12	0.0440067	4842 nitric oxide synthase 1 (neuronal)
GO photoreceptor inner segment	3	12	0.0440067	5132 phosphodiesterase 4
GO response to pH	3	12	0.0440067	27035 NADPH oxidase 1
GO response to pH	3	12	0.0440067	412 steroid sulfatase (microsomal), isozyme S
GO response to pH	3	12	0.0440067	760 carbonic anhydrase II
GO negative regulation of macrophage differentiation	3	12	0.0440067	4792 nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor 3
GO negative regulation of macrophage differentiation	3	12	0.0440067	5465 peroxisome proliferator-activated receptor alpha
GO negative regulation of macrophage differentiation	3	12	0.0440067	9619 ATP-binding cassette, sub-family G (WHITE), member 1
GO positive regulation of interferon-beta production	3	12	0.0440067	7097 toll-like receptor 2
GO positive regulation of interferon-beta production	3	12	0.0440067	7098 toll-like receptor 3
GO positive regulation of interferon-beta production	3	12	0.0440067	7099 toll-like receptor 4
GO metanephros development	5	29	0.0446065	10252 sprouty homolog 1, antagonist of FGF signaling (Drosophila)
GO metanephros development	5	29	0.0446065	157506 retinol dehydrogenase 10 (all-trans)
GO metanephros development	5	29	0.0446065	2303 forkhead box C2 (MFX-1, mesenchyme forkhead 1)
GO metanephros development	5	29	0.0446065	2737 GLI family zinc finger 3
GO metanephros development	5	29	0.0446065	652 bone morphogenetic protein 4
GO protein targeting	5	29	0.0446065	22906 trafficking protein, kinesin binding 1
GO protein targeting	5	29	0.0446065	23303 kinesin family member 13B

GO protein targeting	5	29	0.0446065	5371 promyelocytic leukemia
GO protein targeting	5	29	0.0446065	5873 RAB27A, member RAS oncogene family
GO protein targeting	5	29	0.0446065	9182 Ras association (RalGDS/AF-6) domain family (N-terminal) member 9
GO in utero embryonic development	15	136	0.045041	10568 solute carrier family 34 (sodium phosphate), member 2
GO in utero embryonic development	15	136	0.045041	157506 retinol dehydrogenase 10 (all-trans)
GO in utero embryonic development	15	136	0.045041	1906 endothelin 1
GO in utero embryonic development	15	136	0.045041	2296 forkhead box C1
GO in utero embryonic development	15	136	0.045041	2707 gap junction protein, beta 3, 31kDa
GO in utero embryonic development	15	136	0.045041	2737 GLI family zinc finger 3
GO in utero embryonic development	15	136	0.045041	28982 feline leukemia virus subgroup C cellular receptor 1
GO in utero embryonic development	15	136	0.045041	29123 ankyrin repeat domain 11
GO in utero embryonic development	15	136	0.045041	3726 jun B proto-oncogene
GO in utero embryonic development	15	136	0.045041	4087 SMAD family member 2
GO in utero embryonic development	15	136	0.045041	4851 Notch homolog 1, translocation-associated (Drosophila)
GO in utero embryonic development	15	136	0.045041	5801 protein tyrosine phosphatase, receptor type, R
GO in utero embryonic development	15	136	0.045041	8531 cold shock domain protein A
GO in utero embryonic development	15	136	0.045041	91 activin A receptor, type IB
GO in utero embryonic development	15	136	0.045041	94 activin A receptor type II-like 1
GO Golgi membrane	32	343	0.0456553	10090 uronyl-2-sulfotransferase
GO Golgi membrane	32	343	0.0456553	10282 blocked early in transport 1 homolog (S. cerevisiae)
GO Golgi membrane	32	343	0.0456553	10317 UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 5
GO Golgi membrane	32	343	0.0456553	127845 golgi transport 1 homolog A (S. cerevisiae)
GO Golgi membrane	32	343	0.0456553	1571 cytochrome P450, family 2, subfamily E, polypeptide 1
GO Golgi membrane	32	343	0.0456553	166929 sphingomyelin synthase 2
GO Golgi membrane	32	343	0.0456553	192134 UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 6 (core
GO Golgi membrane	32	343	0.0456553	26035 glucuronic acid epimerase
GO Golgi membrane	32	343	0.0456553	2706 gap junction protein, beta 2, 26kDa
GO Golgi membrane	32	343	0.0456553	27090 ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalact
GO Golgi membrane	32	343	0.0456553	3601 interleukin 15 receptor, alpha
GO Golgi membrane	32	343	0.0456553	374378 UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosami
GO Golgi membrane	32	343	0.0456553	4121 mannosidase, alpha, class 1A, member 1
GO Golgi membrane	32	343	0.0456553	51272 blocked early in transport 1 homolog (S. cerevisiae)-like
GO Golgi membrane	32	343	0.0456553	51313 family with sequence similarity 198, member B
GO Golgi membrane	32	343	0.0456553	5244 ATP-binding cassette, sub-family B (MDR/TAP), member 4
GO Golgi membrane	32	343	0.0456553	53947 alpha 1,4-galactosyltransferase
GO Golgi membrane	32	343	0.0456553	54947 lysophosphatidylcholine acyltransferase 2

GO Golgi membrane	32	343	0.0456553	55638 Golgi-localized protein
GO Golgi membrane	32	343	0.0456553	55808 ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalact
GO Golgi membrane	32	343	0.0456553	57134 mannosidase, alpha, class 1C, member 1
GO Golgi membrane	32	343	0.0456553	5768 quiescin Q6 sulfhydryl oxidase 1
GO Golgi membrane	32	343	0.0456553	6489 ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 1
GO Golgi membrane	32	343	0.0456553	682 basigin (Ok blood group)
GO Golgi membrane	32	343	0.0456553	79689 STEAP family member 4
GO Golgi membrane	32	343	0.0456553	79695 UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosami
GO Golgi membrane	32	343	0.0456553	79971 wntless homolog (Drosophila)
GO Golgi membrane	32	343	0.0456553	8509 N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 2
GO Golgi membrane	32	343	0.0456553	8706 beta-1,3-N-acetylgalactosaminyltransferase 1 (globoside blood group)
GO Golgi membrane	32	343	0.0456553	89866 SEC16 homolog B (S. cerevisiae)
GO Golgi membrane	32	343	0.0456553	9445 integral membrane protein 2B
GO Golgi membrane	32	343	0.0456553	9619 ATP-binding cassette, sub-family G (WHITE), member 1
GO transport vesicle	6	39	0.0474143	5016 oviductal glycoprotein 1, 120kDa
GO transport vesicle	6	39	0.0474143	5122 proprotein convertase subtilisin/kexin type 1
GO transport vesicle	6	39	0.0474143	5284 polymeric immunoglobulin receptor
GO transport vesicle	6	39	0.0474143	6494 signal-induced proliferation-associated 1
GO transport vesicle	6	39	0.0474143	80763 chromosome 12 open reading frame 39
GO transport vesicle	6	39	0.0474143	8082 sarcospan (Kras oncogene-associated gene)
GO calcium ion transport	13	114	0.0474416	1139 cholinergic receptor, nicotinic, alpha 7
GO calcium ion transport	13	114	0.0474416	3709 inositol 1,4,5-triphosphate receptor, type 2
GO calcium ion transport	13	114	0.0474416	493 ATPase, Ca <sup>++</sup> transporting, plasma membrane 4
GO calcium ion transport	13	114	0.0474416	53373 two pore segment channel 1
GO calcium ion transport	13	114	0.0474416	55799 calcium channel, voltage-dependent, alpha 2/delta subunit 3
GO calcium ion transport	13	114	0.0474416	56923 neuromedin U receptor 2
GO calcium ion transport	13	114	0.0474416	7223 transient receptor potential cation channel, subfamily C, member 4
GO calcium ion transport	13	114	0.0474416	774 calcium channel, voltage-dependent, N type, alpha 1B subunit
GO calcium ion transport	13	114	0.0474416	783 calcium channel, voltage-dependent, beta 2 subunit
GO calcium ion transport	13	114	0.0474416	8911 calcium channel, voltage-dependent, T type, alpha 1I subunit
GO calcium ion transport	13	114	0.0474416	8912 calcium channel, voltage-dependent, T type, alpha 1H subunit
GO calcium ion transport	13	114	0.0474416	93589 calcium channel, voltage-dependent, alpha 2/delta subunit 4
GO calcium ion transport	13	114	0.0474416	9914 ATPase, Ca <sup>++</sup> transporting, type 2C, member 2
GO receptor activity	93	1148	0.0476856	10076 protein tyrosine phosphatase, receptor type, U
GO receptor activity	93	1148	0.0476856	10268 receptor (G protein-coupled) activity modifying protein 3
GO receptor activity	93	1148	0.0476856	10288 leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIN

GO receptor activity	93	1148	0.0476856	10507 sema domain, immunoglobulin domain (Ig), transmembrane domain (T
GO receptor activity	93	1148	0.0476856	10913 ectodysplasin A receptor
GO receptor activity	93	1148	0.0476856	115330 G protein-coupled receptor 146
GO receptor activity	93	1148	0.0476856	118429 anthrax toxin receptor 2
GO receptor activity	93	1148	0.0476856	121130 olfactory receptor, family 10, subfamily P, member 1
GO receptor activity	93	1148	0.0476856	130399 activin A receptor, type IC
GO receptor activity	93	1148	0.0476856	143503 olfactory receptor, family 51, subfamily E, member 1
GO receptor activity	93	1148	0.0476856	154 adrenergic, beta-2-, receptor, surface
GO receptor activity	93	1148	0.0476856	1803 dipeptidyl-peptidase 4
GO receptor activity	93	1148	0.0476856	1813 dopamine receptor D2
GO receptor activity	93	1148	0.0476856	1815 dopamine receptor D4
GO receptor activity	93	1148	0.0476856	1839 heparin-binding EGF-like growth factor
GO receptor activity	93	1148	0.0476856	1901 sphingosine-1-phosphate receptor 1
GO receptor activity	93	1148	0.0476856	1902 lysophosphatidic acid receptor 1
GO receptor activity	93	1148	0.0476856	1969 EPH receptor A2
GO receptor activity	93	1148	0.0476856	2044 EPH receptor A5
GO receptor activity	93	1148	0.0476856	2066 v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian)
GO receptor activity	93	1148	0.0476856	2205 Fc fragment of IgE, high affinity I, receptor for; alpha polypeptide
GO receptor activity	93	1148	0.0476856	222545 G protein-coupled receptor, family C, group 6, member A
GO receptor activity	93	1148	0.0476856	223117 sema domain, immunoglobulin domain (Ig), short basic domain, secret
GO receptor activity	93	1148	0.0476856	2263 fibroblast growth factor receptor 2
GO receptor activity	93	1148	0.0476856	22925 phospholipase A2 receptor 1, 180kDa
GO receptor activity	93	1148	0.0476856	23654 plexin B2
GO receptor activity	93	1148	0.0476856	27202 G protein-coupled receptor 77
GO receptor activity	93	1148	0.0476856	27242 tumor necrosis factor receptor superfamily, member 21
GO receptor activity	93	1148	0.0476856	2861 G protein-coupled receptor 37 (endothelin receptor type B-like)
GO receptor activity	93	1148	0.0476856	286133 scavenger receptor class A, member 5 (putative)
GO receptor activity	93	1148	0.0476856	2865 free fatty acid receptor 3
GO receptor activity	93	1148	0.0476856	2867 free fatty acid receptor 2
GO receptor activity	93	1148	0.0476856	28982 feline leukemia virus subgroup C cellular receptor 1
GO receptor activity	93	1148	0.0476856	2911 glutamate receptor, metabotropic 1
GO receptor activity	93	1148	0.0476856	29126 CD274 molecule
GO receptor activity	93	1148	0.0476856	3355 5-hydroxytryptamine (serotonin) receptor 1F
GO receptor activity	93	1148	0.0476856	338557 G protein-coupled receptor 120
GO receptor activity	93	1148	0.0476856	353345 G protein-coupled receptor 141
GO receptor activity	93	1148	0.0476856	3561 interleukin 2 receptor, gamma (severe combined immunodeficiency)

GO receptor activity	93	1148	0.0476856	3570 interleukin 6 receptor
GO receptor activity	93	1148	0.0476856	3587 interleukin 10 receptor, alpha
GO receptor activity	93	1148	0.0476856	3601 interleukin 15 receptor, alpha
GO receptor activity	93	1148	0.0476856	3604 tumor necrosis factor receptor superfamily, member 9
GO receptor activity	93	1148	0.0476856	3643 insulin receptor
GO receptor activity	93	1148	0.0476856	3678 integrin, alpha 5 (fibronectin receptor, alpha polypeptide)
GO receptor activity	93	1148	0.0476856	3687 integrin, alpha X (complement component 3 receptor 4 subunit)
GO receptor activity	93	1148	0.0476856	3689 integrin, beta 2 (complement component 3 receptor 3 and 4 subunit)
GO receptor activity	93	1148	0.0476856	3691 integrin, beta 4
GO receptor activity	93	1148	0.0476856	3696 integrin, beta 8
GO receptor activity	93	1148	0.0476856	3815 v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog
GO receptor activity	93	1148	0.0476856	387509 G protein-coupled receptor 153
GO receptor activity	93	1148	0.0476856	388633 low density lipoprotein receptor class A domain containing 1
GO receptor activity	93	1148	0.0476856	3911 laminin, alpha 5
GO receptor activity	93	1148	0.0476856	392392 olfactory receptor, family 1, subfamily K, member 1
GO receptor activity	93	1148	0.0476856	4038 low density lipoprotein receptor-related protein 4
GO receptor activity	93	1148	0.0476856	4065 lymphocyte antigen 75
GO receptor activity	93	1148	0.0476856	4163 mutated in colorectal cancers
GO receptor activity	93	1148	0.0476856	4179 CD46 molecule, complement regulatory protein
GO receptor activity	93	1148	0.0476856	4306 nuclear receptor subfamily 3, group C, member 2
GO receptor activity	93	1148	0.0476856	4486 macrophage stimulating 1 receptor (c-met-related tyrosine kinase)
GO receptor activity	93	1148	0.0476856	4851 Notch homolog 1, translocation-associated (Drosophila)
GO receptor activity	93	1148	0.0476856	4853 Notch homolog 2 (Drosophila)
GO receptor activity	93	1148	0.0476856	4886 neuropeptide Y receptor Y1
GO receptor activity	93	1148	0.0476856	4889 neuropeptide Y receptor Y5
GO receptor activity	93	1148	0.0476856	5025 purinergic receptor P2X, ligand-gated ion channel, 4
GO receptor activity	93	1148	0.0476856	5362 plexin A2
GO receptor activity	93	1148	0.0476856	54852 progesterin and adipoQ receptor family member V
GO receptor activity	93	1148	0.0476856	56923 neuromedin U receptor 2
GO receptor activity	93	1148	0.0476856	5724 platelet-activating factor receptor
GO receptor activity	93	1148	0.0476856	5732 prostaglandin E receptor 2 (subtype EP2), 53kDa
GO receptor activity	93	1148	0.0476856	5734 prostaglandin E receptor 4 (subtype EP4)
GO receptor activity	93	1148	0.0476856	5737 prostaglandin F receptor (FP)
GO receptor activity	93	1148	0.0476856	57512 G protein-coupled receptor 158
GO receptor activity	93	1148	0.0476856	5789 protein tyrosine phosphatase, receptor type, D
GO receptor activity	93	1148	0.0476856	5799 protein tyrosine phosphatase, receptor type, N polypeptide 2

GO receptor activity	93	1148	0.0476856	5801 protein tyrosine phosphatase, receptor type, R
GO receptor activity	93	1148	0.0476856	6238 ribosome binding protein 1 homolog 180kDa (dog)
GO receptor activity	93	1148	0.0476856	6751 somatostatin receptor 1
GO receptor activity	93	1148	0.0476856	7097 toll-like receptor 2
GO receptor activity	93	1148	0.0476856	7098 toll-like receptor 3
GO receptor activity	93	1148	0.0476856	7099 toll-like receptor 4
GO receptor activity	93	1148	0.0476856	7133 tumor necrosis factor receptor superfamily, member 1B
GO receptor activity	93	1148	0.0476856	7869 sema domain, immunoglobulin domain (Ig), short basic domain, secret
GO receptor activity	93	1148	0.0476856	79098 chromosome 1 open reading frame 116
GO receptor activity	93	1148	0.0476856	79957 progesterin and adipoQ receptor family member VI
GO receptor activity	93	1148	0.0476856	81285 olfactory receptor, family 51, subfamily E, member 2
GO receptor activity	93	1148	0.0476856	81470 olfactory receptor, family 2, subfamily G, member 2
GO receptor activity	93	1148	0.0476856	83661 membrane-spanning 4-domains, subfamily A, member 8B
GO receptor activity	93	1148	0.0476856	8600 tumor necrosis factor (ligand) superfamily, member 11
GO receptor activity	93	1148	0.0476856	8973 cholinergic receptor, nicotinic, alpha 6
GO receptor activity	93	1148	0.0476856	91 activin A receptor, type IB
GO receptor activity	93	1148	0.0476856	94 activin A receptor type II-like 1
GO receptor activity	93	1148	0.0476856	952 CD38 molecule
GO elevation of cytosolic calcium ion con	11	92	0.0488474	1604 CD55 molecule, decay accelerating factor for complement (Cromer blo
GO elevation of cytosolic calcium ion con	11	92	0.0488474	1902 lysophosphatidic acid receptor 1
GO elevation of cytosolic calcium ion con	11	92	0.0488474	1906 endothelin 1
GO elevation of cytosolic calcium ion con	11	92	0.0488474	2769 guanine nucleotide binding protein (G protein), alpha 15 (Gq class)
GO elevation of cytosolic calcium ion con	11	92	0.0488474	3827 kininogen 1
GO elevation of cytosolic calcium ion con	11	92	0.0488474	5367 pro-melanin-concentrating hormone
GO elevation of cytosolic calcium ion con	11	92	0.0488474	56477 chemokine (C-C motif) ligand 28
GO elevation of cytosolic calcium ion con	11	92	0.0488474	56923 neuromedin U receptor 2
GO elevation of cytosolic calcium ion con	11	92	0.0488474	7852 chemokine (C-X-C motif) receptor 4
GO elevation of cytosolic calcium ion con	11	92	0.0488474	799 calcitonin receptor
GO elevation of cytosolic calcium ion con	11	92	0.0488474	952 CD38 molecule
GO brain development	13	115	0.0502916	1152 creatine kinase, brain
GO brain development	13	115	0.0502916	127343 diencephalon/mesencephalon homeobox 1
GO brain development	13	115	0.0502916	1959 early growth response 2
GO brain development	13	115	0.0502916	22859 latrophilin 1
GO brain development	13	115	0.0502916	2290 forkhead box G1
GO brain development	13	115	0.0502916	2296 forkhead box C1
GO brain development	13	115	0.0502916	3400 inhibitor of DNA binding 4, dominant negative helix-loop-helix protein



GO brain development	13	115	0.0502916	5463 POU class 6 homeobox 1
GO brain development	13	115	0.0502916	57453 Down syndrome cell adhesion molecule like 1
GO brain development	13	115	0.0502916	6096 RAR-related orphan receptor B
GO brain development	13	115	0.0502916	7170 tropomyosin 3
GO brain development	13	115	0.0502916	7546 Zic family member 2 (odd-paired homolog, Drosophila)
GO brain development	13	115	0.0502916	8660 insulin receptor substrate 2
GO negative regulation of gene-specific t	8	60	0.0505689	10014 histone deacetylase 5
GO negative regulation of gene-specific t	8	60	0.0505689	4784 nuclear factor I/X (CCAAT-binding transcription factor)
GO negative regulation of gene-specific t	8	60	0.0505689	5187 period homolog 1 (Drosophila)
GO negative regulation of gene-specific t	8	60	0.0505689	5465 peroxisome proliferator-activated receptor alpha
GO negative regulation of gene-specific t	8	60	0.0505689	6256 retinoid X receptor, alpha
GO negative regulation of gene-specific t	8	60	0.0505689	652 bone morphogenetic protein 4
GO negative regulation of gene-specific t	8	60	0.0505689	8864 period homolog 2 (Drosophila)
GO negative regulation of gene-specific t	8	60	0.0505689	9734 histone deacetylase 9
GO adult locomotory behavior	5	30	0.0506306	127343 diencephalon/mesencephalon homeobox 1
GO adult locomotory behavior	5	30	0.0506306	1815 dopamine receptor D4
GO adult locomotory behavior	5	30	0.0506306	4929 nuclear receptor subfamily 4, group A, member 2
GO adult locomotory behavior	5	30	0.0506306	5071 Parkinson disease (autosomal recessive, juvenile) 2, parkin
GO adult locomotory behavior	5	30	0.0506306	6622 synuclein, alpha (non A4 component of amyloid precursor)
GO dorsal/ventral pattern formation	5	30	0.0506306	1906 endothelin 1
GO dorsal/ventral pattern formation	5	30	0.0506306	2290 forkhead box G1
GO dorsal/ventral pattern formation	5	30	0.0506306	57453 Down syndrome cell adhesion molecule like 1
GO dorsal/ventral pattern formation	5	30	0.0506306	84976 dispatched homolog 1 (Drosophila)
GO dorsal/ventral pattern formation	5	30	0.0506306	8646 chordin
GO positive regulation of inflammatory r	4	21	0.0511354	183 angiotensinogen (serpin peptidase inhibitor, clade A, member 8)
GO positive regulation of inflammatory r	4	21	0.0511354	7097 toll-like receptor 2
GO positive regulation of inflammatory r	4	21	0.0511354	7098 toll-like receptor 3
GO positive regulation of inflammatory r	4	21	0.0511354	7099 toll-like receptor 4
GO ventricular cardiac muscle tissue mor	4	21	0.0511354	2296 forkhead box C1
GO ventricular cardiac muscle tissue mor	4	21	0.0511354	2303 forkhead box C2 (MFH-1, mesenchyme forkhead 1)
GO ventricular cardiac muscle tissue mor	4	21	0.0511354	6256 retinoid X receptor, alpha
GO ventricular cardiac muscle tissue mor	4	21	0.0511354	7049 transforming growth factor, beta receptor III
GO negative regulation of gene-specific t	4	21	0.0511354	429 achaete-scute complex homolog 1 (Drosophila)
GO negative regulation of gene-specific t	4	21	0.0511354	4851 Notch homolog 1, translocation-associated (Drosophila)
GO negative regulation of gene-specific t	4	21	0.0511354	652 bone morphogenetic protein 4
GO negative regulation of gene-specific t	4	21	0.0511354	7026 nuclear receptor subfamily 2, group F, member 2

GO proteolysis	38	423	0.0513137	10942	protease, serine, 21 (testisin)
GO proteolysis	38	423	0.0513137	11202	kallikrein-related peptidase 8
GO proteolysis	38	423	0.0513137	1363	carboxypeptidase E
GO proteolysis	38	423	0.0513137	1368	carboxypeptidase M
GO proteolysis	38	423	0.0513137	1508	cathepsin B
GO proteolysis	38	423	0.0513137	1519	cathepsin O
GO proteolysis	38	423	0.0513137	170692	ADAM metallopeptidase with thrombospondin type 1 motif, 18
GO proteolysis	38	423	0.0513137	1803	dipeptidyl-peptidase 4
GO proteolysis	38	423	0.0513137	255738	proprotein convertase subtilisin/kexin type 9
GO proteolysis	38	423	0.0513137	25825	beta-site APP-cleaving enzyme 2
GO proteolysis	38	423	0.0513137	26232	F-box protein 2
GO proteolysis	38	423	0.0513137	26270	F-box protein 6
GO proteolysis	38	423	0.0513137	29108	PYD and CARD domain containing
GO proteolysis	38	423	0.0513137	388743	calpain 8
GO proteolysis	38	423	0.0513137	4316	matrix metallopeptidase 7 (matrilysin, uterine)
GO proteolysis	38	423	0.0513137	5046	proprotein convertase subtilisin/kexin type 6
GO proteolysis	38	423	0.0513137	5122	proprotein convertase subtilisin/kexin type 1
GO proteolysis	38	423	0.0513137	51279	complement component 1, r subcomponent-like
GO proteolysis	38	423	0.0513137	5327	plasminogen activator, tissue
GO proteolysis	38	423	0.0513137	54504	carboxypeptidase, vitellogenic-like
GO proteolysis	38	423	0.0513137	5648	mannan-binding lectin serine peptidase 1 (C4/C2 activating component
GO proteolysis	38	423	0.0513137	56547	matrix metallopeptidase 26
GO proteolysis	38	423	0.0513137	5655	kallikrein-related peptidase 10
GO proteolysis	38	423	0.0513137	56649	transmembrane protease, serine 4
GO proteolysis	38	423	0.0513137	57094	carboxypeptidase A6
GO proteolysis	38	423	0.0513137	5972	renin
GO proteolysis	38	423	0.0513137	629	complement factor B
GO proteolysis	38	423	0.0513137	64699	transmembrane protease, serine 3
GO proteolysis	38	423	0.0513137	7092	tolloid-like 1
GO proteolysis	38	423	0.0513137	715	complement component 1, r subcomponent
GO proteolysis	38	423	0.0513137	717	complement component 2
GO proteolysis	38	423	0.0513137	726	calpain 5
GO proteolysis	38	423	0.0513137	79956	endoplasmic reticulum metallopeptidase 1
GO proteolysis	38	423	0.0513137	834	caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, co
GO proteolysis	38	423	0.0513137	837	caspase 4, apoptosis-related cysteine peptidase
GO proteolysis	38	423	0.0513137	8722	cathepsin F

GO proteolysis	38	423	0.0513137	8751 ADAM metallopeptidase domain 15
GO proteolysis	38	423	0.0513137	9510 ADAM metallopeptidase with thrombospondin type 1 motif, 1
GO response to hydrogen peroxide	6	40	0.0526898	10628 thioredoxin interacting protein
GO response to hydrogen peroxide	6	40	0.0526898	1843 dual specificity phosphatase 1
GO response to hydrogen peroxide	6	40	0.0526898	2066 v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian)
GO response to hydrogen peroxide	6	40	0.0526898	3725 jun oncogene
GO response to hydrogen peroxide	6	40	0.0526898	4151 myoglobin
GO response to hydrogen peroxide	6	40	0.0526898	84919 protein phosphatase 1, regulatory (inhibitor) subunit 15B
GO negative regulation of smooth muscle cell proliferation	3	13	0.0543804	10221 tribbles homolog 1 (Drosophila)
GO negative regulation of smooth muscle cell proliferation	3	13	0.0543804	3486 insulin-like growth factor binding protein 3
GO negative regulation of smooth muscle cell proliferation	3	13	0.0543804	3488 insulin-like growth factor binding protein 5
GO hormone metabolic process	3	13	0.0543804	183 angiotensinogen (serpin peptidase inhibitor, clade A, member 8)
GO hormone metabolic process	3	13	0.0543804	3169 forkhead box A1
GO hormone metabolic process	3	13	0.0543804	54361 wingless-type MMTV integration site family, member 4
GO MAP kinase tyrosine/serine/threonine kinase activity	3	13	0.0543804	1843 dual specificity phosphatase 1
GO MAP kinase tyrosine/serine/threonine kinase activity	3	13	0.0543804	1844 dual specificity phosphatase 2
GO MAP kinase tyrosine/serine/threonine kinase activity	3	13	0.0543804	1847 dual specificity phosphatase 5
GO regulation of inflammatory response	3	13	0.0543804	22904 strawberry notch homolog 2 (Drosophila)
GO regulation of inflammatory response	3	13	0.0543804	50604 interleukin 20
GO regulation of inflammatory response	3	13	0.0543804	604 B-cell CLL/lymphoma 6
GO negative regulation of Wnt receptor signaling pathway	3	13	0.0543804	2737 GLI family zinc finger 3
GO negative regulation of Wnt receptor signaling pathway	3	13	0.0543804	4163 mutated in colorectal cancers
GO negative regulation of Wnt receptor signaling pathway	3	13	0.0543804	7474 wingless-type MMTV integration site family, member 5A
GO embryonic cranial skeleton morphogenesis	3	13	0.0543804	4087 SMAD family member 2
GO embryonic cranial skeleton morphogenesis	3	13	0.0543804	5396 paired related homeobox 1
GO embryonic cranial skeleton morphogenesis	3	13	0.0543804	652 bone morphogenetic protein 4
GO inorganic anion exchanger activity	3	13	0.0543804	55867 solute carrier family 22 (organic anion/urate transporter), member 11
GO inorganic anion exchanger activity	3	13	0.0543804	6521 solute carrier family 4, anion exchanger, member 1 (erythrocyte membrane protein)
GO inorganic anion exchanger activity	3	13	0.0543804	8671 solute carrier family 4, sodium bicarbonate cotransporter, member 4
GO activation of NF-kappaB-inducing kinase activity	3	13	0.0543804	7098 toll-like receptor 3
GO activation of NF-kappaB-inducing kinase activity	3	13	0.0543804	79092 caspase recruitment domain family, member 14
GO activation of NF-kappaB-inducing kinase activity	3	13	0.0543804	9966 tumor necrosis factor (ligand) superfamily, member 15
GO intracellular protein kinase cascade	11	94	0.0555645	150094 salt-inducible kinase 1
GO intracellular protein kinase cascade	11	94	0.0555645	1612 death-associated protein kinase 1
GO intracellular protein kinase cascade	11	94	0.0555645	1813 dopamine receptor D2
GO intracellular protein kinase cascade	11	94	0.0555645	1906 endothelin 1

GO intracellular protein kinase cascade	11	94	0.0555645	23043 TRAF2 and NCK interacting kinase
GO intracellular protein kinase cascade	11	94	0.0555645	23604 death-associated protein kinase 2
GO intracellular protein kinase cascade	11	94	0.0555645	3815 v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog
GO intracellular protein kinase cascade	11	94	0.0555645	51085 MLX interacting protein-like
GO intracellular protein kinase cascade	11	94	0.0555645	7049 transforming growth factor, beta receptor III
GO intracellular protein kinase cascade	11	94	0.0555645	7538 zinc finger protein 36, C3H type, homolog (mouse)
GO intracellular protein kinase cascade	11	94	0.0555645	9263 serine/threonine kinase 17a
GO embryonic development	9	72	0.0559856	1999 E74-like factor 3 (ets domain transcription factor, epithelial-specific )
GO embryonic development	9	72	0.0559856	3911 laminin, alpha 5
GO embryonic development	9	72	0.0559856	4851 Notch homolog 1, translocation-associated (Drosophila)
GO embryonic development	9	72	0.0559856	498 ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subun
GO embryonic development	9	72	0.0559856	5122 proprotein convertase subtilisin/kexin type 1
GO embryonic development	9	72	0.0559856	5950 retinol binding protein 4, plasma
GO embryonic development	9	72	0.0559856	7474 wingless-type MMTV integration site family, member 5A
GO embryonic development	9	72	0.0559856	8796 sciellin
GO embryonic development	9	72	0.0559856	91 activin A receptor, type IB
GO positive regulation of MAPKKK casc	5	31	0.0571075	154 adrenergic, beta-2-, receptor, surface
GO positive regulation of MAPKKK casc	5	31	0.0571075	183 angiotensinogen (serpin peptidase inhibitor, clade A, member 8)
GO positive regulation of MAPKKK casc	5	31	0.0571075	3569 interleukin 6 (interferon, beta 2)
GO positive regulation of MAPKKK casc	5	31	0.0571075	3570 interleukin 6 receptor
GO positive regulation of MAPKKK casc	5	31	0.0571075	3643 insulin receptor
GO heart morphogenesis	5	31	0.0571075	2296 forkhead box C1
GO heart morphogenesis	5	31	0.0571075	2303 forkhead box C2 (MFH-1, mesenchyme forkhead 1)
GO heart morphogenesis	5	31	0.0571075	3643 insulin receptor
GO heart morphogenesis	5	31	0.0571075	6604 SWI/SNF related, matrix associated, actin dependent regulator of chrom
GO heart morphogenesis	5	31	0.0571075	7049 transforming growth factor, beta receptor III
GO negative regulation of Ras protein sig	2	6	0.0582206	10252 sprouty homolog 1, antagonist of FGF signaling (Drosophila)
GO negative regulation of Ras protein sig	2	6	0.0582206	10253 sprouty homolog 2 (Drosophila)
GO prostate epithelial cord arborization i	2	6	0.0582206	10481 homeobox B13
GO prostate epithelial cord arborization i	2	6	0.0582206	3479 insulin-like growth factor 1 (somatomedin C)
GO negative regulation of interleukin-12	2	6	0.0582206	11213 interleukin-1 receptor-associated kinase 3
GO negative regulation of interleukin-12	2	6	0.0582206	64127 nucleotide-binding oligomerization domain containing 2
GO response to amine stimulus	2	6	0.0582206	1373 carbamoyl-phosphate synthetase 1, mitochondrial
GO response to amine stimulus	2	6	0.0582206	1508 cathepsin B
GO negative regulation of protein secreti	2	6	0.0582206	1813 dopamine receptor D2
GO negative regulation of protein secreti	2	6	0.0582206	1815 dopamine receptor D4

GO peristalsis	2	6	0.0582206	1813 dopamine receptor D2
GO peristalsis	2	6	0.0582206	183 angiotensinogen (serpin peptidase inhibitor, clade A, member 8)
GO regulation of synaptic transmission, C	2	6	0.0582206	1813 dopamine receptor D2
GO regulation of synaptic transmission, C	2	6	0.0582206	3845 v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog
GO regulation of dopamine metabolic pr	2	6	0.0582206	1815 dopamine receptor D4
GO regulation of dopamine metabolic pr	2	6	0.0582206	4929 nuclear receptor subfamily 4, group A, member 2
GO positive regulation of fatty acid biosy	2	6	0.0582206	183 angiotensinogen (serpin peptidase inhibitor, clade A, member 8)
GO positive regulation of fatty acid biosy	2	6	0.0582206	51085 MLX interacting protein-like
GO inositol phosphate-mediated signalin	2	6	0.0582206	1906 endothelin 1
GO inositol phosphate-mediated signalin	2	6	0.0582206	56923 neuromedin U receptor 2
GO mitochondrial membrane organizatic	2	6	0.0582206	2055 ceroid-lipofuscinosis, neuronal 8 (epilepsy, progressive with mental ret
GO mitochondrial membrane organizatic	2	6	0.0582206	6622 synuclein, alpha (non A4 component of amyloid precursor)
GO positive regulation of mast cell degra	2	6	0.0582206	2205 Fc fragment of IgE, high affinity I, receptor for; alpha polypeptide
GO positive regulation of mast cell degra	2	6	0.0582206	6850 spleen tyrosine kinase
GO leukotriene metabolic process	2	6	0.0582206	240 arachidonate 5-lipoxygenase
GO leukotriene metabolic process	2	6	0.0582206	4056 leukotriene C4 synthase
GO lipoxygenase activity	2	6	0.0582206	240 arachidonate 5-lipoxygenase
GO lipoxygenase activity	2	6	0.0582206	59344 arachidonate lipoxygenase 3
GO glycosaminoglycan catabolic process	2	6	0.0582206	2517 fucosidase, alpha-L- 1, tissue
GO glycosaminoglycan catabolic process	2	6	0.0582206	2990 glucuronidase, beta
GO heparan sulfate proteoglycan biosynt	2	6	0.0582206	26035 glucuronic acid epimerase
GO heparan sulfate proteoglycan biosynt	2	6	0.0582206	8509 N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 2
GO neuron fate specification	2	6	0.0582206	3169 forkhead box A1
GO neuron fate specification	2	6	0.0582206	429 achaete-scute complex homolog 1 (Drosophila)
GO exocrine pancreas development	2	6	0.0582206	3479 insulin-like growth factor 1 (somatomedin C)
GO exocrine pancreas development	2	6	0.0582206	3643 insulin receptor
GO positive regulation of myoblast differ	2	6	0.0582206	3486 insulin-like growth factor binding protein 3
GO positive regulation of myoblast differ	2	6	0.0582206	91653 Boc homolog (mouse)
GO interleukin-6 receptor binding	2	6	0.0582206	3569 interleukin 6 (interferon, beta 2)
GO interleukin-6 receptor binding	2	6	0.0582206	3570 interleukin 6 receptor
GO positive regulation of acute inflamma	2	6	0.0582206	3569 interleukin 6 (interferon, beta 2)
GO positive regulation of acute inflamma	2	6	0.0582206	4889 neuropeptide Y receptor Y5
GO water transmembrane transporter ac	2	6	0.0582206	358 aquaporin 1 (Colton blood group)
GO water transmembrane transporter ac	2	6	0.0582206	6563 solute carrier family 14 (urea transporter), member 1 (Kidd blood group)
GO SMAD protein nuclear translocation	2	6	0.0582206	3725 jun oncogene
GO SMAD protein nuclear translocation	2	6	0.0582206	5371 promyelocytic leukemia

GO somatic stem cell division	2	6	0.0582206	3815 v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog
GO somatic stem cell division	2	6	0.0582206	4851 Notch homolog 1, translocation-associated (Drosophila)
GO negative regulation of erythrocyte dif	2	6	0.0582206	4005 LIM domain only 2 (rhombotin-like 1)
GO negative regulation of erythrocyte dif	2	6	0.0582206	9935 v-maf musculoaponeurotic fibrosarcoma oncogene homolog B (avian)
GO maintenance of gastrointestinal epith	2	6	0.0582206	4588 mucin 6, oligomeric mucus/gel-forming
GO maintenance of gastrointestinal epith	2	6	0.0582206	5950 retinol binding protein 4, plasma
GO dopamine biosynthetic process	2	6	0.0582206	4929 nuclear receptor subfamily 4, group A, member 2
GO dopamine biosynthetic process	2	6	0.0582206	6622 synuclein, alpha (non A4 component of amyloid precursor)
GO negative regulation of cholesterol stc	2	6	0.0582206	5465 peroxisome proliferator-activated receptor alpha
GO negative regulation of cholesterol stc	2	6	0.0582206	9619 ATP-binding cassette, sub-family G (WHITE), member 1
GO protein thiol-disulfide exchange	2	6	0.0582206	56605 ERO1-like beta ( <i>S. cerevisiae</i> )
GO protein thiol-disulfide exchange	2	6	0.0582206	5768 quiescin Q6 sulfhydryl oxidase 1
GO regulation of branching involved in pi	2	6	0.0582206	6256 retinoid X receptor, alpha
GO regulation of branching involved in pi	2	6	0.0582206	652 bone morphogenetic protein 4
GO branching involved in embryonic plac	2	6	0.0582206	6692 serine peptidase inhibitor, Kunitz type 1
GO branching involved in embryonic plac	2	6	0.0582206	9021 suppressor of cytokine signaling 3
GO cobalt ion transport	2	6	0.0582206	6947 transcobalamin I (vitamin B12 binding protein, R binder family)
GO cobalt ion transport	2	6	0.0582206	6948 transcobalamin II; macrocytic anemia
GO Rho GTPase activator activity	4	22	0.0592421	10435 CDC42 effector protein (Rho GTPase binding) 2
GO Rho GTPase activator activity	4	22	0.0592421	23092 Rho GTPase activating protein 26
GO Rho GTPase activator activity	4	22	0.0592421	3725 jun oncogene
GO Rho GTPase activator activity	4	22	0.0592421	395 Rho GTPase activating protein 6
GO gluconeogenesis	4	22	0.0592421	10891 peroxisome proliferator-activated receptor gamma, coactivator 1 alpha
GO gluconeogenesis	4	22	0.0592421	2026 enolase 2 (gamma, neuronal)
GO gluconeogenesis	4	22	0.0592421	467 activating transcription factor 3
GO gluconeogenesis	4	22	0.0592421	5950 retinol binding protein 4, plasma
GO negative regulation of NF-kappaB tra	4	22	0.0592421	11213 interleukin-1 receptor-associated kinase 3
GO negative regulation of NF-kappaB tra	4	22	0.0592421	4792 nuclear factor of kappa light polypeptide gene enhancer in B-cells inhib
GO negative regulation of NF-kappaB tra	4	22	0.0592421	64127 nucleotide-binding oligomerization domain containing 2
GO negative regulation of NF-kappaB tra	4	22	0.0592421	7001 peroxiredoxin 2
GO cysteine-type endopeptidase inhibito	4	22	0.0592421	1469 cystatin SN
GO cysteine-type endopeptidase inhibito	4	22	0.0592421	1471 cystatin C
GO cysteine-type endopeptidase inhibito	4	22	0.0592421	26998 fetuin B
GO cysteine-type endopeptidase inhibito	4	22	0.0592421	3827 kininogen 1
GO blood vessel remodeling	4	22	0.0592421	183 angiotensinogen (serpin peptidase inhibitor, clade A, member 8)
GO blood vessel remodeling	4	22	0.0592421	2296 forkhead box C1

GO	blood vessel remodeling	4	22	0.0592421	2303	forkhead box C2 (MFH-1, mesenchyme forkhead 1)
GO	blood vessel remodeling	4	22	0.0592421	3479	insulin-like growth factor 1 (somatomedin C)
GO	activation of phospholipase C activity	4	22	0.0592421	1902	lysophosphatidic acid receptor 1
GO	activation of phospholipase C activity	4	22	0.0592421	2769	guanine nucleotide binding protein (G protein), alpha 15 (Gq class)
GO	activation of phospholipase C activity	4	22	0.0592421	395	Rho GTPase activating protein 6
GO	activation of phospholipase C activity	4	22	0.0592421	799	calcitonin receptor
GO	basal plasma membrane	4	22	0.0592421	26119	low density lipoprotein receptor adaptor protein 1
GO	basal plasma membrane	4	22	0.0592421	358	aquaporin 1 (Colton blood group)
GO	basal plasma membrane	4	22	0.0592421	3691	integrin, beta 4
GO	basal plasma membrane	4	22	0.0592421	9962	solute carrier family 23 (nucleobase transporters), member 2
GO	voltage-gated calcium channel compl	4	22	0.0592421	774	calcium channel, voltage-dependent, N type, alpha 1B subunit
GO	voltage-gated calcium channel compl	4	22	0.0592421	783	calcium channel, voltage-dependent, beta 2 subunit
GO	voltage-gated calcium channel compl	4	22	0.0592421	8911	calcium channel, voltage-dependent, T type, alpha 1I subunit
GO	voltage-gated calcium channel compl	4	22	0.0592421	8912	calcium channel, voltage-dependent, T type, alpha 1H subunit
GO	positive regulation of cell migration	8	62	0.0594006	1435	colony stimulating factor 1 (macrophage)
GO	positive regulation of cell migration	8	62	0.0594006	1906	endothelin 1
GO	positive regulation of cell migration	8	62	0.0594006	2066	v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian)
GO	positive regulation of cell migration	8	62	0.0594006	3175	one cut homeobox 1
GO	positive regulation of cell migration	8	62	0.0594006	3643	insulin receptor
GO	positive regulation of cell migration	8	62	0.0594006	3815	v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog
GO	positive regulation of cell migration	8	62	0.0594006	79872	Cas-Br-M (murine) ecotropic retroviral transforming sequence-like 1
GO	positive regulation of cell migration	8	62	0.0594006	8660	insulin receptor substrate 2
GO	extracellular matrix organization	8	62	0.0594006	183	angiotensinogen (serpin peptidase inhibitor, clade A, member 8)
GO	extracellular matrix organization	8	62	0.0594006	1999	E74-like factor 3 (ets domain transcription factor, epithelial-specific )
GO	extracellular matrix organization	8	62	0.0594006	27035	NADPH oxidase 1
GO	extracellular matrix organization	8	62	0.0594006	3491	cysteine-rich, angiogenic inducer, 61
GO	extracellular matrix organization	8	62	0.0594006	3958	lectin, galactoside-binding, soluble, 3
GO	extracellular matrix organization	8	62	0.0594006	4791	nuclear factor of kappa light polypeptide gene enhancer in B-cells 2 (p4
GO	extracellular matrix organization	8	62	0.0594006	6692	serine peptidase inhibitor, Kunitz type 1
GO	extracellular matrix organization	8	62	0.0594006	8434	reversion-inducing-cysteine-rich protein with kazal motifs
GO	G-protein coupled receptor activity	32	352	0.0607328	115330	G protein-coupled receptor 146
GO	G-protein coupled receptor activity	32	352	0.0607328	154	adrenergic, beta-2-, receptor, surface
GO	G-protein coupled receptor activity	32	352	0.0607328	1813	dopamine receptor D2
GO	G-protein coupled receptor activity	32	352	0.0607328	1815	dopamine receptor D4
GO	G-protein coupled receptor activity	32	352	0.0607328	1901	sphingosine-1-phosphate receptor 1
GO	G-protein coupled receptor activity	32	352	0.0607328	1902	lysophosphatidic acid receptor 1

GO	G-protein coupled receptor activity	32	352	0.0607328	2015 egf-like module containing, mucin-like, hormone receptor-like 1
GO	G-protein coupled receptor activity	32	352	0.0607328	222545 G protein-coupled receptor, family C, group 6, member A
GO	G-protein coupled receptor activity	32	352	0.0607328	22859 latrophilin 1
GO	G-protein coupled receptor activity	32	352	0.0607328	23266 latrophilin 2
GO	G-protein coupled receptor activity	32	352	0.0607328	23284 latrophilin 3
GO	G-protein coupled receptor activity	32	352	0.0607328	27202 G protein-coupled receptor 77
GO	G-protein coupled receptor activity	32	352	0.0607328	283383 G protein-coupled receptor 133
GO	G-protein coupled receptor activity	32	352	0.0607328	2861 G protein-coupled receptor 37 (endothelin receptor type B-like)
GO	G-protein coupled receptor activity	32	352	0.0607328	2865 free fatty acid receptor 3
GO	G-protein coupled receptor activity	32	352	0.0607328	2867 free fatty acid receptor 2
GO	G-protein coupled receptor activity	32	352	0.0607328	2911 glutamate receptor, metabotropic 1
GO	G-protein coupled receptor activity	32	352	0.0607328	3355 5-hydroxytryptamine (serotonin) receptor 1F
GO	G-protein coupled receptor activity	32	352	0.0607328	338557 G protein-coupled receptor 120
GO	G-protein coupled receptor activity	32	352	0.0607328	353345 G protein-coupled receptor 141
GO	G-protein coupled receptor activity	32	352	0.0607328	387509 G protein-coupled receptor 153
GO	G-protein coupled receptor activity	32	352	0.0607328	4886 neuropeptide Y receptor Y1
GO	G-protein coupled receptor activity	32	352	0.0607328	4889 neuropeptide Y receptor Y5
GO	G-protein coupled receptor activity	32	352	0.0607328	56923 neuromedin U receptor 2
GO	G-protein coupled receptor activity	32	352	0.0607328	5724 platelet-activating factor receptor
GO	G-protein coupled receptor activity	32	352	0.0607328	5732 prostaglandin E receptor 2 (subtype EP2), 53kDa
GO	G-protein coupled receptor activity	32	352	0.0607328	5734 prostaglandin E receptor 4 (subtype EP4)
GO	G-protein coupled receptor activity	32	352	0.0607328	5737 prostaglandin F receptor (FP)
GO	G-protein coupled receptor activity	32	352	0.0607328	57512 G protein-coupled receptor 158
GO	G-protein coupled receptor activity	32	352	0.0607328	6751 somatostatin receptor 1
GO	G-protein coupled receptor activity	32	352	0.0607328	7852 chemokine (C-X-C motif) receptor 4
GO	G-protein coupled receptor activity	32	352	0.0607328	84059 G protein-coupled receptor 98
GO	anti-apoptosis	18	178	0.061715	10507 sema domain, immunoglobulin domain (Ig), transmembrane domain (T
GO	anti-apoptosis	18	178	0.061715	1612 death-associated protein kinase 1
GO	anti-apoptosis	18	178	0.061715	2296 forkhead box C1
GO	anti-apoptosis	18	178	0.061715	2303 forkhead box C2 (MFH-1, mesenchyme forkhead 1)
GO	anti-apoptosis	18	178	0.061715	3479 insulin-like growth factor 1 (somatomedin C)
GO	anti-apoptosis	18	178	0.061715	4170 myeloid cell leukemia sequence 1 (BCL2-related)
GO	anti-apoptosis	18	178	0.061715	4792 nuclear factor of kappa light polypeptide gene enhancer in B-cells inhib
GO	anti-apoptosis	18	178	0.061715	4853 Notch homolog 2 (Drosophila)
GO	anti-apoptosis	18	178	0.061715	573 BCL2-associated athanogene
GO	anti-apoptosis	18	178	0.061715	627 brain-derived neurotrophic factor



GO anti-apoptosis	18	178	0.061715	6622 synuclein, alpha (non A4 component of amyloid precursor)
GO anti-apoptosis	18	178	0.061715	7001 peroxiredoxin 2
GO anti-apoptosis	18	178	0.061715	79444 baculoviral IAP repeat-containing 7
GO anti-apoptosis	18	178	0.061715	8382 non-metastatic cells 5, protein expressed in (nucleoside-diphosphate k
GO anti-apoptosis	18	178	0.061715	8793 tumor necrosis factor receptor superfamily, member 10d, decoy with t
GO anti-apoptosis	18	178	0.061715	8996 nucleolar protein 3 (apoptosis repressor with CARD domain)
GO anti-apoptosis	18	178	0.061715	9021 suppressor of cytokine signaling 3
GO anti-apoptosis	18	178	0.061715	9214 Fas apoptotic inhibitory molecule 3
GO positive regulation of anti-apoptosis	5	32	0.0640368	1843 dual specificity phosphatase 1
GO positive regulation of anti-apoptosis	5	32	0.0640368	2066 v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian)
GO positive regulation of anti-apoptosis	5	32	0.0640368	3569 interleukin 6 (interferon, beta 2)
GO positive regulation of anti-apoptosis	5	32	0.0640368	3570 interleukin 6 receptor
GO positive regulation of anti-apoptosis	5	32	0.0640368	4889 neuropeptide Y receptor Y5
GO spermatid development	5	32	0.0640368	3306 heat shock 70kDa protein 2
GO spermatid development	5	32	0.0640368	3815 v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog
GO spermatid development	5	32	0.0640368	8382 non-metastatic cells 5, protein expressed in (nucleoside-diphosphate k
GO spermatid development	5	32	0.0640368	9271 piwi-like 1 (Drosophila)
GO spermatid development	5	32	0.0640368	9985 REC8 homolog (yeast)
GO apical part of cell	6	42	0.0642702	358 aquaporin 1 (Colton blood group)
GO apical part of cell	6	42	0.0642702	5025 purinergic receptor P2X, ligand-gated ion channel, 4
GO apical part of cell	6	42	0.0642702	50617 ATPase, H+ transporting, lysosomal V0 subunit a4
GO apical part of cell	6	42	0.0642702	5327 plasminogen activator, tissue
GO apical part of cell	6	42	0.0642702	760 carbonic anhydrase II
GO apical part of cell	6	42	0.0642702	81693 amnionless homolog (mouse)
GO cytokine activity	15	143	0.0644498	10447 family with sequence similarity 3, member C
GO cytokine activity	15	143	0.0644498	1435 colony stimulating factor 1 (macrophage)
GO cytokine activity	15	143	0.0644498	23529 cardiotrophin-like cytokine factor 1
GO cytokine activity	15	143	0.0644498	3569 interleukin 6 (interferon, beta 2)
GO cytokine activity	15	143	0.0644498	4254 KIT ligand
GO cytokine activity	15	143	0.0644498	50604 interleukin 20
GO cytokine activity	15	143	0.0644498	64388 gremlin 2, cysteine knot superfamily, homolog (Xenopus laevis)
GO cytokine activity	15	143	0.0644498	652 bone morphogenetic protein 4
GO cytokine activity	15	143	0.0644498	8600 tumor necrosis factor (ligand) superfamily, member 11
GO cytokine activity	15	143	0.0644498	8740 tumor necrosis factor (ligand) superfamily, member 14
GO cytokine activity	15	143	0.0644498	8744 tumor necrosis factor (ligand) superfamily, member 9
GO cytokine activity	15	143	0.0644498	90865 interleukin 33

GO cytokine activity	15	143	0.0644498	92304 secretoglobin, family 3A, member 1
GO cytokine activity	15	143	0.0644498	9518 growth differentiation factor 15
GO cytokine activity	15	143	0.0644498	9966 tumor necrosis factor (ligand) superfamily, member 15
GO transcription repressor binding	3	14	0.0658037	10014 histone deacetylase 5
GO transcription repressor binding	3	14	0.0658037	2737 GLI family zinc finger 3
GO transcription repressor binding	3	14	0.0658037	9734 histone deacetylase 9
GO response to starvation	3	14	0.0658037	10891 peroxisome proliferator-activated receptor gamma, coactivator 1 alpha
GO response to starvation	3	14	0.0658037	1373 carbamoyl-phosphate synthetase 1, mitochondrial
GO response to starvation	3	14	0.0658037	35 acyl-Coenzyme A dehydrogenase, C-2 to C-3 short chain
GO regulation of sensory perception of p	3	14	0.0658037	154 adrenergic, beta-2-, receptor, surface
GO regulation of sensory perception of p	3	14	0.0658037	2911 glutamate receptor, metabotropic 1
GO regulation of sensory perception of p	3	14	0.0658037	885 cholecystokinin
GO regulation of vasoconstriction	3	14	0.0658037	183 angiotensinogen (serpin peptidase inhibitor, clade A, member 8)
GO regulation of vasoconstriction	3	14	0.0658037	1906 endothelin 1
GO regulation of vasoconstriction	3	14	0.0658037	27345 potassium large conductance calcium-activated channel, subfamily M,
GO regulation of neuronal synaptic plasti	3	14	0.0658037	1959 early growth response 2
GO regulation of neuronal synaptic plasti	3	14	0.0658037	5367 pro-melanin-concentrating hormone
GO regulation of neuronal synaptic plasti	3	14	0.0658037	8553 basic helix-loop-helix family, member e40
GO positive regulation of protein secretic	3	14	0.0658037	2033 E1A binding protein p300
GO positive regulation of protein secretic	3	14	0.0658037	3783 potassium intermediate/small conductance calcium-activated channel,
GO positive regulation of protein secretic	3	14	0.0658037	5122 proprotein convertase subtilisin/kexin type 1
GO artery morphogenesis	3	14	0.0658037	2296 forkhead box C1
GO artery morphogenesis	3	14	0.0658037	2303 forkhead box C2 (MFH-1, mesenchyme forkhead 1)
GO artery morphogenesis	3	14	0.0658037	5396 paired related homeobox 1
GO eye development	3	14	0.0658037	2296 forkhead box C1
GO eye development	3	14	0.0658037	4212 Meis homeobox 2
GO eye development	3	14	0.0658037	5950 retinol binding protein 4, plasma
GO negative regulation of mitotic cell cyc	3	14	0.0658037	2296 forkhead box C1
GO negative regulation of mitotic cell cyc	3	14	0.0658037	5371 promyelocytic leukemia
GO negative regulation of mitotic cell cyc	3	14	0.0658037	5774 protein tyrosine phosphatase, non-receptor type 3
GO sialyltransferase activity	3	14	0.0658037	27090 ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalact
GO sialyltransferase activity	3	14	0.0658037	55808 ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalact
GO sialyltransferase activity	3	14	0.0658037	6489 ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 1
GO DNA damage response, signal transdi	3	14	0.0658037	28996 homeodomain interacting protein kinase 2
GO DNA damage response, signal transdi	3	14	0.0658037	3428 interferon, gamma-inducible protein 16
GO DNA damage response, signal transdi	3	14	0.0658037	5371 promyelocytic leukemia

GO	response to ATP	3	14	0.0658037	5025 purinergic receptor P2X, ligand-gated ion channel, 4
GO	response to ATP	3	14	0.0658037	6402 selectin L
GO	response to ATP	3	14	0.0658037	834 caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, co
GO	proteasome core complex	3	14	0.0658037	5696 proteasome (prosome, macropain) subunit, beta type, 8 (large multifur
GO	proteasome core complex	3	14	0.0658037	5698 proteasome (prosome, macropain) subunit, beta type, 9 (large multifur
GO	proteasome core complex	3	14	0.0658037	5699 proteasome (prosome, macropain) subunit, beta type, 10
GO	guanyl-nucleotide exchange factor ac	13	120	0.0663024	152273 FYVE, RhoGEF and PH domain containing 5
GO	guanyl-nucleotide exchange factor ac	13	120	0.0663024	23179 ral guanine nucleotide dissociation stimulator-like 1
GO	guanyl-nucleotide exchange factor ac	13	120	0.0663024	23263 MCF.2 cell line derived transforming sequence-like
GO	guanyl-nucleotide exchange factor ac	13	120	0.0663024	23348 dedicator of cytokinesis 9
GO	guanyl-nucleotide exchange factor ac	13	120	0.0663024	23365 Rho guanine nucleotide exchange factor (GEF) 12
GO	guanyl-nucleotide exchange factor ac	13	120	0.0663024	389337 Rho guanine nucleotide exchange factor (GEF) 37
GO	guanyl-nucleotide exchange factor ac	13	120	0.0663024	54848 Rho guanine nucleotide exchange factor (GEF) 38
GO	guanyl-nucleotide exchange factor ac	13	120	0.0663024	55160 Rho guanine nucleotide exchange factor (GEF) 10-like
GO	guanyl-nucleotide exchange factor ac	13	120	0.0663024	57139 ral guanine nucleotide dissociation stimulator-like 3
GO	guanyl-nucleotide exchange factor ac	13	120	0.0663024	5900 ral guanine nucleotide dissociation stimulator
GO	guanyl-nucleotide exchange factor ac	13	120	0.0663024	7984 Rho guanine nucleotide exchange factor (GEF) 5
GO	guanyl-nucleotide exchange factor ac	13	120	0.0663024	84033 obscurin, cytoskeletal calmodulin and titin-interacting RhoGEF
GO	guanyl-nucleotide exchange factor ac	13	120	0.0663024	9459 Rac/Cdc42 guanine nucleotide exchange factor (GEF) 6
GO	galactosyltransferase activity	4	23	0.0679884	10317 UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 5
GO	galactosyltransferase activity	4	23	0.0679884	192134 UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 6 (core
GO	galactosyltransferase activity	4	23	0.0679884	53947 alpha 1,4-galactosyltransferase
GO	galactosyltransferase activity	4	23	0.0679884	8706 beta-1,3-N-acetylgalactosaminyltransferase 1 (globoside blood group)
GO	activation of MAPKK activity	4	23	0.0679884	10912 growth arrest and DNA-damage-inducible, gamma
GO	activation of MAPKK activity	4	23	0.0679884	2911 glutamate receptor, metabotropic 1
GO	activation of MAPKK activity	4	23	0.0679884	4616 growth arrest and DNA-damage-inducible, beta
GO	activation of MAPKK activity	4	23	0.0679884	652 bone morphogenetic protein 4
GO	voltage-gated calcium channel activit	4	23	0.0679884	55799 calcium channel, voltage-dependent, alpha 2/delta subunit 3
GO	voltage-gated calcium channel activit	4	23	0.0679884	774 calcium channel, voltage-dependent, N type, alpha 1B subunit
GO	voltage-gated calcium channel activit	4	23	0.0679884	783 calcium channel, voltage-dependent, beta 2 subunit
GO	voltage-gated calcium channel activit	4	23	0.0679884	8911 calcium channel, voltage-dependent, T type, alpha 1I subunit
GO	negative regulation of cell migration i	1	1	0.0683482	10014 histone deacetylase 5
GO	3-alpha(17-beta)-hydroxysteroid deh	1	1	0.0683482	10170 dehydrogenase/reductase (SDR family) member 9
GO	racemase and epimerase activity	1	1	0.0683482	10170 dehydrogenase/reductase (SDR family) member 9
GO	lung growth	1	1	0.0683482	10253 sprouty homolog 2 (Drosophila)
GO	ATP-binding and phosphorylation-dej	1	1	0.0683482	1080 cystic fibrosis transmembrane conductance regulator (ATP-binding cas:

GO channel-conductance-controlling ATP	1	1	0.0683482	1080 cystic fibrosis transmembrane conductance regulator (ATP-binding cas
GO actin modification	1	1	0.0683482	11078 TRIO and F-actin binding protein
GO myosin II binding	1	1	0.0683482	11078 TRIO and F-actin binding protein
GO regulation of synapse organization	1	1	0.0683482	11202 kallikrein-related peptidase 8
GO negative regulation of innate immun	1	1	0.0683482	11213 interleukin-1 receptor-associated kinase 3
GO negative regulation of macrophage c	1	1	0.0683482	11213 interleukin-1 receptor-associated kinase 3
GO positive regulation of macrophage to	1	1	0.0683482	11213 interleukin-1 receptor-associated kinase 3
GO regulation of protein complex disasse	1	1	0.0683482	11213 interleukin-1 receptor-associated kinase 3
GO acyl carnitine transport	1	1	0.0683482	123096 solute carrier family 25, member 29
GO sphinganine metabolic process	1	1	0.0683482	123099 degenerative spermatocyte homolog 2, lipid desaturase (Drosophila)
GO sphingolipid delta-4 desaturase activi	1	1	0.0683482	123099 degenerative spermatocyte homolog 2, lipid desaturase (Drosophila)
GO sphingosine hydroxylase activity	1	1	0.0683482	123099 degenerative spermatocyte homolog 2, lipid desaturase (Drosophila)
GO neuronal RNA granule	1	1	0.0683482	127933 U2AF homology motif (UHM) kinase 1
GO collagen type VIII	1	1	0.0683482	1295 collagen, type VIII, alpha 1
GO carbamoyl phosphate biosynthetic pr	1	1	0.0683482	1373 carbamoyl-phosphate synthetase 1, mitochondrial
GO carbamoyl-phosphate synthase (amn	1	1	0.0683482	1373 carbamoyl-phosphate synthetase 1, mitochondrial
GO carbamoyl-phosphate synthase activi	1	1	0.0683482	1373 carbamoyl-phosphate synthetase 1, mitochondrial
GO citrulline biosynthetic process	1	1	0.0683482	1373 carbamoyl-phosphate synthetase 1, mitochondrial
GO nitric oxide metabolic process	1	1	0.0683482	1373 carbamoyl-phosphate synthetase 1, mitochondrial
GO mammary gland fat development	1	1	0.0683482	1435 colony stimulating factor 1 (macrophage)
GO positive regulation of mononuclear c	1	1	0.0683482	1435 colony stimulating factor 1 (macrophage)
GO regulation of macrophage derived fo	1	1	0.0683482	1435 colony stimulating factor 1 (macrophage)
GO reproductive developmental process	1	1	0.0683482	1435 colony stimulating factor 1 (macrophage)
GO negative regulation of blood vessel re	1	1	0.0683482	1471 cystatin C
GO negative regulation of collagen catab	1	1	0.0683482	1471 cystatin C
GO negative regulation of elastin catabol	1	1	0.0683482	1471 cystatin C
GO negative regulation of histolysis	1	1	0.0683482	1471 cystatin C
GO regulation of tissue remodeling	1	1	0.0683482	1471 cystatin C
GO beta2-adrenergic receptor activity	1	1	0.0683482	154 adrenergic, beta-2-, receptor, surface
GO cellular amide metabolic process	1	1	0.0683482	1559 cytochrome P450, family 2, subfamily C, polypeptide 9
GO urea metabolic process	1	1	0.0683482	1559 cytochrome P450, family 2, subfamily C, polypeptide 9
GO regulation of endothelial cell migratic	1	1	0.0683482	168667 BMP binding endothelial regulator
GO induction of bacterial agglutination	1	1	0.0683482	1755 deleted in malignant brain tumors 1
GO zymogen binding	1	1	0.0683482	1755 deleted in malignant brain tumors 1
GO establishment of localization	1	1	0.0683482	1803 dipeptidyl-peptidase 4
GO invadopodium membrane	1	1	0.0683482	1803 dipeptidyl-peptidase 4

GO	regulation of T cell mediated immuni	1	1	0.0683482	1803 dipeptidyl-peptidase 4
GO	dopamine D2 receptor activity	1	1	0.0683482	1813 dopamine receptor D2
GO	dopamine D4 receptor activity	1	1	0.0683482	1815 dopamine receptor D4
GO	toxin receptor binding	1	1	0.0683482	1822 atrophin 1
GO	angiotensin mediated vasoconstricti	1	1	0.0683482	183 angiotensinogen (serpin peptidase inhibitor, clade A, member 8)
GO	renal response to blood flow involve	1	1	0.0683482	183 angiotensinogen (serpin peptidase inhibitor, clade A, member 8)
GO	response to muscle activity involved i	1	1	0.0683482	183 angiotensinogen (serpin peptidase inhibitor, clade A, member 8)
GO	type 2 angiotensin receptor binding	1	1	0.0683482	183 angiotensinogen (serpin peptidase inhibitor, clade A, member 8)
GO	negative regulation of elastin biosynt	1	1	0.0683482	1839 heparin-binding EGF-like growth factor
GO	activation of phospholipase D activity	1	1	0.0683482	1906 endothelin 1
GO	endothelin A receptor binding	1	1	0.0683482	1906 endothelin 1
GO	negative regulation of nitric-oxide syn	1	1	0.0683482	1906 endothelin 1
GO	protein kinase C deactivation	1	1	0.0683482	1906 endothelin 1
GO	O-glycan processing, core 3	1	1	0.0683482	192134 UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 6 (core
GO	rhombomere 3 formation	1	1	0.0683482	1959 early growth response 2
GO	rhombomere 5 formation	1	1	0.0683482	1959 early growth response 2
GO	axial mesoderm formation	1	1	0.0683482	1969 EPH receptor A2
GO	notochord cell development	1	1	0.0683482	1969 EPH receptor A2
GO	negative regulation of cellular metab	1	1	0.0683482	2033 E1A binding protein p300
GO	positive regulation of cellular metab	1	1	0.0683482	2033 E1A binding protein p300
GO	regulation of angiotensin metabolic p	1	1	0.0683482	2033 E1A binding protein p300
GO	synapse maturation	1	1	0.0683482	2066 v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian)
GO	hemopoietic stem cell proliferation	1	1	0.0683482	2122 MDS1 and EVI1 complex locus
GO	positive regulation of type I hypersen	1	1	0.0683482	2205 Fc fragment of IgE, high affinity I, receptor for; alpha polypeptide
GO	pancreatic D cell differentiation	1	1	0.0683482	222546 regulatory factor X, 6
GO	pancreatic E cell differentiation	1	1	0.0683482	222546 regulatory factor X, 6
GO	cytoskeleton-dependent intracellular	1	1	0.0683482	23095 kinesin family member 1B
GO	latrotoxin receptor activity	1	1	0.0683482	23266 latrophilin 2
GO	low-density lipoprotein receptor cata	1	1	0.0683482	255738 proprotein convertase subtilisin/kexin type 9
GO	glutamate catabolic process	1	1	0.0683482	2571 glutamate decarboxylase 1 (brain, 67kDa)
GO	protein-pyridoxal-5-phosphate linkag	1	1	0.0683482	2571 glutamate decarboxylase 1 (brain, 67kDa)
GO	exocrine system development	1	1	0.0683482	25837 RAB26, member RAS oncogene family
GO	intrinsic to plasma membrane	1	1	0.0683482	25837 RAB26, member RAS oncogene family
GO	racemase and epimerase activity, act	1	1	0.0683482	26035 glucuronic acid epimerase
GO	UDP-glucuronate 5'-epimerase activit	1	1	0.0683482	26035 glucuronic acid epimerase
GO	vitamin transporter activity	1	1	0.0683482	2638 group-specific component (vitamin D binding protein)

GO vitamin transport	1	1	0.0683482	2638 group-specific component (vitamin D binding protein)
GO FADH2 metabolic process	1	1	0.0683482	27035 NADPH oxidase 1
GO intracellular pH elevation	1	1	0.0683482	27035 NADPH oxidase 1
GO (alpha-N-acetylneuraminy-2,3-beta-ξ	1	1	0.0683482	27090 ST6 (alpha-N-acetyl-neuraminy-2,3-beta-galactosyl-1,3)-N-acetylgalact
GO anterior semicircular canal developm	1	1	0.0683482	2737 GLI family zinc finger 3
GO lateral semicircular canal developmei	1	1	0.0683482	2737 GLI family zinc finger 3
GO pallium development	1	1	0.0683482	2737 GLI family zinc finger 3
GO ferritin receptor activity	1	1	0.0683482	286133 scavenger receptor class A, member 5 (putative)
GO iron ion transmembrane transport	1	1	0.0683482	286133 scavenger receptor class A, member 5 (putative)
GO negative regulation of interleukin-10	1	1	0.0683482	28951 tribbles homolog 2 (Drosophila)
GO histidine ammonia-lyase activity	1	1	0.0683482	3034 histidine ammonia-lyase
GO radial spoke	1	1	0.0683482	345895 radial spoke head 4 homolog A (Chlamydomonas)
GO glycolate metabolic process	1	1	0.0683482	3479 insulin-like growth factor 1 (somatomedin C)
GO muscle hypertrophy	1	1	0.0683482	3479 insulin-like growth factor 1 (somatomedin C)
GO myotube cell development	1	1	0.0683482	3479 insulin-like growth factor 1 (somatomedin C)
GO satellite cell maintenance involved in	1	1	0.0683482	3479 insulin-like growth factor 1 (somatomedin C)
GO intussusceptive angiogenesis	1	1	0.0683482	3491 cysteine-rich, angiogenic inducer, 61
GO butyryl-CoA dehydrogenase activity	1	1	0.0683482	35 acyl-Coenzyme A dehydrogenase, C-2 to C-3 short chain
GO glucagon secretion	1	1	0.0683482	3569 interleukin 6 (interferon, beta 2)
GO positive regulation of B cell activator	1	1	0.0683482	3569 interleukin 6 (interferon, beta 2)
GO ciliary neurotrophic factor binding	1	1	0.0683482	3570 interleukin 6 receptor
GO positive regulation of activation of Ja	1	1	0.0683482	3570 interleukin 6 receptor
GO carbon dioxide transmembrane trans	1	1	0.0683482	358 aquaporin 1 (Colton blood group)
GO carbon dioxide transmembrane trans	1	1	0.0683482	358 aquaporin 1 (Colton blood group)
GO cellular hyperosmotic response	1	1	0.0683482	358 aquaporin 1 (Colton blood group)
GO cellular response to inorganic substai	1	1	0.0683482	358 aquaporin 1 (Colton blood group)
GO cellular response to mechanical stimu	1	1	0.0683482	358 aquaporin 1 (Colton blood group)
GO cellular response to nitric oxide	1	1	0.0683482	358 aquaporin 1 (Colton blood group)
GO cellular response to salt stress	1	1	0.0683482	358 aquaporin 1 (Colton blood group)
GO establishment or maintenance of acti	1	1	0.0683482	358 aquaporin 1 (Colton blood group)
GO maintenance of symbiont-containing	1	1	0.0683482	358 aquaporin 1 (Colton blood group)
GO nitric oxide transmembrane transpor	1	1	0.0683482	358 aquaporin 1 (Colton blood group)
GO symbiont-containing vacuole membr	1	1	0.0683482	358 aquaporin 1 (Colton blood group)
GO transepithelial water transport	1	1	0.0683482	358 aquaporin 1 (Colton blood group)
GO insulin receptor activity	1	1	0.0683482	3643 insulin receptor
GO positive regulation of developmental	1	1	0.0683482	3643 insulin receptor

GO transformation of host cell by virus	1	1	0.0683482	3643 insulin receptor
GO leading edge cell differentiation	1	1	0.0683482	3725 jun oncogene
GO regulation of synaptic growth at neur	1	1	0.0683482	375790 agrin
GO stem cell factor receptor activity	1	1	0.0683482	3815 v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog
GO GMP binding	1	1	0.0683482	3845 v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog
GO laminin-5 complex	1	1	0.0683482	3911 laminin, alpha 5
GO morphogenesis of a polarized epithel	1	1	0.0683482	3911 laminin, alpha 5
GO axon extension involved in regenerat	1	1	0.0683482	3913 laminin, beta 2 (laminin 5)
GO positive regulation of phospholipase	1	1	0.0683482	395 Rho GTPase activating protein 6
GO cellular response to vitamin A	1	1	0.0683482	4056 leukotriene C4 synthase
GO steryl-sulfatase activity	1	1	0.0683482	412 steroid sulfatase (microsomal), isozyme S
GO mannosidase activity	1	1	0.0683482	4121 mannosidase, alpha, class 1A, member 1
GO protein channel activity	1	1	0.0683482	4170 myeloid cell leukemia sequence 1 (BCL2-related)
GO inner acrosomal membrane	1	1	0.0683482	4179 CD46 molecule, complement regulatory protein
GO G0 to G1 transition	1	1	0.0683482	4194 Mdm4 p53 binding protein homolog (mouse)
GO double-stranded methylated DNA bir	1	1	0.0683482	4204 methyl CpG binding protein 2 (Rett syndrome)
GO positive regulation of myeloid leukoc	1	1	0.0683482	4254 KIT ligand
GO cellular response to magnetism	1	1	0.0683482	429 achaete-scute complex homolog 1 (Drosophila)
GO lung epithelial cell differentiation	1	1	0.0683482	429 achaete-scute complex homolog 1 (Drosophila)
GO neuroblast fate determination	1	1	0.0683482	429 achaete-scute complex homolog 1 (Drosophila)
GO noradrenergic neuron fate commitm	1	1	0.0683482	429 achaete-scute complex homolog 1 (Drosophila)
GO oligodendrocyte cell fate commitmer	1	1	0.0683482	429 achaete-scute complex homolog 1 (Drosophila)
GO regulation of timing of subpallium ne	1	1	0.0683482	429 achaete-scute complex homolog 1 (Drosophila)
GO response to epidermal growth factor	1	1	0.0683482	429 achaete-scute complex homolog 1 (Drosophila)
GO methylenetetrahydrofolate reductas	1	1	0.0683482	4524 5,10-methylenetetrahydrofolate reductase (NADPH)
GO nitrilase activity	1	1	0.0683482	4817 nitrilase 1
GO aortic valve morphogenesis	1	1	0.0683482	4851 Notch homolog 1, translocation-associated (Drosophila)
GO endocardium morphogenesis	1	1	0.0683482	4851 Notch homolog 1, translocation-associated (Drosophila)
GO foregut morphogenesis	1	1	0.0683482	4851 Notch homolog 1, translocation-associated (Drosophila)
GO regulation of epithelial cell proliferati	1	1	0.0683482	4851 Notch homolog 1, translocation-associated (Drosophila)
GO regulation of somitogenesis	1	1	0.0683482	4851 Notch homolog 1, translocation-associated (Drosophila)
GO generation of ovulation cycle rhythm	1	1	0.0683482	4889 neuropeptide Y receptor Y5
GO 2'-5'-oligoadenylate synthetase activi	1	1	0.0683482	4939 2'-5'-oligoadenylate synthetase 2, 69/71kDa
GO relaxation of cardiac muscle	1	1	0.0683482	5025 purinergic receptor P2X, ligand-gated ion channel, 4
GO protein amino acid hydroxylation	1	1	0.0683482	5053 phenylalanine hydroxylase
GO tetrahydrobiopterin metabolic proce:	1	1	0.0683482	5053 phenylalanine hydroxylase

GO tyrosine biosynthetic process	1	1	0.0683482	5053 phenylalanine hydroxylase
GO interleukin-20 receptor binding	1	1	0.0683482	50604 interleukin 20
GO positive regulation of epidermal cell c	1	1	0.0683482	50604 interleukin 20
GO peptidylamidoglycolate lyase activity	1	1	0.0683482	5066 peptidylglycine alpha-amidating monooxygenase
GO peptidylglycine monooxygenase activ	1	1	0.0683482	5066 peptidylglycine alpha-amidating monooxygenase
GO carbohydrate response element bind	1	1	0.0683482	51085 MLX interacting protein-like
GO glucose mediated signaling pathway	1	1	0.0683482	51085 MLX interacting protein-like
GO negative regulation of oxidative phos	1	1	0.0683482	51085 MLX interacting protein-like
GO spot adherens junction	1	1	0.0683482	5239 phosphoglucomutase 5
GO 1-phosphatidylinositol-4-phosphate 3	1	1	0.0683482	5295 phosphoinositide-3-kinase, regulatory subunit 1 (alpha)
GO branchiomic skeletal muscle develo	1	1	0.0683482	5307 paired-like homeodomain 1
GO hydroxylysine biosynthetic process	1	1	0.0683482	5351 procollagen-lysine 1, 2-oxoglutarate 5-dioxygenase 1
GO granule cell precursor tangential mig	1	1	0.0683482	5362 plexin A2
GO melanin-concentrating hormone acti	1	1	0.0683482	5367 pro-melanin-concentrating hormone
GO type 1 melanin-concentrating hormo	1	1	0.0683482	5367 pro-melanin-concentrating hormone
GO negative regulation of translation in r	1	1	0.0683482	5371 promyelocytic leukemia
GO negative regulation of calcium-depen	1	1	0.0683482	53827 FXD domain containing ion transport regulator 5
GO lactosylceramide 4-alpha-galactosyltr	1	1	0.0683482	53947 alpha 1,4-galactosyltransferase
GO thyroid stimulating hormone secretin	1	1	0.0683482	54361 wingless-type MMTV integration site family, member 4
GO cell fate commitment involved in the	1	1	0.0683482	5460 POU class 5 homeobox 1
GO positive regulation of catenin protein	1	1	0.0683482	5460 POU class 5 homeobox 1
GO regulation of canonical Wnt receptor	1	1	0.0683482	5460 POU class 5 homeobox 1
GO regulation of methylation-dependent	1	1	0.0683482	5460 POU class 5 homeobox 1
GO RNA 5'-end processing	1	1	0.0683482	55124 piwi-like 2 (Drosophila)
GO sphingoid biosynthetic process	1	1	0.0683482	55304 serine palmitoyltransferase, long chain base subunit 3
GO alpha-N-acetylgalactosaminide alpha	1	1	0.0683482	55808 ST6 (alpha-N-acetyl-neuraminy-2,3-beta-galactosyl-1,3)-N-acetylgalact
GO barrier septum formation	1	1	0.0683482	55909 bridging integrator 3
GO unidimensional cell growth	1	1	0.0683482	55909 bridging integrator 3
GO inorganic diphosphate transmembran	1	1	0.0683482	56172 ankylosis, progressive homolog (mouse)
GO asymmetric cell division	1	1	0.0683482	56288 par-3 partitioning defective 3 homolog (C. elegans)
GO negative regulation of complement a	1	1	0.0683482	5648 mannan-binding lectin serine peptidase 1 (C4/C2 activating component)
GO glycoprotein-N-acetylgalactosamine 3	1	1	0.0683482	56913 core 1 synthase, glycoprotein-N-acetylgalactosamine 3-beta-galactosyl
GO neuromedin U binding	1	1	0.0683482	56923 neuromedin U receptor 2
GO columnar/cuboidal epithelial cell dev	1	1	0.0683482	57619 shroom family member 3
GO negative regulation of calcium ion tra	1	1	0.0683482	57620 stromal interaction molecule 2
GO flavin-linked sulfhydryl oxidase activit	1	1	0.0683482	5768 quiescin Q6 sulfhydryl oxidase 1



GO	regulation of mast cell activation	1	1	0.0683482	5791 protein tyrosine phosphatase, receptor type, E
GO	cytotoxic T cell degranulation	1	1	0.0683482	5873 RAB27A, member RAS oncogene family
GO	retinol transporter activity	1	1	0.0683482	5950 retinol binding protein 4, plasma
GO	retinol transport	1	1	0.0683482	5950 retinol binding protein 4, plasma
GO	spermatogonial cell division	1	1	0.0683482	5950 retinol binding protein 4, plasma
GO	response to cGMP	1	1	0.0683482	5972 renin
GO	regulation of germinal center formati	1	1	0.0683482	604 B-cell CLL/lymphoma 6
GO	regulation of memory T cell different	1	1	0.0683482	604 B-cell CLL/lymphoma 6
GO	complement binding	1	1	0.0683482	629 complement factor B
GO	regulation of mitochondrion organiza	1	1	0.0683482	64083 golgi phosphoprotein 3 (coat-protein)
GO	activation of immune response	1	1	0.0683482	64127 nucleotide-binding oligomerization domain containing 2
GO	cytokine production involved in immu	1	1	0.0683482	64127 nucleotide-binding oligomerization domain containing 2
GO	detection of muramyl dipeptide	1	1	0.0683482	64127 nucleotide-binding oligomerization domain containing 2
GO	immunoglobulin production during ir	1	1	0.0683482	64127 nucleotide-binding oligomerization domain containing 2
GO	macrophage inflammatory protein-1	1	1	0.0683482	64127 nucleotide-binding oligomerization domain containing 2
GO	muramyl dipeptide binding	1	1	0.0683482	64127 nucleotide-binding oligomerization domain containing 2
GO	negative regulation of interleukin-18	1	1	0.0683482	64127 nucleotide-binding oligomerization domain containing 2
GO	negative regulation of toll-like recept	1	1	0.0683482	64127 nucleotide-binding oligomerization domain containing 2
GO	glutamate:sodium symporter activity	1	1	0.0683482	6505 solute carrier family 1 (neuronal/epithelial high affinity glutamate trans
GO	branch elongation involved in ureteri	1	1	0.0683482	652 bone morphogenetic protein 4
GO	bronchus development	1	1	0.0683482	652 bone morphogenetic protein 4
GO	bud dilation involved in lung branchir	1	1	0.0683482	652 bone morphogenetic protein 4
GO	epithelial cell proliferation involved i	1	1	0.0683482	652 bone morphogenetic protein 4
GO	intermediate mesodermal cell differe	1	1	0.0683482	652 bone morphogenetic protein 4
GO	mammary gland formation	1	1	0.0683482	652 bone morphogenetic protein 4
GO	negative regulation of branching invc	1	1	0.0683482	652 bone morphogenetic protein 4
GO	negative regulation of glomerulus de	1	1	0.0683482	652 bone morphogenetic protein 4
GO	trachea formation	1	1	0.0683482	652 bone morphogenetic protein 4
GO	creatine transporter activity	1	1	0.0683482	6535 solute carrier family 6 (neurotransmitter transporter, creatine), membe
GO	creatine transport	1	1	0.0683482	6535 solute carrier family 6 (neurotransmitter transporter, creatine), membe
GO	creatine:sodium symporter activity	1	1	0.0683482	6535 solute carrier family 6 (neurotransmitter transporter, creatine), membe
GO	channel inhibitor activity	1	1	0.0683482	6564 solute carrier family 15 (oligopeptide transporter), member 1
GO	negative regulation of amino acid tra	1	1	0.0683482	6564 solute carrier family 15 (oligopeptide transporter), member 1
GO	oligopeptide transporter activity	1	1	0.0683482	6564 solute carrier family 15 (oligopeptide transporter), member 1
GO	antibiotic transporter activity	1	1	0.0683482	6565 solute carrier family 15 (H+/peptide transporter), member 2
GO	antibiotic transport	1	1	0.0683482	6565 solute carrier family 15 (H+/peptide transporter), member 2

GO	dipeptide transporter activity	1	1	0.0683482	6565 solute carrier family 15 (H+/peptide transporter), member 2
GO	dipeptide transport	1	1	0.0683482	6565 solute carrier family 15 (H+/peptide transporter), member 2
GO	high affinity oligopeptide transporter	1	1	0.0683482	6565 solute carrier family 15 (H+/peptide transporter), member 2
GO	negative regulation of dopamine uptake	1	1	0.0683482	6622 synuclein, alpha (non A4 component of amyloid precursor)
GO	negative regulation of monooxygenase activity	1	1	0.0683482	6622 synuclein, alpha (non A4 component of amyloid precursor)
GO	negative regulation of norepinephrine transport	1	1	0.0683482	6622 synuclein, alpha (non A4 component of amyloid precursor)
GO	negative regulation of serotonin uptake	1	1	0.0683482	6622 synuclein, alpha (non A4 component of amyloid precursor)
GO	negative regulation of thrombin receptor activity	1	1	0.0683482	6622 synuclein, alpha (non A4 component of amyloid precursor)
GO	neutral lipid metabolic process	1	1	0.0683482	6622 synuclein, alpha (non A4 component of amyloid precursor)
GO	phospholipase D inhibitor activity	1	1	0.0683482	6622 synuclein, alpha (non A4 component of amyloid precursor)
GO	regulation of acyl-CoA biosynthetic process	1	1	0.0683482	6622 synuclein, alpha (non A4 component of amyloid precursor)
GO	regulation of phospholipase activity	1	1	0.0683482	6622 synuclein, alpha (non A4 component of amyloid precursor)
GO	regulation of synaptic vesicle priming	1	1	0.0683482	6812 syntaxin binding protein 1
GO	thromboxane-A synthase activity	1	1	0.0683482	6916 thromboxane A synthase 1 (platelet)
GO	respiratory burst involved in inflammation	1	1	0.0683482	7001 peroxiredoxin 2
GO	radial pattern formation	1	1	0.0683482	7026 nuclear receptor subfamily 2, group F, member 2
GO	definitive erythrocyte differentiation	1	1	0.0683482	7049 transforming growth factor, beta receptor III
GO	response to luteinizing hormone stimulation	1	1	0.0683482	7049 transforming growth factor, beta receptor III
GO	transforming growth factor beta receptor signaling pathway	1	1	0.0683482	7049 transforming growth factor, beta receptor III
GO	cellular response to bacterial lipopeptide	1	1	0.0683482	7097 toll-like receptor 2
GO	chloramphenicol transport	1	1	0.0683482	7097 toll-like receptor 2
GO	triacylated lipopeptide binding	1	1	0.0683482	7097 toll-like receptor 2
GO	detection of virus	1	1	0.0683482	7098 toll-like receptor 3
GO	detection of fungus	1	1	0.0683482	7099 toll-like receptor 4
GO	innate immune response-activating signaling pathway	1	1	0.0683482	7099 toll-like receptor 4
GO	intestinal epithelial structure maintenance	1	1	0.0683482	7099 toll-like receptor 4
GO	negative regulation of interleukin-17 production	1	1	0.0683482	7099 toll-like receptor 4
GO	negative regulation of interleukin-23 production	1	1	0.0683482	7099 toll-like receptor 4
GO	positive regulation of interleukin-1 production	1	1	0.0683482	7099 toll-like receptor 4
GO	positive regulation of nucleotide-binding site-leucine-rich repeat domain binding	1	1	0.0683482	7099 toll-like receptor 4
GO	positive regulation of nucleotide-binding site-leucine-rich repeat domain binding	1	1	0.0683482	7099 toll-like receptor 4
GO	production of nitric oxide involved in signaling pathway	1	1	0.0683482	7099 toll-like receptor 4
GO	positive regulation of type IIa hypersensitivity	1	1	0.0683482	718 complement component 3
GO	ionotropic glutamate receptor complex assembly	1	1	0.0683482	729993 shisa homolog 9 ( <i>Xenopus laevis</i> )
GO	negative regulation of mesenchymal cell proliferation	1	1	0.0683482	7474 wingless-type MMTV integration site family, member 5A
GO	positive regulation of cytokine secretion	1	1	0.0683482	7474 wingless-type MMTV integration site family, member 5A

GO receptor tyrosine kinase-like orphan	1	1	0.0683482	7474 wingless-type MMTV integration site family, member 5A
GO positive regulation of nuclear-transcr	1	1	0.0683482	7538 zinc finger protein 36, C3H type, homolog (mouse)
GO negative regulation of nuclease activi	1	1	0.0683482	79661 nei endonuclease VIII-like 1 (E. coli)
GO oxidoreductase activity, acting on the	1	1	0.0683482	79802 HHIP-like 2
GO calcitonin binding	1	1	0.0683482	799 calcitonin receptor
GO semicircular canal morphogenesis	1	1	0.0683482	8013 nuclear receptor subfamily 4, group A, member 3
GO vestibular reflex	1	1	0.0683482	8013 nuclear receptor subfamily 4, group A, member 3
GO hydroxypyruvate isomerase activity	1	1	0.0683482	81888 hydroxypyruvate isomerase homolog (E. coli)
GO calcium-dependent cysteine-type enc	1	1	0.0683482	831 calpastatin
GO CMP-N-acetylneuraminate monooxyg	1	1	0.0683482	8418 cytidine monophosphate-N-acetylneuraminic acid hydroxylase (CMP-N
GO patched ligand maturation	1	1	0.0683482	84976 dispatched homolog 1 (Drosophila)
GO negative regulation of skeletal muscl	1	1	0.0683482	8531 cold shock domain protein A
GO ribonuclease T2 activity	1	1	0.0683482	8635 ribonuclease T2
GO BMP signaling pathway involved in sp	1	1	0.0683482	8646 chordin
GO floor plate development	1	1	0.0683482	8646 chordin
GO galactosylgalactosylglucosylceramide	1	1	0.0683482	8706 beta-1,3-N-acetylgalactosaminyltransferase 1 (globoside blood group)
GO positive regulation of protein oligom	1	1	0.0683482	885 cholecystokinin
GO phosphatidic acid binding	1	1	0.0683482	91404 SEC14 and spectrin domains 1
GO negative regulation of Golgi to plasm	1	1	0.0683482	91461 protein kinase domain containing, cytoplasmic homolog (mouse)
GO trans-Golgi network transport vesicle	1	1	0.0683482	9182 Ras association (RalGDS/AF-6) domain family (N-terminal) member 9
GO pyruvate secondary active transmem	1	1	0.0683482	9194 solute carrier family 16, member 7 (monocarboxylic acid transporter 2)
GO pyruvate transport	1	1	0.0683482	9194 solute carrier family 16, member 7 (monocarboxylic acid transporter 2)
GO opsonin receptor activity	1	1	0.0683482	929 CD14 molecule
GO nicotinate phosphoribosyltransferase	1	1	0.0683482	93100 nicotinate phosphoribosyltransferase domain containing 1
GO phosphorus-oxygen lyase activity	1	1	0.0683482	952 CD38 molecule
GO glucose 1-dehydrogenase activity	1	1	0.0683482	9563 hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase)
GO guanine deaminase activity	1	1	0.0683482	9615 guanine deaminase
GO detection of hormone stimulus	1	1	0.0683482	9619 ATP-binding cassette, sub-family G (WHITE), member 1
GO glycoprotein transporter activity	1	1	0.0683482	9619 ATP-binding cassette, sub-family G (WHITE), member 1
GO glycoprotein transport	1	1	0.0683482	9619 ATP-binding cassette, sub-family G (WHITE), member 1
GO regulation of cholesterol esterificatio	1	1	0.0683482	9619 ATP-binding cassette, sub-family G (WHITE), member 1
GO sterol-transporting ATPase activity	1	1	0.0683482	9619 ATP-binding cassette, sub-family G (WHITE), member 1
GO regulation of striated muscle cell diff	1	1	0.0683482	9734 histone deacetylase 9
GO rhombomere 6 development	1	1	0.0683482	9935 v-maf musculoaponeurotic fibrosarcoma oncogene homolog B (avian)
GO cytokine metabolic process	1	1	0.0683482	9966 tumor necrosis factor (ligand) superfamily, member 15
GO meiotic cohesin complex	1	1	0.0683482	9985 REC8 homolog (yeast)

GO	positive regulation of I-kappaB kinase	12	109	0.0686347	10769 polo-like kinase 2 (Drosophila)
GO	positive regulation of I-kappaB kinase	12	109	0.0686347	1902 lysophosphatidic acid receptor 1
GO	positive regulation of I-kappaB kinase	12	109	0.0686347	5071 Parkinson disease (autosomal recessive, juvenile) 2, parkin
GO	positive regulation of I-kappaB kinase	12	109	0.0686347	51523 CXXC finger 5
GO	positive regulation of I-kappaB kinase	12	109	0.0686347	64127 nucleotide-binding oligomerization domain containing 2
GO	positive regulation of I-kappaB kinase	12	109	0.0686347	684 bone marrow stromal cell antigen 2
GO	positive regulation of I-kappaB kinase	12	109	0.0686347	7098 toll-like receptor 3
GO	positive regulation of I-kappaB kinase	12	109	0.0686347	7099 toll-like receptor 4
GO	positive regulation of I-kappaB kinase	12	109	0.0686347	79971 wntless homolog (Drosophila)
GO	positive regulation of I-kappaB kinase	12	109	0.0686347	80833 apolipoprotein L, 3
GO	positive regulation of I-kappaB kinase	12	109	0.0686347	834 caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, co
GO	positive regulation of I-kappaB kinase	12	109	0.0686347	8600 tumor necrosis factor (ligand) superfamily, member 11
GO	cell cortex	9	75	0.0691174	2263 fibroblast growth factor receptor 2
GO	cell cortex	9	75	0.0691174	23048 formin binding protein 1
GO	cell cortex	9	75	0.0691174	3709 inositol 1,4,5-triphosphate receptor, type 2
GO	cell cortex	9	75	0.0691174	53405 chloride intracellular channel 5
GO	cell cortex	9	75	0.0691174	56288 par-3 partitioning defective 3 homolog (C. elegans)
GO	cell cortex	9	75	0.0691174	6622 synuclein, alpha (non A4 component of amyloid precursor)
GO	cell cortex	9	75	0.0691174	6710 spectrin, beta, erythrocytic
GO	cell cortex	9	75	0.0691174	85477 scinderin
GO	cell cortex	9	75	0.0691174	9595 cytohesin 1 interacting protein
GO	calcium-mediated signaling	5	33	0.0714159	10231 regulator of calcineurin 2
GO	calcium-mediated signaling	5	33	0.0714159	1906 endothelin 1
GO	calcium-mediated signaling	5	33	0.0714159	222545 G protein-coupled receptor, family C, group 6, member A
GO	calcium-mediated signaling	5	33	0.0714159	2911 glutamate receptor, metabotropic 1
GO	calcium-mediated signaling	5	33	0.0714159	56923 neuromedin U receptor 2
GO	learning or memory	5	33	0.0714159	1958 early growth response 1
GO	learning or memory	5	33	0.0714159	1959 early growth response 2
GO	learning or memory	5	33	0.0714159	2182 acyl-CoA synthetase long-chain family member 4
GO	learning or memory	5	33	0.0714159	412 steroid sulfatase (microsomal), isozyme S
GO	learning or memory	5	33	0.0714159	627 brain-derived neurotrophic factor
GO	lipid metabolic process	20	206	0.0714555	11343 monoglyceride lipase
GO	lipid metabolic process	20	206	0.0714555	166929 sphingomyelin synthase 2
GO	lipid metabolic process	20	206	0.0714555	2182 acyl-CoA synthetase long-chain family member 4
GO	lipid metabolic process	20	206	0.0714555	23780 apolipoprotein L, 2
GO	lipid metabolic process	20	206	0.0714555	256987 serine incorporator 5

GO lipid metabolic process	20	206	0.0714555	35 acyl-Coenzyme A dehydrogenase, C-2 to C-3 short chain
GO lipid metabolic process	20	206	0.0714555	3949 low density lipoprotein receptor
GO lipid metabolic process	20	206	0.0714555	498 ATP synthase, H <sup>+</sup> transporting, mitochondrial F1 complex, alpha subun
GO lipid metabolic process	20	206	0.0714555	51703 acyl-CoA synthetase long-chain family member 5
GO lipid metabolic process	20	206	0.0714555	5244 ATP-binding cassette, sub-family B (MDR/TAP), member 4
GO lipid metabolic process	20	206	0.0714555	5346 perilipin 1
GO lipid metabolic process	20	206	0.0714555	5465 peroxisome proliferator-activated receptor alpha
GO lipid metabolic process	20	206	0.0714555	55268 enoyl Coenzyme A hydratase domain containing 2
GO lipid metabolic process	20	206	0.0714555	56261 glycerophosphocholine phosphodiesterase GDE1 homolog ( <i>S. cerevisia</i>
GO lipid metabolic process	20	206	0.0714555	5742 prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase a
GO lipid metabolic process	20	206	0.0714555	6489 ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 1
GO lipid metabolic process	20	206	0.0714555	7026 nuclear receptor subfamily 2, group F, member 2
GO lipid metabolic process	20	206	0.0714555	7069 thyroid hormone responsive (SPOT14 homolog, rat)
GO lipid metabolic process	20	206	0.0714555	7941 phospholipase A2, group VII (platelet-activating factor acetylhydrolase,
GO lipid metabolic process	20	206	0.0714555	81544 glycerophosphodiester phosphodiesterase domain containing 5
GO chloride channel complex	7	54	0.073533	1080 cystic fibrosis transmembrane conductance regulator (ATP-binding cas
GO chloride channel complex	7	54	0.073533	1193 chloride intracellular channel 2
GO chloride channel complex	7	54	0.073533	2564 gamma-aminobutyric acid (GABA) A receptor, epsilon
GO chloride channel complex	7	54	0.073533	266675 bestrophin 4
GO chloride channel complex	7	54	0.073533	53405 chloride intracellular channel 5
GO chloride channel complex	7	54	0.073533	5349 FX1D domain containing ion transport regulator 3
GO chloride channel complex	7	54	0.073533	63982 anoctamin 3
GO oxidation reduction	44	515	0.0741864	10170 dehydrogenase/reductase (SDR family) member 9
GO oxidation reduction	44	515	0.0741864	10826 chromosome 5 open reading frame 4
GO oxidation reduction	44	515	0.0741864	112724 retinol dehydrogenase 13 (all-trans/9-cis)
GO oxidation reduction	44	515	0.0741864	123099 degenerative spermatocyte homolog 2, lipid desaturase ( <i>Drosophila</i> )
GO oxidation reduction	44	515	0.0741864	124 alcohol dehydrogenase 1A (class I), alpha polypeptide
GO oxidation reduction	44	515	0.0741864	125 alcohol dehydrogenase 1B (class I), beta polypeptide
GO oxidation reduction	44	515	0.0741864	1558 cytochrome P450, family 2, subfamily C, polypeptide 8
GO oxidation reduction	44	515	0.0741864	1559 cytochrome P450, family 2, subfamily C, polypeptide 9
GO oxidation reduction	44	515	0.0741864	1571 cytochrome P450, family 2, subfamily E, polypeptide 1
GO oxidation reduction	44	515	0.0741864	157506 retinol dehydrogenase 10 (all-trans)
GO oxidation reduction	44	515	0.0741864	195814 short chain dehydrogenase/reductase family 16C, member 5
GO oxidation reduction	44	515	0.0741864	2153 coagulation factor V (proaccelerin, labile factor)
GO oxidation reduction	44	515	0.0741864	23081 lysine (K)-specific demethylase 4C
GO oxidation reduction	44	515	0.0741864	240 arachidonate 5-lipoxygenase

GO oxidation reduction	44	515	0.0741864	254295 phytanoyl-CoA dioxygenase domain containing 1
GO oxidation reduction	44	515	0.0741864	27035 NADPH oxidase 1
GO oxidation reduction	44	515	0.0741864	316 aldehyde oxidase 1
GO oxidation reduction	44	515	0.0741864	3294 hydroxysteroid (17-beta) dehydrogenase 2
GO oxidation reduction	44	515	0.0741864	345275 hydroxysteroid (17-beta) dehydrogenase 13
GO oxidation reduction	44	515	0.0741864	35 acyl-Coenzyme A dehydrogenase, C-2 to C-3 short chain
GO oxidation reduction	44	515	0.0741864	4015 lysyl oxidase
GO oxidation reduction	44	515	0.0741864	4128 monoamine oxidase A
GO oxidation reduction	44	515	0.0741864	4129 monoamine oxidase B
GO oxidation reduction	44	515	0.0741864	4524 5,10-methylenetetrahydrofolate reductase (NADPH)
GO oxidation reduction	44	515	0.0741864	4842 nitric oxide synthase 1 (neuronal)
GO oxidation reduction	44	515	0.0741864	5053 phenylalanine hydroxylase
GO oxidation reduction	44	515	0.0741864	5066 peptidylglycine alpha-amidating monooxygenase
GO oxidation reduction	44	515	0.0741864	5351 procollagen-lysine 1, 2-oxoglutarate 5-dioxygenase 1
GO oxidation reduction	44	515	0.0741864	54681 prolyl 4-hydroxylase, transmembrane (endoplasmic reticulum)
GO oxidation reduction	44	515	0.0741864	55693 lysine (K)-specific demethylase 4D
GO oxidation reduction	44	515	0.0741864	5742 prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and
GO oxidation reduction	44	515	0.0741864	5768 quiescin Q6 sulfhydryl oxidase 1
GO oxidation reduction	44	515	0.0741864	59344 arachidonate lipoxygenase 3
GO oxidation reduction	44	515	0.0741864	622 3-hydroxybutyrate dehydrogenase, type 1
GO oxidation reduction	44	515	0.0741864	64359 nucleoredoxin
GO oxidation reduction	44	515	0.0741864	6916 thromboxane A synthase 1 (platelet)
GO oxidation reduction	44	515	0.0741864	7001 peroxiredoxin 2
GO oxidation reduction	44	515	0.0741864	7404 ubiquitously transcribed tetratricopeptide repeat gene, Y-linked
GO oxidation reduction	44	515	0.0741864	79689 STEAP family member 4
GO oxidation reduction	44	515	0.0741864	84171 lysyl oxidase-like 4
GO oxidation reduction	44	515	0.0741864	8418 cytidine monophosphate-N-acetylneuraminic acid hydroxylase (CMP-N
GO oxidation reduction	44	515	0.0741864	84795 pyridine nucleotide-disulphide oxidoreductase domain 2
GO oxidation reduction	44	515	0.0741864	8514 potassium voltage-gated channel, shaker-related subfamily, beta mem
GO oxidation reduction	44	515	0.0741864	9563 hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase)
GO ubiquitin protein ligase binding	6	44	0.0772264	10221 tribbles homolog 1 (Drosophila)
GO ubiquitin protein ligase binding	6	44	0.0772264	28951 tribbles homolog 2 (Drosophila)
GO ubiquitin protein ligase binding	6	44	0.0772264	4087 SMAD family member 2
GO ubiquitin protein ligase binding	6	44	0.0772264	4792 nuclear factor of kappa light polypeptide gene enhancer in B-cells inhib
GO ubiquitin protein ligase binding	6	44	0.0772264	5371 promyelocytic leukemia
GO ubiquitin protein ligase binding	6	44	0.0772264	91 activin A receptor, type IB

GO drug binding	6	44	0.0772264	154 adrenergic, beta-2-, receptor, surface
GO drug binding	6	44	0.0772264	1559 cytochrome P450, family 2, subfamily C, polypeptide 9
GO drug binding	6	44	0.0772264	1813 dopamine receptor D2
GO drug binding	6	44	0.0772264	1815 dopamine receptor D4
GO drug binding	6	44	0.0772264	5025 purinergic receptor P2X, ligand-gated ion channel, 4
GO drug binding	6	44	0.0772264	5465 peroxisome proliferator-activated receptor alpha
GO hydrolase activity, acting on glycosyl	6	44	0.0772264	2517 fucosidase, alpha-L- 1, tissue
GO hydrolase activity, acting on glycosyl	6	44	0.0772264	3373 hyaluronoglucosaminidase 1
GO hydrolase activity, acting on glycosyl	6	44	0.0772264	4121 mannosidase, alpha, class 1A, member 1
GO hydrolase activity, acting on glycosyl	6	44	0.0772264	57134 mannosidase, alpha, class 1C, member 1
GO hydrolase activity, acting on glycosyl	6	44	0.0772264	79661 nei endonuclease VIII-like 1 (E. coli)
GO hydrolase activity, acting on glycosyl	6	44	0.0772264	952 CD38 molecule
GO response to interleukin-1	4	24	0.0773606	11213 interleukin-1 receptor-associated kinase 3
GO response to interleukin-1	4	24	0.0773606	5122 proprotein convertase subtilisin/kexin type 1
GO response to interleukin-1	4	24	0.0773606	6622 synuclein, alpha (non A4 component of amyloid precursor)
GO response to interleukin-1	4	24	0.0773606	952 CD38 molecule
GO defense response to Gram-positive b	4	24	0.0773606	3569 interleukin 6 (interferon, beta 2)
GO defense response to Gram-positive b	4	24	0.0773606	3570 interleukin 6 receptor
GO defense response to Gram-positive b	4	24	0.0773606	64127 nucleotide-binding oligomerization domain containing 2
GO defense response to Gram-positive b	4	24	0.0773606	7097 toll-like receptor 2
GO response to metal ion	2	7	0.0778892	10397 N-myc downstream regulated 1
GO response to metal ion	2	7	0.0778892	9633 metallothionein-like 5, testis-specific (tesmin)
GO positive regulation of ossification	2	7	0.0778892	10766 transducer of ERBB2, 2
GO positive regulation of ossification	2	7	0.0778892	652 bone morphogenetic protein 4
GO chitin catabolic process	2	7	0.0778892	1117 chitinase 3-like 2
GO chitin catabolic process	2	7	0.0778892	5016 oviductal glycoprotein 1, 120kDa
GO chitinase activity	2	7	0.0778892	1117 chitinase 3-like 2
GO chitinase activity	2	7	0.0778892	5016 oviductal glycoprotein 1, 120kDa
GO retinoic acid binding	2	7	0.0778892	1382 cellular retinoic acid binding protein 2
GO retinoic acid binding	2	7	0.0778892	7026 nuclear receptor subfamily 2, group F, member 2
GO axon regeneration	2	7	0.0778892	1462 versican
GO axon regeneration	2	7	0.0778892	6256 retinoid X receptor, alpha
GO fibril organization	2	7	0.0778892	1471 cystatin C
GO fibril organization	2	7	0.0778892	4586 mucin 5AC, oligomeric mucus/gel-forming
GO dopamine binding	2	7	0.0778892	154 adrenergic, beta-2-, receptor, surface
GO dopamine binding	2	7	0.0778892	1815 dopamine receptor D4

GO negative regulation of peptidyl-serine	2	7	0.0778892	154043 CNKSR family member 3
GO negative regulation of peptidyl-serine	2	7	0.0778892	51085 MLX interacting protein-like
GO exogenous drug catabolic process	2	7	0.0778892	1558 cytochrome P450, family 2, subfamily C, polypeptide 8
GO exogenous drug catabolic process	2	7	0.0778892	1559 cytochrome P450, family 2, subfamily C, polypeptide 9
GO negative regulation of cAMP biosynthesis	2	7	0.0778892	1815 dopamine receptor D4
GO negative regulation of cAMP biosynthesis	2	7	0.0778892	1906 endothelin 1
GO smooth muscle cell differentiation	2	7	0.0778892	183 angiotensinogen (serpin peptidase inhibitor, clade A, member 8)
GO smooth muscle cell differentiation	2	7	0.0778892	54361 wingless-type MMTV integration site family, member 4
GO detection of light stimulus involved in circadian rhythm	2	7	0.0778892	195814 short chain dehydrogenase/reductase family 16C, member 5
GO detection of light stimulus involved in circadian rhythm	2	7	0.0778892	5950 retinol binding protein 4, plasma
GO bHLH transcription factor binding	2	7	0.0778892	2033 E1A binding protein p300
GO bHLH transcription factor binding	2	7	0.0778892	429 achaete-scute complex homolog 1 (Drosophila)
GO embryonic process involved in female sex determination	2	7	0.0778892	2182 acyl-CoA synthetase long-chain family member 4
GO embryonic process involved in female sex determination	2	7	0.0778892	3726 jun B proto-oncogene
GO central nervous system neuron development	2	7	0.0778892	2290 forkhead box G1
GO central nervous system neuron development	2	7	0.0778892	429 achaete-scute complex homolog 1 (Drosophila)
GO negative regulation of T cell receptor signaling pathway	2	7	0.0778892	26191 protein tyrosine phosphatase, non-receptor type 22 (lymphoid)
GO negative regulation of T cell receptor signaling pathway	2	7	0.0778892	53347 ubiquitin associated and SH3 domain containing, A
GO cellular homeostasis	2	7	0.0778892	358 aquaporin 1 (Colton blood group)
GO cellular homeostasis	2	7	0.0778892	4170 myeloid cell leukemia sequence 1 (BCL2-related)
GO pancreatic juice secretion	2	7	0.0778892	358 aquaporin 1 (Colton blood group)
GO pancreatic juice secretion	2	7	0.0778892	6343 secretin
GO positive regulation of interleukin-12 production	2	7	0.0778892	3659 interferon regulatory factor 1
GO positive regulation of interleukin-12 production	2	7	0.0778892	7099 toll-like receptor 4
GO wound healing, spreading of epidermal cells	2	7	0.0778892	3678 integrin, alpha 5 (fibronectin receptor, alpha polypeptide)
GO wound healing, spreading of epidermal cells	2	7	0.0778892	94 activin A receptor type II-like 1
GO positive regulation of Notch signaling	2	7	0.0778892	3815 v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog
GO positive regulation of Notch signaling	2	7	0.0778892	429 achaete-scute complex homolog 1 (Drosophila)
GO response to selenium ion	2	7	0.0778892	4129 monoamine oxidase B
GO response to selenium ion	2	7	0.0778892	6256 retinoid X receptor, alpha
GO negative regulation of myoblast differentiation	2	7	0.0778892	4851 Notch homolog 1, translocation-associated (Drosophila)
GO negative regulation of myoblast differentiation	2	7	0.0778892	652 bone morphogenetic protein 4
GO negative regulation of synaptic transmission	2	7	0.0778892	4889 neuropeptide Y receptor Y5
GO negative regulation of synaptic transmission	2	7	0.0778892	6812 syntaxin binding protein 1
GO aggresome	2	7	0.0778892	5071 Parkinson disease (autosomal recessive, juvenile) 2, parkin
GO aggresome	2	7	0.0778892	79092 caspase recruitment domain family, member 14



GO	3',5'-cyclic-GMP phosphodiesterase a	2	7	0.0778892	5152 phosphodiesterase 9A
GO	3',5'-cyclic-GMP phosphodiesterase a	2	7	0.0778892	5158 phosphodiesterase 6B, cGMP-specific, rod, beta
GO	phototransduction, visible light	2	7	0.0778892	5158 phosphodiesterase 6B, cGMP-specific, rod, beta
GO	phototransduction, visible light	2	7	0.0778892	6101 retinitis pigmentosa 1 (autosomal dominant)
GO	chromatoid body	2	7	0.0778892	55124 piwi-like 2 (Drosophila)
GO	chromatoid body	2	7	0.0778892	9271 piwi-like 1 (Drosophila)
GO	CARD domain binding	2	7	0.0778892	64127 nucleotide-binding oligomerization domain containing 2
GO	CARD domain binding	2	7	0.0778892	79092 caspase recruitment domain family, member 14
GO	negative regulation of interferon-gan	2	7	0.0778892	64127 nucleotide-binding oligomerization domain containing 2
GO	negative regulation of interferon-gan	2	7	0.0778892	7099 toll-like receptor 4
GO	hyperosmotic response	2	7	0.0778892	6750 somatostatin
GO	hyperosmotic response	2	7	0.0778892	7098 toll-like receptor 3
GO	positive regulation of chemokine bio:	2	7	0.0778892	7098 toll-like receptor 3
GO	positive regulation of chemokine bio:	2	7	0.0778892	7474 wingless-type MMTV integration site family, member 5A
GO	positive regulation of interferon-beta	2	7	0.0778892	7098 toll-like receptor 3
GO	positive regulation of interferon-beta	2	7	0.0778892	7099 toll-like receptor 4
GO	regulation of mRNA stability	2	7	0.0778892	7538 zinc finger protein 36, C3H type, homolog (mouse)
GO	regulation of mRNA stability	2	7	0.0778892	799 calcitonin receptor
GO	transmembrane receptor protein ser	2	7	0.0778892	91 activin A receptor, type IB
GO	transmembrane receptor protein ser	2	7	0.0778892	94 activin A receptor type II-like 1
GO	response to biotic stimulus	3	15	0.0782215	10410 interferon induced transmembrane protein 3 (1-8U)
GO	response to biotic stimulus	3	15	0.0782215	646658 transmembrane protein 90A
GO	response to biotic stimulus	3	15	0.0782215	8519 interferon induced transmembrane protein 1 (9-27)
GO	water transport	3	15	0.0782215	1080 cystic fibrosis transmembrane conductance regulator (ATP-binding cas:
GO	water transport	3	15	0.0782215	358 aquaporin 1 (Colton blood group)
GO	water transport	3	15	0.0782215	6563 solute carrier family 14 (urea transporter), member 1 (Kidd blood group)
GO	cellular response to heat	3	15	0.0782215	113278 chromosome 20 open reading frame 54
GO	cellular response to heat	3	15	0.0782215	286133 scavenger receptor class A, member 5 (putative)
GO	cellular response to heat	3	15	0.0782215	6489 ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 1
GO	positive regulation of phagocytosis	3	15	0.0782215	2624 GATA binding protein 2
GO	positive regulation of phagocytosis	3	15	0.0782215	64127 nucleotide-binding oligomerization domain containing 2
GO	positive regulation of phagocytosis	3	15	0.0782215	718 complement component 3
GO	response to vitamin D	3	15	0.0782215	3643 insulin receptor
GO	response to vitamin D	3	15	0.0782215	6256 retinoid X receptor, alpha
GO	response to vitamin D	3	15	0.0782215	7706 tripartite motif-containing 25
GO	polysome	3	15	0.0782215	55124 piwi-like 2 (Drosophila)

GO polysome	3	15	0.0782215	8531 cold shock domain protein A
GO polysome	3	15	0.0782215	9271 piwi-like 1 (Drosophila)
GO phosphatidylinositol-4,5-bisphosphat	3	15	0.0782215	56288 par-3 partitioning defective 3 homolog (C. elegans)
GO phosphatidylinositol-4,5-bisphosphat	3	15	0.0782215	85477 scinderin
GO phosphatidylinositol-4,5-bisphosphat	3	15	0.0782215	91404 SEC14 and spectrin domains 1
GO extrinsic to membrane	5	34	0.0792402	1755 deleted in malignant brain tumors 1
GO extrinsic to membrane	5	34	0.0792402	257019 FERM domain containing 3
GO extrinsic to membrane	5	34	0.0792402	29116 myosin regulatory light chain interacting protein
GO extrinsic to membrane	5	34	0.0792402	5774 protein tyrosine phosphatase, non-receptor type 3
GO extrinsic to membrane	5	34	0.0792402	94025 mucin 16, cell surface associated
GO perikaryon	5	34	0.0792402	2026 enolase 2 (gamma, neuronal)
GO perikaryon	5	34	0.0792402	4692 necdin homolog (mouse)
GO perikaryon	5	34	0.0792402	5152 phosphodiesterase 9A
GO perikaryon	5	34	0.0792402	885 cholecystokinin
GO perikaryon	5	34	0.0792402	8912 calcium channel, voltage-dependent, T type, alpha 1H subunit
GO lipid transport	8	66	0.0798135	2055 ceroid-lipofuscinosis, neuronal 8 (epilepsy, progressive with mental ret
GO lipid transport	8	66	0.0798135	23780 apolipoprotein L, 2
GO lipid transport	8	66	0.0798135	3949 low density lipoprotein receptor
GO lipid transport	8	66	0.0798135	6653 sortilin-related receptor, L(DLR class) A repeats-containing
GO lipid transport	8	66	0.0798135	80830 apolipoprotein L, 6
GO lipid transport	8	66	0.0798135	80833 apolipoprotein L, 3
GO lipid transport	8	66	0.0798135	8542 apolipoprotein L, 1
GO lipid transport	8	66	0.0798135	9619 ATP-binding cassette, sub-family G (WHITE), member 1
GO anatomical structure morphogenesis	11	101	0.083773	10205 myelin protein zero-like 2
GO anatomical structure morphogenesis	11	101	0.083773	1368 carboxypeptidase M
GO anatomical structure morphogenesis	11	101	0.083773	1948 ephrin-B2
GO anatomical structure morphogenesis	11	101	0.083773	1999 E74-like factor 3 (ets domain transcription factor, epithelial-specific )
GO anatomical structure morphogenesis	11	101	0.083773	2201 fibrillin 2
GO anatomical structure morphogenesis	11	101	0.083773	2239 glypican 4
GO anatomical structure morphogenesis	11	101	0.083773	3175 one cut homeobox 1
GO anatomical structure morphogenesis	11	101	0.083773	3491 cysteine-rich, angiogenic inducer, 61
GO anatomical structure morphogenesis	11	101	0.083773	51085 MLX interacting protein-like
GO anatomical structure morphogenesis	11	101	0.083773	5307 paired-like homeodomain 1
GO anatomical structure morphogenesis	11	101	0.083773	5460 POU class 5 homeobox 1
GO glucose homeostasis	6	45	0.084217	222546 regulatory factor X, 6
GO glucose homeostasis	6	45	0.084217	3169 forkhead box A1

GO	glucose homeostasis	6	45	0.084217	3643 insulin receptor
GO	glucose homeostasis	6	45	0.084217	51085 MLX interacting protein-like
GO	glucose homeostasis	6	45	0.084217	5367 pro-melanin-concentrating hormone
GO	glucose homeostasis	6	45	0.084217	5950 retinol binding protein 4, plasma
GO	GTPase activity	19	198	0.0845246	1785 dynamin 2
GO	GTPase activity	19	198	0.0845246	1915 eukaryotic translation elongation factor 1 alpha 1
GO	GTPase activity	19	198	0.0845246	1983 eukaryotic translation initiation factor 5
GO	GTPase activity	19	198	0.0845246	23682 RAB38, member RAS oncogene family
GO	GTPase activity	19	198	0.0845246	2633 guanylate binding protein 1, interferon-inducible, 67kDa
GO	GTPase activity	19	198	0.0845246	2634 guanylate binding protein 2, interferon-inducible
GO	GTPase activity	19	198	0.0845246	2635 guanylate binding protein 3
GO	GTPase activity	19	198	0.0845246	2769 guanine nucleotide binding protein (G protein), alpha 15 (Gq class)
GO	GTPase activity	19	198	0.0845246	379 ADP-ribosylation factor-like 4D
GO	GTPase activity	19	198	0.0845246	3845 v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog
GO	GTPase activity	19	198	0.0845246	387496 RAS-like, family 11, member A
GO	GTPase activity	19	198	0.0845246	4599 myxovirus (influenza virus) resistance 1, interferon-inducible protein p1
GO	GTPase activity	19	198	0.0845246	4600 myxovirus (influenza virus) resistance 2 (mouse)
GO	GTPase activity	19	198	0.0845246	51285 RAS-like, family 12
GO	GTPase activity	19	198	0.0845246	51655 RAS, dexamethasone-induced 1
GO	GTPase activity	19	198	0.0845246	54769 DIRAS family, GTP-binding RAS-like 2
GO	GTPase activity	19	198	0.0845246	5873 RAB27A, member RAS oncogene family
GO	GTPase activity	19	198	0.0845246	85004 RAS-like, estrogen-regulated, growth inhibitor
GO	GTPase activity	19	198	0.0845246	9567 GTP binding protein 1
GO	epidermal growth factor receptor sig	4	25	0.0873408	1839 heparin-binding EGF-like growth factor
GO	epidermal growth factor receptor sig	4	25	0.0873408	819 calcium modulating ligand
GO	epidermal growth factor receptor sig	4	25	0.0873408	8527 diacylglycerol kinase, delta 130kDa
GO	epidermal growth factor receptor sig	4	25	0.0873408	9185 RALBP1 associated Eps domain containing 2
GO	mammary gland development	4	25	0.0873408	2066 v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian)
GO	mammary gland development	4	25	0.0873408	2737 GLI family zinc finger 3
GO	mammary gland development	4	25	0.0873408	3479 insulin-like growth factor 1 (somatomedin C)
GO	mammary gland development	4	25	0.0873408	8660 insulin receptor substrate 2
GO	skeletal system morphogenesis	4	25	0.0873408	29123 ankyrin repeat domain 11
GO	skeletal system morphogenesis	4	25	0.0873408	64651 cysteine-serine-rich nuclear protein 1
GO	skeletal system morphogenesis	4	25	0.0873408	84159 AT rich interactive domain 5B (MRF1-like)
GO	skeletal system morphogenesis	4	25	0.0873408	9496 T-box 4
GO	feeding behavior	4	25	0.0873408	4886 neuropeptide Y receptor Y1

GO feeding behavior	4	25	0.0873408	5367 pro-melanin-concentrating hormone
GO feeding behavior	4	25	0.0873408	56923 neuromedin U receptor 2
GO feeding behavior	4	25	0.0873408	627 brain-derived neurotrophic factor
GO positive regulation of B cell proliferat	4	25	0.0873408	604 B-cell CLL/lymphoma 6
GO positive regulation of B cell proliferat	4	25	0.0873408	7099 toll-like receptor 4
GO positive regulation of B cell proliferat	4	25	0.0873408	8660 insulin receptor substrate 2
GO positive regulation of B cell proliferat	4	25	0.0873408	952 CD38 molecule
GO positive regulation of protein amino a	5	35	0.0875028	2033 E1A binding protein p300
GO positive regulation of protein amino a	5	35	0.0875028	3643 insulin receptor
GO positive regulation of protein amino a	5	35	0.0875028	55600 intelectin 1 (galactofuranose binding)
GO positive regulation of protein amino a	5	35	0.0875028	652 bone morphogenetic protein 4
GO positive regulation of protein amino a	5	35	0.0875028	79092 caspase recruitment domain family, member 14
GO steroid metabolic process	8	68	0.0914049	1559 cytochrome P450, family 2, subfamily C, polypeptide 9
GO steroid metabolic process	8	68	0.0914049	1571 cytochrome P450, family 2, subfamily E, polypeptide 1
GO steroid metabolic process	8	68	0.0914049	1577 cytochrome P450, family 3, subfamily A, polypeptide 5
GO steroid metabolic process	8	68	0.0914049	255738 proprotein convertase subtilisin/kexin type 9
GO steroid metabolic process	8	68	0.0914049	26119 low density lipoprotein receptor adaptor protein 1
GO steroid metabolic process	8	68	0.0914049	3949 low density lipoprotein receptor
GO steroid metabolic process	8	68	0.0914049	6653 sortilin-related receptor, L(DLR class) A repeats-containing
GO steroid metabolic process	8	68	0.0914049	8542 apolipoprotein L, 1
GO regulation of small GTPase mediated	6	46	0.0915452	10156 RAS p21 protein activator 4
GO regulation of small GTPase mediated	6	46	0.0915452	23179 ral guanine nucleotide dissociation stimulator-like 1
GO regulation of small GTPase mediated	6	46	0.0915452	57139 ral guanine nucleotide dissociation stimulator-like 3
GO regulation of small GTPase mediated	6	46	0.0915452	57186 Ral GTPase activating protein, alpha subunit 2 (catalytic)
GO regulation of small GTPase mediated	6	46	0.0915452	5900 ral guanine nucleotide dissociation stimulator
GO regulation of small GTPase mediated	6	46	0.0915452	6494 signal-induced proliferation-associated 1
GO carbonate dehydratase activity	3	16	0.0915718	11238 carbonic anhydrase VB, mitochondrial
GO carbonate dehydratase activity	3	16	0.0915718	760 carbonic anhydrase II
GO carbonate dehydratase activity	3	16	0.0915718	771 carbonic anhydrase XII
GO glycosaminoglycan binding	3	16	0.0915718	1462 versican
GO glycosaminoglycan binding	3	16	0.0915718	50859 sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican)
GO glycosaminoglycan binding	3	16	0.0915718	7049 transforming growth factor, beta receptor III
GO negative regulation of blood pressure	3	16	0.0915718	1813 dopamine receptor D2
GO negative regulation of blood pressure	3	16	0.0915718	5367 pro-melanin-concentrating hormone
GO negative regulation of blood pressure	3	16	0.0915718	5465 peroxisome proliferator-activated receptor alpha
GO antigen binding	3	16	0.0915718	2033 E1A binding protein p300

GO	antigen binding	3	16	0.0915718	3512 immunoglobulin J polypeptide, linker protein for immunoglobulin alpha
GO	antigen binding	3	16	0.0915718	8631 src kinase associated phosphoprotein 1
GO	neurogenesis	3	16	0.0915718	255738 proprotein convertase subtilisin/kexin type 9
GO	neurogenesis	3	16	0.0915718	429 achaete-scute complex homolog 1 (Drosophila)
GO	neurogenesis	3	16	0.0915718	5122 proprotein convertase subtilisin/kexin type 1
GO	carbohydrate binding	3	16	0.0915718	26270 F-box protein 6
GO	carbohydrate binding	3	16	0.0915718	56261 glycerophosphocholine phosphodiesterase GDE1 homolog (S. cerevisia
GO	carbohydrate binding	3	16	0.0915718	6402 selectin L
GO	gap junction	3	16	0.0915718	2707 gap junction protein, beta 3, 31kDa
GO	gap junction	3	16	0.0915718	8531 cold shock domain protein A
GO	gap junction	3	16	0.0915718	9414 tight junction protein 2 (zona occludens 2)
GO	neuron fate commitment	3	16	0.0915718	2737 GLI family zinc finger 3
GO	neuron fate commitment	3	16	0.0915718	4851 Notch homolog 1, translocation-associated (Drosophila)
GO	neuron fate commitment	3	16	0.0915718	652 bone morphogenetic protein 4
GO	negative regulation of protein amino	3	16	0.0915718	3486 insulin-like growth factor binding protein 3
GO	negative regulation of protein amino	3	16	0.0915718	3643 insulin receptor
GO	negative regulation of protein amino	3	16	0.0915718	5071 Parkinson disease (autosomal recessive, juvenile) 2, parkin
GO	negative regulation of endothelial cel	3	16	0.0915718	498 ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subun
GO	negative regulation of endothelial cel	3	16	0.0915718	7026 nuclear receptor subfamily 2, group F, member 2
GO	negative regulation of endothelial cel	3	16	0.0915718	9966 tumor necrosis factor (ligand) superfamily, member 15
GO	regulation of cell growth	7	57	0.0923766	1154 cytokine inducible SH2-containing protein
GO	regulation of cell growth	7	57	0.0923766	183 angiotensinogen (serpin peptidase inhibitor, clade A, member 8)
GO	regulation of cell growth	7	57	0.0923766	3486 insulin-like growth factor binding protein 3
GO	regulation of cell growth	7	57	0.0923766	3488 insulin-like growth factor binding protein 5
GO	regulation of cell growth	7	57	0.0923766	3491 cysteine-rich, angiogenic inducer, 61
GO	regulation of cell growth	7	57	0.0923766	4856 nephroblastoma overexpressed gene
GO	regulation of cell growth	7	57	0.0923766	8839 WNT1 inducible signaling pathway protein 2
GO	liver development	7	57	0.0923766	2033 E1A binding protein p300
GO	liver development	7	57	0.0923766	255738 proprotein convertase subtilisin/kexin type 9
GO	liver development	7	57	0.0923766	3142 H2.0-like homeobox
GO	liver development	7	57	0.0923766	3175 one cut homeobox 1
GO	liver development	7	57	0.0923766	4851 Notch homolog 1, translocation-associated (Drosophila)
GO	liver development	7	57	0.0923766	6256 retinoid X receptor, alpha
GO	liver development	7	57	0.0923766	7049 transforming growth factor, beta receptor III
GO	ion channel activity	15	151	0.0927128	1080 cystic fibrosis transmembrane conductance regulator (ATP-binding cas
GO	ion channel activity	15	151	0.0927128	1139 cholinergic receptor, nicotinic, alpha 7

GO ion channel activity	15	151	0.0927128	2564 gamma-aminobutyric acid (GABA) A receptor, epsilon
GO ion channel activity	15	151	0.0927128	266675 bestrophin 4
GO ion channel activity	15	151	0.0927128	27345 potassium large conductance calcium-activated channel, subfamily M,
GO ion channel activity	15	151	0.0927128	343450 potassium channel, subfamily T, member 2
GO ion channel activity	15	151	0.0927128	3709 inositol 1,4,5-triphosphate receptor, type 2
GO ion channel activity	15	151	0.0927128	3782 potassium intermediate/small conductance calcium-activated channel,
GO ion channel activity	15	151	0.0927128	3783 potassium intermediate/small conductance calcium-activated channel,
GO ion channel activity	15	151	0.0927128	5025 purinergic receptor P2X, ligand-gated ion channel, 4
GO ion channel activity	15	151	0.0927128	5349 FXFD domain containing ion transport regulator 3
GO ion channel activity	15	151	0.0927128	53827 FXFD domain containing ion transport regulator 5
GO ion channel activity	15	151	0.0927128	63982 anoctamin 3
GO ion channel activity	15	151	0.0927128	7223 transient receptor potential cation channel, subfamily C, member 4
GO ion channel activity	15	151	0.0927128	8973 cholinergic receptor, nicotinic, alpha 6
GO calcium ion binding	50	605	0.0935166	1004 cadherin 6, type 2, K-cadherin (fetal kidney)
GO calcium ion binding	50	605	0.0935166	10085 EGF-like repeats and discoidin I-like domains 3
GO calcium ion binding	50	605	0.0935166	1009 cadherin 11, type 2, OB-cadherin (osteoblast)
GO calcium ion binding	50	605	0.0935166	1014 cadherin 16, KSP-cadherin
GO calcium ion binding	50	605	0.0935166	1016 cadherin 18, type 2
GO calcium ion binding	50	605	0.0935166	10516 fibulin 5
GO calcium ion binding	50	605	0.0935166	11199 annexin A10
GO calcium ion binding	50	605	0.0935166	126638 repetin
GO calcium ion binding	50	605	0.0935166	1462 versican
GO calcium ion binding	50	605	0.0935166	1821 dystrophin related protein 2
GO calcium ion binding	50	605	0.0935166	1953 multiple EGF-like-domains 6
GO calcium ion binding	50	605	0.0935166	2015 egf-like module containing, mucin-like, hormone receptor-like 1
GO calcium ion binding	50	605	0.0935166	2200 fibrillin 1
GO calcium ion binding	50	605	0.0935166	2201 fibrillin 2
GO calcium ion binding	50	605	0.0935166	22795 nidogen 2 (osteonidogen)
GO calcium ion binding	50	605	0.0935166	23208 synaptotagmin XI
GO calcium ion binding	50	605	0.0935166	23418 crumbs homolog 1 (Drosophila)
GO calcium ion binding	50	605	0.0935166	255743 nephronectin
GO calcium ion binding	50	605	0.0935166	29943 peptidyl arginine deiminase, type I
GO calcium ion binding	50	605	0.0935166	30008 EGF-containing fibulin-like extracellular matrix protein 2
GO calcium ion binding	50	605	0.0935166	311 annexin A11
GO calcium ion binding	50	605	0.0935166	388743 calpain 8
GO calcium ion binding	50	605	0.0935166	3949 low density lipoprotein receptor

GO calcium ion binding	50	605	0.0935166	4038 low density lipoprotein receptor-related protein 4
GO calcium ion binding	50	605	0.0935166	4121 mannosidase, alpha, class 1A, member 1
GO calcium ion binding	50	605	0.0935166	4851 Notch homolog 1, translocation-associated (Drosophila)
GO calcium ion binding	50	605	0.0935166	4853 Notch homolog 2 (Drosophila)
GO calcium ion binding	50	605	0.0935166	50859 sparco/osteonectin, cwcv and kazal-like domains proteoglycan (testican)
GO calcium ion binding	50	605	0.0935166	5099 protocadherin 7
GO calcium ion binding	50	605	0.0935166	54681 prolyl 4-hydroxylase, transmembrane (endoplasmic reticulum)
GO calcium ion binding	50	605	0.0935166	54947 lysophosphatidylcholine acyltransferase 2
GO calcium ion binding	50	605	0.0935166	5648 mannan-binding lectin serine peptidase 1 (C4/C2 activating component)
GO calcium ion binding	50	605	0.0935166	57134 mannosidase, alpha, class 1C, member 1
GO calcium ion binding	50	605	0.0935166	57493 HEG homolog 1 (zebrafish)
GO calcium ion binding	50	605	0.0935166	57620 stromal interaction molecule 2
GO calcium ion binding	50	605	0.0935166	64093 SPARC related modular calcium binding 1
GO calcium ion binding	50	605	0.0935166	6622 synuclein, alpha (non A4 component of amyloid precursor)
GO calcium ion binding	50	605	0.0935166	6778 signal transducer and activator of transcription 6, interleukin-4 inducible
GO calcium ion binding	50	605	0.0935166	6857 synaptotagmin I
GO calcium ion binding	50	605	0.0935166	7092 tolloid-like 1
GO calcium ion binding	50	605	0.0935166	715 complement component 1, r subcomponent
GO calcium ion binding	50	605	0.0935166	7447 visinin-like 1
GO calcium ion binding	50	605	0.0935166	79180 EF-hand domain family, member D2
GO calcium ion binding	50	605	0.0935166	79987 sushi, von Willebrand factor type A, EGF and pentraxin domain containing
GO calcium ion binding	50	605	0.0935166	80258 EF-hand domain (C-terminal) containing 2
GO calcium ion binding	50	605	0.0935166	83394 PITPNM family member 3
GO calcium ion binding	50	605	0.0935166	83872 hemicentin 1
GO calcium ion binding	50	605	0.0935166	84059 G protein-coupled receptor 98
GO calcium ion binding	50	605	0.0935166	85477 scinderin
GO calcium ion binding	50	605	0.0935166	9185 RALBP1 associated Eps domain containing 2
GO skeletal muscle tissue development	5	36	0.0961953	1508 cathepsin B
GO skeletal muscle tissue development	5	36	0.0961953	2033 E1A binding protein p300
GO skeletal muscle tissue development	5	36	0.0961953	3142 H2.0-like homeobox
GO skeletal muscle tissue development	5	36	0.0961953	4223 mesenchyme homeobox 2
GO skeletal muscle tissue development	5	36	0.0961953	7026 nuclear receptor subfamily 2, group F, member 2
GO ovarian follicle development	5	36	0.0961953	2296 forkhead box C1
GO ovarian follicle development	5	36	0.0961953	4254 KIT ligand
GO ovarian follicle development	5	36	0.0961953	652 bone morphogenetic protein 4
GO ovarian follicle development	5	36	0.0961953	726 calpain 5

GO ovarian follicle development	5	36	0.0961953	79956 endoplasmic reticulum metallopeptidase 1
GO insulin receptor signaling pathway	5	36	0.0961953	2303 forkhead box C2 (MFH-1, mesenchyme forkhead 1)
GO insulin receptor signaling pathway	5	36	0.0961953	3484 insulin-like growth factor binding protein 1
GO insulin receptor signaling pathway	5	36	0.0961953	3643 insulin receptor
GO insulin receptor signaling pathway	5	36	0.0961953	5295 phosphoinositide-3-kinase, regulatory subunit 1 (alpha)
GO insulin receptor signaling pathway	5	36	0.0961953	8660 insulin receptor substrate 2
GO extracellular matrix structural constit	8	69	0.0975449	2200 fibrillin 1
GO extracellular matrix structural constit	8	69	0.0975449	2201 fibrillin 2
GO extracellular matrix structural constit	8	69	0.0975449	30008 EGF-containing fibulin-like extracellular matrix protein 2
GO extracellular matrix structural constit	8	69	0.0975449	4586 mucin 5AC, oligomeric mucus/gel-forming
GO extracellular matrix structural constit	8	69	0.0975449	4588 mucin 6, oligomeric mucus/gel-forming
GO extracellular matrix structural constit	8	69	0.0975449	54361 wingless-type MMTV integration site family, member 4
GO extracellular matrix structural constit	8	69	0.0975449	7477 wingless-type MMTV integration site family, member 7B
GO extracellular matrix structural constit	8	69	0.0975449	8076 microfibrillar associated protein 5
GO negative regulation of apoptosis	14	140	0.0976595	2055 ceroid-lipofuscinosis, neuronal 8 (epilepsy, progressive with mental ret
GO negative regulation of apoptosis	14	140	0.0976595	23529 cardiotrophin-like cytokine factor 1
GO negative regulation of apoptosis	14	140	0.0976595	3569 interleukin 6 (interferon, beta 2)
GO negative regulation of apoptosis	14	140	0.0976595	358 aquaporin 1 (Colton blood group)
GO negative regulation of apoptosis	14	140	0.0976595	415116 pim-3 oncogene
GO negative regulation of apoptosis	14	140	0.0976595	4254 KIT ligand
GO negative regulation of apoptosis	14	140	0.0976595	4286 microphthalmia-associated transcription factor
GO negative regulation of apoptosis	14	140	0.0976595	429 achaete-scute complex homolog 1 (Drosophila)
GO negative regulation of apoptosis	14	140	0.0976595	4851 Notch homolog 1, translocation-associated (Drosophila)
GO negative regulation of apoptosis	14	140	0.0976595	604 B-cell CLL/lymphoma 6
GO negative regulation of apoptosis	14	140	0.0976595	652 bone morphogenetic protein 4
GO negative regulation of apoptosis	14	140	0.0976595	7474 wingless-type MMTV integration site family, member 5A
GO negative regulation of apoptosis	14	140	0.0976595	81788 NIAK family, SNF1-like kinase, 2
GO negative regulation of apoptosis	14	140	0.0976595	8531 cold shock domain protein A
GO cell differentiation	40	474	0.0978325	10076 protein tyrosine phosphatase, receptor type, U
GO cell differentiation	40	474	0.0978325	10507 sema domain, immunoglobulin domain (Ig), transmembrane domain (T
GO cell differentiation	40	474	0.0978325	10752 cell adhesion molecule with homology to L1CAM (close homolog of L1)
GO cell differentiation	40	474	0.0978325	10912 growth arrest and DNA-damage-inducible, gamma
GO cell differentiation	40	474	0.0978325	10913 ectodysplasin A receptor
GO cell differentiation	40	474	0.0978325	130399 activin A receptor, type IC
GO cell differentiation	40	474	0.0978325	1435 colony stimulating factor 1 (macrophage)
GO cell differentiation	40	474	0.0978325	143689 piwi-like 4 (Drosophila)



GO cell differentiation	40	474	0.0978325	1948 ephrin-B2
GO cell differentiation	40	474	0.0978325	2122 MDS1 and EVI1 complex locus
GO cell differentiation	40	474	0.0978325	223117 sema domain, immunoglobulin domain (Ig), short basic domain, secret
GO cell differentiation	40	474	0.0978325	255743 nephronectin
GO cell differentiation	40	474	0.0978325	26281 fibroblast growth factor 20
GO cell differentiation	40	474	0.0978325	26468 LIM homeobox 6
GO cell differentiation	40	474	0.0978325	28959 transmembrane protein 176B
GO cell differentiation	40	474	0.0978325	3142 H2.0-like homeobox
GO cell differentiation	40	474	0.0978325	342035 gliomedin
GO cell differentiation	40	474	0.0978325	3911 laminin, alpha 5
GO cell differentiation	40	474	0.0978325	3958 lectin, galactoside-binding, soluble, 3
GO cell differentiation	40	474	0.0978325	4170 myeloid cell leukemia sequence 1 (BCL2-related)
GO cell differentiation	40	474	0.0978325	4616 growth arrest and DNA-damage-inducible, beta
GO cell differentiation	40	474	0.0978325	4853 Notch homolog 2 (Drosophila)
GO cell differentiation	40	474	0.0978325	4915 neurotrophic tyrosine kinase, receptor, type 2
GO cell differentiation	40	474	0.0978325	51314 thioredoxin domain containing 3 (spermatzoa)
GO cell differentiation	40	474	0.0978325	5367 pro-melanin-concentrating hormone
GO cell differentiation	40	474	0.0978325	54852 progesterin and adipoQ receptor family member V
GO cell differentiation	40	474	0.0978325	54904 Wolf-Hirschhorn syndrome candidate 1-like 1
GO cell differentiation	40	474	0.0978325	55124 piwi-like 2 (Drosophila)
GO cell differentiation	40	474	0.0978325	56913 core 1 synthase, glycoprotein-N-acetylgalactosamine 3-beta-galactosyl
GO cell differentiation	40	474	0.0978325	64359 nucleoredoxin
GO cell differentiation	40	474	0.0978325	7092 tolloid-like 1
GO cell differentiation	40	474	0.0978325	7546 Zic family member 2 (odd-paired homolog, Drosophila)
GO cell differentiation	40	474	0.0978325	79820 cation channel, sperm-associated, beta
GO cell differentiation	40	474	0.0978325	83890 spermatogenesis associated 9
GO cell differentiation	40	474	0.0978325	84033 obscurin, cytoskeletal calmodulin and titin-interacting RhoGEF
GO cell differentiation	40	474	0.0978325	85416 Zic family member 5 (odd-paired homolog, Drosophila)
GO cell differentiation	40	474	0.0978325	8600 tumor necrosis factor (ligand) superfamily, member 11
GO cell differentiation	40	474	0.0978325	91461 protein kinase domain containing, cytoplasmic homolog (mouse)
GO cell differentiation	40	474	0.0978325	9271 piwi-like 1 (Drosophila)
GO cell differentiation	40	474	0.0978325	9633 metallothionein-like 5, testis-specific (tesmin)
GO cellular response to hormone stimul	4	26	0.0979082	1080 cystic fibrosis transmembrane conductance regulator (ATP-binding cas
GO cellular response to hormone stimul	4	26	0.0979082	1843 dual specificity phosphatase 1
GO cellular response to hormone stimul	4	26	0.0979082	2353 FBJ murine osteosarcoma viral oncogene homolog
GO cellular response to hormone stimul	4	26	0.0979082	3726 jun B proto-oncogene

GO branching involved in ureteric bud morphogenesis	4	26	0.0979082	183 angiotensinogen (serpin peptidase inhibitor, clade A, member 8)
GO branching involved in ureteric bud morphogenesis	4	26	0.0979082	2737 GLI family zinc finger 3
GO branching involved in ureteric bud morphogenesis	4	26	0.0979082	3911 laminin, alpha 5
GO branching involved in ureteric bud morphogenesis	4	26	0.0979082	652 bone morphogenetic protein 4
GO negative regulation of epithelial cell proliferation	4	26	0.0979082	4163 mutated in colorectal cancers
GO negative regulation of epithelial cell proliferation	4	26	0.0979082	652 bone morphogenetic protein 4
GO negative regulation of epithelial cell proliferation	4	26	0.0979082	7049 transforming growth factor, beta receptor III
GO negative regulation of epithelial cell proliferation	4	26	0.0979082	7474 wingless-type MMTV integration site family, member 5A
GO chloride channel activity	7	58	0.0992041	1080 cystic fibrosis transmembrane conductance regulator (ATP-binding cassette)
GO chloride channel activity	7	58	0.0992041	1193 chloride intracellular channel 2
GO chloride channel activity	7	58	0.0992041	2564 gamma-aminobutyric acid (GABA) A receptor, epsilon
GO chloride channel activity	7	58	0.0992041	266675 bestrophin 4
GO chloride channel activity	7	58	0.0992041	5349 FXFD domain containing ion transport regulator 3
GO chloride channel activity	7	58	0.0992041	63982 anoctamin 3
GO chloride channel activity	7	58	0.0992041	8542 apolipoprotein L, 1
GO oxidoreductase activity, acting on single substrates	7	58	0.0992041	23081 lysine (K)-specific demethylase 4C
GO oxidoreductase activity, acting on single substrates	7	58	0.0992041	254295 phytanoyl-CoA dioxygenase domain containing 1
GO oxidoreductase activity, acting on single substrates	7	58	0.0992041	5351 procollagen-lysine 1, 2-oxoglutarate 5-dioxygenase 1
GO oxidoreductase activity, acting on single substrates	7	58	0.0992041	54681 prolyl 4-hydroxylase, transmembrane (endoplasmic reticulum)
GO oxidoreductase activity, acting on single substrates	7	58	0.0992041	55693 lysine (K)-specific demethylase 4D
GO oxidoreductase activity, acting on single substrates	7	58	0.0992041	5742 prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and
GO oxidoreductase activity, acting on single substrates	7	58	0.0992041	7404 ubiquitously transcribed tetratricopeptide repeat gene, Y-linked
GO UDP-galactose:beta-N-acetylglucosamine 4-epimerase	2	8	0.0992693	10317 UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 5
GO UDP-galactose:beta-N-acetylglucosamine 4-epimerase	2	8	0.0992693	8706 beta-1,3-N-acetylgalactosaminyltransferase 1 (globoside blood group)
GO phosphate transport	2	8	0.0992693	10568 solute carrier family 34 (sodium phosphate), member 2
GO phosphate transport	2	8	0.0992693	56172 ankylosis, progressive homolog (mouse)
GO regulation of calcium ion-dependent membrane transport	2	8	0.0992693	143425 synaptotagmin IX
GO regulation of calcium ion-dependent membrane transport	2	8	0.0992693	6857 synaptotagmin I
GO secretory granule membrane	2	8	0.0992693	143425 synaptotagmin IX
GO secretory granule membrane	2	8	0.0992693	5873 RAB27A, member RAS oncogene family
GO embryonic viscerocranium morphogenesis	2	8	0.0992693	157506 retinol dehydrogenase 10 (all-trans)
GO embryonic viscerocranium morphogenesis	2	8	0.0992693	2303 forkhead box C2 (MFH-1, mesenchyme forkhead 1)
GO behavioral response to cocaine	2	8	0.0992693	1813 dopamine receptor D2
GO behavioral response to cocaine	2	8	0.0992693	1815 dopamine receptor D4
GO positive regulation of neuroblast proliferation	2	8	0.0992693	1813 dopamine receptor D2
GO positive regulation of neuroblast proliferation	2	8	0.0992693	2290 forkhead box G1

GO	regulation of heart rate	2	8	0.0992693	1813 dopamine receptor D2
GO	regulation of heart rate	2	8	0.0992693	5367 pro-melanin-concentrating hormone
GO	regulation of sodium ion transport	2	8	0.0992693	1813 dopamine receptor D2
GO	regulation of sodium ion transport	2	8	0.0992693	5025 purinergic receptor P2X, ligand-gated ion channel, 4
GO	phosphoinositide 3-kinase cascade	2	8	0.0992693	1906 endothelin 1
GO	phosphoinositide 3-kinase cascade	2	8	0.0992693	5295 phosphoinositide-3-kinase, regulatory subunit 1 (alpha)
GO	cellular response to hydrogen peroxide	2	8	0.0992693	2033 E1A binding protein p300
GO	cellular response to hydrogen peroxide	2	8	0.0992693	358 aquaporin 1 (Colton blood group)
GO	histone acetyltransferase complex	2	8	0.0992693	2033 E1A binding protein p300
GO	histone acetyltransferase complex	2	8	0.0992693	23338 PHD finger protein 15
GO	negative regulation of programmed cell death	2	8	0.0992693	2122 MDS1 and EVI1 complex locus
GO	negative regulation of programmed cell death	2	8	0.0992693	3815 v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog
GO	protein autoprocessing	2	8	0.0992693	255738 proprotein convertase subtilisin/kexin type 9
GO	protein autoprocessing	2	8	0.0992693	5122 proprotein convertase subtilisin/kexin type 1
GO	positive regulation of chondrocyte differentiation	2	8	0.0992693	2737 GLI family zinc finger 3
GO	positive regulation of chondrocyte differentiation	2	8	0.0992693	91461 protein kinase domain containing, cytoplasmic homolog (mouse)
GO	positive regulation of leukocyte chemotaxis	2	8	0.0992693	3569 interleukin 6 (interferon, beta 2)
GO	positive regulation of leukocyte chemotaxis	2	8	0.0992693	3570 interleukin 6 receptor
GO	regulation of embryonic development	2	8	0.0992693	3643 insulin receptor
GO	regulation of embryonic development	2	8	0.0992693	3911 laminin, alpha 5
GO	positive regulation of leukocyte migration	2	8	0.0992693	375056 melanoma inhibitory activity family, member 3
GO	positive regulation of leukocyte migration	2	8	0.0992693	7097 toll-like receptor 2
GO	mannosyl-oligosaccharide 1,2-alpha-mannosidase activity	2	8	0.0992693	4121 mannosidase, alpha, class 1A, member 1
GO	mannosyl-oligosaccharide 1,2-alpha-mannosidase activity	2	8	0.0992693	57134 mannosidase, alpha, class 1C, member 1
GO	glycosphingolipid biosynthetic process	2	8	0.0992693	53947 alpha 1,4-galactosyltransferase
GO	glycosphingolipid biosynthetic process	2	8	0.0992693	6489 ST8 alpha-N-acetyl-neuraminidase alpha-2,8-sialyltransferase 1
GO	glycerophosphodiester phosphodiesterase activity	2	8	0.0992693	56261 glycerophosphocholine phosphodiesterase GDE1 homolog (S. cerevisiae)
GO	glycerophosphodiester phosphodiesterase activity	2	8	0.0992693	81544 glycerophosphodiester phosphodiesterase domain containing 5
GO	phosphatidylinositol-3-phosphate binding	2	8	0.0992693	56288 par-3 partitioning defective 3 homolog (C. elegans)
GO	phosphatidylinositol-3-phosphate binding	2	8	0.0992693	91404 SEC14 and spectrin domains 1
GO	mesonephros development	2	8	0.0992693	5972 renin
GO	mesonephros development	2	8	0.0992693	652 bone morphogenetic protein 4
GO	peptidoglycan binding	2	8	0.0992693	64127 nucleotide-binding oligomerization domain containing 2
GO	peptidoglycan binding	2	8	0.0992693	7097 toll-like receptor 2
GO	positive regulation of endocytosis	2	8	0.0992693	6622 synuclein, alpha (non A4 component of amyloid precursor)
GO	positive regulation of endocytosis	2	8	0.0992693	79872 Cas-Br-M (murine) ecotropic retroviral transforming sequence-like 1

GO	regulation of dopamine secretion	2	8	0.0992693	6622 synuclein, alpha (non A4 component of amyloid precursor)
GO	regulation of dopamine secretion	2	8	0.0992693	8973 cholinergic receptor, nicotinic, alpha 6
GO	syntaxin-1 binding	2	8	0.0992693	6812 syntaxin binding protein 1
GO	syntaxin-1 binding	2	8	0.0992693	6857 synaptotagmin I
GO	cobalamin binding	2	8	0.0992693	6947 transcobalamin I (vitamin B12 binding protein, R binder family)
GO	cobalamin binding	2	8	0.0992693	6948 transcobalamin II; macrocytic anemia
GO	negative regulation of endothelial cell proliferation	2	8	0.0992693	7026 nuclear receptor subfamily 2, group F, member 2
GO	negative regulation of endothelial cell proliferation	2	8	0.0992693	94 activin A receptor type II-like 1
GO	calcium channel complex	2	8	0.0992693	7223 transient receptor potential cation channel, subfamily C, member 4
GO	calcium channel complex	2	8	0.0992693	91404 SEC14 and spectrin domains 1
GO	protein amino acid phosphorylation	41	488	0.099532	10221 tribbles homolog 1 (Drosophila)
GO	protein amino acid phosphorylation	41	488	0.099532	10769 polo-like kinase 2 (Drosophila)
GO	protein amino acid phosphorylation	41	488	0.099532	11200 CHK2 checkpoint homolog (S. pombe)
GO	protein amino acid phosphorylation	41	488	0.099532	11213 interleukin-1 receptor-associated kinase 3
GO	protein amino acid phosphorylation	41	488	0.099532	130399 activin A receptor, type IC
GO	protein amino acid phosphorylation	41	488	0.099532	140901 serine/threonine kinase 35
GO	protein amino acid phosphorylation	41	488	0.099532	150094 salt-inducible kinase 1
GO	protein amino acid phosphorylation	41	488	0.099532	1612 death-associated protein kinase 1
GO	protein amino acid phosphorylation	41	488	0.099532	1969 EPH receptor A2
GO	protein amino acid phosphorylation	41	488	0.099532	197259 mixed lineage kinase domain-like
GO	protein amino acid phosphorylation	41	488	0.099532	2044 EPH receptor A5
GO	protein amino acid phosphorylation	41	488	0.099532	2263 fibroblast growth factor receptor 2
GO	protein amino acid phosphorylation	41	488	0.099532	23043 TRAF2 and NCK interacting kinase
GO	protein amino acid phosphorylation	41	488	0.099532	23387 SIK family kinase 3
GO	protein amino acid phosphorylation	41	488	0.099532	23476 bromodomain containing 4
GO	protein amino acid phosphorylation	41	488	0.099532	23604 death-associated protein kinase 2
GO	protein amino acid phosphorylation	41	488	0.099532	28951 tribbles homolog 2 (Drosophila)
GO	protein amino acid phosphorylation	41	488	0.099532	28996 homeodomain interacting protein kinase 2
GO	protein amino acid phosphorylation	41	488	0.099532	3486 insulin-like growth factor binding protein 3
GO	protein amino acid phosphorylation	41	488	0.099532	375449 microtubule associated serine/threonine kinase family member 4
GO	protein amino acid phosphorylation	41	488	0.099532	415116 pim-3 oncogene
GO	protein amino acid phosphorylation	41	488	0.099532	4293 mitogen-activated protein kinase kinase kinase 9
GO	protein amino acid phosphorylation	41	488	0.099532	4486 macrophage stimulating 1 receptor (c-met-related tyrosine kinase)
GO	protein amino acid phosphorylation	41	488	0.099532	4638 myosin light chain kinase
GO	protein amino acid phosphorylation	41	488	0.099532	4915 neurotrophic tyrosine kinase, receptor, type 2
GO	protein amino acid phosphorylation	41	488	0.099532	5063 p21 protein (Cdc42/Rac)-activated kinase 3

GO protein amino acid phosphorylation	41	488	0.099532	5129 cyclin-dependent kinase 18
GO protein amino acid phosphorylation	41	488	0.099532	5218 cyclin-dependent kinase 14
GO protein amino acid phosphorylation	41	488	0.099532	57118 calcium/calmodulin-dependent protein kinase ID
GO protein amino acid phosphorylation	41	488	0.099532	57147 SCY1-like 3 ( <i>S. cerevisiae</i> )
GO protein amino acid phosphorylation	41	488	0.099532	5791 protein tyrosine phosphatase, receptor type, E
GO protein amino acid phosphorylation	41	488	0.099532	6446 serum/glucocorticoid regulated kinase 1
GO protein amino acid phosphorylation	41	488	0.099532	6850 spleen tyrosine kinase
GO protein amino acid phosphorylation	41	488	0.099532	7474 wingless-type MMTV integration site family, member 5A
GO protein amino acid phosphorylation	41	488	0.099532	81788 NUAK family, SNF1-like kinase, 2
GO protein amino acid phosphorylation	41	488	0.099532	84033 obscurin, cytoskeletal calmodulin and titin-interacting RhoGEF
GO protein amino acid phosphorylation	41	488	0.099532	9064 mitogen-activated protein kinase kinase kinase 6
GO protein amino acid phosphorylation	41	488	0.099532	91 activin A receptor, type IB
GO protein amino acid phosphorylation	41	488	0.099532	91461 protein kinase domain containing, cytoplasmic homolog (mouse)
GO protein amino acid phosphorylation	41	488	0.099532	9263 serine/threonine kinase 17a
GO protein amino acid phosphorylation	41	488	0.099532	94 activin A receptor type II-like 1
GO endoplasmic reticulum	70	880	0.1021424	10162 lysophosphatidylcholine acyltransferase 3
GO endoplasmic reticulum	70	880	0.1021424	10170 dehydrogenase/reductase (SDR family) member 9
GO endoplasmic reticulum	70	880	0.1021424	10282 blocked early in transport 1 homolog ( <i>S. cerevisiae</i> )
GO endoplasmic reticulum	70	880	0.1021424	10317 UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 5
GO endoplasmic reticulum	70	880	0.1021424	10439 olfactomedin 1
GO endoplasmic reticulum	70	880	0.1021424	10826 chromosome 5 open reading frame 4
GO endoplasmic reticulum	70	880	0.1021424	11322 transmembrane channel-like 6
GO endoplasmic reticulum	70	880	0.1021424	116844 leucine-rich alpha-2-glycoprotein 1
GO endoplasmic reticulum	70	880	0.1021424	118429 anthrax toxin receptor 2
GO endoplasmic reticulum	70	880	0.1021424	121506 endoplasmic reticulum protein 27
GO endoplasmic reticulum	70	880	0.1021424	123 perilipin 2
GO endoplasmic reticulum	70	880	0.1021424	123099 degenerative spermatocyte homolog 2, lipid desaturase ( <i>Drosophila</i> )
GO endoplasmic reticulum	70	880	0.1021424	130367 sphingosine-1-phosphate phosphatase 2
GO endoplasmic reticulum	70	880	0.1021424	147138 transmembrane channel-like 8
GO endoplasmic reticulum	70	880	0.1021424	1558 cytochrome P450, family 2, subfamily C, polypeptide 8
GO endoplasmic reticulum	70	880	0.1021424	1559 cytochrome P450, family 2, subfamily C, polypeptide 9
GO endoplasmic reticulum	70	880	0.1021424	1571 cytochrome P450, family 2, subfamily E, polypeptide 1
GO endoplasmic reticulum	70	880	0.1021424	157506 retinol dehydrogenase 10 (all-trans)
GO endoplasmic reticulum	70	880	0.1021424	1577 cytochrome P450, family 3, subfamily A, polypeptide 5
GO endoplasmic reticulum	70	880	0.1021424	163590 torsin A interacting protein 2
GO endoplasmic reticulum	70	880	0.1021424	165679 chromosome 3 open reading frame 57

GO	endoplasmic reticulum	70	880	0.1021424	1803 dipeptidyl-peptidase 4
GO	endoplasmic reticulum	70	880	0.1021424	195814 short chain dehydrogenase/reductase family 16C, member 5
GO	endoplasmic reticulum	70	880	0.1021424	2055 ceroid-lipofuscinosis, neuronal 8 (epilepsy, progressive with mental ret
GO	endoplasmic reticulum	70	880	0.1021424	2182 acyl-CoA synthetase long-chain family member 4
GO	endoplasmic reticulum	70	880	0.1021424	22901 arylsulfatase G
GO	endoplasmic reticulum	70	880	0.1021424	256987 serine incorporator 5
GO	endoplasmic reticulum	70	880	0.1021424	25825 beta-site APP-cleaving enzyme 2
GO	endoplasmic reticulum	70	880	0.1021424	25956 SEC31 homolog B ( <i>S. cerevisiae</i> )
GO	endoplasmic reticulum	70	880	0.1021424	2861 G protein-coupled receptor 37 (endothelin receptor type B-like)
GO	endoplasmic reticulum	70	880	0.1021424	3601 interleukin 15 receptor, alpha
GO	endoplasmic reticulum	70	880	0.1021424	375056 melanoma inhibitory activity family, member 3
GO	endoplasmic reticulum	70	880	0.1021424	387923 stress-associated endoplasmic reticulum protein family member 2
GO	endoplasmic reticulum	70	880	0.1021424	3913 laminin, beta 2 (laminin S)
GO	endoplasmic reticulum	70	880	0.1021424	4056 leukotriene C4 synthase
GO	endoplasmic reticulum	70	880	0.1021424	405753 dual oxidase maturation factor 2
GO	endoplasmic reticulum	70	880	0.1021424	407738 family with sequence similarity 19 (chemokine (C-C motif)-like), membr
GO	endoplasmic reticulum	70	880	0.1021424	412 steroid sulfatase (microsomal), isozyme S
GO	endoplasmic reticulum	70	880	0.1021424	4121 mannosidase, alpha, class 1A, member 1
GO	endoplasmic reticulum	70	880	0.1021424	4306 nuclear receptor subfamily 3, group C, member 2
GO	endoplasmic reticulum	70	880	0.1021424	48 aconitase 1, soluble
GO	endoplasmic reticulum	70	880	0.1021424	4939 2'-5'-oligoadenylate synthetase 2, 69/71kDa
GO	endoplasmic reticulum	70	880	0.1021424	5046 proprotein convertase subtilisin/kexin type 6
GO	endoplasmic reticulum	70	880	0.1021424	5071 Parkinson disease (autosomal recessive, juvenile) 2, parkin
GO	endoplasmic reticulum	70	880	0.1021424	5152 phosphodiesterase 9A
GO	endoplasmic reticulum	70	880	0.1021424	51703 acyl-CoA synthetase long-chain family member 5
GO	endoplasmic reticulum	70	880	0.1021424	51754 transmembrane protein 8B
GO	endoplasmic reticulum	70	880	0.1021424	5351 procollagen-lysine 1, 2-oxoglutarate 5-dioxygenase 1
GO	endoplasmic reticulum	70	880	0.1021424	54463 family with sequence similarity 134, member B
GO	endoplasmic reticulum	70	880	0.1021424	54681 prolyl 4-hydroxylase, transmembrane (endoplasmic reticulum)
GO	endoplasmic reticulum	70	880	0.1021424	54894 ring finger protein 43
GO	endoplasmic reticulum	70	880	0.1021424	54947 lysophosphatidylcholine acyltransferase 2
GO	endoplasmic reticulum	70	880	0.1021424	55080 TAP binding protein-like
GO	endoplasmic reticulum	70	880	0.1021424	55304 serine palmitoyltransferase, long chain base subunit 3
GO	endoplasmic reticulum	70	880	0.1021424	56605 ERO1-like beta ( <i>S. cerevisiae</i> )
GO	endoplasmic reticulum	70	880	0.1021424	5742 prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase a
GO	endoplasmic reticulum	70	880	0.1021424	57620 stromal interaction molecule 2

GO	endoplasmic reticulum	70	880	0.1021424	6238 ribosome binding protein 1 homolog 180kDa (dog)
GO	endoplasmic reticulum	70	880	0.1021424	6446 serum/glucocorticoid regulated kinase 1
GO	endoplasmic reticulum	70	880	0.1021424	64699 transmembrane protease, serine 3
GO	endoplasmic reticulum	70	880	0.1021424	7098 toll-like receptor 3
GO	endoplasmic reticulum	70	880	0.1021424	7869 sema domain, immunoglobulin domain (Ig), short basic domain, secret
GO	endoplasmic reticulum	70	880	0.1021424	79152 fatty acid 2-hydroxylase
GO	endoplasmic reticulum	70	880	0.1021424	79956 endoplasmic reticulum metalloproteinase 1
GO	endoplasmic reticulum	70	880	0.1021424	819 calcium modulating ligand
GO	endoplasmic reticulum	70	880	0.1021424	84879 major facilitator superfamily domain containing 2A
GO	endoplasmic reticulum	70	880	0.1021424	89866 SEC16 homolog B ( <i>S. cerevisiae</i> )
GO	endoplasmic reticulum	70	880	0.1021424	90993 cAMP responsive element binding protein 3-like 1
GO	endoplasmic reticulum	70	880	0.1021424	9563 hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase)
GO	endoplasmic reticulum	70	880	0.1021424	9619 ATP-binding cassette, sub-family G (WHITE), member 1
GO	heparin binding	11	105	0.1032557	1839 heparin-binding EGF-like growth factor
GO	heparin binding	11	105	0.1032557	2263 fibroblast growth factor receptor 2
GO	heparin binding	11	105	0.1032557	3491 cysteine-rich, angiogenic inducer, 61
GO	heparin binding	11	105	0.1032557	3827 kininogen 1
GO	heparin binding	11	105	0.1032557	5046 proprotein convertase subtilisin/kexin type 6
GO	heparin binding	11	105	0.1032557	6372 chemokine (C-X-C motif) ligand 6 (granulocyte chemotactic protein 2)
GO	heparin binding	11	105	0.1032557	6402 selectin L
GO	heparin binding	11	105	0.1032557	652 bone morphogenetic protein 4
GO	heparin binding	11	105	0.1032557	7049 transforming growth factor, beta receptor III
GO	heparin binding	11	105	0.1032557	8646 chordin
GO	heparin binding	11	105	0.1032557	9510 ADAM metalloproteinase with thrombospondin type 1 motif, 1
GO	response to ethanol	8	70	0.1039122	1508 cathepsin B
GO	response to ethanol	8	70	0.1039122	1571 cytochrome P450, family 2, subfamily E, polypeptide 1
GO	response to ethanol	8	70	0.1039122	2033 E1A binding protein p300
GO	response to ethanol	8	70	0.1039122	3570 interleukin 6 receptor
GO	response to ethanol	8	70	0.1039122	3643 insulin receptor
GO	response to ethanol	8	70	0.1039122	4129 monoamine oxidase B
GO	response to ethanol	8	70	0.1039122	5950 retinol binding protein 4, plasma
GO	response to ethanol	8	70	0.1039122	7099 toll-like receptor 4
GO	oxygen binding	5	37	0.1053072	1558 cytochrome P450, family 2, subfamily C, polypeptide 8
GO	oxygen binding	5	37	0.1053072	1559 cytochrome P450, family 2, subfamily C, polypeptide 9
GO	oxygen binding	5	37	0.1053072	1571 cytochrome P450, family 2, subfamily E, polypeptide 1
GO	oxygen binding	5	37	0.1053072	1577 cytochrome P450, family 3, subfamily A, polypeptide 5

GO oxygen binding	5	37	0.1053072	4151 myoglobin
GO positive regulation of pathway-restric	3	17	0.1057881	11030 RNA binding protein with multiple splicing
GO positive regulation of pathway-restric	3	17	0.1057881	652 bone morphogenetic protein 4
GO positive regulation of pathway-restric	3	17	0.1057881	91 activin A receptor, type IB
GO aspartic-type endopeptidase activity	3	17	0.1057881	121665 signal peptide peptidase 3
GO aspartic-type endopeptidase activity	3	17	0.1057881	25825 beta-site APP-cleaving enzyme 2
GO aspartic-type endopeptidase activity	3	17	0.1057881	5972 renin
GO sphingolipid metabolic process	3	17	0.1057881	166929 sphingomyelin synthase 2
GO sphingolipid metabolic process	3	17	0.1057881	6489 ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 1
GO sphingolipid metabolic process	3	17	0.1057881	79152 fatty acid 2-hydroxylase
GO social behavior	3	17	0.1057881	1815 dopamine receptor D4
GO social behavior	3	17	0.1057881	2055 ceroid-lipofuscinosis, neuronal 8 (epilepsy, progressive with mental ret
GO social behavior	3	17	0.1057881	3845 v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog
GO actin filament capping	3	17	0.1057881	2039 erythrocyte membrane protein band 4.9 (dematin)
GO actin filament capping	3	17	0.1057881	6710 spectrin, beta, erythrocytic
GO actin filament capping	3	17	0.1057881	85477 scinderin
GO negative regulation of osteoblast diff	3	17	0.1057881	4851 Notch homolog 1, translocation-associated (Drosophila)
GO negative regulation of osteoblast diff	3	17	0.1057881	8313 axin 2
GO negative regulation of osteoblast diff	3	17	0.1057881	8646 chordin
GO transcription corepressor activity	14	142	0.106427	10346 tripartite motif-containing 22
GO transcription corepressor activity	14	142	0.106427	1822 atrophin 1
GO transcription corepressor activity	14	142	0.106427	28996 homeodomain interacting protein kinase 2
GO transcription corepressor activity	14	142	0.106427	3400 inhibitor of DNA binding 4, dominant negative helix-loop-helix protein
GO transcription corepressor activity	14	142	0.106427	3726 jun B proto-oncogene
GO transcription corepressor activity	14	142	0.106427	4204 methyl CpG binding protein 2 (Rett syndrome)
GO transcription corepressor activity	14	142	0.106427	4212 Meis homeobox 2
GO transcription corepressor activity	14	142	0.106427	467 activating transcription factor 3
GO transcription corepressor activity	14	142	0.106427	4783 nuclear factor, interleukin 3 regulated
GO transcription corepressor activity	14	142	0.106427	7026 nuclear receptor subfamily 2, group F, member 2
GO transcription corepressor activity	14	142	0.106427	8531 cold shock domain protein A
GO transcription corepressor activity	14	142	0.106427	9572 nuclear receptor subfamily 1, group D, member 1
GO transcription corepressor activity	14	142	0.106427	9734 histone deacetylase 9
GO transcription corepressor activity	14	142	0.106427	9971 nuclear receptor subfamily 1, group H, member 4
GO negative regulation of signal transduc	6	48	0.1071947	115265 DNA-damage-inducible transcript 4-like
GO negative regulation of signal transduc	6	48	0.1071947	1154 cytokine inducible SH2-containing protein
GO negative regulation of signal transduc	6	48	0.1071947	3486 insulin-like growth factor binding protein 3



GO	negative regulation of signal transduc	6	48	0.1071947	6004 regulator of G-protein signaling 16
GO	negative regulation of signal transduc	6	48	0.1071947	8786 regulator of G-protein signaling 11
GO	negative regulation of signal transduc	6	48	0.1071947	9021 suppressor of cytokine signaling 3
GO	adherens junction	4	27	0.109039	143098 membrane protein, palmitoylated 7 (MAGUK p55 subfamily member 7)
GO	adherens junction	4	27	0.109039	5318 plakophilin 2
GO	adherens junction	4	27	0.109039	57619 shroom family member 3
GO	adherens junction	4	27	0.109039	9414 tight junction protein 2 (zona occludens 2)
GO	endocytic vesicle	4	27	0.109039	1803 dipeptidyl-peptidase 4
GO	endocytic vesicle	4	27	0.109039	1902 lysophosphatidic acid receptor 1
GO	endocytic vesicle	4	27	0.109039	338557 G protein-coupled receptor 120
GO	endocytic vesicle	4	27	0.109039	9788 metastasis suppressor 1
GO	positive regulation of fibroblast prolif	4	27	0.109039	183 angiotensinogen (serpin peptidase inhibitor, clade A, member 8)
GO	positive regulation of fibroblast prolif	4	27	0.109039	3479 insulin-like growth factor 1 (somatomedin C)
GO	positive regulation of fibroblast prolif	4	27	0.109039	358 aquaporin 1 (Colton blood group)
GO	positive regulation of fibroblast prolif	4	27	0.109039	7474 wingless-type MMTV integration site family, member 5A
GO	SH2 domain binding	4	27	0.109039	3643 insulin receptor
GO	SH2 domain binding	4	27	0.109039	55824 phosphoprotein associated with glycosphingolipid microdomains 1
GO	SH2 domain binding	4	27	0.109039	8631 src kinase associated phosphoprotein 1
GO	SH2 domain binding	4	27	0.109039	9143 synaptogyrin 3
GO	transmembrane receptor protein tyrosi	8	71	0.1105047	2044 EPH receptor A5
GO	transmembrane receptor protein tyrosi	8	71	0.1105047	2066 v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian)
GO	transmembrane receptor protein tyrosi	8	71	0.1105047	3815 v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog
GO	transmembrane receptor protein tyrosi	8	71	0.1105047	4486 macrophage stimulating 1 receptor (c-met-related tyrosine kinase)
GO	transmembrane receptor protein tyrosi	8	71	0.1105047	4915 neurotrophic tyrosine kinase, receptor, type 2
GO	transmembrane receptor protein tyrosi	8	71	0.1105047	55816 docking protein 5
GO	transmembrane receptor protein tyrosi	8	71	0.1105047	9019 myelin protein zero-like 1
GO	transmembrane receptor protein tyrosi	8	71	0.1105047	9788 metastasis suppressor 1
GO	GTPase activator activity	15	156	0.1137977	10156 RAS p21 protein activator 4
GO	GTPase activator activity	15	156	0.1137977	1124 chimerin (chimaerin) 2
GO	GTPase activator activity	15	156	0.1137977	126432 Ras and Rab interactor-like
GO	GTPase activator activity	15	156	0.1137977	23092 Rho GTPase activating protein 26
GO	GTPase activator activity	15	156	0.1137977	23365 Rho guanine nucleotide exchange factor (GEF) 12
GO	GTPase activator activity	15	156	0.1137977	259173 ALS2 C-terminal like
GO	GTPase activator activity	15	156	0.1137977	395 Rho GTPase activating protein 6
GO	GTPase activator activity	15	156	0.1137977	55200 pleckstrin homology domain containing, family G (with RhoGef domain
GO	GTPase activator activity	15	156	0.1137977	55357 TBC1 domain family, member 2

GO	GTPase activator activity	15	156	0.1137977	57186 Ral GTPase activating protein, alpha subunit 2 (catalytic)
GO	GTPase activator activity	15	156	0.1137977	57636 Rho GTPase activating protein 23
GO	GTPase activator activity	15	156	0.1137977	6004 regulator of G-protein signaling 16
GO	GTPase activator activity	15	156	0.1137977	6494 signal-induced proliferation-associated 1
GO	GTPase activator activity	15	156	0.1137977	8786 regulator of G-protein signaling 11
GO	GTPase activator activity	15	156	0.1137977	9459 Rac/Cdc42 guanine nucleotide exchange factor (GEF) 6
GO	positive regulation of angiogenesis	5	38	0.1148267	1139 cholinergic receptor, nicotinic, alpha 7
GO	positive regulation of angiogenesis	5	38	0.1148267	2624 GATA binding protein 2
GO	positive regulation of angiogenesis	5	38	0.1148267	358 aquaporin 1 (Colton blood group)
GO	positive regulation of angiogenesis	5	38	0.1148267	718 complement component 3
GO	positive regulation of angiogenesis	5	38	0.1148267	7474 wingless-type MMTV integration site family, member 5A
GO	digestion	6	49	0.1155039	10891 peroxisome proliferator-activated receptor gamma, coactivator 1 alpha
GO	digestion	6	49	0.1155039	4586 mucin 5AC, oligomeric mucus/gel-forming
GO	digestion	6	49	0.1155039	6564 solute carrier family 15 (oligopeptide transporter), member 1
GO	digestion	6	49	0.1155039	6750 somatostatin
GO	digestion	6	49	0.1155039	6751 somatostatin receptor 1
GO	digestion	6	49	0.1155039	7032 trefoil factor 2
GO	phospholipid binding	6	49	0.1155039	1373 carbamoyl-phosphate synthetase 1, mitochondrial
GO	phospholipid binding	6	49	0.1155039	5724 platelet-activating factor receptor
GO	phospholipid binding	6	49	0.1155039	6857 synaptotagmin I
GO	phospholipid binding	6	49	0.1155039	7941 phospholipase A2, group VII (platelet-activating factor acetylhydrolase,
GO	phospholipid binding	6	49	0.1155039	9619 ATP-binding cassette, sub-family G (WHITE), member 1
GO	phospholipid binding	6	49	0.1155039	9892 synaptosomal-associated protein, 91kDa homolog (mouse)
GO	tight junction	8	72	0.1173196	1364 claudin 4
GO	tight junction	8	72	0.1173196	143098 membrane protein, palmitoylated 7 (MAGUK p55 subfamily member 7)
GO	tight junction	8	72	0.1173196	154810 angiomin like 1
GO	tight junction	8	72	0.1173196	27134 tight junction protein 3 (zona occludens 3)
GO	tight junction	8	72	0.1173196	55870 ash1 (absent, small, or homeotic)-like (Drosophila)
GO	tight junction	8	72	0.1173196	56288 par-3 partitioning defective 3 homolog (C. elegans)
GO	tight junction	8	72	0.1173196	9071 claudin 10
GO	tight junction	8	72	0.1173196	9414 tight junction protein 2 (zona occludens 2)
GO	actin filament organization	4	28	0.1207066	10435 CDC42 effector protein (Rho GTPase binding) 2
GO	actin filament organization	4	28	0.1207066	27295 PDZ and LIM domain 3
GO	actin filament organization	4	28	0.1207066	395 Rho GTPase activating protein 6
GO	actin filament organization	4	28	0.1207066	55909 bridging integrator 3
GO	memory	4	28	0.1207066	11202 kallikrein-related peptidase 8

GO memory	4	28	0.1207066	1139 cholinergic receptor, nicotinic, alpha 7
GO memory	4	28	0.1207066	3678 integrin, alpha 5 (fibronectin receptor, alpha polypeptide)
GO memory	4	28	0.1207066	834 caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, co
GO positive regulation of DNA replicati	4	28	0.1207066	3479 insulin-like growth factor 1 (somatomedin C)
GO positive regulation of DNA replicati	4	28	0.1207066	3643 insulin receptor
GO positive regulation of DNA replicati	4	28	0.1207066	3725 jun oncogene
GO positive regulation of DNA replicati	4	28	0.1207066	4254 KIT ligand
GO sensory perception of pain	4	28	0.1207066	4692 necdin homolog (mouse)
GO sensory perception of pain	4	28	0.1207066	4886 neuropeptide Y receptor Y1
GO sensory perception of pain	4	28	0.1207066	5025 purinergic receptor P2X, ligand-gated ion channel, 4
GO sensory perception of pain	4	28	0.1207066	54463 family with sequence similarity 134, member B
GO beta-amyloid binding	3	18	0.1208002	1139 cholinergic receptor, nicotinic, alpha 7
GO beta-amyloid binding	3	18	0.1208002	1471 cystatin C
GO beta-amyloid binding	3	18	0.1208002	9445 integral membrane protein 2B
GO cornified envelope	3	18	0.1208002	126638 repetin
GO cornified envelope	3	18	0.1208002	6706 small proline-rich protein 2G
GO cornified envelope	3	18	0.1208002	8796 sciellin
GO integral to membrane of membrane t	3	18	0.1208002	148229 ATPase, class I, type 8B, member 3
GO integral to membrane of membrane t	3	18	0.1208002	195814 short chain dehydrogenase/reductase family 16C, member 5
GO integral to membrane of membrane t	3	18	0.1208002	412 steroid sulfatase (microsomal), isozyme S
GO establishment or maintenance of cell	3	18	0.1208002	23418 crumbs homolog 1 (Drosophila)
GO establishment or maintenance of cell	3	18	0.1208002	56288 par-3 partitioning defective 3 homolog (C. elegans)
GO establishment or maintenance of cell	3	18	0.1208002	9892 synaptosomal-associated protein, 91kDa homolog (mouse)
GO polypeptide N-acetylgalactosaminylt	3	18	0.1208002	2589 UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosami
GO polypeptide N-acetylgalactosaminylt	3	18	0.1208002	374378 UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosami
GO polypeptide N-acetylgalactosaminylt	3	18	0.1208002	79695 UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosami
GO inner ear development	3	18	0.1208002	2737 GLI family zinc finger 3
GO inner ear development	3	18	0.1208002	627 brain-derived neurotrophic factor
GO inner ear development	3	18	0.1208002	84059 G protein-coupled receptor 98
GO inward rectifier potassium channel ac	3	18	0.1208002	3759 potassium inwardly-rectifying channel, subfamily J, member 2
GO inward rectifier potassium channel ac	3	18	0.1208002	3773 potassium inwardly-rectifying channel, subfamily J, member 16
GO inward rectifier potassium channel ac	3	18	0.1208002	3775 potassium channel, subfamily K, member 1
GO cytoskeleton organization	7	61	0.1212818	152273 FYVE, RhoGEF and PH domain containing 5
GO cytoskeleton organization	7	61	0.1212818	2039 erythrocyte membrane protein band 4.9 (dematin)
GO cytoskeleton organization	7	61	0.1212818	23043 TRAF2 and NCK interacting kinase
GO cytoskeleton organization	7	61	0.1212818	3814 KiSS-1 metastasis-suppressor

GO cytoskeleton organization	7	61	0.1212818	3911 laminin, alpha 5
GO cytoskeleton organization	7	61	0.1212818	3983 actin binding LIM protein 1
GO cytoskeleton organization	7	61	0.1212818	6494 signal-induced proliferation-associated 1
GO axonogenesis	7	61	0.1212818	1813 dopamine receptor D2
GO axonogenesis	7	61	0.1212818	26050 SLIT and NTRK-like family, member 5
GO axonogenesis	7	61	0.1212818	4851 Notch homolog 1, translocation-associated (Drosophila)
GO axonogenesis	7	61	0.1212818	56288 par-3 partitioning defective 3 homolog (C. elegans)
GO axonogenesis	7	61	0.1212818	57453 Down syndrome cell adhesion molecule like 1
GO axonogenesis	7	61	0.1212818	885 cholecystokinin
GO axonogenesis	7	61	0.1212818	9892 synaptosomal-associated protein, 91kDa homolog (mouse)
GO NADPH oxidase complex	2	9	0.1220356	10811 NADPH oxidase activator 1
GO NADPH oxidase complex	2	9	0.1220356	27035 NADPH oxidase 1
GO intracellular part	2	9	0.1220356	112 adenylate cyclase 6
GO intracellular part	2	9	0.1220356	154 adrenergic, beta-2-, receptor, surface
GO negative regulation of interleukin-6 p	2	9	0.1220356	11213 interleukin-1 receptor-associated kinase 3
GO negative regulation of interleukin-6 p	2	9	0.1220356	7099 toll-like receptor 4
GO negative regulation of protein catabolism	2	9	0.1220356	11213 interleukin-1 receptor-associated kinase 3
GO negative regulation of protein catabolism	2	9	0.1220356	4194 Mdm4 p53 binding protein homolog (mouse)
GO embryonic foregut morphogenesis	2	9	0.1220356	116113 forkhead box P4
GO embryonic foregut morphogenesis	2	9	0.1220356	4087 SMAD family member 2
GO retinal binding	2	9	0.1220356	1382 cellular retinoic acid binding protein 2
GO retinal binding	2	9	0.1220356	5950 retinol binding protein 4, plasma
GO respiratory burst	2	9	0.1220356	1604 CD55 molecule, decay accelerating factor for complement (Cromer blood group)
GO respiratory burst	2	9	0.1220356	27035 NADPH oxidase 1
GO associative learning	2	9	0.1220356	1813 dopamine receptor D2
GO associative learning	2	9	0.1220356	2055 ceroid-lipofuscinosis, neuronal 8 (epilepsy, progressive with mental retardation)
GO phosphoinositide metabolic process	2	9	0.1220356	1813 dopamine receptor D2
GO phosphoinositide metabolic process	2	9	0.1220356	83394 PITPNM family member 3
GO low-density lipoprotein particle remodeling	2	9	0.1220356	183 angiotensinogen (serpin peptidase inhibitor, clade A, member 8)
GO low-density lipoprotein particle remodeling	2	9	0.1220356	9619 ATP-binding cassette, sub-family G (WHITE), member 1
GO telencephalon development	2	9	0.1220356	2066 v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian)
GO telencephalon development	2	9	0.1220356	652 bone morphogenetic protein 4
GO fucosyltransferase activity	2	9	0.1220356	2525 fucosyltransferase 3 (galactoside 3(4)-L-fucosyltransferase, Lewis blood group antigen synthase)
GO fucosyltransferase activity	2	9	0.1220356	2526 fucosyltransferase 4 (alpha (1,3) fucosyltransferase, myeloid-specific)
GO detection of calcium ion	2	9	0.1220356	27345 potassium large conductance calcium-activated channel, subfamily M, member 1
GO detection of calcium ion	2	9	0.1220356	6857 synaptotagmin I

GO	regulation of MAPKKK cascade	2	9	0.1220356	2911 glutamate receptor, metabotropic 1
GO	regulation of MAPKKK cascade	2	9	0.1220356	5972 renin
GO	phospholipase binding	2	9	0.1220356	395 Rho GTPase activating protein 6
GO	phospholipase binding	2	9	0.1220356	6622 synuclein, alpha (non A4 component of amyloid precursor)
GO	neuropeptide Y receptor activity	2	9	0.1220356	4886 neuropeptide Y receptor Y1
GO	neuropeptide Y receptor activity	2	9	0.1220356	4889 neuropeptide Y receptor Y5
GO	calcium-transporting ATPase activity	2	9	0.1220356	493 ATPase, Ca <sup>++</sup> transporting, plasma membrane 4
GO	calcium-transporting ATPase activity	2	9	0.1220356	9914 ATPase, Ca <sup>++</sup> transporting, type 2C, member 2
GO	ATP hydrolysis coupled proton transp	2	9	0.1220356	50617 ATPase, H <sup>+</sup> transporting, lysosomal V0 subunit a4
GO	ATP hydrolysis coupled proton transp	2	9	0.1220356	8992 ATPase, H <sup>+</sup> transporting, lysosomal 9kDa, V0 subunit e1
GO	GTP biosynthetic process	2	9	0.1220356	51314 thioredoxin domain containing 3 (spermatzoa)
GO	GTP biosynthetic process	2	9	0.1220356	8382 non-metastatic cells 5, protein expressed in (nucleoside-diphosphate k
GO	nucleoside diphosphate kinase activit	2	9	0.1220356	51314 thioredoxin domain containing 3 (spermatzoa)
GO	nucleoside diphosphate kinase activit	2	9	0.1220356	8382 non-metastatic cells 5, protein expressed in (nucleoside-diphosphate k
GO	UTP biosynthetic process	2	9	0.1220356	51314 thioredoxin domain containing 3 (spermatzoa)
GO	UTP biosynthetic process	2	9	0.1220356	8382 non-metastatic cells 5, protein expressed in (nucleoside-diphosphate k
GO	lipopolysaccharide binding	2	9	0.1220356	7099 toll-like receptor 4
GO	lipopolysaccharide binding	2	9	0.1220356	929 CD14 molecule
GO	M band	2	9	0.1220356	84033 obscurin, cytoskeletal calmodulin and titin-interacting RhoGEF
GO	M band	2	9	0.1220356	8736 myomesin 1, 185kDa
GO	male meiosis I	2	9	0.1220356	8900 cyclin A1
GO	male meiosis I	2	9	0.1220356	9985 REC8 homolog (yeast)
GO	RNA polymerase II transcription factc	5	39	0.1247403	2296 forkhead box C1
GO	RNA polymerase II transcription factc	5	39	0.1247403	2303 forkhead box C2 (MFH-1, mesenchyme forkhead 1)
GO	RNA polymerase II transcription factc	5	39	0.1247403	3725 jun oncogene
GO	RNA polymerase II transcription factc	5	39	0.1247403	4286 microphthalmia-associated transcription factor
GO	RNA polymerase II transcription factc	5	39	0.1247403	4784 nuclear factor I/X (CCAAT-binding transcription factor)
GO	peptidase inhibitor activity	9	85	0.1256783	1469 cystatin SN
GO	peptidase inhibitor activity	9	85	0.1256783	1471 cystatin C
GO	peptidase inhibitor activity	9	85	0.1256783	153218 serine peptidase inhibitor, Kazal type 13 (putative)
GO	peptidase inhibitor activity	9	85	0.1256783	23145 SCO-spondin homolog (Bos taurus)
GO	peptidase inhibitor activity	9	85	0.1256783	3827 kininogen 1
GO	peptidase inhibitor activity	9	85	0.1256783	404203 serine peptidase inhibitor, Kazal type 6
GO	peptidase inhibitor activity	9	85	0.1256783	6692 serine peptidase inhibitor, Kunitz type 1
GO	peptidase inhibitor activity	9	85	0.1256783	80760 inter-alpha (globulin) inhibitor H5
GO	peptidase inhibitor activity	9	85	0.1256783	89778 serpin peptidase inhibitor, clade B (ovalbumin), member 11 (gene/pse)

GO	Golgi apparatus	62	784	0.1273212	10090 uronyl-2-sulfotransferase
GO	Golgi apparatus	62	784	0.1273212	10282 blocked early in transport 1 homolog ( <i>S. cerevisiae</i> )
GO	Golgi apparatus	62	784	0.1273212	10317 UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 5
GO	Golgi apparatus	62	784	0.1273212	127845 golgi transport 1 homolog A ( <i>S. cerevisiae</i> )
GO	Golgi apparatus	62	784	0.1273212	129049 small G protein signaling modulator 1
GO	Golgi apparatus	62	784	0.1273212	152273 FYVE, RhoGEF and PH domain containing 5
GO	Golgi apparatus	62	784	0.1273212	166929 sphingomyelin synthase 2
GO	Golgi apparatus	62	784	0.1273212	1803 dipeptidyl-peptidase 4
GO	Golgi apparatus	62	784	0.1273212	192134 UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 6 (core
GO	Golgi apparatus	62	784	0.1273212	2525 fucosyltransferase 3 (galactoside 3(4)-L-fucosyltransferase, Lewis blood
GO	Golgi apparatus	62	784	0.1273212	2526 fucosyltransferase 4 (alpha (1,3) fucosyltransferase, myeloid-specific)
GO	Golgi apparatus	62	784	0.1273212	25825 beta-site APP-cleaving enzyme 2
GO	Golgi apparatus	62	784	0.1273212	2589 UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosami
GO	Golgi apparatus	62	784	0.1273212	26035 glucuronic acid epimerase
GO	Golgi apparatus	62	784	0.1273212	27090 ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalact
GO	Golgi apparatus	62	784	0.1273212	2752 glutamate-ammonia ligase (glutamine synthetase)
GO	Golgi apparatus	62	784	0.1273212	2801 golgin A2
GO	Golgi apparatus	62	784	0.1273212	3601 interleukin 15 receptor, alpha
GO	Golgi apparatus	62	784	0.1273212	374378 UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosami
GO	Golgi apparatus	62	784	0.1273212	3790 potassium voltage-gated channel, delayed-rectifier, subfamily S, memb
GO	Golgi apparatus	62	784	0.1273212	388743 calpain 8
GO	Golgi apparatus	62	784	0.1273212	412 steroid sulfatase (microsomal), isozyme S
GO	Golgi apparatus	62	784	0.1273212	4121 mannosidase, alpha, class 1A, member 1
GO	Golgi apparatus	62	784	0.1273212	4794 nuclear factor of kappa light polypeptide gene enhancer in B-cells inhib
GO	Golgi apparatus	62	784	0.1273212	48 aconitase 1, soluble
GO	Golgi apparatus	62	784	0.1273212	4851 Notch homolog 1, translocation-associated ( <i>Drosophila</i> )
GO	Golgi apparatus	62	784	0.1273212	5071 Parkinson disease (autosomal recessive, juvenile) 2, parkin
GO	Golgi apparatus	62	784	0.1273212	51272 blocked early in transport 1 homolog ( <i>S. cerevisiae</i> )-like
GO	Golgi apparatus	62	784	0.1273212	51280 golgi membrane protein 1
GO	Golgi apparatus	62	784	0.1273212	51313 family with sequence similarity 198, member B
GO	Golgi apparatus	62	784	0.1273212	5152 phosphodiesterase 9A
GO	Golgi apparatus	62	784	0.1273212	53405 chloride intracellular channel 5
GO	Golgi apparatus	62	784	0.1273212	53947 alpha 1,4-galactosyltransferase
GO	Golgi apparatus	62	784	0.1273212	54361 wingless-type MMTV integration site family, member 4
GO	Golgi apparatus	62	784	0.1273212	54463 family with sequence similarity 134, member B
GO	Golgi apparatus	62	784	0.1273212	54947 lysophosphatidylcholine acyltransferase 2

GO Golgi apparatus	62	784	0.1273212	55275 vacuolar protein sorting 53 homolog ( <i>S. cerevisiae</i> )
GO Golgi apparatus	62	784	0.1273212	55638 Golgi-localized protein
GO Golgi apparatus	62	784	0.1273212	55808 ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalact
GO Golgi apparatus	62	784	0.1273212	57134 mannosidase, alpha, class 1C, member 1
GO Golgi apparatus	62	784	0.1273212	57147 SCY1-like 3 ( <i>S. cerevisiae</i> )
GO Golgi apparatus	62	784	0.1273212	5742 prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and
GO Golgi apparatus	62	784	0.1273212	5768 quiescin Q6 sulfhydryl oxidase 1
GO Golgi apparatus	62	784	0.1273212	5801 protein tyrosine phosphatase, receptor type, R
GO Golgi apparatus	62	784	0.1273212	5873 RAB27A, member RAS oncogene family
GO Golgi apparatus	62	784	0.1273212	64083 golgi phosphoprotein 3 (coat-protein)
GO Golgi apparatus	62	784	0.1273212	646658 transmembrane protein 90A
GO Golgi apparatus	62	784	0.1273212	6484 ST3 beta-galactoside alpha-2,3-sialyltransferase 4
GO Golgi apparatus	62	784	0.1273212	6489 ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 1
GO Golgi apparatus	62	784	0.1273212	684 bone marrow stromal cell antigen 2
GO Golgi apparatus	62	784	0.1273212	79656 BEN domain containing 5
GO Golgi apparatus	62	784	0.1273212	79689 STEAP family member 4
GO Golgi apparatus	62	784	0.1273212	79695 UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosami
GO Golgi apparatus	62	784	0.1273212	79971 wntless homolog ( <i>Drosophila</i> )
GO Golgi apparatus	62	784	0.1273212	8509 N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 2
GO Golgi apparatus	62	784	0.1273212	8706 beta-1,3-N-acetylgalactosaminyltransferase 1 (globoside blood group)
GO Golgi apparatus	62	784	0.1273212	89866 SEC16 homolog B ( <i>S. cerevisiae</i> )
GO Golgi apparatus	62	784	0.1273212	91461 protein kinase domain containing, cytoplasmic homolog (mouse)
GO Golgi apparatus	62	784	0.1273212	9435 carbohydrate (N-acetylglucosamine-6-O) sulfotransferase 2
GO Golgi apparatus	62	784	0.1273212	9445 integral membrane protein 2B
GO Golgi apparatus	62	784	0.1273212	9619 ATP-binding cassette, sub-family G (WHITE), member 1
GO Golgi apparatus	62	784	0.1273212	9832 janus kinase and microtubule interacting protein 2
GO embryonic axis specification	1	2	0.1320282	10023 frequently rearranged in advanced T-cell lymphomas
GO coreceptor, soluble ligand activity	1	2	0.1320282	10268 receptor (G protein-coupled) activity modifying protein 3
GO mast cell activation	1	2	0.1320282	10397 N-myc downstream regulated 1
GO endoplasmic reticulum Sec complex	1	2	0.1320282	1080 cystic fibrosis transmembrane conductance regulator (ATP-binding cas
GO iodide transport	1	2	0.1320282	1080 cystic fibrosis transmembrane conductance regulator (ATP-binding cas
GO superoxide-generating NADPH oxidase	1	2	0.1320282	10811 NADPH oxidase activator 1
GO positive regulation of gluconeogenesis	1	2	0.1320282	10891 peroxisome proliferator-activated receptor gamma, coactivator 1 alpha
GO prenylated protein tyrosine phosphatase	1	2	0.1320282	11156 protein tyrosine phosphatase type IVA, member 3
GO negative regulation of axon regeneration	1	2	0.1320282	11202 kallikrein-related peptidase 8
GO negative regulation of protein complex assembly	1	2	0.1320282	11213 interleukin-1 receptor-associated kinase 3

GO negative regulation of toll-like recept	1	2	0.1320282	11213 interleukin-1 receptor-associated kinase 3
GO heme transport	1	2	0.1320282	113235 solute carrier family 46 (folate transporter), member 1
GO chloride channel regulator activity	1	2	0.1320282	1139 cholinergic receptor, nicotinic, alpha 7
GO acyl carnitine transporter activity	1	2	0.1320282	123096 solute carrier family 25, member 29
GO myosin II complex	1	2	0.1320282	134549 shroom family member 1
GO insulin processing	1	2	0.1320282	1363 carboxypeptidase E
GO anion homeostasis	1	2	0.1320282	1373 carbamoyl-phosphate synthetase 1, mitochondrial
GO response to oleic acid	1	2	0.1320282	1373 carbamoyl-phosphate synthetase 1, mitochondrial
GO complement receptor activity	1	2	0.1320282	1380 complement component (3d/Epstein Barr virus) receptor 2
GO macrophage colony stimulating facto	1	2	0.1320282	1435 colony stimulating factor 1 (macrophage)
GO positive regulation of odontogenesis	1	2	0.1320282	1435 colony stimulating factor 1 (macrophage)
GO heat generation	1	2	0.1320282	154 adrenergic, beta-2-, receptor, surface
GO negative regulation of smooth muscle	1	2	0.1320282	154 adrenergic, beta-2-, receptor, surface
GO positive regulation of skeletal muscle	1	2	0.1320282	154 adrenergic, beta-2-, receptor, surface
GO vasodilation by norepinephrine-epine	1	2	0.1320282	154 adrenergic, beta-2-, receptor, surface
GO (S)-limonene 6-monooxygenase activ	1	2	0.1320282	1559 cytochrome P450, family 2, subfamily C, polypeptide 9
GO (S)-limonene 7-monooxygenase activ	1	2	0.1320282	1559 cytochrome P450, family 2, subfamily C, polypeptide 9
GO 4-hydroxyacetophenone monooxyge	1	2	0.1320282	1559 cytochrome P450, family 2, subfamily C, polypeptide 9
GO monocarboxylic acid metabolic proce	1	2	0.1320282	1559 cytochrome P450, family 2, subfamily C, polypeptide 9
GO primary lung bud formation	1	2	0.1320282	157506 retinol dehydrogenase 10 (all-trans)
GO retinoic acid biosynthetic process	1	2	0.1320282	157506 retinol dehydrogenase 10 (all-trans)
GO alkaloid catabolic process	1	2	0.1320282	1577 cytochrome P450, family 3, subfamily A, polypeptide 5
GO ceramide cholinephosphotransferase	1	2	0.1320282	166929 sphingomyelin synthase 2
GO sphingomyelin synthase activity	1	2	0.1320282	166929 sphingomyelin synthase 2
GO transferrin transport	1	2	0.1320282	1785 dynamin 2
GO negative regulation of dopamine rece	1	2	0.1320282	1813 dopamine receptor D2
GO neurological system process involved	1	2	0.1320282	1813 dopamine receptor D2
GO positive regulation of sodium:hydrog	1	2	0.1320282	1815 dopamine receptor D4
GO acetyltransferase activator activity	1	2	0.1320282	183 angiotensinogen (serpin peptidase inhibitor, clade A, member 8)
GO brain renin-angiotensin system	1	2	0.1320282	183 angiotensinogen (serpin peptidase inhibitor, clade A, member 8)
GO positive regulation of NAD(P)H oxida	1	2	0.1320282	183 angiotensinogen (serpin peptidase inhibitor, clade A, member 8)
GO regulation of blood vessel size by ren	1	2	0.1320282	183 angiotensinogen (serpin peptidase inhibitor, clade A, member 8)
GO regulation of renal output by angiot	1	2	0.1320282	183 angiotensinogen (serpin peptidase inhibitor, clade A, member 8)
GO renin-angiotensin regulation of ald	1	2	0.1320282	183 angiotensinogen (serpin peptidase inhibitor, clade A, member 8)
GO smooth muscle cell proliferation	1	2	0.1320282	183 angiotensinogen (serpin peptidase inhibitor, clade A, member 8)
GO positive regulation of prostaglandin- $\epsilon$	1	2	0.1320282	1906 endothelin 1



GO	rhythmic excitation	1	2	0.1320282	1906 endothelin 1
GO	beta-1,3-galactosyl-O-glycosyl-glycop	1	2	0.1320282	192134 UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 6 (core
GO	cellular response to heparin	1	2	0.1320282	1958 early growth response 1
GO	cellular response to mycophenolic ac	1	2	0.1320282	1958 early growth response 1
GO	rhythmic behavior	1	2	0.1320282	1959 early growth response 2
GO	notochord formation	1	2	0.1320282	1969 EPH receptor A2
GO	protein-DNA complex assembly	1	2	0.1320282	2033 E1A binding protein p300
GO	cellular protein catabolic process	1	2	0.1320282	2055 ceroid-lipofuscinosis, neuronal 8 (epilepsy, progressive with mental ret
GO	glutamate uptake involved in synapti	1	2	0.1320282	2055 ceroid-lipofuscinosis, neuronal 8 (epilepsy, progressive with mental ret
GO	negative regulation of transferase acti	1	2	0.1320282	2055 ceroid-lipofuscinosis, neuronal 8 (epilepsy, progressive with mental ret
GO	response to interleukin-15	1	2	0.1320282	2182 acyl-CoA synthetase long-chain family member 4
GO	IgE receptor activity	1	2	0.1320282	2205 Fc fragment of IgE, high affinity I, receptor for; alpha polypeptide
GO	pancreatic A cell differentiation	1	2	0.1320282	222546 regulatory factor X, 6
GO	pancreatic B cell differentiation	1	2	0.1320282	222546 regulatory factor X, 6
GO	dolichol kinase activity	1	2	0.1320282	22901 arylsulfatase G
GO	lacrimal gland development	1	2	0.1320282	2296 forkhead box C1
GO	paraxial mesodermal cell fate commi	1	2	0.1320282	2303 forkhead box C2 (MFH-1, mesenchyme forkhead 1)
GO	arachidonate 5-lipoxygenase activity	1	2	0.1320282	240 arachidonate 5-lipoxygenase
GO	alpha-L-fucosidase activity	1	2	0.1320282	2517 fucosidase, alpha-L- 1, tissue
GO	negative regulation of receptor recyc	1	2	0.1320282	255738 proprotein convertase subtilisin/kexin type 9
GO	glutamate decarboxylation to succina	1	2	0.1320282	2571 glutamate decarboxylase 1 (brain, 67kDa)
GO	negative regulation of amyloid precu	1	2	0.1320282	25825 beta-site APP-cleaving enzyme 2
GO	glucagon receptor activity	1	2	0.1320282	2642 glucagon receptor
GO	forebrain neuron fate commitment	1	2	0.1320282	26468 LIM homeobox 6
GO	hydrogen peroxide metabolic proces	1	2	0.1320282	27035 NADPH oxidase 1
GO	positive regulation of integrin biosynt	1	2	0.1320282	27035 NADPH oxidase 1
GO	voltage-gated proton channel activity	1	2	0.1320282	27035 NADPH oxidase 1
GO	glycolipid metabolic process	1	2	0.1320282	27090 ST6 (alpha-N-acetyl-neuraminy-2,3-beta-galactosyl-1,3)-N-acetylgalact
GO	purine nucleotide metabolic process	1	2	0.1320282	271 adenosine monophosphate deaminase 2
GO	glutaminase activity	1	2	0.1320282	27165 glutaminase 2 (liver, mitochondrial)
GO	C5a anaphylatoxin receptor activity	1	2	0.1320282	27202 G protein-coupled receptor 77
GO	artery development	1	2	0.1320282	2737 GLI family zinc finger 3
GO	smoothened signaling pathway invol	1	2	0.1320282	2737 GLI family zinc finger 3
GO	smoothened signaling pathway invol	1	2	0.1320282	2737 GLI family zinc finger 3
GO	DNA nucleotidylexotransferase activi	1	2	0.1320282	27434 polymerase (DNA directed), mu
GO	glutamate-ammonia ligase activity	1	2	0.1320282	2752 glutamate-ammonia ligase (glutamine synthetase)

GO	glutamine biosynthetic process	1	2	0.1320282	2752	glutamate-ammonia ligase (glutamine synthetase)
GO	voluntary musculoskeletal movement	1	2	0.1320282	28996	homeodomain interacting protein kinase 2
GO	Pyrin domain binding	1	2	0.1320282	29108	PYD and CARD domain containing
GO	cytokinesis, completion of separation	1	2	0.1320282	311	annexin A11
GO	aldehyde oxidase activity	1	2	0.1320282	316	aldehyde oxidase 1
GO	xanthine dehydrogenase activity	1	2	0.1320282	316	aldehyde oxidase 1
GO	epithelial-mesenchymal signaling inv	1	2	0.1320282	3169	forkhead box A1
GO	20-alpha-hydroxysteroid dehydrogen	1	2	0.1320282	3294	hydroxysteroid (17-beta) dehydrogenase 2
GO	hyaluronan catabolic process	1	2	0.1320282	3373	hyaluronoglucosaminidase 1
GO	hormone secretion	1	2	0.1320282	338557	G protein-coupled receptor 120
GO	cilium movement	1	2	0.1320282	345895	radial spoke head 4 homolog A (Chlamydomonas)
GO	regulation of steroid hormone recept	1	2	0.1320282	3479	insulin-like growth factor 1 (somatomedin C)
GO	Type I pneumocyte differentiation	1	2	0.1320282	3479	insulin-like growth factor 1 (somatomedin C)
GO	protein tyrosine phosphatase activati	1	2	0.1320282	3486	insulin-like growth factor binding protein 3
GO	interleukin-2 binding	1	2	0.1320282	3561	interleukin 2 receptor, gamma (severe combined immunodeficiency)
GO	interleukin-4 receptor activity	1	2	0.1320282	3561	interleukin 2 receptor, gamma (severe combined immunodeficiency)
GO	interleukin-7 receptor activity	1	2	0.1320282	3561	interleukin 2 receptor, gamma (severe combined immunodeficiency)
GO	neutrophil apoptosis	1	2	0.1320282	3569	interleukin 6 (interferon, beta 2)
GO	regulation of vascular endothelial grc	1	2	0.1320282	3569	interleukin 6 (interferon, beta 2)
GO	interleukin-6 binding	1	2	0.1320282	3570	interleukin 6 receptor
GO	interleukin-6 receptor activity	1	2	0.1320282	3570	interleukin 6 receptor
GO	cellular response to copper ion	1	2	0.1320282	358	aquaporin 1 (Colton blood group)
GO	cellular response to mercury ion	1	2	0.1320282	358	aquaporin 1 (Colton blood group)
GO	cerebrospinal fluid secretion	1	2	0.1320282	358	aquaporin 1 (Colton blood group)
GO	glycerol transmembrane transporter	1	2	0.1320282	358	aquaporin 1 (Colton blood group)
GO	intracellular cGMP activated cation cl	1	2	0.1320282	358	aquaporin 1 (Colton blood group)
GO	positive regulation of saliva secretion	1	2	0.1320282	358	aquaporin 1 (Colton blood group)
GO	renal water transport	1	2	0.1320282	358	aquaporin 1 (Colton blood group)
GO	interleukin-10 receptor activity	1	2	0.1320282	3587	interleukin 10 receptor, alpha
GO	3-phosphoinositide-dependent prote	1	2	0.1320282	3643	insulin receptor
GO	positive regulation of respiratory bur	1	2	0.1320282	3643	insulin receptor
GO	ganglioside metabolic process	1	2	0.1320282	3696	integrin, beta 8
GO	cellular response to potassium ion st	1	2	0.1320282	3725	jun oncogene
GO	acetylcholine receptor regulator activ	1	2	0.1320282	375790	agrin
GO	lymphoid progenitor cell differentiati	1	2	0.1320282	3815	v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog
GO	positive regulation of transcription fr	1	2	0.1320282	387496	RAS-like, family 11, member A

GO laminin-3 complex	1	2	0.1320282	3913 laminin, beta 2 (laminin S)
GO clathrin-coated endocytic vesicle mer	1	2	0.1320282	3949 low density lipoprotein receptor
GO phospholipase activator activity	1	2	0.1320282	395 Rho GTPase activating protein 6
GO leukotriene-C4 synthase activity	1	2	0.1320282	4056 leukotriene C4 synthase
GO paraxial mesoderm morphogenesis	1	2	0.1320282	4087 SMAD family member 2
GO cellular biogenic amine metabolic pro	1	2	0.1320282	4128 monoamine oxidase A
GO negative regulation of serotonin secr	1	2	0.1320282	4129 monoamine oxidase B
GO positive regulation of dopamine metab	1	2	0.1320282	4129 monoamine oxidase B
GO response to aluminum ion	1	2	0.1320282	4129 monoamine oxidase B
GO slow-twitch skeletal muscle fiber con	1	2	0.1320282	4151 myoglobin
GO negative regulation of mast cell apop	1	2	0.1320282	4254 KIT ligand
GO positive regulation of mast cell prolif	1	2	0.1320282	4254 KIT ligand
GO cerebral cortex GABAergic interneurc	1	2	0.1320282	429 achaete-scute complex homolog 1 (Drosophila)
GO olfactory pit development	1	2	0.1320282	429 achaete-scute complex homolog 1 (Drosophila)
GO subpallium neuron fate commitment	1	2	0.1320282	429 achaete-scute complex homolog 1 (Drosophila)
GO macrophage colony stimulating facto	1	2	0.1320282	4486 macrophage stimulating 1 receptor (c-met-related tyrosine kinase)
GO Bcl3/NF-kappaB2 complex	1	2	0.1320282	4791 nuclear factor of kappa light polypeptide gene enhancer in B-cells 2 (p4
GO follicular dendritic cell differentiation	1	2	0.1320282	4791 nuclear factor of kappa light polypeptide gene enhancer in B-cells 2 (p4
GO nucleotide-binding oligomerization d	1	2	0.1320282	4792 nuclear factor of kappa light polypeptide gene enhancer in B-cells inhib
GO D-serine transport	1	2	0.1320282	4794 nuclear factor of kappa light polypeptide gene enhancer in B-cells inhib
GO aconitate hydratase activity	1	2	0.1320282	48 aconitase 1, soluble
GO iron-responsive element binding	1	2	0.1320282	48 aconitase 1, soluble
GO negative regulation of photoreceptor	1	2	0.1320282	4851 Notch homolog 1, translocation-associated (Drosophila)
GO positive regulation of transcription of	1	2	0.1320282	4851 Notch homolog 1, translocation-associated (Drosophila)
GO response to insecticide	1	2	0.1320282	4929 nuclear receptor subfamily 4, group A, member 2
GO nerve growth factor production	1	2	0.1320282	5046 proprotein convertase subtilisin/kexin type 6
GO dopamine uptake	1	2	0.1320282	5071 Parkinson disease (autosomal recessive, juvenile) 2, parkin
GO negative regulation of actin filament	1	2	0.1320282	5071 Parkinson disease (autosomal recessive, juvenile) 2, parkin
GO negative regulation of release of cyto	1	2	0.1320282	5071 Parkinson disease (autosomal recessive, juvenile) 2, parkin
GO protein K63-linked ubiquitination	1	2	0.1320282	5071 Parkinson disease (autosomal recessive, juvenile) 2, parkin
GO embryonic body morphogenesis	1	2	0.1320282	50937 Cdon homolog (mouse)
GO response to chlorate	1	2	0.1320282	5122 proprotein convertase subtilisin/kexin type 1
GO detection of light stimulus	1	2	0.1320282	5158 phosphodiesterase 6B, cGMP-specific, rod, beta
GO positive regulation of plasma membr	1	2	0.1320282	51703 acyl-CoA synthetase long-chain family member 5
GO cytoplasmic cyclin-dependent proteir	1	2	0.1320282	5218 cyclin-dependent kinase 14
GO myoblast cell fate commitment	1	2	0.1320282	5307 paired-like homeodomain 1

GO PML body organization	1	2	0.1320282	5371 promyelocytic leukemia
GO regulation of MHC class I biosynthetic	1	2	0.1320282	5371 promyelocytic leukemia
GO anatomical structure development	1	2	0.1320282	54361 wingless-type MMTV integration site family, member 4
GO embryonic epithelial tube formation	1	2	0.1320282	54361 wingless-type MMTV integration site family, member 4
GO somatotropin secreting cell differenti	1	2	0.1320282	54361 wingless-type MMTV integration site family, member 4
GO hydroxymethylglutaryl-CoA lyase acti	1	2	0.1320282	54511 3-hydroxymethyl-3-methylglutaryl-Coenzyme A lyase-like 1
GO BMP signaling pathway involved in h	1	2	0.1320282	5460 POU class 5 homeobox 1
GO cardiac cell fate determination	1	2	0.1320282	5460 POU class 5 homeobox 1
GO negative regulation of gene silencing	1	2	0.1320282	5460 POU class 5 homeobox 1
GO negative regulation of receptor biosy	1	2	0.1320282	5465 peroxisome proliferator-activated receptor alpha
GO 1-alkylglycerophosphocholine O-acet	1	2	0.1320282	54947 lysophosphatidylcholine acyltransferase 2
GO germ-line stem cell maintenance	1	2	0.1320282	55124 piwi-like 2 (Drosophila)
GO establishment of epithelial cell polari	1	2	0.1320282	56288 par-3 partitioning defective 3 homolog (C. elegans)
GO oxidoreductase activity, acting on sul	1	2	0.1320282	56605 ERO1-like beta (S. cerevisiae)
GO activation of phospholipase A2 activit	1	2	0.1320282	56923 neuromedin U receptor 2
GO neuromedin U receptor activity	1	2	0.1320282	56923 neuromedin U receptor 2
GO inositol trisphosphate biosynthetic pr	1	2	0.1320282	5724 platelet-activating factor receptor
GO prostaglandin F receptor activity	1	2	0.1320282	5737 prostaglandin F receptor (FP)
GO negative regulation of epinephrine se	1	2	0.1320282	5742 prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase a
GO negative regulation of norepinephrin	1	2	0.1320282	5742 prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase a
GO prostaglandin-endoperoxide synthas	1	2	0.1320282	5742 prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase a
GO cellular pigment accumulation	1	2	0.1320282	57619 shroom family member 3
GO myosin V binding	1	2	0.1320282	5873 RAB27A, member RAS oncogene family
GO natural killer cell degranulation	1	2	0.1320282	5873 RAB27A, member RAS oncogene family
GO embryonic retina morphogenesis in c	1	2	0.1320282	5950 retinol binding protein 4, plasma
GO female genitalia morphogenesis	1	2	0.1320282	5950 retinol binding protein 4, plasma
GO angiotensin maturation	1	2	0.1320282	5972 renin
GO negative regulation of isotype switch	1	2	0.1320282	604 B-cell CLL/lymphoma 6
GO negative regulation of mast cell cytok	1	2	0.1320282	604 B-cell CLL/lymphoma 6
GO regulation of Rho GTPase activity	1	2	0.1320282	604 B-cell CLL/lymphoma 6
GO 3-hydroxybutyrate dehydrogenase ac	1	2	0.1320282	622 3-hydroxybutyrate dehydrogenase, type 1
GO vitamin metabolic process	1	2	0.1320282	6256 retinoid X receptor, alpha
GO 3-oxoacid CoA-transferase activity	1	2	0.1320282	64064 3-oxoacid CoA transferase 2
GO ketone body catabolic process	1	2	0.1320282	64064 3-oxoacid CoA transferase 2
GO positive regulation of biosynthetic pr	1	2	0.1320282	64127 nucleotide-binding oligomerization domain containing 2
GO regulation of neutrophil chemotaxis	1	2	0.1320282	64127 nucleotide-binding oligomerization domain containing 2

GO protein-disulfide reductase activity	1	2	0.1320282	64359 nucleoredoxin
GO cardiac septum development	1	2	0.1320282	652 bone morphogenetic protein 4
GO cloacal septation	1	2	0.1320282	652 bone morphogenetic protein 4
GO positive regulation of kidney develop	1	2	0.1320282	652 bone morphogenetic protein 4
GO telencephalon regionalization	1	2	0.1320282	652 bone morphogenetic protein 4
GO urea transmembrane transporter act	1	2	0.1320282	6563 solute carrier family 14 (urea transporter), member 1 (Kidd blood group)
GO proton-dependent oligopeptide seco	1	2	0.1320282	6564 solute carrier family 15 (oligopeptide transporter), member 1
GO negative regulation of exocytosis	1	2	0.1320282	6622 synuclein, alpha (non A4 component of amyloid precursor)
GO negative regulation of platelet-derive	1	2	0.1320282	6622 synuclein, alpha (non A4 component of amyloid precursor)
GO positive regulation of inositol phosph	1	2	0.1320282	6622 synuclein, alpha (non A4 component of amyloid precursor)
GO regulation of glutamate secretion	1	2	0.1320282	6622 synuclein, alpha (non A4 component of amyloid precursor)
GO positive regulation of isotype switchi	1	2	0.1320282	6778 signal transducer and activator of transcription 6, interleukin-4 inducec
GO platelet degranulation	1	2	0.1320282	6812 syntaxin binding protein 1
GO syntaxin-2 binding	1	2	0.1320282	6812 syntaxin binding protein 1
GO lactate transmembrane transporter a	1	2	0.1320282	682 basigin (Ok blood group)
GO B cell receptor complex	1	2	0.1320282	6850 spleen tyrosine kinase
GO beta selection	1	2	0.1320282	6850 spleen tyrosine kinase
GO homeostasis of number of cells	1	2	0.1320282	7001 peroxiredoxin 2
GO negative regulation of oxygen and re	1	2	0.1320282	7001 peroxiredoxin 2
GO negative regulation of T cell different	1	2	0.1320282	7001 peroxiredoxin 2
GO regulation of transcription involved ir	1	2	0.1320282	7026 nuclear receptor subfamily 2, group F, member 2
GO response to follicle-stimulating horm	1	2	0.1320282	7049 transforming growth factor, beta receptor III
GO cell surface pattern recognition recep	1	2	0.1320282	7097 toll-like receptor 2
GO cellular response to diacylated bacter	1	2	0.1320282	7097 toll-like receptor 2
GO cellular response to triacylated bacte	1	2	0.1320282	7097 toll-like receptor 2
GO detection of diacylated bacterial lipo	1	2	0.1320282	7097 toll-like receptor 2
GO detection of triacylated bacterial lipo	1	2	0.1320282	7097 toll-like receptor 2
GO positive regulation of interleukin-18 r	1	2	0.1320282	7097 toll-like receptor 2
GO response to bacterial lipoprotein	1	2	0.1320282	7097 toll-like receptor 2
GO Toll-like receptor 1-Toll-like receptor	1	2	0.1320282	7097 toll-like receptor 2
GO response to lipoteichoic acid	1	2	0.1320282	7099 toll-like receptor 4
GO positive regulation of activation of m	1	2	0.1320282	718 complement component 3
GO cellular response to interferon-gamrr	1	2	0.1320282	7474 wingless-type MMTV integration site family, member 5A
GO hypophysis morphogenesis	1	2	0.1320282	7474 wingless-type MMTV integration site family, member 5A
GO lateral sprouting involved in mamma	1	2	0.1320282	7474 wingless-type MMTV integration site family, member 5A
GO positive regulation of response to cyt	1	2	0.1320282	7474 wingless-type MMTV integration site family, member 5A

GO myosin light chain binding	1	2	0.1320282	7852 chemokine (C-X-C motif) receptor 4
GO regulation of chemotaxis	1	2	0.1320282	7852 chemokine (C-X-C motif) receptor 4
GO Stn1-Ten1 complex	1	2	0.1320282	80169 chromosome 17 open reading frame 68
GO receptor recycling	1	2	0.1320282	819 calcium modulating ligand
GO positive regulation of circadian sleep,	1	2	0.1320282	834 caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, co
GO stereocilia ankle link complex	1	2	0.1320282	84059 G protein-coupled receptor 98
GO actin nucleation	1	2	0.1320282	85477 scinderin
GO positive regulation of secretion	1	2	0.1320282	85477 scinderin
GO two-component response regulator $\alpha$	1	2	0.1320282	8622 phosphodiesterase 8B
GO striated muscle thick filament	1	2	0.1320282	8736 myomesin 1, 185kDa
GO initial segment	1	2	0.1320282	885 cholecystokinin
GO pantothenate metabolic process	1	2	0.1320282	8875 vanin 2
GO ATPase activity, coupled to transmembrane	1	2	0.1320282	8992 ATPase, H <sup>+</sup> transporting, lysosomal 9kDa, V0 subunit e1
GO adenylylsulfate kinase activity	1	2	0.1320282	9060 3'-phosphoadenosine 5'-phosphosulfate synthase 2
GO sulfate adenylyltransferase (ATP) activity	1	2	0.1320282	9060 3'-phosphoadenosine 5'-phosphosulfate synthase 2
GO activin receptor activity	1	2	0.1320282	91 activin A receptor, type IB
GO development of primary female sex organ	1	2	0.1320282	91 activin A receptor, type IB
GO positive regulation of transporter activity	1	2	0.1320282	9143 synaptogyrin 3
GO lipoteichoic acid binding	1	2	0.1320282	929 CD14 molecule
GO nicotinamide metabolic process	1	2	0.1320282	93100 nicotinate phosphoribosyltransferase domain containing 1
GO leg morphogenesis	1	2	0.1320282	9496 T-box 4
GO 6-phosphogluconolactonase activity	1	2	0.1320282	9563 hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase)
GO glucose-6-phosphate dehydrogenase	1	2	0.1320282	9563 hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase)
GO positive regulation of cholesterol biosynthesis	1	2	0.1320282	9619 ATP-binding cassette, sub-family G (WHITE), member 1
GO toxin transporter activity	1	2	0.1320282	9619 ATP-binding cassette, sub-family G (WHITE), member 1
GO regulation of skeletal muscle fiber development	1	2	0.1320282	9734 histone deacetylase 9
GO microspike assembly	1	2	0.1320282	9788 metastasis suppressor 1
GO clathrin heavy chain binding	1	2	0.1320282	9892 synaptosomal-associated protein, 91kDa homolog (mouse)
GO positive regulation of embryonic development	1	2	0.1320282	9904 RNA binding motif protein 19
GO sensory organ development	1	2	0.1320282	9935 v-maf musculoaponeurotic fibrosarcoma oncogene homolog B (avian)
GO L-ascorbate:sodium symporter activity	1	2	0.1320282	9962 solute carrier family 23 (nucleobase transporters), member 2
GO L-ascorbic acid metabolic process	1	2	0.1320282	9962 solute carrier family 23 (nucleobase transporters), member 2
GO L-ascorbic acid transporter activity	1	2	0.1320282	9962 solute carrier family 23 (nucleobase transporters), member 2
GO L-ascorbic acid transport	1	2	0.1320282	9962 solute carrier family 23 (nucleobase transporters), member 2
GO molecular hydrogen transport	1	2	0.1320282	9962 solute carrier family 23 (nucleobase transporters), member 2
GO nucleobase transmembrane transporter activity	1	2	0.1320282	9962 solute carrier family 23 (nucleobase transporters), member 2

GO nucleobase transport	1	2	0.1320282	9962 solute carrier family 23 (nucleobase transporters), member 2
GO sodium-dependent L-ascorbate transp	1	2	0.1320282	9962 solute carrier family 23 (nucleobase transporters), member 2
GO sodium-dependent multivitamin tran	1	2	0.1320282	9962 solute carrier family 23 (nucleobase transporters), member 2
GO transepithelial L-ascorbic acid transp	1	2	0.1320282	9962 solute carrier family 23 (nucleobase transporters), member 2
GO regulation of carbohydrate metabolic	1	2	0.1320282	9971 nuclear receptor subfamily 1, group H, member 4
GO respiratory gaseous exchange	4	29	0.1328826	1080 cystic fibrosis transmembrane conductance regulator (ATP-binding cas
GO respiratory gaseous exchange	4	29	0.1328826	1906 endothelin 1
GO respiratory gaseous exchange	4	29	0.1328826	4692 necdin homolog (mouse)
GO respiratory gaseous exchange	4	29	0.1328826	9935 v-maf musculoaponeurotic fibrosarcoma oncogene homolog B (avian)
GO positive regulation of ERK1 and ERK2	4	29	0.1328826	168667 BMP binding endothelial regulator
GO positive regulation of ERK1 and ERK2	4	29	0.1328826	64127 nucleotide-binding oligomerization domain containing 2
GO positive regulation of ERK1 and ERK2	4	29	0.1328826	652 bone morphogenetic protein 4
GO positive regulation of ERK1 and ERK2	4	29	0.1328826	7099 toll-like receptor 4
GO negative regulation of neuron apoptc	6	51	0.1330528	183 angiotensinogen (serpin peptidase inhibitor, clade A, member 8)
GO negative regulation of neuron apoptc	6	51	0.1330528	28996 homeodomain interacting protein kinase 2
GO negative regulation of neuron apoptc	6	51	0.1330528	3845 v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog
GO negative regulation of neuron apoptc	6	51	0.1330528	4929 nuclear receptor subfamily 4, group A, member 2
GO negative regulation of neuron apoptc	6	51	0.1330528	627 brain-derived neurotrophic factor
GO negative regulation of neuron apoptc	6	51	0.1330528	6622 synuclein, alpha (non A4 component of amyloid precursor)
GO male gonad development	5	40	0.1350332	54361 wingless-type MMTV integration site family, member 4
GO male gonad development	5	40	0.1350332	5950 retinol binding protein 4, plasma
GO male gonad development	5	40	0.1350332	5972 renin
GO male gonad development	5	40	0.1350332	7474 wingless-type MMTV integration site family, member 5A
GO male gonad development	5	40	0.1350332	8531 cold shock domain protein A
GO regulation of signal transduction	3	19	0.1365361	10252 sprouty homolog 1, antagonist of FGF signaling (Drosophila)
GO regulation of signal transduction	3	19	0.1365361	10253 sprouty homolog 2 (Drosophila)
GO regulation of signal transduction	3	19	0.1365361	154043 CNKSR family member 3
GO lipid particle	3	19	0.1365361	123 perilipin 2
GO lipid particle	3	19	0.1365361	5346 perilipin 1
GO lipid particle	3	19	0.1365361	57104 patatin-like phospholipase domain containing 2
GO protein amino acid O-linked glycosyla	3	19	0.1365361	22906 trafficking protein, kinesin binding 1
GO protein amino acid O-linked glycosyla	3	19	0.1365361	2589 UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosami
GO protein amino acid O-linked glycosyla	3	19	0.1365361	3949 low density lipoprotein receptor
GO negative regulation of cell differentia	3	19	0.1365361	2737 GLI family zinc finger 3
GO negative regulation of cell differentia	3	19	0.1365361	54361 wingless-type MMTV integration site family, member 4
GO negative regulation of cell differentia	3	19	0.1365361	604 B-cell CLL/lymphoma 6

GO spleen development	3	19	0.1365361	28982 feline leukemia virus subgroup C cellular receptor 1
GO spleen development	3	19	0.1365361	3175 one cut homeobox 1
GO spleen development	3	19	0.1365361	4791 nuclear factor of kappa light polypeptide gene enhancer in B-cells 2 (p4
GO protein heterodimerization activity	18	199	0.1365571	11213 interleukin-1 receptor-associated kinase 3
GO protein heterodimerization activity	18	199	0.1365571	116113 forkhead box P4
GO protein heterodimerization activity	18	199	0.1365571	127343 diencephalon/mesencephalon homeobox 1
GO protein heterodimerization activity	18	199	0.1365571	2026 enolase 2 (gamma, neuronal)
GO protein heterodimerization activity	18	199	0.1365571	22807 IKAROS family zinc finger 2 (Helios)
GO protein heterodimerization activity	18	199	0.1365571	2353 FBJ murine osteosarcoma viral oncogene homolog
GO protein heterodimerization activity	18	199	0.1365571	3164 nuclear receptor subfamily 4, group A, member 1
GO protein heterodimerization activity	18	199	0.1365571	3725 jun oncogene
GO protein heterodimerization activity	18	199	0.1365571	4056 leukotriene C4 synthase
GO protein heterodimerization activity	18	199	0.1365571	4170 myeloid cell leukemia sequence 1 (BCL2-related)
GO protein heterodimerization activity	18	199	0.1365571	4929 nuclear receptor subfamily 4, group A, member 2
GO protein heterodimerization activity	18	199	0.1365571	5025 purinergic receptor P2X, ligand-gated ion channel, 4
GO protein heterodimerization activity	18	199	0.1365571	51085 MLX interacting protein-like
GO protein heterodimerization activity	18	199	0.1365571	5371 promyelocytic leukemia
GO protein heterodimerization activity	18	199	0.1365571	57186 Ral GTPase activating protein, alpha subunit 2 (catalytic)
GO protein heterodimerization activity	18	199	0.1365571	7097 toll-like receptor 2
GO protein heterodimerization activity	18	199	0.1365571	8527 diacylglycerol kinase, delta 130kDa
GO protein heterodimerization activity	18	199	0.1365571	9619 ATP-binding cassette, sub-family G (WHITE), member 1
GO defense response	7	63	0.1372825	1471 cystatin C
GO defense response	7	63	0.1372825	3783 potassium intermediate/small conductance calcium-activated channel,
GO defense response	7	63	0.1372825	4486 macrophage stimulating 1 receptor (c-met-related tyrosine kinase)
GO defense response	7	63	0.1372825	4599 myxovirus (influenza virus) resistance 1, interferon-inducible protein p:
GO defense response	7	63	0.1372825	4600 myxovirus (influenza virus) resistance 2 (mouse)
GO defense response	7	63	0.1372825	64127 nucleotide-binding oligomerization domain containing 2
GO defense response	7	63	0.1372825	819 calcium modulating ligand
GO cell surface receptor linked signaling	15	161	0.1375077	10288 leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM
GO cell surface receptor linked signaling	15	161	0.1375077	154 adrenergic, beta-2-, receptor, surface
GO cell surface receptor linked signaling	15	161	0.1375077	1906 endothelin 1
GO cell surface receptor linked signaling	15	161	0.1375077	2205 Fc fragment of IgE, high affinity I, receptor for; alpha polypeptide
GO cell surface receptor linked signaling	15	161	0.1375077	23529 cardiotrophin-like cytokine factor 1
GO cell surface receptor linked signaling	15	161	0.1375077	29126 CD274 molecule
GO cell surface receptor linked signaling	15	161	0.1375077	4684 neural cell adhesion molecule 1
GO cell surface receptor linked signaling	15	161	0.1375077	5362 plexin A2



GO	cell surface receptor linked signaling	15	161	0.1375077	573 BCL2-associated athanogene
GO	cell surface receptor linked signaling	15	161	0.1375077	6750 somatostatin
GO	cell surface receptor linked signaling	15	161	0.1375077	6751 somatostatin receptor 1
GO	cell surface receptor linked signaling	15	161	0.1375077	682 basigin (Ok blood group)
GO	cell surface receptor linked signaling	15	161	0.1375077	7133 tumor necrosis factor receptor superfamily, member 1B
GO	cell surface receptor linked signaling	15	161	0.1375077	8519 interferon induced transmembrane protein 1 (9-27)
GO	cell surface receptor linked signaling	15	161	0.1375077	929 CD14 molecule
GO	actin binding	24	278	0.141386	11078 TRIO and F-actin binding protein
GO	actin binding	24	278	0.141386	2039 erythrocyte membrane protein band 4.9 (dematin)
GO	actin binding	24	278	0.141386	22998 LIM and calponin homology domains 1
GO	actin binding	24	278	0.141386	23500 dishevelled associated activator of morphogenesis 2
GO	actin binding	24	278	0.141386	2638 group-specific component (vitamin D binding protein)
GO	actin binding	24	278	0.141386	3983 actin binding LIM protein 1
GO	actin binding	24	278	0.141386	4638 myosin light chain kinase
GO	actin binding	24	278	0.141386	4645 myosin VB
GO	actin binding	24	278	0.141386	51168 myosin XVA
GO	actin binding	24	278	0.141386	5304 prolactin-induced protein
GO	actin binding	24	278	0.141386	53827 FXFD domain containing ion transport regulator 5
GO	actin binding	24	278	0.141386	55740 enabled homolog (Drosophila)
GO	actin binding	24	278	0.141386	57619 shroom family member 3
GO	actin binding	24	278	0.141386	6521 solute carrier family 4, anion exchanger, member 1 (erythrocyte memb
GO	actin binding	24	278	0.141386	6710 spectrin, beta, erythrocytic
GO	actin binding	24	278	0.141386	7111 tropomodulin 1
GO	actin binding	24	278	0.141386	7170 tropomyosin 3
GO	actin binding	24	278	0.141386	7464 coronin, actin binding protein, 2A
GO	actin binding	24	278	0.141386	7852 chemokine (C-X-C motif) receptor 4
GO	actin binding	24	278	0.141386	79789 calmin (calponin-like, transmembrane)
GO	actin binding	24	278	0.141386	85462 FH2 domain containing 1
GO	actin binding	24	278	0.141386	85477 scinderin
GO	actin binding	24	278	0.141386	9087 thymosin beta 4, Y-linked
GO	actin binding	24	278	0.141386	9749 phosphatase and actin regulator 2
GO	monooxygenase activity	6	52	0.1422747	1558 cytochrome P450, family 2, subfamily C, polypeptide 8
GO	monooxygenase activity	6	52	0.1422747	1559 cytochrome P450, family 2, subfamily C, polypeptide 9
GO	monooxygenase activity	6	52	0.1422747	1571 cytochrome P450, family 2, subfamily E, polypeptide 1
GO	monooxygenase activity	6	52	0.1422747	1577 cytochrome P450, family 3, subfamily A, polypeptide 5
GO	monooxygenase activity	6	52	0.1422747	5066 peptidylglycine alpha-amidating monooxygenase

GO	monooxygenase activity	6	52	0.1422747	6916 thromboxane A synthase 1 (platelet)
GO	central nervous system development	10	100	0.1450876	10231 regulator of calcineurin 2
GO	central nervous system development	10	100	0.1450876	127343 diencephalon/mesencephalon homeobox 1
GO	central nervous system development	10	100	0.1450876	1821 dystrophin related protein 2
GO	central nervous system development	10	100	0.1450876	1822 atrophin 1
GO	central nervous system development	10	100	0.1450876	4692 necdin homolog (mouse)
GO	central nervous system development	10	100	0.1450876	5071 Parkinson disease (autosomal recessive, juvenile) 2, parkin
GO	central nervous system development	10	100	0.1450876	56923 neuromedin U receptor 2
GO	central nervous system development	10	100	0.1450876	57453 Down syndrome cell adhesion molecule like 1
GO	central nervous system development	10	100	0.1450876	8646 chordin
GO	central nervous system development	10	100	0.1450876	91 activin A receptor, type IB
GO	one-carbon metabolic process	4	30	0.1455367	11238 carbonic anhydrase VB, mitochondrial
GO	one-carbon metabolic process	4	30	0.1455367	23382 adenosylhomocysteinase-like 2
GO	one-carbon metabolic process	4	30	0.1455367	760 carbonic anhydrase II
GO	one-carbon metabolic process	4	30	0.1455367	771 carbonic anhydrase XII
GO	response to organic nitrogen	4	30	0.1455367	1571 cytochrome P450, family 2, subfamily E, polypeptide 1
GO	response to organic nitrogen	4	30	0.1455367	205 adenylate kinase 3-like 1
GO	response to organic nitrogen	4	30	0.1455367	5742 prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase a)
GO	response to organic nitrogen	4	30	0.1455367	6750 somatostatin
GO	insulin receptor binding	4	30	0.1455367	3479 insulin-like growth factor 1 (somatomedin C)
GO	insulin receptor binding	4	30	0.1455367	5295 phosphoinositide-3-kinase, regulatory subunit 1 (alpha)
GO	insulin receptor binding	4	30	0.1455367	55816 docking protein 5
GO	insulin receptor binding	4	30	0.1455367	8660 insulin receptor substrate 2
GO	negative regulation of protein kinase	5	41	0.1456895	10221 tribbles homolog 1 (Drosophila)
GO	negative regulation of protein kinase	5	41	0.1456895	10912 growth arrest and DNA-damage-inducible, gamma
GO	negative regulation of protein kinase	5	41	0.1456895	28951 tribbles homolog 2 (Drosophila)
GO	negative regulation of protein kinase	5	41	0.1456895	4616 growth arrest and DNA-damage-inducible, beta
GO	negative regulation of protein kinase	5	41	0.1456895	64798 DEP domain containing 6
GO	cholesterol homeostasis	5	41	0.1456895	255738 proprotein convertase subtilisin/kexin type 9
GO	cholesterol homeostasis	5	41	0.1456895	26119 low density lipoprotein receptor adaptor protein 1
GO	cholesterol homeostasis	5	41	0.1456895	29116 myosin regulatory light chain interacting protein
GO	cholesterol homeostasis	5	41	0.1456895	3949 low density lipoprotein receptor
GO	cholesterol homeostasis	5	41	0.1456895	9619 ATP-binding cassette, sub-family G (WHITE), member 1
GO	death receptor binding	2	10	0.145899	10116 fem-1 homolog b (C. elegans)
GO	death receptor binding	2	10	0.145899	9966 tumor necrosis factor (ligand) superfamily, member 15
GO	negative regulation of ossification	2	10	0.145899	154 adrenergic, beta-2-, receptor, surface

GO	negative regulation of ossification	2	10	0.145899	799 calcitonin receptor
GO	phagocytic vesicle membrane	2	10	0.145899	1755 deleted in malignant brain tumors 1
GO	phagocytic vesicle membrane	2	10	0.145899	80223 RAB11 family interacting protein 1 (class I)
GO	receptor internalization	2	10	0.145899	1785 dynamin 2
GO	receptor internalization	2	10	0.145899	6622 synuclein, alpha (non A4 component of amyloid precursor)
GO	elevation of cytosolic calcium ion con	2	10	0.145899	1813 dopamine receptor D2
GO	elevation of cytosolic calcium ion con	2	10	0.145899	1906 endothelin 1
GO	cytoplasmic part	2	10	0.145899	183 angiotensinogen (serpin peptidase inhibitor, clade A, member 8)
GO	cytoplasmic part	2	10	0.145899	5972 renin
GO	negative regulation of blood coagulat	2	10	0.145899	1906 endothelin 1
GO	negative regulation of blood coagulat	2	10	0.145899	3827 kininogen 1
GO	negative regulation of hormone secre	2	10	0.145899	1906 endothelin 1
GO	negative regulation of hormone secre	2	10	0.145899	4886 neuropeptide Y receptor Y1
GO	heparan sulfate proteoglycan binding	2	10	0.145899	2239 glypican 4
GO	heparan sulfate proteoglycan binding	2	10	0.145899	2262 glypican 5
GO	vascular endothelial growth factor re	2	10	0.145899	2296 forkhead box C1
GO	vascular endothelial growth factor re	2	10	0.145899	2303 forkhead box C2 (MFH-1, mesenchyme forkhead 1)
GO	regulation of exocytosis	2	10	0.145899	25837 RAB26, member RAS oncogene family
GO	regulation of exocytosis	2	10	0.145899	6857 synaptotagmin I
GO	phosphotyrosine binding	2	10	0.145899	26119 low density lipoprotein receptor adaptor protein 1
GO	phosphotyrosine binding	2	10	0.145899	5774 protein tyrosine phosphatase, non-receptor type 3
GO	limb morphogenesis	2	10	0.145899	2737 GLI family zinc finger 3
GO	limb morphogenesis	2	10	0.145899	28982 feline leukemia virus subgroup C cellular receptor 1
GO	positive regulation of glycogen biosyr	2	10	0.145899	3643 insulin receptor
GO	positive regulation of glycogen biosyr	2	10	0.145899	8660 insulin receptor substrate 2
GO	lipoprotein binding	2	10	0.145899	3949 low density lipoprotein receptor
GO	lipoprotein binding	2	10	0.145899	7097 toll-like receptor 2
GO	receptor tyrosine kinase binding	2	10	0.145899	399694 SHC (Src homology 2 domain containing) family, member 4
GO	receptor tyrosine kinase binding	2	10	0.145899	83394 PITPNM family member 3
GO	transforming growth factor beta rece	2	10	0.145899	4087 SMAD family member 2
GO	transforming growth factor beta rece	2	10	0.145899	7049 transforming growth factor, beta receptor III
GO	limb development	2	10	0.145899	4223 mesenchyme homeobox 2
GO	limb development	2	10	0.145899	7026 nuclear receptor subfamily 2, group F, member 2
GO	CTP biosynthetic process	2	10	0.145899	51314 thioredoxin domain containing 3 (spermatozoa)
GO	CTP biosynthetic process	2	10	0.145899	8382 non-metastatic cells 5, protein expressed in (nucleoside-diphosphate k
GO	transforming growth factor beta bind	2	10	0.145899	7049 transforming growth factor, beta receptor III

GO transforming growth factor beta binc	2	10	0.145899	94 activin A receptor type II-like 1
GO potassium ion transport	14	151	0.1514828	157855 potassium channel, subfamily U, member 1
GO potassium ion transport	14	151	0.1514828	27345 potassium large conductance calcium-activated channel, subfamily M,
GO potassium ion transport	14	151	0.1514828	343450 potassium channel, subfamily T, member 2
GO potassium ion transport	14	151	0.1514828	358 aquaporin 1 (Colton blood group)
GO potassium ion transport	14	151	0.1514828	3759 potassium inwardly-rectifying channel, subfamily J, member 2
GO potassium ion transport	14	151	0.1514828	3773 potassium inwardly-rectifying channel, subfamily J, member 16
GO potassium ion transport	14	151	0.1514828	3775 potassium channel, subfamily K, member 1
GO potassium ion transport	14	151	0.1514828	3782 potassium intermediate/small conductance calcium-activated channel,
GO potassium ion transport	14	151	0.1514828	3783 potassium intermediate/small conductance calcium-activated channel,
GO potassium ion transport	14	151	0.1514828	3786 potassium voltage-gated channel, KQT-like subfamily, member 3
GO potassium ion transport	14	151	0.1514828	3790 potassium voltage-gated channel, delayed-rectifier, subfamily S, memb
GO potassium ion transport	14	151	0.1514828	84561 solute carrier family 12 (potassium/chloride transporters), member 8
GO potassium ion transport	14	151	0.1514828	8514 potassium voltage-gated channel, shaker-related subfamily, beta mem
GO potassium ion transport	14	151	0.1514828	8645 potassium channel, subfamily K, member 5
GO GTP binding	29	347	0.1522536	115273 RAB42, member RAS oncogene family
GO GTP binding	29	347	0.1522536	1785 dynamin 2
GO GTP binding	29	347	0.1522536	1915 eukaryotic translation elongation factor 1 alpha 1
GO GTP binding	29	347	0.1522536	1983 eukaryotic translation initiation factor 5
GO GTP binding	29	347	0.1522536	205 adenylate kinase 3-like 1
GO GTP binding	29	347	0.1522536	23348 dedicator of cytokinesis 9
GO GTP binding	29	347	0.1522536	23682 RAB38, member RAS oncogene family
GO GTP binding	29	347	0.1522536	25837 RAB26, member RAS oncogene family
GO GTP binding	29	347	0.1522536	26157 GTPase, IMAP family member 2
GO GTP binding	29	347	0.1522536	2633 guanylate binding protein 1, interferon-inducible, 67kDa
GO GTP binding	29	347	0.1522536	2634 guanylate binding protein 2, interferon-inducible
GO GTP binding	29	347	0.1522536	2635 guanylate binding protein 3
GO GTP binding	29	347	0.1522536	2769 guanine nucleotide binding protein (G protein), alpha 15 (Gq class)
GO GTP binding	29	347	0.1522536	3643 insulin receptor
GO GTP binding	29	347	0.1522536	379 ADP-ribosylation factor-like 4D
GO GTP binding	29	347	0.1522536	3845 v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog
GO GTP binding	29	347	0.1522536	387496 RAS-like, family 11, member A
GO GTP binding	29	347	0.1522536	392509 ADP-ribosylation factor-like 13A
GO GTP binding	29	347	0.1522536	4599 myxovirus (influenza virus) resistance 1, interferon-inducible protein p
GO GTP binding	29	347	0.1522536	4600 myxovirus (influenza virus) resistance 2 (mouse)
GO GTP binding	29	347	0.1522536	51285 RAS-like, family 12

GO	GTP binding	29	347	0.1522536	51655 RAS, dexamethasone-induced 1
GO	GTP binding	29	347	0.1522536	54769 DIRAS family, GTP-binding RAS-like 2
GO	GTP binding	29	347	0.1522536	56923 neuromedin U receptor 2
GO	GTP binding	29	347	0.1522536	57799 RAB40C, member RAS oncogene family
GO	GTP binding	29	347	0.1522536	5873 RAB27A, member RAS oncogene family
GO	GTP binding	29	347	0.1522536	7984 Rho guanine nucleotide exchange factor (GEF) 5
GO	GTP binding	29	347	0.1522536	85004 RAS-like, estrogen-regulated, growth inhibitor
GO	GTP binding	29	347	0.1522536	9567 GTP binding protein 1
GO	B cell activation	3	20	0.1529228	10014 histone deacetylase 5
GO	B cell activation	3	20	0.1529228	684 bone marrow stromal cell antigen 2
GO	B cell activation	3	20	0.1529228	9734 histone deacetylase 9
GO	positive regulation of bone mineraliz	3	20	0.1529228	154 adrenergic, beta-2-, receptor, surface
GO	positive regulation of bone mineraliz	3	20	0.1529228	652 bone morphogenetic protein 4
GO	positive regulation of bone mineraliz	3	20	0.1529228	91461 protein kinase domain containing, cytoplasmic homolog (mouse)
GO	adult walking behavior	3	20	0.1529228	1813 dopamine receptor D2
GO	adult walking behavior	3	20	0.1529228	2055 ceroid-lipofuscinosis, neuronal 8 (epilepsy, progressive with mental ret
GO	adult walking behavior	3	20	0.1529228	28996 homeodomain interacting protein kinase 2
GO	response to amphetamine	3	20	0.1529228	1813 dopamine receptor D2
GO	response to amphetamine	3	20	0.1529228	1815 dopamine receptor D4
GO	response to amphetamine	3	20	0.1529228	4929 nuclear receptor subfamily 4, group A, member 2
GO	positive regulation of mitosis	3	20	0.1529228	1906 endothelin 1
GO	positive regulation of mitosis	3	20	0.1529228	3479 insulin-like growth factor 1 (somatomedin C)
GO	positive regulation of mitosis	3	20	0.1529228	3643 insulin receptor
GO	positive regulation of neuron apopto	3	20	0.1529228	255738 proprotein convertase subtilisin/kexin type 9
GO	positive regulation of neuron apopto	3	20	0.1529228	3725 jun oncogene
GO	positive regulation of neuron apopto	3	20	0.1529228	429 achaete-scute complex homolog 1 (Drosophila)
GO	tissue regeneration	3	20	0.1529228	3484 insulin-like growth factor binding protein 1
GO	tissue regeneration	3	20	0.1529228	4851 Notch homolog 1, translocation-associated (Drosophila)
GO	tissue regeneration	3	20	0.1529228	4853 Notch homolog 2 (Drosophila)
GO	response to steroid hormone stimulu	3	20	0.1529228	4015 lysyl oxidase
GO	response to steroid hormone stimulu	3	20	0.1529228	4129 monoamine oxidase B
GO	response to steroid hormone stimulu	3	20	0.1529228	6750 somatostatin
GO	L-ascorbic acid binding	3	20	0.1529228	5066 peptidylglycine alpha-amidating monooxygenase
GO	L-ascorbic acid binding	3	20	0.1529228	5351 procollagen-lysine 1, 2-oxoglutarate 5-dioxygenase 1
GO	L-ascorbic acid binding	3	20	0.1529228	54681 prolyl 4-hydroxylase, transmembrane (endoplasmic reticulum)
GO	actin cytoskeleton organization	11	114	0.1558943	10435 CDC42 effector protein (Rho GTPase binding) 2

GO	actin cytoskeleton organization	11	114	0.1558943	152273 FYVE, RhoGEF and PH domain containing 5
GO	actin cytoskeleton organization	11	114	0.1558943	23092 Rho GTPase activating protein 26
GO	actin cytoskeleton organization	11	114	0.1558943	23500 dishevelled associated activator of morphogenesis 2
GO	actin cytoskeleton organization	11	114	0.1558943	3845 v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog
GO	actin cytoskeleton organization	11	114	0.1558943	57619 shroom family member 3
GO	actin cytoskeleton organization	11	114	0.1558943	604 B-cell CLL/lymphoma 6
GO	actin cytoskeleton organization	11	114	0.1558943	81788 NUAK family, SNF1-like kinase, 2
GO	actin cytoskeleton organization	11	114	0.1558943	85462 FH2 domain containing 1
GO	actin cytoskeleton organization	11	114	0.1558943	9087 thymosin beta 4, Y-linked
GO	actin cytoskeleton organization	11	114	0.1558943	9788 metastasis suppressor 1
GO	regulation of cell cycle	5	42	0.1566921	10912 growth arrest and DNA-damage-inducible, gamma
GO	regulation of cell cycle	5	42	0.1566921	2122 MDS1 and EVI1 complex locus
GO	regulation of cell cycle	5	42	0.1566921	3725 jun oncogene
GO	regulation of cell cycle	5	42	0.1566921	3726 jun B proto-oncogene
GO	regulation of cell cycle	5	42	0.1566921	4616 growth arrest and DNA-damage-inducible, beta
GO	calcium-dependent protein binding	4	31	0.1586374	1755 deleted in malignant brain tumors 1
GO	calcium-dependent protein binding	4	31	0.1586374	311 annexin A11
GO	calcium-dependent protein binding	4	31	0.1586374	5648 mannan-binding lectin serine peptidase 1 (C4/C2 activating component
GO	calcium-dependent protein binding	4	31	0.1586374	6857 synaptotagmin I
GO	transcription from RNA polymerase II	16	178	0.1591611	1999 E74-like factor 3 (ets domain transcription factor, epithelial-specific )
GO	transcription from RNA polymerase II	16	178	0.1591611	2115 ets variant 1
GO	transcription from RNA polymerase II	16	178	0.1591611	23650 tripartite motif-containing 29
GO	transcription from RNA polymerase II	16	178	0.1591611	3131 hepatic leukemia factor
GO	transcription from RNA polymerase II	16	178	0.1591611	3659 interferon regulatory factor 1
GO	transcription from RNA polymerase II	16	178	0.1591611	4783 nuclear factor, interleukin 3 regulated
GO	transcription from RNA polymerase II	16	178	0.1591611	4784 nuclear factor I/X (CCAAT-binding transcription factor)
GO	transcription from RNA polymerase II	16	178	0.1591611	51621 Kruppel-like factor 13
GO	transcription from RNA polymerase II	16	178	0.1591611	5465 peroxisome proliferator-activated receptor alpha
GO	transcription from RNA polymerase II	16	178	0.1591611	55870 ash1 (absent, small, or homeotic)-like (Drosophila)
GO	transcription from RNA polymerase II	16	178	0.1591611	6239 ras responsive element binding protein 1
GO	transcription from RNA polymerase II	16	178	0.1591611	7227 trichorhinophalangeal syndrome I
GO	transcription from RNA polymerase II	16	178	0.1591611	80714 pre-B-cell leukemia homeobox 4
GO	transcription from RNA polymerase II	16	178	0.1591611	8462 Kruppel-like factor 11
GO	transcription from RNA polymerase II	16	178	0.1591611	8543 LIM domain only 4
GO	transcription from RNA polymerase II	16	178	0.1591611	8848 TSC22 domain family, member 1
GO	Wnt receptor signaling pathway	9	90	0.161066	10023 frequently rearranged in advanced T-cell lymphomas

GO	Wnt receptor signaling pathway	9	90	0.161066	23043 TRAF2 and NCK interacting kinase
GO	Wnt receptor signaling pathway	9	90	0.161066	4163 mutated in colorectal cancers
GO	Wnt receptor signaling pathway	9	90	0.161066	4286 microphthalmia-associated transcription factor
GO	Wnt receptor signaling pathway	9	90	0.161066	5218 cyclin-dependent kinase 14
GO	Wnt receptor signaling pathway	9	90	0.161066	64359 nucleoredoxin
GO	Wnt receptor signaling pathway	9	90	0.161066	7089 transducin-like enhancer of split 2 (E(sp1) homolog, Drosophila)
GO	Wnt receptor signaling pathway	9	90	0.161066	7090 transducin-like enhancer of split 3 (E(sp1) homolog, Drosophila)
GO	Wnt receptor signaling pathway	9	90	0.161066	79971 wntless homolog (Drosophila)
GO	serine-type endopeptidase inhibitor a	9	90	0.161066	153218 serine peptidase inhibitor, Kazal type 13 (putative)
GO	serine-type endopeptidase inhibitor a	9	90	0.161066	183 angiotensinogen (serpin peptidase inhibitor, clade A, member 8)
GO	serine-type endopeptidase inhibitor a	9	90	0.161066	404203 serine peptidase inhibitor, Kazal type 6
GO	serine-type endopeptidase inhibitor a	9	90	0.161066	6590 secretory leukocyte peptidase inhibitor
GO	serine-type endopeptidase inhibitor a	9	90	0.161066	6690 serine peptidase inhibitor, Kazal type 1
GO	serine-type endopeptidase inhibitor a	9	90	0.161066	6692 serine peptidase inhibitor, Kunitz type 1
GO	serine-type endopeptidase inhibitor a	9	90	0.161066	80760 inter-alpha (globulin) inhibitor H5
GO	serine-type endopeptidase inhibitor a	9	90	0.161066	8434 reversion-inducing-cysteine-rich protein with kazal motifs
GO	serine-type endopeptidase inhibitor a	9	90	0.161066	89778 serpin peptidase inhibitor, clade B (ovalbumin), member 11 (gene/pset
GO	calmodulin binding	13	140	0.1611272	1612 death-associated protein kinase 1
GO	calmodulin binding	13	140	0.1611272	23604 death-associated protein kinase 2
GO	calmodulin binding	13	140	0.1611272	3782 potassium intermediate/small conductance calcium-activated channel,
GO	calmodulin binding	13	140	0.1611272	3783 potassium intermediate/small conductance calcium-activated channel,
GO	calmodulin binding	13	140	0.1611272	4638 myosin light chain kinase
GO	calmodulin binding	13	140	0.1611272	4645 myosin VB
GO	calmodulin binding	13	140	0.1611272	4842 nitric oxide synthase 1 (neuronal)
GO	calmodulin binding	13	140	0.1611272	493 ATPase, Ca <sup>++</sup> transporting, plasma membrane 4
GO	calmodulin binding	13	140	0.1611272	51168 myosin XVA
GO	calmodulin binding	13	140	0.1611272	5136 phosphodiesterase 1A, calmodulin-dependent
GO	calmodulin binding	13	140	0.1611272	57118 calcium/calmodulin-dependent protein kinase ID
GO	calmodulin binding	13	140	0.1611272	6004 regulator of G-protein signaling 16
GO	calmodulin binding	13	140	0.1611272	6857 synaptotagmin I
GO	cysteine-type endopeptidase activity	6	54	0.1615628	1508 cathepsin B
GO	cysteine-type endopeptidase activity	6	54	0.1615628	1519 cathepsin O
GO	cysteine-type endopeptidase activity	6	54	0.1615628	29108 PYD and CARD domain containing
GO	cysteine-type endopeptidase activity	6	54	0.1615628	834 caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, co
GO	cysteine-type endopeptidase activity	6	54	0.1615628	837 caspase 4, apoptosis-related cysteine peptidase
GO	cysteine-type endopeptidase activity	6	54	0.1615628	8722 cathepsin F

GO protein localization	6	54	0.1615628	1813 dopamine receptor D2
GO protein localization	6	54	0.1615628	259173 ALS2 C-terminal like
GO protein localization	6	54	0.1615628	53405 chloride intracellular channel 5
GO protein localization	6	54	0.1615628	55909 bridging integrator 3
GO protein localization	6	54	0.1615628	604 B-cell CLL/lymphoma 6
GO protein localization	6	54	0.1615628	81693 amnionless homolog (mouse)
GO endocytosis	10	103	0.1657623	1785 dynamin 2
GO endocytosis	10	103	0.1657623	22925 phospholipase A2 receptor 1, 180kDa
GO endocytosis	10	103	0.1657623	23048 formin binding protein 1
GO endocytosis	10	103	0.1657623	26119 low density lipoprotein receptor adaptor protein 1
GO endocytosis	10	103	0.1657623	286133 scavenger receptor class A, member 5 (putative)
GO endocytosis	10	103	0.1657623	3845 v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog
GO endocytosis	10	103	0.1657623	3949 low density lipoprotein receptor
GO endocytosis	10	103	0.1657623	4038 low density lipoprotein receptor-related protein 4
GO endocytosis	10	103	0.1657623	4065 lymphocyte antigen 75
GO endocytosis	10	103	0.1657623	8527 diacylglycerol kinase, delta 130kDa
GO inner ear morphogenesis	5	43	0.168023	10253 sprouty homolog 2 (Drosophila)
GO inner ear morphogenesis	5	43	0.168023	2290 forkhead box G1
GO inner ear morphogenesis	5	43	0.168023	51168 myosin XVA
GO inner ear morphogenesis	5	43	0.168023	5396 paired related homeobox 1
GO inner ear morphogenesis	5	43	0.168023	9935 v-maf musculoaponeurotic fibrosarcoma oncogene homolog B (avian)
GO Notch signaling pathway	5	43	0.168023	2296 forkhead box C1
GO Notch signaling pathway	5	43	0.168023	2303 forkhead box C2 (MFH-1, mesenchyme forkhead 1)
GO Notch signaling pathway	5	43	0.168023	429 achaete-scute complex homolog 1 (Drosophila)
GO Notch signaling pathway	5	43	0.168023	4851 Notch homolog 1, translocation-associated (Drosophila)
GO Notch signaling pathway	5	43	0.168023	4853 Notch homolog 2 (Drosophila)
GO glucose metabolic process	5	43	0.168023	3175 one cut homeobox 1
GO glucose metabolic process	5	43	0.168023	4886 neuropeptide Y receptor Y1
GO glucose metabolic process	5	43	0.168023	5239 phosphoglucomutase 5
GO glucose metabolic process	5	43	0.168023	8660 insulin receptor substrate 2
GO glucose metabolic process	5	43	0.168023	9563 hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase)
GO angiogenesis	11	116	0.1691608	10481 homeobox B13
GO angiogenesis	11	116	0.1691608	1295 collagen, type VIII, alpha 1
GO angiogenesis	11	116	0.1691608	27035 NADPH oxidase 1
GO angiogenesis	11	116	0.1691608	3678 integrin, alpha 5 (fibronectin receptor, alpha polypeptide)
GO angiogenesis	11	116	0.1691608	3725 jun oncogene



GO angiogenesis	11	116	0.1691608	3911 laminin, alpha 5
GO angiogenesis	11	116	0.1691608	4223 mesenchyme homeobox 2
GO angiogenesis	11	116	0.1691608	56913 core 1 synthase, glycoprotein-N-acetylgalactosamine 3-beta-galactosyl
GO angiogenesis	11	116	0.1691608	5787 protein tyrosine phosphatase, receptor type, B
GO angiogenesis	11	116	0.1691608	652 bone morphogenetic protein 4
GO angiogenesis	11	116	0.1691608	94 activin A receptor type II-like 1
GO synaptic transmission	15	167	0.169308	2571 glutamate decarboxylase 1 (brain, 67kDa)
GO synaptic transmission	15	167	0.169308	27345 potassium large conductance calcium-activated channel, subfamily M,
GO synaptic transmission	15	167	0.169308	2911 glutamate receptor, metabotropic 1
GO synaptic transmission	15	167	0.169308	3355 5-hydroxytryptamine (serotonin) receptor 1F
GO synaptic transmission	15	167	0.169308	3786 potassium voltage-gated channel, KQT-like subfamily, member 3
GO synaptic transmission	15	167	0.169308	4359 myelin protein zero
GO synaptic transmission	15	167	0.169308	4889 neuropeptide Y receptor Y5
GO synaptic transmission	15	167	0.169308	5367 pro-melanin-concentrating hormone
GO synaptic transmission	15	167	0.169308	6505 solute carrier family 1 (neuronal/epithelial high affinity glutamate trans
GO synaptic transmission	15	167	0.169308	6750 somatostatin
GO synaptic transmission	15	167	0.169308	6857 synaptotagmin I
GO synaptic transmission	15	167	0.169308	774 calcium channel, voltage-dependent, N type, alpha 1B subunit
GO synaptic transmission	15	167	0.169308	783 calcium channel, voltage-dependent, beta 2 subunit
GO synaptic transmission	15	167	0.169308	8973 cholinergic receptor, nicotinic, alpha 6
GO synaptic transmission	15	167	0.169308	9892 synaptosomal-associated protein, 91kDa homolog (mouse)
GO microsome	19	219	0.1693996	10170 dehydrogenase/reductase (SDR family) member 9
GO microsome	19	219	0.1693996	154 adrenergic, beta-2-, receptor, surface
GO microsome	19	219	0.1693996	1558 cytochrome P450, family 2, subfamily C, polypeptide 8
GO microsome	19	219	0.1693996	1559 cytochrome P450, family 2, subfamily C, polypeptide 9
GO microsome	19	219	0.1693996	1571 cytochrome P450, family 2, subfamily E, polypeptide 1
GO microsome	19	219	0.1693996	157506 retinol dehydrogenase 10 (all-trans)
GO microsome	19	219	0.1693996	1577 cytochrome P450, family 3, subfamily A, polypeptide 5
GO microsome	19	219	0.1693996	2182 acyl-CoA synthetase long-chain family member 4
GO microsome	19	219	0.1693996	2911 glutamate receptor, metabotropic 1
GO microsome	19	219	0.1693996	3643 insulin receptor
GO microsome	19	219	0.1693996	3709 inositol 1,4,5-triphosphate receptor, type 2
GO microsome	19	219	0.1693996	4056 leukotriene C4 synthase
GO microsome	19	219	0.1693996	412 steroid sulfatase (microsomal), isozyme S
GO microsome	19	219	0.1693996	4939 2'-5'-oligoadenylate synthetase 2, 69/71kDa
GO microsome	19	219	0.1693996	55080 TAP binding protein-like

GO	microsome	19	219	0.1693996	5742 prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase a
GO	microsome	19	219	0.1693996	79152 fatty acid 2-hydroxylase
GO	microsome	19	219	0.1693996	952 CD38 molecule
GO	microsome	19	219	0.1693996	9563 hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase)
GO	protein kinase inhibitor activity	3	21	0.1698873	10221 tribbles homolog 1 (Drosophila)
GO	protein kinase inhibitor activity	3	21	0.1698873	28951 tribbles homolog 2 (Drosophila)
GO	protein kinase inhibitor activity	3	21	0.1698873	9021 suppressor of cytokine signaling 3
GO	calcium-dependent phospholipid bin	3	21	0.1698873	11199 annexin A10
GO	calcium-dependent phospholipid bin	3	21	0.1698873	23208 synaptotagmin XI
GO	calcium-dependent phospholipid bin	3	21	0.1698873	311 annexin A11
GO	Wnt receptor signaling pathway, calc	3	21	0.1698873	54361 wingless-type MMTV integration site family, member 4
GO	Wnt receptor signaling pathway, calc	3	21	0.1698873	7474 wingless-type MMTV integration site family, member 5A
GO	Wnt receptor signaling pathway, calc	3	21	0.1698873	7477 wingless-type MMTV integration site family, member 7B
GO	threonine-type endopeptidase activit	3	21	0.1698873	5696 proteasome (prosome, macropain) subunit, beta type, 8 (large multifur
GO	threonine-type endopeptidase activit	3	21	0.1698873	5698 proteasome (prosome, macropain) subunit, beta type, 9 (large multifur
GO	threonine-type endopeptidase activit	3	21	0.1698873	5699 proteasome (prosome, macropain) subunit, beta type, 10
GO	polysaccharide binding	2	11	0.1706035	10216 proteoglycan 4
GO	polysaccharide binding	2	11	0.1706035	157869 chromosome 8 open reading frame 84
GO	morphogenesis of an epithelium	2	11	0.1706035	10481 homeobox B13
GO	morphogenesis of an epithelium	2	11	0.1706035	760 carbonic anhydrase II
GO	ceramide biosynthetic process	2	11	0.1706035	123099 degenerative spermatocyte homolog 2, lipid desaturase (Drosophila)
GO	ceramide biosynthetic process	2	11	0.1706035	2055 ceroid-lipofuscinosis, neuronal 8 (epilepsy, progressive with mental ret
GO	retinol binding	2	11	0.1706035	1382 cellular retinoic acid binding protein 2
GO	retinol binding	2	11	0.1706035	5950 retinol binding protein 4, plasma
GO	DNA methylation involved in gamete	2	11	0.1706035	143689 piwi-like 4 (Drosophila)
GO	DNA methylation involved in gamete	2	11	0.1706035	55124 piwi-like 2 (Drosophila)
GO	cell recognition	2	11	0.1706035	1462 versican
GO	cell recognition	2	11	0.1706035	3911 laminin, alpha 5
GO	guanylate kinase activity	2	11	0.1706035	1741 discs, large homolog 3 (Drosophila)
GO	guanylate kinase activity	2	11	0.1706035	9414 tight junction protein 2 (zona occludens 2)
GO	T cell costimulation	2	11	0.1706035	1803 dipeptidyl-peptidase 4
GO	T cell costimulation	2	11	0.1706035	8740 tumor necrosis factor (ligand) superfamily, member 14
GO	long-chain fatty acid-CoA ligase activi	2	11	0.1706035	2182 acyl-CoA synthetase long-chain family member 4
GO	long-chain fatty acid-CoA ligase activi	2	11	0.1706035	51703 acyl-CoA synthetase long-chain family member 5
GO	regulation of blood vessel size	2	11	0.1706035	2296 forkhead box C1
GO	regulation of blood vessel size	2	11	0.1706035	2303 forkhead box C2 (MFH-1, mesenchyme forkhead 1)

GO	kinesin binding	2	11	0.1706035	23095 kinesin family member 1B
GO	kinesin binding	2	11	0.1706035	6622 synuclein, alpha (non A4 component of amyloid precursor)
GO	Rho GTPase binding	2	11	0.1706035	23348 dedicator of cytokinesis 9
GO	Rho GTPase binding	2	11	0.1706035	23500 dishevelled associated activator of morphogenesis 2
GO	positive regulation of DNA binding	2	11	0.1706035	23476 bromodomain containing 4
GO	positive regulation of DNA binding	2	11	0.1706035	28996 homeodomain interacting protein kinase 2
GO	low-density lipoprotein receptor binding	2	11	0.1706035	255738 proprotein convertase subtilisin/kexin type 9
GO	low-density lipoprotein receptor binding	2	11	0.1706035	6857 synaptotagmin I
GO	protein maturation by peptide bond formation	2	11	0.1706035	255738 proprotein convertase subtilisin/kexin type 9
GO	protein maturation by peptide bond formation	2	11	0.1706035	5046 proprotein convertase subtilisin/kexin type 6
GO	gap junction channel activity	2	11	0.1706035	2706 gap junction protein, beta 2, 26kDa
GO	gap junction channel activity	2	11	0.1706035	2707 gap junction protein, beta 3, 31kDa
GO	laminin binding	2	11	0.1706035	27076 LY6/PLAUR domain containing 3
GO	laminin binding	2	11	0.1706035	375790 agrin
GO	regulation of neurotransmitter secretion	2	11	0.1706035	27345 potassium large conductance calcium-activated channel, subfamily M,
GO	regulation of neurotransmitter secretion	2	11	0.1706035	5071 Parkinson disease (autosomal recessive, juvenile) 2, parkin
GO	cell volume homeostasis	2	11	0.1706035	358 aquaporin 1 (Colton blood group)
GO	cell volume homeostasis	2	11	0.1706035	3783 potassium intermediate/small conductance calcium-activated channel,
GO	hemidesmosome assembly	2	11	0.1706035	3691 integrin, beta 4
GO	hemidesmosome assembly	2	11	0.1706035	3914 laminin, beta 3
GO	negative regulation of DNA binding	2	11	0.1706035	3725 jun oncogene
GO	negative regulation of DNA binding	2	11	0.1706035	4792 nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor 3
GO	somatic stem cell maintenance	2	11	0.1706035	3815 v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog
GO	somatic stem cell maintenance	2	11	0.1706035	5460 POU class 5 homeobox 1
GO	vasodilation	2	11	0.1706035	3827 kininogen 1
GO	vasodilation	2	11	0.1706035	5025 purinergic receptor P2X, ligand-gated ion channel, 4
GO	3',5'-cyclic-nucleotide phosphodiesterase activity	2	11	0.1706035	5152 phosphodiesterase 9A
GO	3',5'-cyclic-nucleotide phosphodiesterase activity	2	11	0.1706035	8622 phosphodiesterase 8B
GO	face morphogenesis	2	11	0.1706035	64651 cysteine-serine-rich nuclear protein 1
GO	face morphogenesis	2	11	0.1706035	84159 AT rich interactive domain 5B (MRF1-like)
GO	phosphatidylserine binding	2	11	0.1706035	85477 scinderin
GO	phosphatidylserine binding	2	11	0.1706035	91404 SEC14 and spectrin domains 1
GO	activin binding	2	11	0.1706035	91 activin A receptor, type IB
GO	activin binding	2	11	0.1706035	94 activin A receptor type II-like 1
GO	protein amino acid autophosphorylation	8	79	0.1709253	11213 interleukin-1 receptor-associated kinase 3
GO	protein amino acid autophosphorylation	8	79	0.1709253	127933 U2AF homology motif (UHM) kinase 1

GO	protein amino acid autophosphorylat	8	79	0.1709253	23043 TRAF2 and NCK interacting kinase
GO	protein amino acid autophosphorylat	8	79	0.1709253	3643 insulin receptor
GO	protein amino acid autophosphorylat	8	79	0.1709253	3815 v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog
GO	protein amino acid autophosphorylat	8	79	0.1709253	4293 mitogen-activated protein kinase kinase kinase 9
GO	protein amino acid autophosphorylat	8	79	0.1709253	6850 spleen tyrosine kinase
GO	protein amino acid autophosphorylat	8	79	0.1709253	91 activin A receptor, type IB
GO	ossification	6	55	0.1716065	1009 cadherin 11, type 2, OB-cadherin (osteoblast)
GO	ossification	6	55	0.1716065	2296 forkhead box C1
GO	ossification	6	55	0.1716065	2303 forkhead box C2 (MFH-1, mesenchyme forkhead 1)
GO	ossification	6	55	0.1716065	50617 ATPase, H+ transporting, lysosomal V0 subunit a4
GO	ossification	6	55	0.1716065	8600 tumor necrosis factor (ligand) superfamily, member 11
GO	ossification	6	55	0.1716065	91461 protein kinase domain containing, cytoplasmic homolog (mouse)
GO	neural tube closure	4	32	0.1721517	57619 shroom family member 3
GO	neural tube closure	4	32	0.1721517	7546 Zic family member 2 (odd-paired homolog, Drosophila)
GO	neural tube closure	4	32	0.1721517	85416 Zic family member 5 (odd-paired homolog, Drosophila)
GO	neural tube closure	4	32	0.1721517	8543 LIM domain only 4
GO	regulation of transcription from RNA	18	207	0.1748127	1628 D site of albumin promoter (albumin D-box) binding protein
GO	regulation of transcription from RNA	18	207	0.1748127	22906 trafficking protein, kinesin binding 1
GO	regulation of transcription from RNA	18	207	0.1748127	2353 FBJ murine osteosarcoma viral oncogene homolog
GO	regulation of transcription from RNA	18	207	0.1748127	3175 one cut homeobox 1
GO	regulation of transcription from RNA	18	207	0.1748127	3400 inhibitor of DNA binding 4, dominant negative helix-loop-helix protein
GO	regulation of transcription from RNA	18	207	0.1748127	3726 jun B proto-oncogene
GO	regulation of transcription from RNA	18	207	0.1748127	4613 v-myc myelocytomatosis viral related oncogene, neuroblastoma derive
GO	regulation of transcription from RNA	18	207	0.1748127	4778 nuclear factor (erythroid-derived 2), 45kDa
GO	regulation of transcription from RNA	18	207	0.1748127	4802 nuclear transcription factor Y, gamma
GO	regulation of transcription from RNA	18	207	0.1748127	55140 elongation protein 3 homolog ( <i>S. cerevisiae</i> )
GO	regulation of transcription from RNA	18	207	0.1748127	6604 SWI/SNF related, matrix associated, actin dependent regulator of chromatin
GO	regulation of transcription from RNA	18	207	0.1748127	6778 signal transducer and activator of transcription 6, interleukin-4 induced
GO	regulation of transcription from RNA	18	207	0.1748127	687 Kruppel-like factor 9
GO	regulation of transcription from RNA	18	207	0.1748127	6921 transcription elongation factor B (SIII), polypeptide 1 (15kDa, elongin C)
GO	regulation of transcription from RNA	18	207	0.1748127	6941 transcription factor 19
GO	regulation of transcription from RNA	18	207	0.1748127	7008 thyrotrophic embryonic factor
GO	regulation of transcription from RNA	18	207	0.1748127	7022 transcription factor AP-2 gamma (activating enhancer binding protein 2)
GO	regulation of transcription from RNA	18	207	0.1748127	7026 nuclear receptor subfamily 2, group F, member 2
GO	response to hormone stimulus	5	44	0.1796636	2303 forkhead box C2 (MFH-1, mesenchyme forkhead 1)
GO	response to hormone stimulus	5	44	0.1796636	4151 myoglobin

GO response to hormone stimulus	5	44	0.1796636	6096 RAR-related orphan receptor B
GO response to hormone stimulus	5	44	0.1796636	85004 RAS-like, estrogen-regulated, growth inhibitor
GO response to hormone stimulus	5	44	0.1796636	952 CD38 molecule
GO cell-cell junction	6	56	0.1819008	10076 protein tyrosine phosphatase, receptor type, U
GO cell-cell junction	6	56	0.1819008	11187 plakophilin 3
GO cell-cell junction	6	56	0.1819008	3678 integrin, alpha 5 (fibronectin receptor, alpha polypeptide)
GO cell-cell junction	6	56	0.1819008	5318 plakophilin 2
GO cell-cell junction	6	56	0.1819008	56288 par-3 partitioning defective 3 homolog (C. elegans)
GO cell-cell junction	6	56	0.1819008	57863 cell adhesion molecule 3
GO lysosome	13	144	0.1858123	10268 receptor (G protein-coupled) activity modifying protein 3
GO lysosome	13	144	0.1858123	1508 cathepsin B
GO lysosome	13	144	0.1858123	1519 cathepsin O
GO lysosome	13	144	0.1858123	154 adrenergic, beta-2-, receptor, surface
GO lysosome	13	144	0.1858123	22901 arylsulfatase G
GO lysosome	13	144	0.1858123	23048 formin binding protein 1
GO lysosome	13	144	0.1858123	2517 fucosidase, alpha-L- 1, tissue
GO lysosome	13	144	0.1858123	255738 proprotein convertase subtilisin/kexin type 9
GO lysosome	13	144	0.1858123	2990 glucuronidase, beta
GO lysosome	13	144	0.1858123	3373 hyaluronoglucosaminidase 1
GO lysosome	13	144	0.1858123	412 steroid sulfatase (microsomal), isozyme S
GO lysosome	13	144	0.1858123	5873 RAB27A, member RAS oncogene family
GO lysosome	13	144	0.1858123	8722 cathepsin F
GO JNK cascade	4	33	0.1860463	10221 tribbles homolog 1 (Drosophila)
GO JNK cascade	4	33	0.1860463	148170 CDC42 effector protein (Rho GTPase binding) 5
GO JNK cascade	4	33	0.1860463	7474 wingless-type MMTV integration site family, member 5A
GO JNK cascade	4	33	0.1860463	9459 Rac/Cdc42 guanine nucleotide exchange factor (GEF) 6
GO acrosomal vesicle	4	33	0.1860463	148229 ATPase, class I, type 8B, member 3
GO acrosomal vesicle	4	33	0.1860463	3815 v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog
GO acrosomal vesicle	4	33	0.1860463	4851 Notch homolog 1, translocation-associated (Drosophila)
GO acrosomal vesicle	4	33	0.1860463	799 calcitonin receptor
GO T cell activation	4	33	0.1860463	1803 dipeptidyl-peptidase 4
GO T cell activation	4	33	0.1860463	23303 kinesin family member 13B
GO T cell activation	4	33	0.1860463	84941 hematopoietic SH2 domain containing
GO T cell activation	4	33	0.1860463	8740 tumor necrosis factor (ligand) superfamily, member 14
GO potassium channel activity	4	33	0.1860463	358 aquaporin 1 (Colton blood group)
GO potassium channel activity	4	33	0.1860463	3775 potassium channel, subfamily K, member 1

GO potassium channel activity	4	33	0.1860463	3786 potassium voltage-gated channel, KQT-like subfamily, member 3
GO potassium channel activity	4	33	0.1860463	8645 potassium channel, subfamily K, member 5
GO determination of left/right symmetry	4	33	0.1860463	4851 Notch homolog 1, translocation-associated (Drosophila)
GO determination of left/right symmetry	4	33	0.1860463	4853 Notch homolog 2 (Drosophila)
GO determination of left/right symmetry	4	33	0.1860463	5308 paired-like homeodomain 2
GO determination of left/right symmetry	4	33	0.1860463	84976 dispatched homolog 1 (Drosophila)
GO positive regulation of translation	3	22	0.1873576	2033 E1A binding protein p300
GO positive regulation of translation	3	22	0.1873576	3569 interleukin 6 (interferon, beta 2)
GO positive regulation of translation	3	22	0.1873576	55124 piwi-like 2 (Drosophila)
GO multicellular organism growth	3	22	0.1873576	28982 feline leukemia virus subgroup C cellular receptor 1
GO multicellular organism growth	3	22	0.1873576	29123 ankyrin repeat domain 11
GO multicellular organism growth	3	22	0.1873576	84159 AT rich interactive domain 5B (MRF1-like)
GO positive regulation of neuron differer	3	22	0.1873576	3169 forkhead box A1
GO positive regulation of neuron differer	3	22	0.1873576	429 achaete-scute complex homolog 1 (Drosophila)
GO positive regulation of neuron differer	3	22	0.1873576	627 brain-derived neurotrophic factor
GO mesoderm formation	3	22	0.1873576	4087 SMAD family member 2
GO mesoderm formation	3	22	0.1873576	8013 nuclear receptor subfamily 4, group A, member 3
GO mesoderm formation	3	22	0.1873576	8646 chordin
GO regulation of ubiquitin-protein ligase	1	3	0.1913587	10116 fem-1 homolog b (C. elegans)
GO progesterone metabolic process	1	3	0.1913587	10170 dehydrogenase/reductase (SDR family) member 9
GO double-stranded RNA adenosine dea	1	3	0.1913587	104 adenosine deaminase, RNA-specific, B1 (RED1 homolog rat)
GO polo kinase kinase activity	1	3	0.1913587	10769 polo-like kinase 2 (Drosophila)
GO negative regulation of myelination	1	3	0.1913587	11202 kallikrein-related peptidase 8
GO heme transporter activity	1	3	0.1913587	113235 solute carrier family 46 (folate transporter), member 1
GO cellular chloride ion homeostasis	1	3	0.1913587	1152 creatine kinase, brain
GO creatine kinase activity	1	3	0.1913587	1152 creatine kinase, brain
GO regulation of protein export from nuc	1	3	0.1913587	127933 U2AF homology motif (UHM) kinase 1
GO sphingosine metabolic process	1	3	0.1913587	130367 sphingosine-1-phosphate phosphotase 2
GO kininogen binding	1	3	0.1913587	1508 cathepsin B
GO response to interleukin-4	1	3	0.1913587	1508 cathepsin B
GO adenylate cyclase binding	1	3	0.1913587	154 adrenergic, beta-2-, receptor, surface
GO desensitization of G-protein coupled	1	3	0.1913587	154 adrenergic, beta-2-, receptor, surface
GO diet induced thermogenesis	1	3	0.1913587	154 adrenergic, beta-2-, receptor, surface
GO norepinephrine binding	1	3	0.1913587	154 adrenergic, beta-2-, receptor, surface
GO organic acid metabolic process	1	3	0.1913587	1558 cytochrome P450, family 2, subfamily C, polypeptide 8
GO oxidoreductase activity, acting on pai	1	3	0.1913587	1571 cytochrome P450, family 2, subfamily E, polypeptide 1

GO	Gram-negative bacterial cell surface l	1	3	0.1913587	1755 deleted in malignant brain tumors 1
GO	regulation of cell-cell adhesion media	1	3	0.1913587	1803 dipeptidyl-peptidase 4
GO	branching morphogenesis of a nerve	1	3	0.1913587	1813 dopamine receptor D2
GO	ovarian follicle rupture	1	3	0.1913587	183 angiotensinogen (serpin peptidase inhibitor, clade A, member 8)
GO	regulation of natriuresis	1	3	0.1913587	183 angiotensinogen (serpin peptidase inhibitor, clade A, member 8)
GO	regulation of norepinephrine secretio	1	3	0.1913587	183 angiotensinogen (serpin peptidase inhibitor, clade A, member 8)
GO	endothelin B receptor binding	1	3	0.1913587	1906 endothelin 1
GO	rhombomere 3 development	1	3	0.1913587	1959 early growth response 2
GO	regulation of blood vessel endothelia	1	3	0.1913587	1969 EPH receptor A2
GO	N-terminal peptidyl-lysine acetylatio	1	3	0.1913587	2033 E1A binding protein p300
GO	positive regulation of protein import	1	3	0.1913587	2033 E1A binding protein p300
GO	age-dependent response to oxidative	1	3	0.1913587	2055 ceroid-lipofuscinosis, neuronal 8 (epilepsy, progressive with mental ret
GO	macrophage activation during immur	1	3	0.1913587	22904 strawberry notch homolog 2 (Drosophila)
GO	transforming growth factor beta rece	1	3	0.1913587	2331 fibromodulin
GO	adenosylhomocysteinase activity	1	3	0.1913587	23382 adenosylhomocysteinase-like 2
GO	conditioned taste aversion	1	3	0.1913587	2353 FBJ murine osteosarcoma viral oncogene homolog
GO	3-galactosyl-N-acetylglucosaminide 4	1	3	0.1913587	2525 fucosyltransferase 3 (galactoside 3(4)-L-fucosyltransferase, Lewis blood
GO	apolipoprotein receptor binding	1	3	0.1913587	255738 proprotein convertase subtilisin/kexin type 9
GO	positive regulation of receptor intern	1	3	0.1913587	255738 proprotein convertase subtilisin/kexin type 9
GO	very-low-density lipoprotein receptor	1	3	0.1913587	255738 proprotein convertase subtilisin/kexin type 9
GO	phosphatidylserine metabolic proces	1	3	0.1913587	256987 serine incorporator 5
GO	protein amino acid O-linked glycosyla	1	3	0.1913587	2589 UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosami
GO	protein amino acid O-linked glycosyla	1	3	0.1913587	2589 UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosami
GO	heparin biosynthetic process	1	3	0.1913587	26035 glucuronic acid epimerase
GO	cerebral cortex tangential migration	1	3	0.1913587	26468 LIM homeobox 6
GO	AMP deaminase activity	1	3	0.1913587	271 adenosine monophosphate deaminase 2
GO	forebrain dorsal/ventral pattern form	1	3	0.1913587	2737 GLI family zinc finger 3
GO	smoothened signaling pathway invol	1	3	0.1913587	2737 GLI family zinc finger 3
GO	tube development	1	3	0.1913587	2737 GLI family zinc finger 3
GO	activation of phospholipase C activity	1	3	0.1913587	2769 guanine nucleotide binding protein (G protein), alpha 15 (Gq class)
GO	bone development	1	3	0.1913587	29123 ankyrin repeat domain 11
GO	beta-glucuronidase activity	1	3	0.1913587	2990 glucuronidase, beta
GO	cilium axoneme assembly	1	3	0.1913587	345895 radial spoke head 4 homolog A (Chlamydomonas)
GO	myoblast proliferation	1	3	0.1913587	3479 insulin-like growth factor 1 (somatomedin C)
GO	negative regulation of androgen rece	1	3	0.1913587	3479 insulin-like growth factor 1 (somatomedin C)
GO	negative regulation of smooth muscl	1	3	0.1913587	3479 insulin-like growth factor 1 (somatomedin C)

GO Type II pneumocyte differentiation	1	3	0.1913587	3479 insulin-like growth factor 1 (somatomedin C)
GO skeletal muscle tissue growth	1	3	0.1913587	3488 insulin-like growth factor binding protein 5
GO interleukin-2 receptor activity	1	3	0.1913587	3561 interleukin 2 receptor, gamma (severe combined immunodeficiency)
GO negative regulation of chemokine bic	1	3	0.1913587	3569 interleukin 6 (interferon, beta 2)
GO cellular response to cAMP	1	3	0.1913587	358 aquaporin 1 (Colton blood group)
GO cellular response to retinoic acid	1	3	0.1913587	358 aquaporin 1 (Colton blood group)
GO cellular response to stress	1	3	0.1913587	358 aquaporin 1 (Colton blood group)
GO glycerol transport	1	3	0.1913587	358 aquaporin 1 (Colton blood group)
GO multicellular organismal water home	1	3	0.1913587	358 aquaporin 1 (Colton blood group)
GO potassium ion transmembrane transp	1	3	0.1913587	358 aquaporin 1 (Colton blood group)
GO insulin receptor complex	1	3	0.1913587	3643 insulin receptor
GO PTB domain binding	1	3	0.1913587	3643 insulin receptor
GO CD8-positive, alpha-beta T cell differ	1	3	0.1913587	3659 interferon regulatory factor 1
GO alphav-beta3 integrin-vitronectin con	1	3	0.1913587	3678 integrin, alpha 5 (fibronectin receptor, alpha polypeptide)
GO vascular endothelial growth factor re	1	3	0.1913587	3678 integrin, alpha 5 (fibronectin receptor, alpha polypeptide)
GO inositol 1,4,5-trisphosphate-sensitive	1	3	0.1913587	3709 inositol 1,4,5-triphosphate receptor, type 2
GO inositol-1,4,5-trisphosphate receptor	1	3	0.1913587	3709 inositol 1,4,5-triphosphate receptor, type 2
GO osteoblast proliferation	1	3	0.1913587	3726 jun B proto-oncogene
GO positive regulation of transcription fr	1	3	0.1913587	3726 jun B proto-oncogene
GO clustering of voltage-gated sodium ch	1	3	0.1913587	375790 agrin
GO neurotransmitter receptor metabolic	1	3	0.1913587	375790 agrin
GO small conductance calcium-activated	1	3	0.1913587	3782 potassium intermediate/small conductance calcium-activated channel,
GO myeloid progenitor cell differentiat	1	3	0.1913587	3815 v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog
GO positive regulation of long-term neur	1	3	0.1913587	3815 v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog
GO laminin-10 complex	1	3	0.1913587	3911 laminin, alpha 5
GO negative regulation of stress fiber ass	1	3	0.1913587	395 Rho GTPase activating protein 6
GO IgE binding	1	3	0.1913587	3958 lectin, galactoside-binding, soluble, 3
GO actinin binding	1	3	0.1913587	4008 LIM domain 7
GO elastic fiber assembly	1	3	0.1913587	4015 lysyl oxidase
GO activin responsive factor complex	1	3	0.1913587	4087 SMAD family member 2
GO zygotic specification of dorsal/ventra	1	3	0.1913587	4087 SMAD family member 2
GO negative regulation of epithelial cell r	1	3	0.1913587	4163 mutated in colorectal cancers
GO somite specification	1	3	0.1913587	4223 mesenchyme homeobox 2
GO positive regulation of melanocyte dif	1	3	0.1913587	4254 KIT ligand
GO stem cell factor receptor binding	1	3	0.1913587	4254 KIT ligand
GO spinal cord oligodendrocyte cell fate	1	3	0.1913587	429 achaete-scute complex homolog 1 (Drosophila)



GO myosin light chain kinase activity	1	3	0.1913587	4638 myosin light chain kinase
GO ionotropic glutamate receptor bindin	1	3	0.1913587	4645 myosin VB
GO axon extension involved in developm	1	3	0.1913587	4692 necdin homolog (mouse)
GO I-kappaB/NF-kappaB complex	1	3	0.1913587	4792 nuclear factor of kappa light polypeptide gene enhancer in B-cells inhib
GO regulation of NF-kappaB import into i	1	3	0.1913587	4792 nuclear factor of kappa light polypeptide gene enhancer in B-cells inhib
GO multicellular organismal response to	1	3	0.1913587	4842 nitric oxide synthase 1 (neuronal)
GO negative regulation of calcium ion tra	1	3	0.1913587	4842 nitric oxide synthase 1 (neuronal)
GO nitric-oxide synthase activity	1	3	0.1913587	4842 nitric oxide synthase 1 (neuronal)
GO tetrahydrobiopterin binding	1	3	0.1913587	4842 nitric oxide synthase 1 (neuronal)
GO neurotrophin binding	1	3	0.1913587	4915 neurotrophic tyrosine kinase, receptor, type 2
GO phenylalanine 4-monooxygenase acti	1	3	0.1913587	5053 phenylalanine hydroxylase
GO rRNA methyltransferase activity	1	3	0.1913587	51093 chromosome 1 open reading frame 66
GO rRNA modification	1	3	0.1913587	51093 chromosome 1 open reading frame 66
GO calmodulin-dependent cyclic-nucleot	1	3	0.1913587	5136 phosphodiesterase 1A, calmodulin-dependent
GO cell-substrate junction	1	3	0.1913587	5239 phosphoglucomutase 5
GO growth hormone receptor signaling p	1	3	0.1913587	5295 phosphoinositide-3-kinase, regulatory subunit 1 (alpha)
GO phosphoinositide 3-kinase regulator ;	1	3	0.1913587	5295 phosphoinositide-3-kinase, regulatory subunit 1 (alpha)
GO smooth muscle cell migration	1	3	0.1913587	5327 plasminogen activator, tissue
GO procollagen-lysine 5-dioxygenase act	1	3	0.1913587	5351 procollagen-lysine 1, 2-oxoglutarate 5-dioxygenase 1
GO centrosome localization	1	3	0.1913587	5362 plexin A2
GO limb bud formation	1	3	0.1913587	5362 plexin A2
GO negative regulation of synaptic transp	1	3	0.1913587	5367 pro-melanin-concentrating hormone
GO positive regulation of circadian sleep,	1	3	0.1913587	5367 pro-melanin-concentrating hormone
GO cobalt ion binding	1	3	0.1913587	5371 promyelocytic leukemia
GO mesenchymal to epithelial transition	1	3	0.1913587	54361 wingless-type MMTV integration site family, member 4
GO tertiary branching involved in mamm	1	3	0.1913587	54361 wingless-type MMTV integration site family, member 4
GO miRNA binding	1	3	0.1913587	5460 POU class 5 homeobox 1
GO response to nematode	1	3	0.1913587	55600 intelectin 1 (galactofuranose binding)
GO DNA damage induced protein phospho	1	3	0.1913587	5608 mitogen-activated protein kinase kinase 6
GO inorganic phosphate transmembrane	1	3	0.1913587	56172 ankylosis, progressive homolog (mouse)
GO outer membrane	1	3	0.1913587	56172 ankylosis, progressive homolog (mouse)
GO intracellular calcium activated chloric	1	3	0.1913587	56923 neuromedin U receptor 2
GO reduction of food intake in response	1	3	0.1913587	56923 neuromedin U receptor 2
GO activation of Ral GTPase activity	1	3	0.1913587	57186 Ral GTPase activating protein, alpha subunit 2 (catalytic)
GO Ral GTPase activator activity	1	3	0.1913587	57186 Ral GTPase activating protein, alpha subunit 2 (catalytic)
GO platelet activating factor receptor act	1	3	0.1913587	5724 platelet-activating factor receptor

GO chaperone cofactor-dependent prote	1	3	0.1913587	573 BCL2-associated athanogene
GO somatic diversification of immunoglo	1	3	0.1913587	57379 activation-induced cytidine deaminase
GO cyclooxygenase pathway	1	3	0.1913587	5742 prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase a
GO uterus development	1	3	0.1913587	5950 retinol binding protein 4, plasma
GO midgut development	1	3	0.1913587	6256 retinoid X receptor, alpha
GO retinoid-X receptor activity	1	3	0.1913587	6256 retinoid X receptor, alpha
GO ventricular cardiac muscle cell differe	1	3	0.1913587	6256 retinoid X receptor, alpha
GO vitamin D response element binding	1	3	0.1913587	6256 retinoid X receptor, alpha
GO regulation of retinal cell programme	1	3	0.1913587	627 brain-derived neurotrophic factor
GO detection of biotic stimulus	1	3	0.1913587	64127 nucleotide-binding oligomerization domain containing 2
GO innate immune response in mucosa	1	3	0.1913587	64127 nucleotide-binding oligomerization domain containing 2
GO positive regulation of interleukin-17 p	1	3	0.1913587	64127 nucleotide-binding oligomerization domain containing 2
GO beta-galactoside alpha-2,3-sialyltrans	1	3	0.1913587	6484 ST3 beta-galactoside alpha-2,3-sialyltransferase 4
GO cellular response to water deprivatio	1	3	0.1913587	6494 signal-induced proliferation-associated 1
GO Rap GTPase activator activity	1	3	0.1913587	6494 signal-induced proliferation-associated 1
GO D-aspartate import	1	3	0.1913587	6505 solute carrier family 1 (neuronal/epithelial high affinity glutamate trans
GO endocardial cushion development	1	3	0.1913587	652 bone morphogenetic protein 4
GO positive regulation of cartilage develo	1	3	0.1913587	652 bone morphogenetic protein 4
GO prostate gland morphogenesis	1	3	0.1913587	652 bone morphogenetic protein 4
GO renal system process	1	3	0.1913587	652 bone morphogenetic protein 4
GO specification of organ position	1	3	0.1913587	652 bone morphogenetic protein 4
GO trachea development	1	3	0.1913587	652 bone morphogenetic protein 4
GO protein anchor	1	3	0.1913587	6521 solute carrier family 4, anion exchanger, member 1 (erythrocyte memb
GO basic amino acid transmembrane tra	1	3	0.1913587	6542 solute carrier family 7 (cationic amino acid transporter, y+ system), me
GO mitochondrial ATP synthesis coupled	1	3	0.1913587	6622 synuclein, alpha (non A4 component of amyloid precursor)
GO negative regulation of histone acetyl	1	3	0.1913587	6622 synuclein, alpha (non A4 component of amyloid precursor)
GO positive regulation of neurotransmitt	1	3	0.1913587	6622 synuclein, alpha (non A4 component of amyloid precursor)
GO intrinsic to internal side of plasma me	1	3	0.1913587	6710 spectrin, beta, erythrocytic
GO clathrin sculpted acetylcholine transp	1	3	0.1913587	6857 synaptotagmin I
GO thioredoxin peroxidase activity	1	3	0.1913587	7001 peroxiredoxin 2
GO cardiac epithelial to mesenchymal tra	1	3	0.1913587	7049 transforming growth factor, beta receptor III
GO inhibin-beta glycan-ActRII complex	1	3	0.1913587	7049 transforming growth factor, beta receptor III
GO response to molecule of fungal origin	1	3	0.1913587	7097 toll-like receptor 2
GO detection of lipopolysaccharide	1	3	0.1913587	7099 toll-like receptor 4
GO positive regulation of interferon-alph	1	3	0.1913587	7099 toll-like receptor 4
GO myofibril assembly	1	3	0.1913587	7111 tropomodulin 1

GO	granulosa cell differentiation	1	3	0.1913587	726 calpain 5
GO	cellular response to calcium ion	1	3	0.1913587	7474 wingless-type MMTV integration site family, member 5A
GO	epithelial cell proliferation involved in	1	3	0.1913587	7474 wingless-type MMTV integration site family, member 5A
GO	frizzled binding	1	3	0.1913587	7474 wingless-type MMTV integration site family, member 5A
GO	positive regulation of protein kinase C	1	3	0.1913587	7474 wingless-type MMTV integration site family, member 5A
GO	positive regulation of T cell chemotaxis	1	3	0.1913587	7474 wingless-type MMTV integration site family, member 5A
GO	regulation of branching involved in morphogenesis	1	3	0.1913587	7474 wingless-type MMTV integration site family, member 5A
GO	acetate-CoA ligase activity	1	3	0.1913587	79611 acyl-CoA synthetase short-chain family member 3
GO	calcitonin receptor activity	1	3	0.1913587	799 calcitonin receptor
GO	microtubule-based flagellum part	1	3	0.1913587	799 calcitonin receptor
GO	positive regulation of interleukin-1 alpha	1	3	0.1913587	834 caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, co
GO	inner ear receptor stereocilium organ	1	3	0.1913587	84059 G protein-coupled receptor 98
GO	fibroblast migration	1	3	0.1913587	84159 AT rich interactive domain 5B (MRF1-like)
GO	peptide transporter activity	1	3	0.1913587	84976 dispatched homolog 1 (Drosophila)
GO	peptide transport	1	3	0.1913587	84976 dispatched homolog 1 (Drosophila)
GO	diacylglycerol metabolic process	1	3	0.1913587	8527 diacylglycerol kinase, delta 130kDa
GO	second-messenger-mediated signaling	1	3	0.1913587	8527 diacylglycerol kinase, delta 130kDa
GO	positive regulation of megakaryocyte	1	3	0.1913587	85477 scinderin
GO	syndecan binding	1	3	0.1913587	8646 chordin
GO	sodium:bicarbonate symporter activity	1	3	0.1913587	8671 solute carrier family 4, sodium bicarbonate cotransporter, member 4
GO	axon hillock	1	3	0.1913587	885 cholecystokinin
GO	pantetheine hydrolase activity	1	3	0.1913587	8875 vanin 2
GO	spongiotrophoblast differentiation	1	3	0.1913587	9021 suppressor of cytokine signaling 3
GO	sulfate assimilation	1	3	0.1913587	9060 3'-phosphoadenosine 5'-phosphosulfate synthase 2
GO	regulation of actin polymerization or	1	3	0.1913587	9087 thymosin beta 4, Y-linked
GO	positive regulation of activin receptor	1	3	0.1913587	91 activin A receptor, type IB
GO	phosphatidylinositol-4-phosphate binding	1	3	0.1913587	91404 SEC14 and spectrin domains 1
GO	transforming growth factor beta receptor	1	3	0.1913587	94 activin A receptor type II-like 1
GO	intrinsic to Golgi membrane	1	3	0.1913587	9435 carbohydrate (N-acetylglucosamine-6-O) sulfotransferase 2
GO	NAD+ nucleosidase activity	1	3	0.1913587	952 CD38 molecule
GO	histone H3 deacetylation	1	3	0.1913587	9734 histone deacetylase 9
GO	histone H4 deacetylation	1	3	0.1913587	9734 histone deacetylase 9
GO	rhombomere 5 development	1	3	0.1913587	9935 v-maf musculoaponeurotic fibrosarcoma oncogene homolog B (avian)
GO	receptor binding	18	211	0.195819	10417 spondin 2, extracellular matrix protein
GO	receptor binding	18	211	0.195819	10507 sema domain, immunoglobulin domain (Ig), transmembrane domain (T
GO	receptor binding	18	211	0.195819	112 adenylate cyclase 6

GO receptor binding	18	211	0.195819	1803 dipeptidyl-peptidase 4
GO receptor binding	18	211	0.195819	23529 cardiotrophin-like cytokine factor 1
GO receptor binding	18	211	0.195819	23780 apolipoprotein L, 2
GO receptor binding	18	211	0.195819	30010 neurexophilin 1
GO receptor binding	18	211	0.195819	3827 kininogen 1
GO receptor binding	18	211	0.195819	4692 necdin homolog (mouse)
GO receptor binding	18	211	0.195819	5025 purinergic receptor P2X, ligand-gated ion channel, 4
GO receptor binding	18	211	0.195819	55600 intelectin 1 (galactofuranose binding)
GO receptor binding	18	211	0.195819	5972 renin
GO receptor binding	18	211	0.195819	6604 SWI/SNF related, matrix associated, actin dependent regulator of chromatin
GO receptor binding	18	211	0.195819	718 complement component 3
GO receptor binding	18	211	0.195819	8740 tumor necrosis factor (ligand) superfamily, member 14
GO receptor binding	18	211	0.195819	8744 tumor necrosis factor (ligand) superfamily, member 9
GO receptor binding	18	211	0.195819	9788 metastasis suppressor 1
GO receptor binding	18	211	0.195819	9966 tumor necrosis factor (ligand) superfamily, member 15
GO cholesterol transport	2	12	0.1959229	1080 cystic fibrosis transmembrane conductance regulator (ATP-binding cassette)
GO cholesterol transport	2	12	0.1959229	3949 low density lipoprotein receptor
GO Rac GTPase binding	2	12	0.1959229	10811 NADPH oxidase activator 1
GO Rac GTPase binding	2	12	0.1959229	27035 NADPH oxidase 1
GO microvillus membrane	2	12	0.1959229	112 adenylate cyclase 6
GO microvillus membrane	2	12	0.1959229	8842 prominin 1
GO keratinocyte proliferation	2	12	0.1959229	11202 kallikrein-related peptidase 8
GO keratinocyte proliferation	2	12	0.1959229	195814 short chain dehydrogenase/reductase family 16C, member 5
GO positive regulation of macrophage de	2	12	0.1959229	1435 colony stimulating factor 1 (macrophage)
GO positive regulation of macrophage de	2	12	0.1959229	183 angiotensinogen (serpin peptidase inhibitor, clade A, member 8)
GO lysosphingolipid and lysophosphatidi	2	12	0.1959229	1901 sphingosine-1-phosphate receptor 1
GO lysosphingolipid and lysophosphatidi	2	12	0.1959229	1902 lysophosphatidic acid receptor 1
GO neuromuscular synaptic transmission	2	12	0.1959229	1960 early growth response 3
GO neuromuscular synaptic transmission	2	12	0.1959229	23095 kinesin family member 1B
GO eye photoreceptor cell development	2	12	0.1959229	23418 crumbs homolog 1 (Drosophila)
GO eye photoreceptor cell development	2	12	0.1959229	6096 RAR-related orphan receptor B
GO positive regulation of caspase activity	2	12	0.1959229	29108 PYD and CARD domain containing
GO positive regulation of caspase activity	2	12	0.1959229	83595 SRY (sex determining region Y)-box 7
GO tissue homeostasis	2	12	0.1959229	29123 ankyrin repeat domain 11
GO tissue homeostasis	2	12	0.1959229	5025 purinergic receptor P2X, ligand-gated ion channel, 4
GO insulin receptor substrate binding	2	12	0.1959229	3643 insulin receptor

GO	insulin receptor substrate binding	2	12	0.1959229	5295 phosphoinositide-3-kinase, regulatory subunit 1 (alpha)
GO	low-density lipoprotein particle	2	12	0.1959229	3949 low density lipoprotein receptor
GO	low-density lipoprotein particle	2	12	0.1959229	6653 sortilin-related receptor, L(DLR class) A repeats-containing
GO	melanocyte differentiation	2	12	0.1959229	4286 microphthalmia-associated transcription factor
GO	melanocyte differentiation	2	12	0.1959229	5873 RAB27A, member RAS oncogene family
GO	positive regulation of calcium ion tra	2	12	0.1959229	5025 purinergic receptor P2X, ligand-gated ion channel, 4
GO	positive regulation of calcium ion tra	2	12	0.1959229	57620 stromal interaction molecule 2
GO	retinoic acid receptor signaling pathv	2	12	0.1959229	5371 promyelocytic leukemia
GO	retinoic acid receptor signaling pathv	2	12	0.1959229	6256 retinoid X receptor, alpha
GO	positive regulation of stress-activatec	2	12	0.1959229	64127 nucleotide-binding oligomerization domain containing 2
GO	positive regulation of stress-activatec	2	12	0.1959229	7099 toll-like receptor 4
GO	anion transmembrane transporter ac	2	12	0.1959229	6521 solute carrier family 4, anion exchanger, member 1 (erythrocyte memb
GO	anion transmembrane transporter ac	2	12	0.1959229	8671 solute carrier family 4, sodium bicarbonate cotransporter, member 4
GO	caspase inhibitor activity	2	12	0.1959229	6622 synuclein, alpha (non A4 component of amyloid precursor)
GO	caspase inhibitor activity	2	12	0.1959229	8740 tumor necrosis factor (ligand) superfamily, member 14
GO	protein tyrosine phosphatase activity	8	82	0.1967798	10076 protein tyrosine phosphatase, receptor type, U
GO	protein tyrosine phosphatase activity	8	82	0.1967798	1844 dual specificity phosphatase 2
GO	protein tyrosine phosphatase activity	8	82	0.1967798	1847 dual specificity phosphatase 5
GO	protein tyrosine phosphatase activity	8	82	0.1967798	26191 protein tyrosine phosphatase, non-receptor type 22 (lymphoid)
GO	protein tyrosine phosphatase activity	8	82	0.1967798	54961 slingshot homolog 3 (Drosophila)
GO	protein tyrosine phosphatase activity	8	82	0.1967798	5774 protein tyrosine phosphatase, non-receptor type 3
GO	protein tyrosine phosphatase activity	8	82	0.1967798	5801 protein tyrosine phosphatase, receptor type, R
GO	protein tyrosine phosphatase activity	8	82	0.1967798	8556 CDC14 cell division cycle 14 homolog A (S. cerevisiae)
GO	positive regulation of transcription	13	146	0.1987917	10891 peroxisome proliferator-activated receptor gamma, coactivator 1 alpha
GO	positive regulation of transcription	13	146	0.1987917	1958 early growth response 1
GO	positive regulation of transcription	13	146	0.1987917	222546 regulatory factor X, 6
GO	positive regulation of transcription	13	146	0.1987917	2353 FBJ murine osteosarcoma viral oncogene homolog
GO	positive regulation of transcription	13	146	0.1987917	2737 GLI family zinc finger 3
GO	positive regulation of transcription	13	146	0.1987917	285704 RGM domain family, member B
GO	positive regulation of transcription	13	146	0.1987917	3725 jun oncogene
GO	positive regulation of transcription	13	146	0.1987917	4087 SMAD family member 2
GO	positive regulation of transcription	13	146	0.1987917	4778 nuclear factor (erythroid-derived 2), 45kDa
GO	positive regulation of transcription	13	146	0.1987917	5465 peroxisome proliferator-activated receptor alpha
GO	positive regulation of transcription	13	146	0.1987917	6256 retinoid X receptor, alpha
GO	positive regulation of transcription	13	146	0.1987917	7026 nuclear receptor subfamily 2, group F, member 2
GO	positive regulation of transcription	13	146	0.1987917	94 activin A receptor type II-like 1

GO sulfotransferase activity	4	34	0.2002871	10090 uronyl-2-sulfotransferase
GO sulfotransferase activity	4	34	0.2002871	6819 sulfotransferase family, cytosolic, 1C, member 2
GO sulfotransferase activity	4	34	0.2002871	8509 N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 2
GO sulfotransferase activity	4	34	0.2002871	9435 carbohydrate (N-acetylglucosamine-6-O) sulfotransferase 2
GO PML body	4	34	0.2002871	11200 CHK2 checkpoint homolog ( <i>S. pombe</i> )
GO PML body	4	34	0.2002871	28996 homeodomain interacting protein kinase 2
GO PML body	4	34	0.2002871	5371 promyelocytic leukemia
GO PML body	4	34	0.2002871	81603 tripartite motif-containing 8
GO activation of protein kinase C activity	4	34	0.2002871	1906 endothelin 1
GO activation of protein kinase C activity	4	34	0.2002871	56288 par-3 partitioning defective 3 homolog ( <i>C. elegans</i> )
GO activation of protein kinase C activity	4	34	0.2002871	8527 diacylglycerol kinase, delta 130kDa
GO activation of protein kinase C activity	4	34	0.2002871	885 cholecystokinin
GO humoral immune response	4	34	0.2002871	29760 B-cell linker
GO humoral immune response	4	34	0.2002871	3569 interleukin 6 (interferon, beta 2)
GO humoral immune response	4	34	0.2002871	5699 proteasome (prosome, macropain) subunit, beta type, 10
GO humoral immune response	4	34	0.2002871	684 bone marrow stromal cell antigen 2
GO response to calcium ion	5	46	0.2037956	10628 thioredoxin interacting protein
GO response to calcium ion	5	46	0.2037956	1843 dual specificity phosphatase 1
GO response to calcium ion	5	46	0.2037956	2033 E1A binding protein p300
GO response to calcium ion	5	46	0.2037956	311 annexin A11
GO response to calcium ion	5	46	0.2037956	5122 proprotein convertase subtilisin/kexin type 1
GO Z disc	5	46	0.2037956	11155 LIM domain binding 3
GO Z disc	5	46	0.2037956	27295 PDZ and LIM domain 3
GO Z disc	5	46	0.2037956	5239 phosphoglucomutase 5
GO Z disc	5	46	0.2037956	6521 solute carrier family 4, anion exchanger, member 1 (erythrocyte memb
GO Z disc	5	46	0.2037956	84033 obscurin, cytoskeletal calmodulin and titin-interacting RhoGEF
GO regulation of ARF GTPase activity	3	23	0.205263	116984 ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 2
GO regulation of ARF GTPase activity	3	23	0.205263	3268 ArfGAP with FG repeats 2
GO regulation of ARF GTPase activity	3	23	0.205263	55616 ArfGAP with SH3 domain, ankyrin repeat and PH domain 3
GO developmental growth	3	23	0.205263	127343 diencephalon/mesencephalon homeobox 1
GO developmental growth	3	23	0.205263	2737 GLI family zinc finger 3
GO developmental growth	3	23	0.205263	4087 SMAD family member 2
GO neuromuscular process controlling b	3	23	0.205263	2055 ceroid-lipofuscinosis, neuronal 8 (epilepsy, progressive with mental ret
GO neuromuscular process controlling b	3	23	0.205263	53405 chloride intracellular channel 5
GO neuromuscular process controlling b	3	23	0.205263	8013 nuclear receptor subfamily 4, group A, member 3
GO cell maturation	3	23	0.205263	2624 GATA binding protein 2

GO cell maturation	3	23	0.205263	26468 LIM homeobox 6
GO cell maturation	3	23	0.205263	5972 renin
GO positive regulation of osteoblast diffe	3	23	0.205263	3569 interleukin 6 (interferon, beta 2)
GO positive regulation of osteoblast diffe	3	23	0.205263	3570 interleukin 6 receptor
GO positive regulation of osteoblast diffe	3	23	0.205263	652 bone morphogenetic protein 4
GO steroid binding	3	23	0.205263	4306 nuclear receptor subfamily 3, group C, member 2
GO steroid binding	3	23	0.205263	54852 progesterin and adiponQ receptor family member V
GO steroid binding	3	23	0.205263	6256 retinoid X receptor, alpha
GO positive regulation of insulin secretio	3	23	0.205263	5950 retinol binding protein 4, plasma
GO positive regulation of insulin secretio	3	23	0.205263	8660 insulin receptor substrate 2
GO positive regulation of insulin secretio	3	23	0.205263	952 CD38 molecule
GO neurotransmitter secretion	3	23	0.205263	6857 synaptotagmin I
GO neurotransmitter secretion	3	23	0.205263	8938 BAI1-associated protein 3
GO neurotransmitter secretion	3	23	0.205263	9892 synaptosomal-associated protein, 91kDa homolog (mouse)
GO blood coagulation	7	71	0.2103789	2153 coagulation factor V (proaccelerin, labile factor)
GO blood coagulation	7	71	0.2103789	22915 multimerin 1
GO blood coagulation	7	71	0.2103789	30008 EGF-containing fibulin-like extracellular matrix protein 2
GO blood coagulation	7	71	0.2103789	3587 interleukin 10 receptor, alpha
GO blood coagulation	7	71	0.2103789	5327 plasminogen activator, tissue
GO blood coagulation	7	71	0.2103789	5873 RAB27A, member RAS oncogene family
GO blood coagulation	7	71	0.2103789	725 complement component 4 binding protein, beta
GO FAD binding	7	71	0.2103789	27035 NADPH oxidase 1
GO FAD binding	7	71	0.2103789	316 aldehyde oxidase 1
GO FAD binding	7	71	0.2103789	35 acyl-Coenzyme A dehydrogenase, C-2 to C-3 short chain
GO FAD binding	7	71	0.2103789	4129 monoamine oxidase B
GO FAD binding	7	71	0.2103789	4842 nitric oxide synthase 1 (neuronal)
GO FAD binding	7	71	0.2103789	56605 ERO1-like beta ( <i>S. cerevisiae</i> )
GO FAD binding	7	71	0.2103789	79689 STEAP family member 4
GO positive regulation of transcription, C	11	122	0.2120286	10891 peroxisome proliferator-activated receptor gamma, coactivator 1 alpha
GO positive regulation of transcription, C	11	122	0.2120286	2114 v-ets erythroblastosis virus E26 oncogene homolog 2 (avian)
GO positive regulation of transcription, C	11	122	0.2120286	2122 MDS1 and EVI1 complex locus
GO positive regulation of transcription, C	11	122	0.2120286	2296 forkhead box C1
GO positive regulation of transcription, C	11	122	0.2120286	2303 forkhead box C2 (MFH-1, mesenchyme forkhead 1)
GO positive regulation of transcription, C	11	122	0.2120286	28996 homeodomain interacting protein kinase 2
GO positive regulation of transcription, C	11	122	0.2120286	4087 SMAD family member 2
GO positive regulation of transcription, C	11	122	0.2120286	4802 nuclear transcription factor Y, gamma

GO	positive regulation of transcription, D	11	122	0.2120286	51085 MLX interacting protein-like
GO	positive regulation of transcription, D	11	122	0.2120286	55810 forkhead box J2
GO	positive regulation of transcription, D	11	122	0.2120286	6604 SWI/SNF related, matrix associated, actin dependent regulator of chromatin
GO	organ regeneration	4	35	0.21484	10076 protein tyrosine phosphatase, receptor type, U
GO	organ regeneration	4	35	0.21484	8013 nuclear receptor subfamily 4, group A, member 3
GO	organ regeneration	4	35	0.21484	8531 cold shock domain protein A
GO	organ regeneration	4	35	0.21484	9021 suppressor of cytokine signaling 3
GO	embryonic limb morphogenesis	4	35	0.21484	2201 fibrillin 2
GO	embryonic limb morphogenesis	4	35	0.21484	4853 Notch homolog 2 (Drosophila)
GO	embryonic limb morphogenesis	4	35	0.21484	5396 paired related homeobox 1
GO	embryonic limb morphogenesis	4	35	0.21484	7474 wingless-type MMTV integration site family, member 5A
GO	extracellular matrix	4	35	0.21484	2263 fibroblast growth factor receptor 2
GO	extracellular matrix	4	35	0.21484	4856 nephroblastoma overexpressed gene
GO	extracellular matrix	4	35	0.21484	5046 proprotein convertase subtilisin/kexin type 6
GO	extracellular matrix	4	35	0.21484	5327 plasminogen activator, tissue
GO	binding	39	500	0.2156733	10170 dehydrogenase/reductase (SDR family) member 9
GO	binding	39	500	0.2156733	11187 plakophilin 3
GO	binding	39	500	0.2156733	112724 retinol dehydrogenase 13 (all-trans/9-cis)
GO	binding	39	500	0.2156733	123096 solute carrier family 25, member 29
GO	binding	39	500	0.2156733	125 alcohol dehydrogenase 1B (class I), beta polypeptide
GO	binding	39	500	0.2156733	1462 versican
GO	binding	39	500	0.2156733	157506 retinol dehydrogenase 10 (all-trans)
GO	binding	39	500	0.2156733	157855 potassium channel, subfamily U, member 1
GO	binding	39	500	0.2156733	195814 short chain dehydrogenase/reductase family 16C, member 5
GO	binding	39	500	0.2156733	2201 fibrillin 2
GO	binding	39	500	0.2156733	22925 phospholipase A2 receptor 1, 180kDa
GO	binding	39	500	0.2156733	23331 tetratricopeptide repeat domain 28
GO	binding	39	500	0.2156733	23382 adenosylhomocysteinase-like 2
GO	binding	39	500	0.2156733	257019 FERM domain containing 3
GO	binding	39	500	0.2156733	316 aldehyde oxidase 1
GO	binding	39	500	0.2156733	3294 hydroxysteroid (17-beta) dehydrogenase 2
GO	binding	39	500	0.2156733	339766 HEAT repeat containing 7B1
GO	binding	39	500	0.2156733	3437 interferon-induced protein with tetratricopeptide repeats 3
GO	binding	39	500	0.2156733	345275 hydroxysteroid (17-beta) dehydrogenase 13
GO	binding	39	500	0.2156733	3823 killer cell lectin-like receptor subfamily C, member 3
GO	binding	39	500	0.2156733	399671 HEAT repeat containing 4



GO binding	39	500	0.2156733	4065 lymphocyte antigen 75
GO binding	39	500	0.2156733	4246 secretoglobin, family 2A, member 1
GO binding	39	500	0.2156733	50865 heme binding protein 1
GO binding	39	500	0.2156733	51309 armadillo repeat containing, X-linked 1
GO binding	39	500	0.2156733	5318 plakophilin 2
GO binding	39	500	0.2156733	54436 SH3 domain and tetratricopeptide repeats 1
GO binding	39	500	0.2156733	55130 armadillo repeat containing 4
GO binding	39	500	0.2156733	55761 tetratricopeptide repeat domain 17
GO binding	39	500	0.2156733	622 3-hydroxybutyrate dehydrogenase, type 1
GO binding	39	500	0.2156733	7404 ubiquitously transcribed tetratricopeptide repeat gene, Y-linked
GO binding	39	500	0.2156733	79689 STEAP family member 4
GO binding	39	500	0.2156733	8013 nuclear receptor subfamily 4, group A, member 3
GO binding	39	500	0.2156733	83857 transmembrane and tetratricopeptide repeat containing 1
GO binding	39	500	0.2156733	93349 SP140 nuclear body protein-like
GO binding	39	500	0.2156733	9481 solute carrier family 25, member 27
GO binding	39	500	0.2156733	952 CD38 molecule
GO binding	39	500	0.2156733	9563 hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase)
GO binding	39	500	0.2156733	9823 armadillo repeat containing, X-linked 2
GO hydrolase activity, acting on acid anhydrides	5	47	0.2162467	148229 ATPase, class I, type 8B, member 3
GO hydrolase activity, acting on acid anhydrides	5	47	0.2162467	493 ATPase, Ca <sup>++</sup> transporting, plasma membrane 4
GO hydrolase activity, acting on acid anhydrides	5	47	0.2162467	498 ATP synthase, H <sup>+</sup> transporting, mitochondrial F1 complex, alpha subunit
GO hydrolase activity, acting on acid anhydrides	5	47	0.2162467	79895 ATPase, class I, type 8B, member 4
GO hydrolase activity, acting on acid anhydrides	5	47	0.2162467	9914 ATPase, Ca <sup>++</sup> transporting, type 2C, member 2
GO SH3 domain binding	9	97	0.217539	1815 dopamine receptor D4
GO SH3 domain binding	9	97	0.217539	23092 Rho GTPase activating protein 26
GO SH3 domain binding	9	97	0.217539	395 Rho GTPase activating protein 6
GO SH3 domain binding	9	97	0.217539	5063 p21 protein (Cdc42/Rac)-activated kinase 3
GO SH3 domain binding	9	97	0.217539	55740 enabled homolog (Drosophila)
GO SH3 domain binding	9	97	0.217539	6452 SH3-domain binding protein 2
GO SH3 domain binding	9	97	0.217539	80115 BAI1-associated protein 2-like 2
GO SH3 domain binding	9	97	0.217539	8751 ADAM metalloproteinase domain 15
GO SH3 domain binding	9	97	0.217539	9788 metastasis suppressor 1
GO heme binding	10	110	0.2189991	1558 cytochrome P450, family 2, subfamily C, polypeptide 8
GO heme binding	10	110	0.2189991	1559 cytochrome P450, family 2, subfamily C, polypeptide 9
GO heme binding	10	110	0.2189991	1571 cytochrome P450, family 2, subfamily E, polypeptide 1
GO heme binding	10	110	0.2189991	1577 cytochrome P450, family 3, subfamily A, polypeptide 5

GO heme binding	10	110	0.2189991	4151 myoglobin
GO heme binding	10	110	0.2189991	4842 nitric oxide synthase 1 (neuronal)
GO heme binding	10	110	0.2189991	50865 heme binding protein 1
GO heme binding	10	110	0.2189991	5742 prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and
GO heme binding	10	110	0.2189991	6916 thromboxane A synthase 1 (platelet)
GO heme binding	10	110	0.2189991	79152 fatty acid 2-hydroxylase
GO transferase activity, transferring glyco	13	149	0.2190026	10317 UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 5
GO transferase activity, transferring glyco	13	149	0.2190026	192134 UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 6 (core
GO transferase activity, transferring glyco	13	149	0.2190026	2525 fucosyltransferase 3 (galactoside 3(4)-L-fucosyltransferase, Lewis blood
GO transferase activity, transferring glyco	13	149	0.2190026	2526 fucosyltransferase 4 (alpha (1,3) fucosyltransferase, myeloid-specific)
GO transferase activity, transferring glyco	13	149	0.2190026	2589 UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosami
GO transferase activity, transferring glyco	13	149	0.2190026	374378 UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosami
GO transferase activity, transferring glyco	13	149	0.2190026	53947 alpha 1,4-galactosyltransferase
GO transferase activity, transferring glyco	13	149	0.2190026	56913 core 1 synthase, glycoprotein-N-acetylgalactosamine 3-beta-galactosyl
GO transferase activity, transferring glyco	13	149	0.2190026	79668 poly (ADP-ribose) polymerase family, member 8
GO transferase activity, transferring glyco	13	149	0.2190026	79695 UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosami
GO transferase activity, transferring glyco	13	149	0.2190026	84875 poly (ADP-ribose) polymerase family, member 10
GO transferase activity, transferring glyco	13	149	0.2190026	8706 beta-1,3-N-acetylgalactosaminyltransferase 1 (globoside blood group)
GO transferase activity, transferring glyco	13	149	0.2190026	93100 nicotinate phosphoribosyltransferase domain containing 1
GO response to nutrient	7	72	0.2204007	2182 acyl-CoA synthetase long-chain family member 4
GO response to nutrient	7	72	0.2204007	240 arachidonate 5-lipoxygenase
GO response to nutrient	7	72	0.2204007	2642 glucagon receptor
GO response to nutrient	7	72	0.2204007	51703 acyl-CoA synthetase long-chain family member 5
GO response to nutrient	7	72	0.2204007	6256 retinoid X receptor, alpha
GO response to nutrient	7	72	0.2204007	6750 somatostatin
GO response to nutrient	7	72	0.2204007	6751 somatostatin receptor 1
GO histone deacetylase activity	2	13	0.2216579	10014 histone deacetylase 5
GO histone deacetylase activity	2	13	0.2216579	9734 histone deacetylase 9
GO bone mineralization	2	13	0.2216579	10117 enamelin
GO bone mineralization	2	13	0.2216579	7071 Kruppel-like factor 10
GO induction of an organ	2	13	0.2216579	10252 sprouty homolog 1, antagonist of FGF signaling (Drosophila)
GO induction of an organ	2	13	0.2216579	652 bone morphogenetic protein 4
GO positive regulation of actin filament p	2	13	0.2216579	10435 CDC42 effector protein (Rho GTPase binding) 2
GO positive regulation of actin filament p	2	13	0.2216579	148170 CDC42 effector protein (Rho GTPase binding) 5
GO superoxide metabolic process	2	13	0.2216579	10811 NADPH oxidase activator 1
GO superoxide metabolic process	2	13	0.2216579	27035 NADPH oxidase 1

GO	acetylcholine receptor activity	2	13	0.2216579	1139	cholinergic receptor, nicotinic, alpha 7
GO	acetylcholine receptor activity	2	13	0.2216579	8973	cholinergic receptor, nicotinic, alpha 6
GO	lipid storage	2	13	0.2216579	123	perilipin 2
GO	lipid storage	2	13	0.2216579	130399	activin A receptor, type IC
GO	carboxypeptidase activity	2	13	0.2216579	1363	carboxypeptidase E
GO	carboxypeptidase activity	2	13	0.2216579	1368	carboxypeptidase M
GO	positive regulation of phosphoinositid	2	13	0.2216579	183	angiotensinogen (serpin peptidase inhibitor, clade A, member 8)
GO	positive regulation of phosphoinositid	2	13	0.2216579	3479	insulin-like growth factor 1 (somatomedin C)
GO	middle ear morphogenesis	2	13	0.2216579	1906	endothelin 1
GO	middle ear morphogenesis	2	13	0.2216579	5396	paired related homeobox 1
GO	positive regulation of smooth muscle	2	13	0.2216579	1906	endothelin 1
GO	positive regulation of smooth muscle	2	13	0.2216579	5742	prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and
GO	negative regulation of proteolysis	2	13	0.2216579	2055	ceroid-lipofuscinosis, neuronal 8 (epilepsy, progressive with mental ret
GO	negative regulation of proteolysis	2	13	0.2216579	5327	plasminogen activator, tissue
GO	positive regulation vascular endothel	2	13	0.2216579	27035	NADPH oxidase 1
GO	positive regulation vascular endothel	2	13	0.2216579	718	complement component 3
GO	camera-type eye morphogenesis	2	13	0.2216579	2737	GLI family zinc finger 3
GO	camera-type eye morphogenesis	2	13	0.2216579	652	bone morphogenetic protein 4
GO	negative regulation of fat cell differer	2	13	0.2216579	28951	tribbles homolog 2 (Drosophila)
GO	negative regulation of fat cell differer	2	13	0.2216579	7474	wingless-type MMTV integration site family, member 5A
GO	labyrinthine layer blood vessel develk	2	13	0.2216579	3491	cysteine-rich, angiogenic inducer, 61
GO	labyrinthine layer blood vessel develk	2	13	0.2216579	3726	jun B proto-oncogene
GO	MAP kinase kinase activity	2	13	0.2216579	4293	mitogen-activated protein kinase kinase kinase 9
GO	MAP kinase kinase activity	2	13	0.2216579	5608	mitogen-activated protein kinase kinase 6
GO	RNA catabolic process	2	13	0.2216579	4939	2'-5'-oligoadenylate synthetase 2, 69/71kDa
GO	RNA catabolic process	2	13	0.2216579	8635	ribonuclease T2
GO	synaptic transmission, glutamatergic	2	13	0.2216579	5071	Parkinson disease (autosomal recessive, juvenile) 2, parkin
GO	synaptic transmission, glutamatergic	2	13	0.2216579	5327	plasminogen activator, tissue
GO	oogenesis	2	13	0.2216579	54852	progesterin and adipoQ receptor family member V
GO	oogenesis	2	13	0.2216579	55124	piwi-like 2 (Drosophila)
GO	protein targeting to membrane	2	13	0.2216579	56288	par-3 partitioning defective 3 homolog (C. elegans)
GO	protein targeting to membrane	2	13	0.2216579	64108	receptor (chemosensory) transporter protein 4
GO	T cell proliferation	2	13	0.2216579	7001	peroxiredoxin 2
GO	T cell proliferation	2	13	0.2216579	8740	tumor necrosis factor (ligand) superfamily, member 14
GO	ARF GTPase activator activity	3	24	0.2235348	116984	ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 2
GO	ARF GTPase activator activity	3	24	0.2235348	3268	ArfGAP with FG repeats 2

GO	ARF GTPase activator activity	3	24	0.2235348	55616 ArfGAP with SH3 domain, ankyrin repeat and PH domain 3
GO	G-protein signaling, coupled to cAMP	3	24	0.2235348	154 adrenergic, beta-2-, receptor, surface
GO	G-protein signaling, coupled to cAMP	3	24	0.2235348	2642 glucagon receptor
GO	G-protein signaling, coupled to cAMP	3	24	0.2235348	5734 prostaglandin E receptor 4 (subtype EP4)
GO	negative regulation of inflammatory r	3	24	0.2235348	154 adrenergic, beta-2-, receptor, surface
GO	negative regulation of inflammatory r	3	24	0.2235348	7133 tumor necrosis factor receptor superfamily, member 1B
GO	negative regulation of inflammatory r	3	24	0.2235348	7538 zinc finger protein 36, C3H type, homolog (mouse)
GO	visual learning	3	24	0.2235348	1813 dopamine receptor D2
GO	visual learning	3	24	0.2235348	3815 v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog
GO	visual learning	3	24	0.2235348	3845 v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog
GO	lung alveolus development	3	24	0.2235348	3479 insulin-like growth factor 1 (somatomedin C)
GO	lung alveolus development	3	24	0.2235348	652 bone morphogenetic protein 4
GO	lung alveolus development	3	24	0.2235348	91461 protein kinase domain containing, cytoplasmic homolog (mouse)
GO	response to gamma radiation	3	24	0.2235348	3570 interleukin 6 receptor
GO	response to gamma radiation	3	24	0.2235348	5371 promyelocytic leukemia
GO	response to gamma radiation	3	24	0.2235348	9021 suppressor of cytokine signaling 3
GO	learning	3	24	0.2235348	3725 jun oncogene
GO	learning	3	24	0.2235348	5071 Parkinson disease (autosomal recessive, juvenile) 2, parkin
GO	learning	3	24	0.2235348	5577 protein kinase, cAMP-dependent, regulatory, type II, beta
GO	proteolysis involved in cellular protei	3	24	0.2235348	5696 proteasome (prosome, macropain) subunit, beta type, 8 (large multifur
GO	proteolysis involved in cellular protei	3	24	0.2235348	5698 proteasome (prosome, macropain) subunit, beta type, 9 (large multifur
GO	proteolysis involved in cellular protei	3	24	0.2235348	5699 proteasome (prosome, macropain) subunit, beta type, 10
GO	fatty acid biosynthetic process	5	48	0.2289272	10826 chromosome 5 open reading frame 4
GO	fatty acid biosynthetic process	5	48	0.2289272	123099 degenerative spermatocyte homolog 2, lipid desaturase (Drosophila)
GO	fatty acid biosynthetic process	5	48	0.2289272	5742 prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase a
GO	fatty acid biosynthetic process	5	48	0.2289272	6916 thromboxane A synthase 1 (platelet)
GO	fatty acid biosynthetic process	5	48	0.2289272	79152 fatty acid 2-hydroxylase
GO	phosphoprotein phosphatase activity	4	36	0.2296705	10106 CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) sma
GO	phosphoprotein phosphatase activity	4	36	0.2296705	23035 PH domain and leucine rich repeat protein phosphatase 2
GO	phosphoprotein phosphatase activity	4	36	0.2296705	23371 tensin like C1 domain containing phosphatase (tensin 2)
GO	phosphoprotein phosphatase activity	4	36	0.2296705	8556 CDC14 cell division cycle 14 homolog A (S. cerevisiae)
GO	somitogenesis	4	36	0.2296705	2033 E1A binding protein p300
GO	somitogenesis	4	36	0.2296705	2296 forkhead box C1
GO	somitogenesis	4	36	0.2296705	5362 plexin A2
GO	somitogenesis	4	36	0.2296705	8313 axin 2
GO	response to organic substance	4	36	0.2296705	760 carbonic anhydrase II

GO response to organic substance	4	36	0.2296705	8527 diacylglycerol kinase, delta 130kDa
GO response to organic substance	4	36	0.2296705	9414 tight junction protein 2 (zona occludens 2)
GO response to organic substance	4	36	0.2296705	9619 ATP-binding cassette, sub-family G (WHITE), member 1
GO response to stress	10	112	0.2353436	10912 growth arrest and DNA-damage-inducible, gamma
GO response to stress	10	112	0.2353436	23043 TRAF2 and NCK interacting kinase
GO response to stress	10	112	0.2353436	27035 NADPH oxidase 1
GO response to stress	10	112	0.2353436	4616 growth arrest and DNA-damage-inducible, beta
GO response to stress	10	112	0.2353436	5025 purinergic receptor P2X, ligand-gated ion channel, 4
GO response to stress	10	112	0.2353436	5972 renin
GO response to stress	10	112	0.2353436	6446 serum/glucocorticoid regulated kinase 1
GO response to stress	10	112	0.2353436	760 carbonic anhydrase II
GO response to stress	10	112	0.2353436	8600 tumor necrosis factor (ligand) superfamily, member 11
GO response to stress	10	112	0.2353436	9537 tumor protein p53 inducible protein 11
GO female pregnancy	6	61	0.2366756	2353 FBJ murine osteosarcoma viral oncogene homolog
GO female pregnancy	6	61	0.2366756	412 steroid sulfatase (microsomal), isozyme S
GO female pregnancy	6	61	0.2366756	5016 oviductal glycoprotein 1, 120kDa
GO female pregnancy	6	61	0.2366756	53405 chloride intracellular channel 5
GO female pregnancy	6	61	0.2366756	6256 retinoid X receptor, alpha
GO female pregnancy	6	61	0.2366756	952 CD38 molecule
GO phospholipid biosynthetic process	5	49	0.2418162	10162 lysophosphatidylcholine acyltransferase 3
GO phospholipid biosynthetic process	5	49	0.2418162	154141 membrane bound O-acyltransferase domain containing 1
GO phospholipid biosynthetic process	5	49	0.2418162	256987 serine incorporator 5
GO phospholipid biosynthetic process	5	49	0.2418162	51703 acyl-CoA synthetase long-chain family member 5
GO phospholipid biosynthetic process	5	49	0.2418162	54947 lysophosphatidylcholine acyltransferase 2
GO wound healing	5	49	0.2418162	2331 fibromodulin
GO wound healing	5	49	0.2418162	375056 melanoma inhibitory activity family, member 3
GO wound healing	5	49	0.2418162	4015 lysyl oxidase
GO wound healing	5	49	0.2418162	5465 peroxisome proliferator-activated receptor alpha
GO wound healing	5	49	0.2418162	7474 wingless-type MMTV integration site family, member 5A
GO metallopeptidase activity	3	25	0.2421067	1363 carboxypeptidase E
GO metallopeptidase activity	3	25	0.2421067	1368 carboxypeptidase M
GO metallopeptidase activity	3	25	0.2421067	57094 carboxypeptidase A6
GO protein phosphatase binding	3	25	0.2421067	3643 insulin receptor
GO protein phosphatase binding	3	25	0.2421067	5295 phosphoinositide-3-kinase, regulatory subunit 1 (alpha)
GO protein phosphatase binding	3	25	0.2421067	8660 insulin receptor substrate 2
GO leukocyte cell-cell adhesion	3	25	0.2421067	3678 integrin, alpha 5 (fibronectin receptor, alpha polypeptide)

GO leukocyte cell-cell adhesion	3	25	0.2421067	3689 integrin, beta 2 (complement component 3 receptor 3 and 4 subunit)
GO leukocyte cell-cell adhesion	3	25	0.2421067	6850 spleen tyrosine kinase
GO symporter activity	10	113	0.2436812	10568 solute carrier family 34 (sodium phosphate), member 2
GO symporter activity	10	113	0.2436812	151473 solute carrier family 16, member 14 (monocarboxylic acid transporter)
GO symporter activity	10	113	0.2436812	6505 solute carrier family 1 (neuronal/epithelial high affinity glutamate transporter)
GO symporter activity	10	113	0.2436812	6535 solute carrier family 6 (neurotransmitter transporter, creatine), member 1
GO symporter activity	10	113	0.2436812	6564 solute carrier family 15 (oligopeptide transporter), member 1
GO symporter activity	10	113	0.2436812	6565 solute carrier family 15 (H <sup>+</sup> /peptide transporter), member 2
GO symporter activity	10	113	0.2436812	84561 solute carrier family 12 (potassium/chloride transporters), member 8
GO symporter activity	10	113	0.2436812	8671 solute carrier family 4, sodium bicarbonate cotransporter, member 4
GO symporter activity	10	113	0.2436812	9194 solute carrier family 16, member 7 (monocarboxylic acid transporter 2)
GO symporter activity	10	113	0.2436812	9962 solute carrier family 23 (nucleobase transporters), member 2
GO activation of adenylate cyclase activity	4	37	0.2447449	112 adenylate cyclase 6
GO activation of adenylate cyclase activity	4	37	0.2447449	154 adrenergic, beta-2-, receptor, surface
GO activation of adenylate cyclase activity	4	37	0.2447449	2642 glucagon receptor
GO activation of adenylate cyclase activity	4	37	0.2447449	799 calcitonin receptor
GO protein amino acid sulfation	1	4	0.2466366	10090 uronyl-2-sulfotransferase
GO CTD phosphatase activity	1	4	0.2466366	10106 CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small
GO branching involved in prostate gland	1	4	0.2466366	10116 fem-1 homolog b (C. elegans)
GO 9-cis-retinoic acid biosynthetic process	1	4	0.2466366	10170 dehydrogenase/reductase (SDR family) member 9
GO base conversion or substitution editing	1	4	0.2466366	104 adenosine deaminase, RNA-specific, B1 (RED1 homolog rat)
GO regulation of respiratory burst	1	4	0.2466366	10811 NADPH oxidase activator 1
GO cellular glucose homeostasis	1	4	0.2466366	10891 peroxisome proliferator-activated receptor gamma, coactivator 1 alpha
GO positive regulation of histone acetylation	1	4	0.2466366	10891 peroxisome proliferator-activated receptor gamma, coactivator 1 alpha
GO DNA damage response, signal transduction	1	4	0.2466366	11200 CHK2 checkpoint homolog (S. pombe)
GO mammary duct terminal end bud growth	1	4	0.2466366	1435 colony stimulating factor 1 (macrophage)
GO piP-body	1	4	0.2466366	143689 piwi-like 4 (Drosophila)
GO negative regulation of peptidase activity	1	4	0.2466366	1471 cystatin C
GO heterocycle metabolic process	1	4	0.2466366	1571 cytochrome P450, family 2, subfamily E, polypeptide 1
GO nose development	1	4	0.2466366	157506 retinol dehydrogenase 10 (all-trans)
GO sphingomyelin biosynthetic process	1	4	0.2466366	166929 sphingomyelin synthase 2
GO zymogen granule membrane	1	4	0.2466366	1755 deleted in malignant brain tumors 1
GO regulation of cAMP metabolic process	1	4	0.2466366	1813 dopamine receptor D2
GO regulation of dopamine uptake	1	4	0.2466366	1813 dopamine receptor D2
GO positive regulation of kinase activity	1	4	0.2466366	1815 dopamine receptor D4
GO JUN kinase binding	1	4	0.2466366	1822 atrophin 1

GO toxin metabolic process	1	4	0.2466366	1822 atrophin 1
GO astrocyte activation	1	4	0.2466366	183 angiotensinogen (serpin peptidase inhibitor, clade A, member 8)
GO peptide hormone secretion	1	4	0.2466366	1906 endothelin 1
GO positive regulation of cell size	1	4	0.2466366	1906 endothelin 1
GO vein smooth muscle contraction	1	4	0.2466366	1906 endothelin 1
GO eukaryotic translation elongation factor 1 alpha 1	1	4	0.2466366	1915 eukaryotic translation elongation factor 1 alpha 1
GO facial nerve structural organization	1	4	0.2466366	1959 early growth response 2
GO Schwann cell differentiation	1	4	0.2466366	1959 early growth response 2
GO phosphopyruvate hydratase activity	1	4	0.2466366	2026 enolase 2 (gamma, neuronal)
GO phosphopyruvate hydratase complex	1	4	0.2466366	2026 enolase 2 (gamma, neuronal)
GO peroxisome proliferator activated receptor gamma 1	1	4	0.2466366	2033 E1A binding protein p300
GO response to cobalt ion	1	4	0.2466366	2033 E1A binding protein p300
GO histone demethylase activity (H3-K9 specific)	1	4	0.2466366	23081 lysine (K)-specific demethylase 4C
GO cAMP response element binding protein 1	1	4	0.2466366	23373 CREB regulated transcription coactivator 1
GO lipoxygenase pathway	1	4	0.2466366	240 arachidonate 5-lipoxygenase
GO inner ear receptor cell differentiation	1	4	0.2466366	26281 fibroblast growth factor 20
GO cerebral cortex radially oriented cell division	1	4	0.2466366	26468 LIM homeobox 6
GO forebrain neuron development	1	4	0.2466366	26468 LIM homeobox 6
GO NADP metabolic process	1	4	0.2466366	27035 NADPH oxidase 1
GO regulation of systemic arterial blood pressure	1	4	0.2466366	27035 NADPH oxidase 1
GO optic nerve morphogenesis	1	4	0.2466366	2737 GLI family zinc finger 3
GO positive regulation of T-helper 1 cell differentiation	1	4	0.2466366	3142 H2.0-like homeobox
GO positive regulation of estrogen receptor signaling pathway	1	4	0.2466366	3169 forkhead box A1
GO testosterone 17-beta-dehydrogenase	1	4	0.2466366	3294 hydroxysteroid (17-beta) dehydrogenase 2
GO chondroitin sulfate proteoglycan biosynthesis	1	4	0.2466366	3479 insulin-like growth factor 1 (somatomedin C)
GO lung lobe morphogenesis	1	4	0.2466366	3479 insulin-like growth factor 1 (somatomedin C)
GO positive regulation of granule cell precursor cell division	1	4	0.2466366	3479 insulin-like growth factor 1 (somatomedin C)
GO water homeostasis	1	4	0.2466366	3479 insulin-like growth factor 1 (somatomedin C)
GO ciliary neurotrophic factor receptor signaling pathway	1	4	0.2466366	3570 interleukin 6 receptor
GO lateral ventricle development	1	4	0.2466366	358 aquaporin 1 (Colton blood group)
GO insulin-like growth factor II binding	1	4	0.2466366	3643 insulin receptor
GO regulation of gene-specific transcription	1	4	0.2466366	3643 insulin receptor
GO cell-cell adhesion mediated by integrin	1	4	0.2466366	3678 integrin, alpha 5 (fibronectin receptor, alpha polypeptide)
GO cell-substrate junction assembly	1	4	0.2466366	3678 integrin, alpha 5 (fibronectin receptor, alpha polypeptide)
GO calcium ion transmembrane transport	1	4	0.2466366	3709 inositol 1,4,5-triphosphate receptor, type 2
GO platelet dense tubular network membrane	1	4	0.2466366	3709 inositol 1,4,5-triphosphate receptor, type 2

GO positive regulation by host of viral tra	1	4	0.2466366	3725 jun oncogene
GO saliva secretion	1	4	0.2466366	3783 potassium intermediate/small conductance calcium-activated channel,
GO myeloid leukocyte differentiation	1	4	0.2466366	3815 v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog
GO positive regulation of Rac protein sig	1	4	0.2466366	3845 v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog
GO response to mineralocorticoid stimul	1	4	0.2466366	3845 v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog
GO very-low-density lipoprotein recepto	1	4	0.2466366	3949 low density lipoprotein receptor
GO dopamine catabolic process	1	4	0.2466366	4128 monoamine oxidase A
GO androgen binding	1	4	0.2466366	4246 secretoglobin, family 2A, member 1
GO bone remodeling	1	4	0.2466366	4286 microphthalmia-associated transcription factor
GO JUN kinase kinase kinase activity	1	4	0.2466366	4293 mitogen-activated protein kinase kinase kinase 9
GO cell-cell junction maintenance	1	4	0.2466366	4359 myelin protein zero
GO negative regulation of lipid storage	1	4	0.2466366	4792 nuclear factor of kappa light polypeptide gene enhancer in B-cells inhib
GO toll-like receptor 4 signaling pathway	1	4	0.2466366	4792 nuclear factor of kappa light polypeptide gene enhancer in B-cells inhib
GO CCAAT-binding factor complex	1	4	0.2466366	4802 nuclear transcription factor Y, gamma
GO arginine binding	1	4	0.2466366	4842 nitric oxide synthase 1 (neuronal)
GO compartment pattern formation	1	4	0.2466366	4851 Notch homolog 1, translocation-associated (Drosophila)
GO positive regulation of glial cell differe	1	4	0.2466366	4851 Notch homolog 1, translocation-associated (Drosophila)
GO regulation of neurogenesis	1	4	0.2466366	4851 Notch homolog 1, translocation-associated (Drosophila)
GO regulation of developmental process	1	4	0.2466366	4853 Notch homolog 2 (Drosophila)
GO neurotrophin receptor activity	1	4	0.2466366	4915 neurotrophic tyrosine kinase, receptor, type 2
GO regulation of respiratory gaseous exc	1	4	0.2466366	4929 nuclear receptor subfamily 4, group A, member 2
GO ADP biosynthetic process	1	4	0.2466366	498 ATP synthase, H <sup>+</sup> transporting, mitochondrial F1 complex, alpha subun
GO mitochondrial proton-transporting A <sup>-</sup>	1	4	0.2466366	498 ATP synthase, H <sup>+</sup> transporting, mitochondrial F1 complex, alpha subun
GO nerve growth factor processing	1	4	0.2466366	5046 proprotein convertase subtilisin/kexin type 6
GO regulation of BMP signaling pathway	1	4	0.2466366	5046 proprotein convertase subtilisin/kexin type 6
GO secretion by cell	1	4	0.2466366	5046 proprotein convertase subtilisin/kexin type 6
GO catecholamine biosynthetic process	1	4	0.2466366	5053 phenylalanine hydroxylase
GO aggresome assembly	1	4	0.2466366	5071 Parkinson disease (autosomal recessive, juvenile) 2, parkin
GO norepinephrine metabolic process	1	4	0.2466366	5071 Parkinson disease (autosomal recessive, juvenile) 2, parkin
GO positive regulation of lipid biosynthes	1	4	0.2466366	51085 MLX interacting protein-like
GO rRNA (adenine-N6,N6 <sup>-</sup> )-dimethyltran	1	4	0.2466366	51093 chromosome 1 open reading frame 66
GO cGMP-mediated signaling	1	4	0.2466366	5152 phosphodiesterase 9A
GO intercalated disc	1	4	0.2466366	5239 phosphoglucomutase 5
GO phosphoglucomutase activity	1	4	0.2466366	5239 phosphoglucomutase 5
GO ErbB-3 class receptor binding	1	4	0.2466366	5295 phosphoinositide-3-kinase, regulatory subunit 1 (alpha)
GO auditory receptor cell stereocilium or	1	4	0.2466366	53405 chloride intracellular channel 5



GO positive regulation of histone deacetylase activity	1	4	0.2466366	5371 promyelocytic leukemia
GO tube morphogenesis	1	4	0.2466366	54361 wingless-type MMTV integration site family, member 4
GO regulation of fatty acid metabolic process	1	4	0.2466366	5465 peroxisome proliferator-activated receptor alpha
GO platelet activating factor biosynthetic process	1	4	0.2466366	54947 lysophosphatidylcholine acyltransferase 2
GO pi-body	1	4	0.2466366	55124 piwi-like 2 (Drosophila)
GO phosphorylase kinase regulator activity	1	4	0.2466366	55140 elongation protein 3 homolog (S. cerevisiae)
GO transmembrane receptor protein tyrosine kinase activity	1	4	0.2466366	55816 docking protein 5
GO tight junction assembly	1	4	0.2466366	56288 par-3 partitioning defective 3 homolog (C. elegans)
GO calcium- and calmodulin-dependent protein kinase activity	1	4	0.2466366	57118 calcium/calmodulin-dependent protein kinase ID
GO activation of store-operated calcium channel activity	1	4	0.2466366	57620 stromal interaction molecule 2
GO embryonic organ morphogenesis	1	4	0.2466366	5950 retinol binding protein 4, plasma
GO negative regulation of cardiac muscle cell proliferation	1	4	0.2466366	5950 retinol binding protein 4, plasma
GO vagina development	1	4	0.2466366	5950 retinol binding protein 4, plasma
GO melatonin receptor activity	1	4	0.2466366	6096 RAR-related orphan receptor B
GO retinoic acid receptor activity	1	4	0.2466366	6256 retinoid X receptor, alpha
GO mechanoreceptor differentiation	1	4	0.2466366	627 brain-derived neurotrophic factor
GO regulation of metabolic process	1	4	0.2466366	627 brain-derived neurotrophic factor
GO positive regulation of TOR signaling pathway	1	4	0.2466366	64083 golgi phosphoprotein 3 (coat-protein)
GO positive regulation of humoral immune response	1	4	0.2466366	64127 nucleotide-binding oligomerization domain containing 2
GO negative regulation of TOR signaling pathway	1	4	0.2466366	64798 DEP domain containing 6
GO alpha-N-acetylneuraminic acid biosynthetic process	1	4	0.2466366	6489 ST8 alpha-N-acetyl-neuraminidase alpha-2,8-sialyltransferase 1
GO L-glutamate import	1	4	0.2466366	6505 solute carrier family 1 (neuronal/epithelial high affinity glutamate transporter)
GO lens induction in camera-type eye	1	4	0.2466366	652 bone morphogenetic protein 4
GO negative regulation of mitosis	1	4	0.2466366	652 bone morphogenetic protein 4
GO positive regulation of cell death	1	4	0.2466366	652 bone morphogenetic protein 4
GO chloride transmembrane transporter activity	1	4	0.2466366	6521 solute carrier family 4, anion exchanger, member 1 (erythrocyte membrane)
GO urea transport	1	4	0.2466366	6563 solute carrier family 14 (urea transporter), member 1 (Kidd blood group)
GO arachidonic acid binding	1	4	0.2466366	6622 synuclein, alpha (non A4 component of amyloid precursor)
GO platelet aggregation	1	4	0.2466366	6812 syntaxin binding protein 1
GO synaptic vesicle maturation	1	4	0.2466366	6812 syntaxin binding protein 1
GO positive regulation of gamma-delta T cell chemotaxis	1	4	0.2466366	6850 spleen tyrosine kinase
GO chromaffin granule membrane	1	4	0.2466366	6857 synaptotagmin I
GO progesterone receptor signaling pathway	1	4	0.2466366	687 Kruppel-like factor 9
GO positive regulation of interferon-alpha/beta signaling pathway	1	4	0.2466366	7098 toll-like receptor 3
GO positive regulation of platelet activation	1	4	0.2466366	7099 toll-like receptor 4
GO muscle thin filament tropomyosin	1	4	0.2466366	7170 tropomyosin 3

GO luteinization	1	4	0.2466366	726 calpain 5
GO dendritic spine membrane	1	4	0.2466366	729993 shisa homolog 9 (Xenopus laevis)
GO gene expression	1	4	0.2466366	7597 zinc finger and BTB domain containing 25
GO positive regulation of cellular pH red	1	4	0.2466366	760 carbonic anhydrase II
GO positive regulation of adenylate cycl	1	4	0.2466366	799 calcitonin receptor
GO cellular response to glucose starvatio	1	4	0.2466366	81788 NUAK family, SNF1-like kinase, 2
GO maintenance of organ identity	1	4	0.2466366	84059 G protein-coupled receptor 98
GO blood vessel maturation	1	4	0.2466366	8434 reversion-inducing-cysteine-rich protein with kazal motifs
GO peripheral to membrane of membrar	1	4	0.2466366	8434 reversion-inducing-cysteine-rich protein with kazal motifs
GO protein phosphatase type 1 complex	1	4	0.2466366	84919 protein phosphatase 1, regulatory (inhibitor) subunit 15B
GO [heparan sulfate]-glucosamine N-sulf	1	4	0.2466366	8509 N-deacetylase/N-sulfotransferase (heparan glucosaminy) 2
GO actin filament severing	1	4	0.2466366	85477 scinderin
GO cyclic nucleotide metabolic process	1	4	0.2466366	8622 phosphodiesterase 8B
GO negative regulation of plasma membr	1	4	0.2466366	8660 insulin receptor substrate 2
GO positive regulation of glucose metabo	1	4	0.2466366	8660 insulin receptor substrate 2
GO release of cytoplasmic sequestered N	1	4	0.2466366	8740 tumor necrosis factor (ligand) superfamily, member 14
GO positive regulation of mitochondrial c	1	4	0.2466366	885 cholecystokinin
GO cellular response to protein stimulus	1	4	0.2466366	8900 cyclin A1
GO vacuolar acidification	1	4	0.2466366	8992 ATPase, H+ transporting, lysosomal 9kDa, V0 subunit e1
GO sequestering of actin monomers	1	4	0.2466366	9087 thymosin beta 4, Y-linked
GO phosphatidylinositol-5-phosphate bir	1	4	0.2466366	91404 SEC14 and spectrin domains 1
GO long term synaptic depression	1	4	0.2466366	952 CD38 molecule
GO response to hydroperoxide	1	4	0.2466366	952 CD38 molecule
GO thrombospondin receptor activity	1	4	0.2466366	961 CD47 molecule
GO intracellular cholesterol transport	1	4	0.2466366	9619 ATP-binding cassette, sub-family G (WHITE), member 1
GO phospholipid transporter activity	1	4	0.2466366	9619 ATP-binding cassette, sub-family G (WHITE), member 1
GO peptidyl-lysine deacetylation	1	4	0.2466366	9734 histone deacetylase 9
GO positive regulation of cell migration i	1	4	0.2466366	9734 histone deacetylase 9
GO clathrin coat	1	4	0.2466366	9892 synaptosomal-associated protein, 91kDa homolog (mouse)
GO regulation of protein transport	1	4	0.2466366	9892 synaptosomal-associated protein, 91kDa homolog (mouse)
GO lateral element	1	4	0.2466366	9985 REC8 homolog (yeast)
GO temperature homeostasis	2	14	0.2476336	10891 peroxisome proliferator-activated receptor gamma, coactivator 1 alpha
GO temperature homeostasis	2	14	0.2476336	1813 dopamine receptor D2
GO glutamine metabolic process	2	14	0.2476336	1373 carbamoyl-phosphate synthetase 1, mitochondrial
GO glutamine metabolic process	2	14	0.2476336	27165 glutaminase 2 (liver, mitochondrial)
GO endosome to lysosome transport	2	14	0.2476336	154 adrenergic, beta-2-, receptor, surface

GO	endosome to lysosome transport	2	14	0.2476336	22906	trafficking protein, kinesin binding 1
GO	behavioral fear response	2	14	0.2476336	1815	dopamine receptor D4
GO	behavioral fear response	2	14	0.2476336	885	cholecystokinin
GO	nitric oxide mediated signal transduc	2	14	0.2476336	183	angiotensinogen (serpin peptidase inhibitor, clade A, member 8)
GO	nitric oxide mediated signal transduc	2	14	0.2476336	51655	RAS, dexamethasone-induced 1
GO	response to testosterone stimulus	2	14	0.2476336	1843	dual specificity phosphatase 1
GO	response to testosterone stimulus	2	14	0.2476336	3643	insulin receptor
GO	protein-chromophore linkage	2	14	0.2476336	22795	nidogen 2 (osteonidogen)
GO	protein-chromophore linkage	2	14	0.2476336	83872	hemicentin 1
GO	sulfur metabolic process	2	14	0.2476336	22901	arylsulfatase G
GO	sulfur metabolic process	2	14	0.2476336	9435	carbohydrate (N-acetylglucosamine-6-O) sulfotransferase 2
GO	embryonic heart tube development	2	14	0.2476336	2296	forkhead box C1
GO	embryonic heart tube development	2	14	0.2476336	2303	forkhead box C2 (MFH-1, mesenchyme forkhead 1)
GO	calmodulin-dependent protein kinase	2	14	0.2476336	23604	death-associated protein kinase 2
GO	calmodulin-dependent protein kinase	2	14	0.2476336	57118	calcium/calmodulin-dependent protein kinase ID
GO	regulation of action potential in neur	2	14	0.2476336	27345	potassium large conductance calcium-activated channel, subfamily M,
GO	regulation of action potential in neur	2	14	0.2476336	5025	purinergic receptor P2X, ligand-gated ion channel, 4
GO	positive regulation of protein catabol	2	14	0.2476336	29116	myosin regulatory light chain interacting protein
GO	positive regulation of protein catabol	2	14	0.2476336	7474	wingless-type MMTV integration site family, member 5A
GO	neuroblast proliferation	2	14	0.2476336	3400	inhibitor of DNA binding 4, dominant negative helix-loop-helix protein
GO	neuroblast proliferation	2	14	0.2476336	429	achaete-scute complex homolog 1 (Drosophila)
GO	transmembrane transporter activity	2	14	0.2476336	358	aquaporin 1 (Colton blood group)
GO	transmembrane transporter activity	2	14	0.2476336	498	ATP synthase, H <sup>+</sup> transporting, mitochondrial F1 complex, alpha subun
GO	ATP catabolic process	2	14	0.2476336	368	ATP-binding cassette, sub-family C (CFTR/MRP), member 6
GO	ATP catabolic process	2	14	0.2476336	498	ATP synthase, H <sup>+</sup> transporting, mitochondrial F1 complex, alpha subun
GO	decidualization	2	14	0.2476336	3726	jun B proto-oncogene
GO	decidualization	2	14	0.2476336	682	basigin (Ok blood group)
GO	cell fate specification	2	14	0.2476336	4851	Notch homolog 1, translocation-associated (Drosophila)
GO	cell fate specification	2	14	0.2476336	50937	Cdon homolog (mouse)
GO	dystrophin-associated glycoprotein c	2	14	0.2476336	5239	phosphoglucomutase 5
GO	dystrophin-associated glycoprotein c	2	14	0.2476336	8082	sarcospan (Kras oncogene-associated gene)
GO	pathway-restricted SMAD protein ph	2	14	0.2476336	652	bone morphogenetic protein 4
GO	pathway-restricted SMAD protein ph	2	14	0.2476336	7049	transforming growth factor, beta receptor III
GO	single-stranded RNA binding	2	14	0.2476336	7538	zinc finger protein 36, C3H type, homolog (mouse)
GO	single-stranded RNA binding	2	14	0.2476336	9271	piwi-like 1 (Drosophila)
GO	transcription factor complex	12	140	0.249175	10481	homeobox B13

GO transcription factor complex	12	140	0.249175	127343 diencephalon/mesencephalon homeobox 1
GO transcription factor complex	12	140	0.249175	2033 E1A binding protein p300
GO transcription factor complex	12	140	0.249175	2353 FBJ murine osteosarcoma viral oncogene homolog
GO transcription factor complex	12	140	0.249175	3725 jun oncogene
GO transcription factor complex	12	140	0.249175	4087 SMAD family member 2
GO transcription factor complex	12	140	0.249175	51085 MLX interacting protein-like
GO transcription factor complex	12	140	0.249175	5308 paired-like homeodomain 2
GO transcription factor complex	12	140	0.249175	5460 POU class 5 homeobox 1
GO transcription factor complex	12	140	0.249175	8543 LIM domain only 4
GO transcription factor complex	12	140	0.249175	9734 histone deacetylase 9
GO transcription factor complex	12	140	0.249175	9935 v-maf musculoaponeurotic fibrosarcoma oncogene homolog B (avian)
GO fatty acid metabolic process	7	75	0.2514152	2182 acyl-CoA synthetase long-chain family member 4
GO fatty acid metabolic process	7	75	0.2514152	35 acyl-Coenzyme A dehydrogenase, C-2 to C-3 short chain
GO fatty acid metabolic process	7	75	0.2514152	51703 acyl-CoA synthetase long-chain family member 5
GO fatty acid metabolic process	7	75	0.2514152	5465 peroxisome proliferator-activated receptor alpha
GO fatty acid metabolic process	7	75	0.2514152	55268 enoyl Coenzyme A hydratase domain containing 2
GO fatty acid metabolic process	7	75	0.2514152	5577 protein kinase, cAMP-dependent, regulatory, type II, beta
GO fatty acid metabolic process	7	75	0.2514152	6622 synuclein, alpha (non A4 component of amyloid precursor)
GO promoter binding	9	101	0.2528355	10014 histone deacetylase 5
GO promoter binding	9	101	0.2528355	2033 E1A binding protein p300
GO promoter binding	9	101	0.2528355	222546 regulatory factor X, 6
GO promoter binding	9	101	0.2528355	2353 FBJ murine osteosarcoma viral oncogene homolog
GO promoter binding	9	101	0.2528355	3169 forkhead box A1
GO promoter binding	9	101	0.2528355	3725 jun oncogene
GO promoter binding	9	101	0.2528355	4087 SMAD family member 2
GO promoter binding	9	101	0.2528355	5460 POU class 5 homeobox 1
GO promoter binding	9	101	0.2528355	7026 nuclear receptor subfamily 2, group F, member 2
GO response to oxidative stress	9	101	0.2528355	10628 thioredoxin interacting protein
GO response to oxidative stress	9	101	0.2528355	1843 dual specificity phosphatase 1
GO response to oxidative stress	9	101	0.2528355	5742 prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase a)
GO response to oxidative stress	9	101	0.2528355	7001 peroxiredoxin 2
GO response to oxidative stress	9	101	0.2528355	7099 toll-like receptor 4
GO response to oxidative stress	9	101	0.2528355	79661 nei endonuclease VIII-like 1 (E. coli)
GO response to oxidative stress	9	101	0.2528355	84919 protein phosphatase 1, regulatory (inhibitor) subunit 15B
GO response to oxidative stress	9	101	0.2528355	93100 nicotinate phosphoribosyltransferase domain containing 1
GO response to oxidative stress	9	101	0.2528355	9962 solute carrier family 23 (nucleobase transporters), member 2

GO chloride transport	5	50	0.2548929	1193 chloride intracellular channel 2
GO chloride transport	5	50	0.2548929	53405 chloride intracellular channel 5
GO chloride transport	5	50	0.2548929	5349 FXYD domain containing ion transport regulator 3
GO chloride transport	5	50	0.2548929	6521 solute carrier family 4, anion exchanger, member 1 (erythrocyte memb
GO chloride transport	5	50	0.2548929	8542 apolipoprotein L, 1
GO activation of caspase activity	5	50	0.2548929	29108 PYD and CARD domain containing
GO activation of caspase activity	5	50	0.2548929	3429 interferon, alpha-inducible protein 27
GO activation of caspase activity	5	50	0.2548929	5371 promyelocytic leukemia
GO activation of caspase activity	5	50	0.2548929	885 cholecystokinin
GO activation of caspase activity	5	50	0.2548929	9966 tumor necrosis factor (ligand) superfamily, member 15
GO Golgi cisterna membrane	6	63	0.2598704	2525 fucosyltransferase 3 (galactoside 3(4)-L-fucosyltransferase, Lewis blood
GO Golgi cisterna membrane	6	63	0.2598704	2526 fucosyltransferase 4 (alpha (1,3) fucosyltransferase, myeloid-specific)
GO Golgi cisterna membrane	6	63	0.2598704	2589 UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosami
GO Golgi cisterna membrane	6	63	0.2598704	2801 golgin A2
GO Golgi cisterna membrane	6	63	0.2598704	64083 golgi phosphoprotein 3 (coat-protein)
GO Golgi cisterna membrane	6	63	0.2598704	6484 ST3 beta-galactoside alpha-2,3-sialyltransferase 4
GO positive regulation of gene expression	4	38	0.2600294	1435 colony stimulating factor 1 (macrophage)
GO positive regulation of gene expression	4	38	0.2600294	2033 E1A binding protein p300
GO positive regulation of gene expression	4	38	0.2600294	3815 v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog
GO positive regulation of gene expression	4	38	0.2600294	652 bone morphogenetic protein 4
GO collagen fibril organization	3	26	0.2609152	2296 forkhead box C1
GO collagen fibril organization	3	26	0.2609152	2303 forkhead box C2 (MFH-1, mesenchyme forkhead 1)
GO collagen fibril organization	3	26	0.2609152	4015 lysyl oxidase
GO GDP binding	3	26	0.2609152	3845 v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog
GO GDP binding	3	26	0.2609152	57799 RAB40C, member RAS oncogene family
GO GDP binding	3	26	0.2609152	85004 RAS-like, estrogen-regulated, growth inhibitor
GO NAD+ ADP-ribosyltransferase activity	3	26	0.2609152	79668 poly (ADP-ribose) polymerase family, member 8
GO NAD+ ADP-ribosyltransferase activity	3	26	0.2609152	83666 poly (ADP-ribose) polymerase family, member 9
GO NAD+ ADP-ribosyltransferase activity	3	26	0.2609152	84875 poly (ADP-ribose) polymerase family, member 10
GO hemopoiesis	5	51	0.2681363	1435 colony stimulating factor 1 (macrophage)
GO hemopoiesis	5	51	0.2681363	3428 interferon, gamma-inducible protein 16
GO hemopoiesis	5	51	0.2681363	3815 v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog
GO hemopoiesis	5	51	0.2681363	4254 KIT ligand
GO hemopoiesis	5	51	0.2681363	4853 Notch homolog 2 (Drosophila)
GO copper ion binding	5	51	0.2681363	2153 coagulation factor V (proaccelerin, labile factor)
GO copper ion binding	5	51	0.2681363	4015 lysyl oxidase

GO copper ion binding	5	51	0.2681363	5025 purinergic receptor P2X, ligand-gated ion channel, 4
GO copper ion binding	5	51	0.2681363	5066 peptidylglycine alpha-amidating monooxygenase
GO copper ion binding	5	51	0.2681363	84171 lysyl oxidase-like 4
GO forebrain development	5	51	0.2681363	2290 forkhead box G1
GO forebrain development	5	51	0.2681363	4851 Notch homolog 1, translocation-associated (Drosophila)
GO forebrain development	5	51	0.2681363	7026 nuclear receptor subfamily 2, group F, member 2
GO forebrain development	5	51	0.2681363	85416 Zic family member 5 (odd-paired homolog, Drosophila)
GO forebrain development	5	51	0.2681363	8646 chordin
GO protein complex binding	8	90	0.2724198	1373 carbamoyl-phosphate synthetase 1, mitochondrial
GO protein complex binding	8	90	0.2724198	1508 cathepsin B
GO protein complex binding	8	90	0.2724198	154 adrenergic, beta-2-, receptor, surface
GO protein complex binding	8	90	0.2724198	2033 E1A binding protein p300
GO protein complex binding	8	90	0.2724198	3643 insulin receptor
GO protein complex binding	8	90	0.2724198	3914 laminin, beta 3
GO protein complex binding	8	90	0.2724198	4792 nuclear factor of kappa light polypeptide gene enhancer in B-cells inhib
GO protein complex binding	8	90	0.2724198	5122 proprotein convertase subtilisin/kexin type 1
GO response to nicotine	2	15	0.273697	1139 cholinergic receptor, nicotinic, alpha 7
GO response to nicotine	2	15	0.273697	3775 potassium channel, subfamily K, member 1
GO voltage-gated chloride channel activi	2	15	0.273697	1193 chloride intracellular channel 2
GO voltage-gated chloride channel activi	2	15	0.273697	53405 chloride intracellular channel 5
GO actin filament bundle assembly	2	15	0.273697	134549 shroom family member 1
GO actin filament bundle assembly	2	15	0.273697	2039 erythrocyte membrane protein band 4.9 (dematin)
GO embryonic forelimb morphogenesis	2	15	0.273697	1382 cellular retinoic acid binding protein 2
GO embryonic forelimb morphogenesis	2	15	0.273697	157506 retinol dehydrogenase 10 (all-trans)
GO phospholipid-translocating ATPase ac	2	15	0.273697	148229 ATPase, class I, type 8B, member 3
GO phospholipid-translocating ATPase ac	2	15	0.273697	79895 ATPase, class I, type 8B, member 4
GO positive regulation of catalytic activit	2	15	0.273697	183 angiotensinogen (serpin peptidase inhibitor, clade A, member 8)
GO positive regulation of catalytic activit	2	15	0.273697	4929 nuclear receptor subfamily 4, group A, member 2
GO digestive tract development	2	15	0.273697	2033 E1A binding protein p300
GO digestive tract development	2	15	0.273697	9971 nuclear receptor subfamily 1, group H, member 4
GO cellular component organization	2	15	0.273697	23500 dishevelled associated activator of morphogenesis 2
GO cellular component organization	2	15	0.273697	85462 FH2 domain containing 1
GO cellular response to extracellular stir	2	15	0.273697	2353 FBJ murine osteosarcoma viral oncogene homolog
GO cellular response to extracellular stir	2	15	0.273697	4929 nuclear receptor subfamily 4, group A, member 2
GO myeloid cell differentiation	2	15	0.273697	3428 interferon, gamma-inducible protein 16
GO myeloid cell differentiation	2	15	0.273697	5371 promyelocytic leukemia

GO neuromuscular junction developmen	2	15	0.273697	375790 agrin
GO neuromuscular junction developmen	2	15	0.273697	783 calcium channel, voltage-dependent, beta 2 subunit
GO hair follicle development	2	15	0.273697	3911 laminin, alpha 5
GO hair follicle development	2	15	0.273697	91 activin A receptor, type IB
GO chondrocyte differentiation	2	15	0.273697	4209 myocyte enhancer factor 2D
GO chondrocyte differentiation	2	15	0.273697	7474 wingless-type MMTV integration site family, member 5A
GO ATPase binding	2	15	0.273697	50617 ATPase, H+ transporting, lysosomal V0 subunit a4
GO ATPase binding	2	15	0.273697	5774 protein tyrosine phosphatase, non-receptor type 3
GO oxidoreductase activity, acting on pai	2	15	0.273697	5351 procollagen-lysine 1, 2-oxoglutarate 5-dioxygenase 1
GO oxidoreductase activity, acting on pai	2	15	0.273697	54681 prolyl 4-hydroxylase, transmembrane (endoplasmic reticulum)
GO regulation of protein amino acid pho:	2	15	0.273697	5577 protein kinase, cAMP-dependent, regulatory, type II, beta
GO regulation of protein amino acid pho:	2	15	0.273697	9021 suppressor of cytokine signaling 3
GO regulation of immune response	2	15	0.273697	604 B-cell CLL/lymphoma 6
GO regulation of immune response	2	15	0.273697	6850 spleen tyrosine kinase
GO positive regulation of cytokine secret	2	15	0.273697	834 caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, co
GO positive regulation of cytokine secret	2	15	0.273697	9966 tumor necrosis factor (ligand) superfamily, member 15
GO epithelial cell differentiation	4	39	0.275491	10170 dehydrogenase/reductase (SDR family) member 9
GO epithelial cell differentiation	4	39	0.275491	1755 deleted in malignant brain tumors 1
GO epithelial cell differentiation	4	39	0.275491	1999 E74-like factor 3 (ets domain transcription factor, epithelial-specific )
GO epithelial cell differentiation	4	39	0.275491	3169 forkhead box A1
GO ER-Golgi intermediate compartment	4	39	0.275491	2055 ceroid-lipofuscinosis, neuronal 8 (epilepsy, progressive with mental ret
GO ER-Golgi intermediate compartment	4	39	0.275491	2706 gap junction protein, beta 2, 26kDa
GO ER-Golgi intermediate compartment	4	39	0.275491	285704 RGM domain family, member B
GO ER-Golgi intermediate compartment	4	39	0.275491	4121 mannosidase, alpha, class 1A, member 1
GO cytoskeletal protein binding	4	39	0.275491	257019 FERM domain containing 3
GO cytoskeletal protein binding	4	39	0.275491	27295 PDZ and LIM domain 3
GO cytoskeletal protein binding	4	39	0.275491	29116 myosin regulatory light chain interacting protein
GO cytoskeletal protein binding	4	39	0.275491	5774 protein tyrosine phosphatase, non-receptor type 3
GO interspecies interaction between org	22	280	0.278823	10346 tripartite motif-containing 22
GO interspecies interaction between org	22	280	0.278823	1755 deleted in malignant brain tumors 1
GO interspecies interaction between org	22	280	0.278823	1948 ephrin-B2
GO interspecies interaction between org	22	280	0.278823	2033 E1A binding protein p300
GO interspecies interaction between org	22	280	0.278823	23373 CREB regulated transcription coactivator 1
GO interspecies interaction between org	22	280	0.278823	3561 interleukin 2 receptor, gamma (severe combined immunodeficiency)
GO interspecies interaction between org	22	280	0.278823	3665 interferon regulatory factor 7
GO interspecies interaction between org	22	280	0.278823	3678 integrin, alpha 5 (fibronectin receptor, alpha polypeptide)

GO interspecies interaction between org	22	280	0.278823	3949 low density lipoprotein receptor
GO interspecies interaction between org	22	280	0.278823	4179 CD46 molecule, complement regulatory protein
GO interspecies interaction between org	22	280	0.278823	4792 nuclear factor of kappa light polypeptide gene enhancer in B-cells inhib
GO interspecies interaction between org	22	280	0.278823	5295 phosphoinositide-3-kinase, regulatory subunit 1 (alpha)
GO interspecies interaction between org	22	280	0.278823	5371 promyelocytic leukemia
GO interspecies interaction between org	22	280	0.278823	5696 proteasome (prosome, macropain) subunit, beta type, 8 (large multifur
GO interspecies interaction between org	22	280	0.278823	5698 proteasome (prosome, macropain) subunit, beta type, 9 (large multifur
GO interspecies interaction between org	22	280	0.278823	5699 proteasome (prosome, macropain) subunit, beta type, 10
GO interspecies interaction between org	22	280	0.278823	6256 retinoid X receptor, alpha
GO interspecies interaction between org	22	280	0.278823	64135 interferon induced with helicase C domain 1
GO interspecies interaction between org	22	280	0.278823	6850 spleen tyrosine kinase
GO interspecies interaction between org	22	280	0.278823	6921 transcription elongation factor B (SIII), polypeptide 1 (15kDa, elongin C
GO interspecies interaction between org	22	280	0.278823	7706 tripartite motif-containing 25
GO interspecies interaction between org	22	280	0.278823	7852 chemokine (C-X-C motif) receptor 4
GO ATP synthesis coupled proton transp	3	27	0.2798997	10312 T-cell, immune regulator 1, ATPase, H+ transporting, lysosomal V0 subu
GO ATP synthesis coupled proton transp	3	27	0.2798997	50617 ATPase, H+ transporting, lysosomal V0 subunit a4
GO ATP synthesis coupled proton transp	3	27	0.2798997	8992 ATPase, H+ transporting, lysosomal 9kDa, V0 subunit e1
GO enzyme inhibitor activity	3	27	0.2798997	10628 thioredoxin interacting protein
GO enzyme inhibitor activity	3	27	0.2798997	50859 sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican)
GO enzyme inhibitor activity	3	27	0.2798997	7076 TIMP metalloproteinase inhibitor 1
GO negative regulation of neuron differe	3	27	0.2798997	2290 forkhead box G1
GO negative regulation of neuron differe	3	27	0.2798997	3400 inhibitor of DNA binding 4, dominant negative helix-loop-helix protein
GO negative regulation of neuron differe	3	27	0.2798997	429 achaete-scute complex homolog 1 (Drosophila)
GO cell-cell adherens junction	3	27	0.2798997	4008 LIM domain 7
GO cell-cell adherens junction	3	27	0.2798997	5239 phosphoglucomutase 5
GO cell-cell adherens junction	3	27	0.2798997	56288 par-3 partitioning defective 3 homolog (C. elegans)
GO negative regulation of cell growth	8	91	0.2824202	183 angiotensinogen (serpin peptidase inhibitor, clade A, member 8)
GO negative regulation of cell growth	8	91	0.2824202	5371 promyelocytic leukemia
GO negative regulation of cell growth	8	91	0.2824202	604 B-cell CLL/lymphoma 6
GO negative regulation of cell growth	8	91	0.2824202	6494 signal-induced proliferation-associated 1
GO negative regulation of cell growth	8	91	0.2824202	85004 RAS-like, estrogen-regulated, growth inhibitor
GO negative regulation of cell growth	8	91	0.2824202	91 activin A receptor, type IB
GO negative regulation of cell growth	8	91	0.2824202	92304 secretoglobin, family 3A, member 1
GO negative regulation of cell growth	8	91	0.2824202	94 activin A receptor type II-like 1
GO ubiquitin-protein ligase activity	12	145	0.2881057	10116 fem-1 homolog b (C. elegans)
GO ubiquitin-protein ligase activity	12	145	0.2881057	134111 ubiquitin-conjugating enzyme E2Q family-like 1



GO	ubiquitin-protein ligase activity	12	145	0.2881057	151636 deltex 3-like (Drosophila)
GO	ubiquitin-protein ligase activity	12	145	0.2881057	154214 ring finger protein 217
GO	ubiquitin-protein ligase activity	12	145	0.2881057	255488 ring finger protein 144B
GO	ubiquitin-protein ligase activity	12	145	0.2881057	26232 F-box protein 2
GO	ubiquitin-protein ligase activity	12	145	0.2881057	26270 F-box protein 6
GO	ubiquitin-protein ligase activity	12	145	0.2881057	29116 myosin regulatory light chain interacting protein
GO	ubiquitin-protein ligase activity	12	145	0.2881057	4008 LIM domain 7
GO	ubiquitin-protein ligase activity	12	145	0.2881057	5071 Parkinson disease (autosomal recessive, juvenile) 2, parkin
GO	ubiquitin-protein ligase activity	12	145	0.2881057	7706 tripartite motif-containing 25
GO	ubiquitin-protein ligase activity	12	145	0.2881057	79872 Cas-Br-M (murine) ecotropic retroviral transforming sequence-like 1
GO	dendritic spine	4	40	0.2910974	2911 glutamate receptor, metabotropic 1
GO	dendritic spine	4	40	0.2910974	4645 myosin VB
GO	dendritic spine	4	40	0.2910974	4842 nitric oxide synthase 1 (neuronal)
GO	dendritic spine	4	40	0.2910974	5025 purinergic receptor P2X, ligand-gated ion channel, 4
GO	hormone activity	7	79	0.2945924	1114 chromogranin B (secretogranin 1)
GO	hormone activity	7	79	0.2945924	183 angiotensinogen (serpin peptidase inhibitor, clade A, member 8)
GO	hormone activity	7	79	0.2945924	1906 endothelin 1
GO	hormone activity	7	79	0.2945924	3479 insulin-like growth factor 1 (somatomedin C)
GO	hormone activity	7	79	0.2945924	6343 secretin
GO	hormone activity	7	79	0.2945924	6750 somatostatin
GO	hormone activity	7	79	0.2945924	885 cholecystokinin
GO	response to wounding	5	53	0.2950409	10481 homeobox B13
GO	response to wounding	5	53	0.2950409	11202 kallikrein-related peptidase 8
GO	response to wounding	5	53	0.2950409	1462 versican
GO	response to wounding	5	53	0.2950409	1508 cathepsin B
GO	response to wounding	5	53	0.2950409	5460 POU class 5 homeobox 1
GO	ATP biosynthetic process	5	53	0.2950409	148229 ATPase, class I, type 8B, member 3
GO	ATP biosynthetic process	5	53	0.2950409	493 ATPase, Ca <sup>++</sup> transporting, plasma membrane 4
GO	ATP biosynthetic process	5	53	0.2950409	498 ATP synthase, H <sup>+</sup> transporting, mitochondrial F1 complex, alpha subun
GO	ATP biosynthetic process	5	53	0.2950409	79895 ATPase, class I, type 8B, member 4
GO	ATP biosynthetic process	5	53	0.2950409	9914 ATPase, Ca <sup>++</sup> transporting, type 2C, member 2
GO	negative regulation of myotube differ	1	5	0.2981385	10014 histone deacetylase 5
GO	mitogen-activated protein kinase kin	1	5	0.2981385	10221 tribbles homolog 1 (Drosophila)
GO	mRNA modification	1	5	0.2981385	104 adenosine deaminase, RNA-specific, B1 (RED1 homolog rat)
GO	opioid peptide activity	1	5	0.2981385	10435 CDC42 effector protein (Rho GTPase binding) 2
GO	positive regulation of protein comple	1	5	0.2981385	10435 CDC42 effector protein (Rho GTPase binding) 2

GO sodium ion binding	1	5	0.2981385	10568 solute carrier family 34 (sodium phosphate), member 2
GO sodium-dependent phosphate transp	1	5	0.2981385	10568 solute carrier family 34 (sodium phosphate), member 2
GO transepithelial chloride transport	1	5	0.2981385	1080 cystic fibrosis transmembrane conductance regulator (ATP-binding cas
GO respiratory electron transport chain	1	5	0.2981385	10891 peroxisome proliferator-activated receptor gamma, coactivator 1 alpha
GO barbed-end actin filament capping	1	5	0.2981385	11078 TRIO and F-actin binding protein
GO calcium- and calmodulin-responsive a	1	5	0.2981385	112 adenylyate cyclase 6
GO interleukin-1-mediated signaling pat	1	5	0.2981385	11213 interleukin-1 receptor-associated kinase 3
GO negative regulation of cytokine-medi	1	5	0.2981385	11213 interleukin-1 receptor-associated kinase 3
GO folic acid transporter activity	1	5	0.2981385	113235 solute carrier family 46 (folate transporter), member 1
GO toxin binding	1	5	0.2981385	1139 cholinergic receptor, nicotinic, alpha 7
GO regulation of neuron apoptosis	1	5	0.2981385	121665 signal peptide peptidase 3
GO ethanol oxidation	1	5	0.2981385	125 alcohol dehydrogenase 1B (class I), beta polypeptide
GO sphingosine-1-phosphate phosphatas	1	5	0.2981385	130367 sphingosine-1-phosphate phosphotase 2
GO monocyte activation	1	5	0.2981385	1435 colony stimulating factor 1 (macrophage)
GO positive regulation of macrophage di	1	5	0.2981385	1435 colony stimulating factor 1 (macrophage)
GO positive regulation of heart contracti	1	5	0.2981385	154 adrenergic, beta-2-, receptor, surface
GO positive regulation of potassium ion t	1	5	0.2981385	154 adrenergic, beta-2-, receptor, surface
GO oxidoreductase activity, acting on pai	1	5	0.2981385	1571 cytochrome P450, family 2, subfamily E, polypeptide 1
GO embryonic camera-type eye develop	1	5	0.2981385	157506 retinol dehydrogenase 10 (all-trans)
GO activation of phospholipase C activity	1	5	0.2981385	1813 dopamine receptor D2
GO circadian regulation of gene expressi	1	5	0.2981385	1813 dopamine receptor D2
GO G-protein signaling, coupled to cGMP	1	5	0.2981385	183 angiotensinogen (serpin peptidase inhibitor, clade A, member 8)
GO type 1 angiotensin receptor binding	1	5	0.2981385	183 angiotensinogen (serpin peptidase inhibitor, clade A, member 8)
GO artery smooth muscle contraction	1	5	0.2981385	1906 endothelin 1
GO leukocyte activation	1	5	0.2981385	1906 endothelin 1
GO regulation of systemic arterial blood	1	5	0.2981385	1906 endothelin 1
GO mammary gland involution	1	5	0.2981385	1999 E74-like factor 3 (ets domain transcription factor, epithelial-specific )
GO transmembrane-ephrin receptor acti	1	5	0.2981385	2044 EPH receptor A5
GO musculoskeletal movement	1	5	0.2981385	2055 ceroid-lipofuscinosis, neuronal 8 (epilepsy, progressive with mental ret
GO fibroblast growth factor receptor acti	1	5	0.2981385	2263 fibroblast growth factor receptor 2
GO axon midline choice point recognitior	1	5	0.2981385	2290 forkhead box G1
GO cell morphogenesis involved in neurc	1	5	0.2981385	2290 forkhead box G1
GO glycosaminoglycan metabolic proces	1	5	0.2981385	2296 forkhead box C1
GO mesenchymal cell differentiation	1	5	0.2981385	2296 forkhead box C1
GO lymphangiogenesis	1	5	0.2981385	2303 forkhead box C2 (MFH-1, mesenchyme forkhead 1)
GO activation of JNKK activity	1	5	0.2981385	23043 TRAF2 and NCK interacting kinase

GO anterograde axon cargo transport	1	5	0.2981385	23095 kinesin family member 1B
GO response to gravity	1	5	0.2981385	2353 FBJ murine osteosarcoma viral oncogene homolog
GO lysosomal transport	1	5	0.2981385	255738 proprotein convertase subtilisin/kexin type 9
GO regulation of receptor activity	1	5	0.2981385	255738 proprotein convertase subtilisin/kexin type 9
GO positive regulation of transferase acti	1	5	0.2981385	256987 serine incorporator 5
GO ER to Golgi transport vesicle membra	1	5	0.2981385	25956 SEC31 homolog B (S. cerevisiae)
GO AP-1 adaptor complex	1	5	0.2981385	26119 low density lipoprotein receptor adaptor protein 1
GO SCF-dependent proteasomal ubiquiti	1	5	0.2981385	26270 F-box protein 6
GO vitamin D binding	1	5	0.2981385	2638 group-specific component (vitamin D binding protein)
GO purine base metabolic process	1	5	0.2981385	271 adenosine monophosphate deaminase 2
GO positive regulation of protein import	1	5	0.2981385	2737 GLI family zinc finger 3
GO spinal cord dorsal/ventral patterning	1	5	0.2981385	2737 GLI family zinc finger 3
GO virion binding	1	5	0.2981385	28996 homeodomain interacting protein kinase 2
GO virus-host interaction	1	5	0.2981385	28996 homeodomain interacting protein kinase 2
GO peptidyl-citrulline biosynthetic proce	1	5	0.2981385	29943 peptidyl arginine deiminase, type I
GO protein-arginine deiminase activity	1	5	0.2981385	29943 peptidyl arginine deiminase, type I
GO azurophil granule	1	5	0.2981385	311 annexin A11
GO S100 alpha binding	1	5	0.2981385	311 annexin A11
GO cell killing	1	5	0.2981385	3192 heterogeneous nuclear ribonucleoprotein U (scaffold attachment facto
GO CRD-mediated mRNA stability complx	1	5	0.2981385	3192 heterogeneous nuclear ribonucleoprotein U (scaffold attachment facto
GO CRD-mediated mRNA stabilization	1	5	0.2981385	3192 heterogeneous nuclear ribonucleoprotein U (scaffold attachment facto
GO negative regulation of astrocyte diffe	1	5	0.2981385	3400 inhibitor of DNA binding 4, dominant negative helix-loop-helix protein
GO monocyte differentiation	1	5	0.2981385	3428 interferon, gamma-inducible protein 16
GO motile secondary cilium	1	5	0.2981385	345895 radial spoke head 4 homolog A (Chlamydomonas)
GO negative regulation of insulin-like gro	1	5	0.2981385	3488 insulin-like growth factor binding protein 5
GO chorio-allantoic fusion	1	5	0.2981385	3491 cysteine-rich, angiogenic inducer, 61
GO ciliary neurotrophic factor-mediated	1	5	0.2981385	3570 interleukin 6 receptor
GO negative regulation of interleukin-8 p	1	5	0.2981385	3570 interleukin 6 receptor
GO negative regulation of protein amino	1	5	0.2981385	3725 jun oncogene
GO glycosphingolipid metabolic process	1	5	0.2981385	3815 v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog
GO regulation of developmental pigment	1	5	0.2981385	3815 v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog
GO lipoprotein catabolic process	1	5	0.2981385	3949 low density lipoprotein receptor
GO low-density lipoprotein particle clear	1	5	0.2981385	3949 low density lipoprotein receptor
GO positive regulation of GTPase activity	1	5	0.2981385	395 Rho GTPase activating protein 6
GO pericardium development	1	5	0.2981385	4087 SMAD family member 2
GO primary microRNA processing	1	5	0.2981385	4087 SMAD family member 2

GO	regulation of binding	1	5	0.2981385	4087 SMAD family member 2
GO	transforming growth factor beta rece	1	5	0.2981385	4087 SMAD family member 2
GO	steroid catabolic process	1	5	0.2981385	412 steroid sulfatase (microsomal), isozyme S
GO	sulfuric ester hydrolase activity	1	5	0.2981385	412 steroid sulfatase (microsomal), isozyme S
GO	regulation of osteoclast differentiat	1	5	0.2981385	4286 microphthalmia-associated transcription factor
GO	E-box binding	1	5	0.2981385	429 achaete-scute complex homolog 1 (Drosophila)
GO	spinal cord association neuron differ	1	5	0.2981385	429 achaete-scute complex homolog 1 (Drosophila)
GO	nerve growth factor receptor signalin	1	5	0.2981385	4692 necdin homolog (mouse)
GO	germinal center formation	1	5	0.2981385	4791 nuclear factor of kappa light polypeptide gene enhancer in B-cells 2 (p4
GO	negative regulation of Notch signalin	1	5	0.2981385	4792 nuclear factor of kappa light polypeptide gene enhancer in B-cells inhib
GO	sprouting angiogenesis	1	5	0.2981385	4851 Notch homolog 1, translocation-associated (Drosophila)
GO	reduction of cytosolic calcium ion cor	1	5	0.2981385	4886 neuropeptide Y receptor Y1
GO	negative regulation of cardiac muscle	1	5	0.2981385	5025 purinergic receptor P2X, ligand-gated ion channel, 4
GO	positive regulation of prostaglandin s	1	5	0.2981385	5025 purinergic receptor P2X, ligand-gated ion channel, 4
GO	nerve growth factor binding	1	5	0.2981385	5046 proprotein convertase subtilisin/kexin type 6
GO	peptide metabolic process	1	5	0.2981385	5066 peptidylglycine alpha-amidating monooxygenase
GO	negative regulation of cell cycle arres	1	5	0.2981385	51085 MLX interacting protein-like
GO	glycolipid binding	1	5	0.2981385	51228 glycolipid transfer protein
GO	glycolipid transporter activity	1	5	0.2981385	51228 glycolipid transfer protein
GO	positive regulation of triglyceride bio	1	5	0.2981385	51703 acyl-CoA synthetase long-chain family member 5
GO	positive regulation of establishment (	1	5	0.2981385	5295 phosphoinositide-3-kinase, regulatory subunit 1 (alpha)
GO	regulation of cytokine production	1	5	0.2981385	53347 ubiquitin associated and SH3 domain containing, A
GO	positive regulation of defense respon	1	5	0.2981385	5371 promyelocytic leukemia
GO	microvillus assembly	1	5	0.2981385	53827 FXYD domain containing ion transport regulator 5
GO	positive regulation of smoothed sig	1	5	0.2981385	5396 paired related homeobox 1
GO	oocyte development	1	5	0.2981385	54361 wingless-type MMTV integration site family, member 4
GO	serine-type carboxypeptidase activity	1	5	0.2981385	54504 carboxypeptidase, vitellogenic-like
GO	DNA-directed RNA polymerase II, hol	1	5	0.2981385	55140 elongation protein 3 homolog ( <i>S. cerevisiae</i> )
GO	cellular amino acid and derivative me	1	5	0.2981385	55432 YOD1 OTU deubiquinating enzyme 1 homolog ( <i>S. cerevisiae</i> )
GO	regulation of T cell activation	1	5	0.2981385	55824 phosphoprotein associated with glycosphingolipid microdomains 1
GO	sodium-independent organic anion tr	1	5	0.2981385	55867 solute carrier family 22 (organic anion/urate transporter), member 11
GO	regulation of bone mineralization	1	5	0.2981385	56172 ankylosis, progressive homolog (mouse)
GO	positive regulation of triglyceride cat	1	5	0.2981385	57104 patatin-like phospholipase domain containing 2
GO	melanosome localization	1	5	0.2981385	5873 RAB27A, member RAS oncogene family
GO	ammonium transmembrane transpor	1	5	0.2981385	6006 Rh blood group, CcEe antigens
GO	negative regulation of Rho protein sig	1	5	0.2981385	604 B-cell CLL/lymphoma 6

GO	glutamate secretion	1	5	0.2981385	627	brain-derived neurotrophic factor
GO	negative regulation of neuroblast prc	1	5	0.2981385	627	brain-derived neurotrophic factor
GO	neuron recognition	1	5	0.2981385	627	brain-derived neurotrophic factor
GO	detection of chemical stimulus involv	1	5	0.2981385	64108	receptor (chemosensory) transporter protein 4
GO	thioredoxin-disulfide reductase activi	1	5	0.2981385	64359	nucleoredoxin
GO	BMP receptor binding	1	5	0.2981385	652	bone morphogenetic protein 4
GO	mesenchymal to epithelial transition	1	5	0.2981385	652	bone morphogenetic protein 4
GO	negative regulation of chondrocyte d	1	5	0.2981385	652	bone morphogenetic protein 4
GO	negative regulation of oligodendrocy	1	5	0.2981385	652	bone morphogenetic protein 4
GO	positive regulation of branching invol	1	5	0.2981385	652	bone morphogenetic protein 4
GO	regulation of smooth muscle cell diff	1	5	0.2981385	652	bone morphogenetic protein 4
GO	tongue morphogenesis	1	5	0.2981385	652	bone morphogenetic protein 4
GO	anion exchanger activity	1	5	0.2981385	6521	solute carrier family 4, anion exchanger, member 1 (erythrocyte memb
GO	cellular ion homeostasis	1	5	0.2981385	6521	solute carrier family 4, anion exchanger, member 1 (erythrocyte memb
GO	oligopeptide transport	1	5	0.2981385	6564	solute carrier family 15 (oligopeptide transporter), member 1
GO	drug transport	1	5	0.2981385	6565	solute carrier family 15 (H+/peptide transporter), member 2
GO	long-term synaptic potentiation	1	5	0.2981385	6622	synuclein, alpha (non A4 component of amyloid precursor)
GO	positive regulation of receptor recycl	1	5	0.2981385	6622	synuclein, alpha (non A4 component of amyloid precursor)
GO	regulation of locomotion	1	5	0.2981385	6622	synuclein, alpha (non A4 component of amyloid precursor)
GO	regulation of macrophage activation	1	5	0.2981385	6622	synuclein, alpha (non A4 component of amyloid precursor)
GO	tau protein binding	1	5	0.2981385	6622	synuclein, alpha (non A4 component of amyloid precursor)
GO	spectrin-associated cytoskeleton	1	5	0.2981385	6710	spectrin, beta, erythrocytic
GO	induction of apoptosis by hormones	1	5	0.2981385	6750	somatostatin
GO	somatostatin receptor activity	1	5	0.2981385	6751	somatostatin receptor 1
GO	definitive hemopoiesis	1	5	0.2981385	7049	transforming growth factor, beta receptor III
GO	negative regulation of cellular compc	1	5	0.2981385	7049	transforming growth factor, beta receptor III
GO	response to prostaglandin E stimulus	1	5	0.2981385	7049	transforming growth factor, beta receptor III
GO	toll-like receptor signaling pathway	1	5	0.2981385	7099	toll-like receptor 4
GO	regulation of short-term neuronal syr	1	5	0.2981385	729993	shisa homolog 9 (Xenopus laevis)
GO	mammary gland branching involved i	1	5	0.2981385	7474	wingless-type MMTV integration site family, member 5A
GO	1-alkyl-2-acetyl-glycerophosphocholin	1	5	0.2981385	7941	phospholipase A2, group VII (platelet-activating factor acetylhydrolase,
GO	intramembranous ossification	1	5	0.2981385	8313	axin 2
GO	phosphatidylinositol transporter acti	1	5	0.2981385	83394	PITPNM family member 3
GO	endoderm formation	1	5	0.2981385	83595	SRY (sex determining region Y)-box 7
GO	muscle organ morphogenesis	1	5	0.2981385	84159	AT rich interactive domain 5B (MRF1-like)
GO	negative regulation of kinase activity	1	5	0.2981385	8660	insulin receptor substrate 2

GO	regulation of calcium ion transport via	1	5	0.2981385	91404	SEC14 and spectrin domains 1
GO	secondary active monocarboxylate transporter	1	5	0.2981385	9194	solute carrier family 16, member 7 (monocarboxylic acid transporter 2)
GO	peptidoglycan receptor activity	1	5	0.2981385	929	CD14 molecule
GO	N-acetylglucosamine 6-O-sulfotransferase	1	5	0.2981385	9435	carbohydrate (N-acetylglucosamine-6-O) sulfotransferase 2
GO	cellular metal ion homeostasis	1	5	0.2981385	9633	metallothionein-like 5, testis-specific (tesmin)
GO	nitric-oxide synthase binding	1	5	0.2981385	9722	nitric oxide synthase 1 (neuronal) adaptor protein
GO	segment specification	1	5	0.2981385	9935	v-maf musculoaponeurotic fibrosarcoma oncogene homolog B (avian)
GO	synapsis	1	5	0.2981385	9985	REC8 homolog (yeast)
GO	camera-type eye development	3	28	0.2990029	2296	forkhead box C1
GO	camera-type eye development	3	28	0.2990029	2303	forkhead box C2 (MFH-1, mesenchyme forkhead 1)
GO	camera-type eye development	3	28	0.2990029	4286	microphthalmia-associated transcription factor
GO	single fertilization	3	28	0.2990029	4179	CD46 molecule, complement regulatory protein
GO	single fertilization	3	28	0.2990029	4486	macrophage stimulating 1 receptor (c-met-related tyrosine kinase)
GO	single fertilization	3	28	0.2990029	5016	oviductal glycoprotein 1, 120kDa
GO	positive regulation of axonogenesis	2	16	0.2997149	10507	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM)
GO	positive regulation of axonogenesis	2	16	0.2997149	23654	plexin B2
GO	vitamin D receptor binding	2	16	0.2997149	10766	transducer of ERBB2, 2
GO	vitamin D receptor binding	2	16	0.2997149	6256	retinoid X receptor, alpha
GO	nicotinic acetylcholine-activated cation channel activity	2	16	0.2997149	1139	cholinergic receptor, nicotinic, alpha 7
GO	nicotinic acetylcholine-activated cation channel activity	2	16	0.2997149	8973	cholinergic receptor, nicotinic, alpha 6
GO	nicotinic acetylcholine-gated receptor activity	2	16	0.2997149	1139	cholinergic receptor, nicotinic, alpha 7
GO	nicotinic acetylcholine-gated receptor activity	2	16	0.2997149	8973	cholinergic receptor, nicotinic, alpha 6
GO	phosphatidylinositol-3,4,5-trisphosphatase	2	16	0.2997149	116984	ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 2
GO	phosphatidylinositol-3,4,5-trisphosphatase	2	16	0.2997149	56288	par-3 partitioning defective 3 homolog (C. elegans)
GO	negative regulation of insulin secretory granule biogenesis	2	16	0.2997149	130399	activin A receptor, type IC
GO	negative regulation of insulin secretory granule biogenesis	2	16	0.2997149	8622	phosphodiesterase 8B
GO	receptor complex	2	16	0.2997149	1435	colony stimulating factor 1 (macrophage)
GO	receptor complex	2	16	0.2997149	154	adrenergic, beta-2-, receptor, surface
GO	gamete generation	2	16	0.2997149	158800	Rhox homeobox family, member 1
GO	gamete generation	2	16	0.2997149	54361	wingless-type MMTV integration site family, member 4
GO	response to morphine	2	16	0.2997149	1813	dopamine receptor D2
GO	response to morphine	2	16	0.2997149	5122	proprotein convertase subtilisin/kexin type 1
GO	lateral plasma membrane	2	16	0.2997149	2706	gap junction protein, beta 2, 26kDa
GO	lateral plasma membrane	2	16	0.2997149	368	ATP-binding cassette, sub-family C (CFTR/MRP), member 6
GO	smoothened signaling pathway	2	16	0.2997149	28996	homeodomain interacting protein kinase 2
GO	smoothened signaling pathway	2	16	0.2997149	50937	Cdon homolog (mouse)

GO response to nutrient levels	2	16	0.2997149	3643 insulin receptor
GO response to nutrient levels	2	16	0.2997149	5122 proprotein convertase subtilisin/kexin type 1
GO internal side of plasma membrane	2	16	0.2997149	3815 v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog
GO internal side of plasma membrane	2	16	0.2997149	5239 phosphoglucomutase 5
GO calcium-dependent cysteine-type enc	2	16	0.2997149	388743 calpain 8
GO calcium-dependent cysteine-type enc	2	16	0.2997149	726 calpain 5
GO response to axon injury	2	16	0.2997149	4056 leukotriene C4 synthase
GO response to axon injury	2	16	0.2997149	5122 proprotein convertase subtilisin/kexin type 1
GO mitochondrial envelope	2	16	0.2997149	4129 monoamine oxidase B
GO mitochondrial envelope	2	16	0.2997149	9804 translocase of outer mitochondrial membrane 20 homolog (yeast)
GO eukaryotic cell surface binding	2	16	0.2997149	498 ATP synthase, H <sup>+</sup> transporting, mitochondrial F1 complex, alpha subun
GO eukaryotic cell surface binding	2	16	0.2997149	5046 proprotein convertase subtilisin/kexin type 6
GO stereocilium	2	16	0.2997149	51168 myosin XVA
GO stereocilium	2	16	0.2997149	53405 chloride intracellular channel 5
GO mRNA binding	4	41	0.3068172	104 adenosine deaminase, RNA-specific, B1 (RED1 homolog rat)
GO mRNA binding	4	41	0.3068172	55124 piwi-like 2 (Drosophila)
GO mRNA binding	4	41	0.3068172	7538 zinc finger protein 36, C3H type, homolog (mouse)
GO mRNA binding	4	41	0.3068172	9271 piwi-like 1 (Drosophila)
GO cellular defense response	5	54	0.3086611	10288 leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM
GO cellular defense response	5	54	0.3086611	10312 T-cell, immune regulator 1, ATPase, H <sup>+</sup> transporting, lysosomal V0 subu
GO cellular defense response	5	54	0.3086611	3823 killer cell lectin-like receptor subfamily C, member 3
GO cellular defense response	5	54	0.3086611	3959 lectin, galactoside-binding, soluble, 3 binding protein
GO cellular defense response	5	54	0.3086611	9214 Fas apoptotic inhibitory molecule 3
GO proton transport	5	54	0.3086611	10312 T-cell, immune regulator 1, ATPase, H <sup>+</sup> transporting, lysosomal V0 subu
GO proton transport	5	54	0.3086611	27035 NADPH oxidase 1
GO proton transport	5	54	0.3086611	498 ATP synthase, H <sup>+</sup> transporting, mitochondrial F1 complex, alpha subun
GO proton transport	5	54	0.3086611	50617 ATPase, H <sup>+</sup> transporting, lysosomal V0 subunit a4
GO proton transport	5	54	0.3086611	8992 ATPase, H <sup>+</sup> transporting, lysosomal 9kDa, V0 subunit e1
GO basolateral plasma membrane	9	107	0.3088619	1048 carcinoembryonic antigen-related cell adhesion molecule 5
GO basolateral plasma membrane	9	107	0.3088619	1080 cystic fibrosis transmembrane conductance regulator (ATP-binding cas:
GO basolateral plasma membrane	9	107	0.3088619	2066 v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian)
GO basolateral plasma membrane	9	107	0.3088619	3570 interleukin 6 receptor
GO basolateral plasma membrane	9	107	0.3088619	358 aquaporin 1 (Colton blood group)
GO basolateral plasma membrane	9	107	0.3088619	6521 solute carrier family 4, anion exchanger, member 1 (erythrocyte memb
GO basolateral plasma membrane	9	107	0.3088619	760 carbonic anhydrase II
GO basolateral plasma membrane	9	107	0.3088619	8671 solute carrier family 4, sodium bicarbonate cotransporter, member 4

GO basolateral plasma membrane	9	107	0.3088619	9962 solute carrier family 23 (nucleobase transporters), member 2
GO actin cytoskeleton	11	134	0.3088761	11078 TRIO and F-actin binding protein
GO actin cytoskeleton	11	134	0.3088761	1612 death-associated protein kinase 1
GO actin cytoskeleton	11	134	0.3088761	2039 erythrocyte membrane protein band 4.9 (dematin)
GO actin cytoskeleton	11	134	0.3088761	27295 PDZ and LIM domain 3
GO actin cytoskeleton	11	134	0.3088761	395 Rho GTPase activating protein 6
GO actin cytoskeleton	11	134	0.3088761	3983 actin binding LIM protein 1
GO actin cytoskeleton	11	134	0.3088761	4778 nuclear factor (erythroid-derived 2), 45kDa
GO actin cytoskeleton	11	134	0.3088761	53405 chloride intracellular channel 5
GO actin cytoskeleton	11	134	0.3088761	6622 synuclein, alpha (non A4 component of amyloid precursor)
GO actin cytoskeleton	11	134	0.3088761	6710 spectrin, beta, erythrocytic
GO actin cytoskeleton	11	134	0.3088761	9788 metastasis suppressor 1
GO cell proliferation	22	286	0.3132056	10216 proteoglycan 4
GO cell proliferation	22	286	0.3132056	1435 colony stimulating factor 1 (macrophage)
GO cell proliferation	22	286	0.3132056	2013 epithelial membrane protein 2
GO cell proliferation	22	286	0.3132056	2066 v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian)
GO cell proliferation	22	286	0.3132056	2239 glypican 4
GO cell proliferation	22	286	0.3132056	2303 forkhead box C2 (MFH-1, mesenchyme forkhead 1)
GO cell proliferation	22	286	0.3132056	2752 glutamate-ammonia ligase (glutamine synthetase)
GO cell proliferation	22	286	0.3132056	29126 CD274 molecule
GO cell proliferation	22	286	0.3132056	3428 interferon, gamma-inducible protein 16
GO cell proliferation	22	286	0.3132056	3491 cysteine-rich, angiogenic inducer, 61
GO cell proliferation	22	286	0.3132056	3601 interleukin 15 receptor, alpha
GO cell proliferation	22	286	0.3132056	3911 laminin, alpha 5
GO cell proliferation	22	286	0.3132056	4194 Mdm4 p53 binding protein homolog (mouse)
GO cell proliferation	22	286	0.3132056	4254 KIT ligand
GO cell proliferation	22	286	0.3132056	64083 golgi phosphoprotein 3 (coat-protein)
GO cell proliferation	22	286	0.3132056	6494 signal-induced proliferation-associated 1
GO cell proliferation	22	286	0.3132056	684 bone marrow stromal cell antigen 2
GO cell proliferation	22	286	0.3132056	6850 spleen tyrosine kinase
GO cell proliferation	22	286	0.3132056	6941 transcription factor 19
GO cell proliferation	22	286	0.3132056	7071 Kruppel-like factor 10
GO cell proliferation	22	286	0.3132056	8556 CDC14 cell division cycle 14 homolog A (S. cerevisiae)
GO cell proliferation	22	286	0.3132056	8744 tumor necrosis factor (ligand) superfamily, member 9
GO histone deacetylase complex	3	29	0.3181706	10014 histone deacetylase 5
GO histone deacetylase complex	3	29	0.3181706	2122 MDS1 and EVI1 complex locus



GO histone deacetylase complex	3	29	0.3181706	9734 histone deacetylase 9
GO protein kinase C binding	3	29	0.3181706	10014 histone deacetylase 5
GO protein kinase C binding	3	29	0.3181706	112464 protein kinase C, delta binding protein
GO protein kinase C binding	3	29	0.3181706	9734 histone deacetylase 9
GO keratinocyte differentiation	3	29	0.3181706	10628 thioredoxin interacting protein
GO keratinocyte differentiation	3	29	0.3181706	6706 small proline-rich protein 2G
GO keratinocyte differentiation	3	29	0.3181706	8796 sciellin
GO transcriptional repressor complex	3	29	0.3181706	2117 ets variant 3
GO transcriptional repressor complex	3	29	0.3181706	2737 GLI family zinc finger 3
GO transcriptional repressor complex	3	29	0.3181706	7464 coronin, actin binding protein, 2A
GO behavior	3	29	0.3181706	2354 FBJ murine osteosarcoma viral oncogene homolog B
GO behavior	3	29	0.3181706	4128 monoamine oxidase A
GO behavior	3	29	0.3181706	5367 pro-melanin-concentrating hormone
GO protein homooligomerization	6	68	0.3200702	2040 stomatin
GO protein homooligomerization	6	68	0.3200702	5025 purinergic receptor P2X, ligand-gated ion channel, 4
GO protein homooligomerization	6	68	0.3200702	6505 solute carrier family 1 (neuronal/epithelial high affinity glutamate transp
GO protein homooligomerization	6	68	0.3200702	6857 synaptotagmin I
GO protein homooligomerization	6	68	0.3200702	8527 diacylglycerol kinase, delta 130kDa
GO protein homooligomerization	6	68	0.3200702	8600 tumor necrosis factor (ligand) superfamily, member 11
GO post-embryonic development	5	55	0.3223666	4087 SMAD family member 2
GO post-embryonic development	5	55	0.3223666	4929 nuclear receptor subfamily 4, group A, member 2
GO post-embryonic development	5	55	0.3223666	64651 cysteine-serine-rich nuclear protein 1
GO post-embryonic development	5	55	0.3223666	652 bone morphogenetic protein 4
GO post-embryonic development	5	55	0.3223666	84159 AT rich interactive domain 5B (MRF1-like)
GO chemokine activity	4	42	0.3226198	2921 chemokine (C-X-C motif) ligand 3
GO chemokine activity	4	42	0.3226198	56477 chemokine (C-C motif) ligand 28
GO chemokine activity	4	42	0.3226198	6372 chemokine (C-X-C motif) ligand 6 (granulocyte chemotactic protein 2)
GO chemokine activity	4	42	0.3226198	6374 chemokine (C-X-C motif) ligand 5
GO histone deacetylation	2	17	0.3255718	10014 histone deacetylase 5
GO histone deacetylation	2	17	0.3255718	9734 histone deacetylase 9
GO positive regulation of cell-substrate a	2	17	0.3255718	10085 EGF-like repeats and discoidin I-like domains 3
GO positive regulation of cell-substrate a	2	17	0.3255718	3491 cysteine-rich, angiogenic inducer, 61
GO positive regulation of proteasomal uk	2	17	0.3255718	10221 tribbles homolog 1 (Drosophila)
GO positive regulation of proteasomal uk	2	17	0.3255718	28951 tribbles homolog 2 (Drosophila)
GO activation of protein kinase A activity	2	17	0.3255718	112 adenylate cyclase 6
GO activation of protein kinase A activity	2	17	0.3255718	5577 protein kinase, cAMP-dependent, regulatory, type II, beta

GO DNA damage response, signal transdu	2	17	0.3255718	11200 CHK2 checkpoint homolog ( <i>S. pombe</i> )
GO DNA damage response, signal transdu	2	17	0.3255718	5371 promyelocytic leukemia
GO regulation of pH	2	17	0.3255718	1906 endothelin 1
GO regulation of pH	2	17	0.3255718	50617 ATPase, H+ transporting, lysosomal V0 subunit a4
GO regulation of angiogenesis	2	17	0.3255718	1969 EPH receptor A2
GO regulation of angiogenesis	2	17	0.3255718	3569 interleukin 6 (interferon, beta 2)
GO NF-kappaB binding	2	17	0.3255718	2033 E1A binding protein p300
GO NF-kappaB binding	2	17	0.3255718	4792 nuclear factor of kappa light polypeptide gene enhancer in B-cells inhib
GO rough endoplasmic reticulum	2	17	0.3255718	255738 proprotein convertase subtilisin/kexin type 9
GO rough endoplasmic reticulum	2	17	0.3255718	5122 proprotein convertase subtilisin/kexin type 1
GO anchored to plasma membrane	2	17	0.3255718	27076 LY6/PLAUR domain containing 3
GO anchored to plasma membrane	2	17	0.3255718	285704 RGM domain family, member B
GO nuclear body	2	17	0.3255718	28996 homeodomain interacting protein kinase 2
GO nuclear body	2	17	0.3255718	6239 ras responsive element binding protein 1
GO caspase activator activity	2	17	0.3255718	29108 PYD and CARD domain containing
GO caspase activator activity	2	17	0.3255718	834 caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, co
GO 2 iron, 2 sulfur cluster binding	2	17	0.3255718	316 aldehyde oxidase 1
GO 2 iron, 2 sulfur cluster binding	2	17	0.3255718	8418 cytidine monophosphate-N-acetylneuraminic acid hydroxylase (CMP-N
GO fatty acid binding	2	17	0.3255718	338557 G protein-coupled receptor 120
GO fatty acid binding	2	17	0.3255718	6622 synuclein, alpha (non A4 component of amyloid precursor)
GO positive regulation of cell differentiat	2	17	0.3255718	3726 jun B proto-oncogene
GO positive regulation of cell differentiat	2	17	0.3255718	9021 suppressor of cytokine signaling 3
GO embryonic pattern specification	2	17	0.3255718	4087 SMAD family member 2
GO embryonic pattern specification	2	17	0.3255718	84976 dispatched homolog 1 ( <i>Drosophila</i> )
GO embryonic hindlimb morphogenesis	2	17	0.3255718	4851 Notch homolog 1, translocation-associated ( <i>Drosophila</i> )
GO embryonic hindlimb morphogenesis	2	17	0.3255718	5307 paired-like homeodomain 1
GO epithelial to mesenchymal transition	2	17	0.3255718	4851 Notch homolog 1, translocation-associated ( <i>Drosophila</i> )
GO epithelial to mesenchymal transition	2	17	0.3255718	7049 transforming growth factor, beta receptor III
GO regulation of excitatory postsynaptic	2	17	0.3255718	5025 purinergic receptor P2X, ligand-gated ion channel, 4
GO regulation of excitatory postsynaptic	2	17	0.3255718	6622 synuclein, alpha (non A4 component of amyloid precursor)
GO glycerol metabolic process	2	17	0.3255718	56261 glycerophosphocholine phosphodiesterase GDE1 homolog ( <i>S. cerevisia</i>
GO glycerol metabolic process	2	17	0.3255718	81544 glycerophosphodiester phosphodiesterase domain containing 5
GO negative regulation of insulin receptc	2	17	0.3255718	5791 protein tyrosine phosphatase, receptor type, E
GO negative regulation of insulin receptc	2	17	0.3255718	9021 suppressor of cytokine signaling 3
GO coreceptor activity	2	17	0.3255718	7049 transforming growth factor, beta receptor III
GO coreceptor activity	2	17	0.3255718	7852 chemokine (C-X-C motif) receptor 4

GO myofibril	2	17	0.3255718	7111 tropomodulin 1
GO myofibril	2	17	0.3255718	84033 obscurin, cytoskeletal calmodulin and titin-interacting RhoGEF
GO ribonuclease activity	2	17	0.3255718	85441 peroxisomal proliferator-activated receptor A interacting complex 285
GO ribonuclease activity	2	17	0.3255718	8635 ribonuclease T2
GO cell junction	29	387	0.3299174	1139 cholinergic receptor, nicotinic, alpha 7
GO cell junction	29	387	0.3299174	1364 claudin 4
GO cell junction	29	387	0.3299174	143098 membrane protein, palmitoylated 7 (MAGUK p55 subfamily member 7)
GO cell junction	29	387	0.3299174	143425 synaptotagmin IX
GO cell junction	29	387	0.3299174	154810 angiomin like 1
GO cell junction	29	387	0.3299174	1785 dynamin 2
GO cell junction	29	387	0.3299174	1803 dipeptidyl-peptidase 4
GO cell junction	29	387	0.3299174	23092 Rho GTPase activating protein 26
GO cell junction	29	387	0.3299174	23208 synaptotagmin XI
GO cell junction	29	387	0.3299174	23371 tensin like C1 domain containing phosphatase (tensin 2)
GO cell junction	29	387	0.3299174	2564 gamma-aminobutyric acid (GABA) A receptor, epsilon
GO cell junction	29	387	0.3299174	2706 gap junction protein, beta 2, 26kDa
GO cell junction	29	387	0.3299174	2707 gap junction protein, beta 3, 31kDa
GO cell junction	29	387	0.3299174	27134 tight junction protein 3 (zona occludens 3)
GO cell junction	29	387	0.3299174	399694 SHC (Src homology 2 domain containing) family, member 4
GO cell junction	29	387	0.3299174	5025 purinergic receptor P2X, ligand-gated ion channel, 4
GO cell junction	29	387	0.3299174	5318 plakophilin 2
GO cell junction	29	387	0.3299174	55740 enabled homolog (Drosophila)
GO cell junction	29	387	0.3299174	55870 ash1 (absent, small, or homeotic)-like (Drosophila)
GO cell junction	29	387	0.3299174	57619 shroom family member 3
GO cell junction	29	387	0.3299174	6857 synaptotagmin I
GO cell junction	29	387	0.3299174	729993 shisa homolog 9 (Xenopus laevis)
GO cell junction	29	387	0.3299174	7706 tripartite motif-containing 25
GO cell junction	29	387	0.3299174	8082 sarcospan (Kras oncogene-associated gene)
GO cell junction	29	387	0.3299174	83604 transmembrane protein 47
GO cell junction	29	387	0.3299174	8973 cholinergic receptor, nicotinic, alpha 6
GO cell junction	29	387	0.3299174	9071 claudin 10
GO cell junction	29	387	0.3299174	9143 synaptogyrin 3
GO cell junction	29	387	0.3299174	9414 tight junction protein 2 (zona occludens 2)
GO cell death	10	123	0.331858	11202 kallikrein-related peptidase 8
GO cell death	10	123	0.331858	1822 atrophin 1
GO cell death	10	123	0.331858	2055 ceroid-lipofuscinosis, neuronal 8 (epilepsy, progressive with mental ret

GO cell death	10	123	0.331858	2521 fused in sarcoma
GO cell death	10	123	0.331858	3373 hyaluronoglucosaminidase 1
GO cell death	10	123	0.331858	6622 synuclein, alpha (non A4 component of amyloid precursor)
GO cell death	10	123	0.331858	7133 tumor necrosis factor receptor superfamily, member 1B
GO cell death	10	123	0.331858	79152 fatty acid 2-hydroxylase
GO cell death	10	123	0.331858	8313 axin 2
GO cell death	10	123	0.331858	834 caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, co
GO transcription coactivator activity	15	192	0.3336553	10891 peroxisome proliferator-activated receptor gamma, coactivator 1 alpha
GO transcription coactivator activity	15	192	0.3336553	11030 RNA binding protein with multiple splicing
GO transcription coactivator activity	15	192	0.3336553	1999 E74-like factor 3 (ets domain transcription factor, epithelial-specific )
GO transcription coactivator activity	15	192	0.3336553	2033 E1A binding protein p300
GO transcription coactivator activity	15	192	0.3336553	3725 jun oncogene
GO transcription coactivator activity	15	192	0.3336553	3726 jun B proto-oncogene
GO transcription coactivator activity	15	192	0.3336553	4778 nuclear factor (erythroid-derived 2), 45kDa
GO transcription coactivator activity	15	192	0.3336553	4791 nuclear factor of kappa light polypeptide gene enhancer in B-cells 2 (p4
GO transcription coactivator activity	15	192	0.3336553	4802 nuclear transcription factor Y, gamma
GO transcription coactivator activity	15	192	0.3336553	5371 promyelocytic leukemia
GO transcription coactivator activity	15	192	0.3336553	5396 paired related homeobox 1
GO transcription coactivator activity	15	192	0.3336553	6256 retinoid X receptor, alpha
GO transcription coactivator activity	15	192	0.3336553	6604 SWI/SNF related, matrix associated, actin dependent regulator of chrom
GO transcription coactivator activity	15	192	0.3336553	85441 peroxisomal proliferator-activated receptor A interacting complex 285
GO transcription coactivator activity	15	192	0.3336553	9971 nuclear receptor subfamily 1, group H, member 4
GO transporter activity	22	290	0.3368005	10312 T-cell, immune regulator 1, ATPase, H+ transporting, lysosomal V0 sub
GO transporter activity	22	290	0.3368005	113235 solute carrier family 46 (folate transporter), member 1
GO transporter activity	22	290	0.3368005	123096 solute carrier family 25, member 29
GO transporter activity	22	290	0.3368005	1382 cellular retinoic acid binding protein 2
GO transporter activity	22	290	0.3368005	143425 synaptotagmin IX
GO transporter activity	22	290	0.3368005	23208 synaptotagmin XI
GO transporter activity	22	290	0.3368005	28231 solute carrier organic anion transporter family, member 4A1
GO transporter activity	22	290	0.3368005	28982 feline leukemia virus subgroup C cellular receptor 1
GO transporter activity	22	290	0.3368005	368 ATP-binding cassette, sub-family C (CFTR/MRP), member 6
GO transporter activity	22	290	0.3368005	5243 ATP-binding cassette, sub-family B (MDR/TAP), member 1
GO transporter activity	22	290	0.3368005	55867 solute carrier family 22 (organic anion/urate transporter), member 11
GO transporter activity	22	290	0.3368005	5950 retinol binding protein 4, plasma
GO transporter activity	22	290	0.3368005	63027 solute carrier family 22, member 23
GO transporter activity	22	290	0.3368005	6521 solute carrier family 4, anion exchanger, member 1 (erythrocyte memb

GO transporter activity	22	290	0.3368005	6564 solute carrier family 15 (oligopeptide transporter), member 1
GO transporter activity	22	290	0.3368005	6565 solute carrier family 15 (H+/peptide transporter), member 2
GO transporter activity	22	290	0.3368005	6857 synaptotagmin I
GO transporter activity	22	290	0.3368005	8671 solute carrier family 4, sodium bicarbonate cotransporter, member 4
GO transporter activity	22	290	0.3368005	8992 ATPase, H+ transporting, lysosomal 9kDa, V0 subunit e1
GO transporter activity	22	290	0.3368005	9182 Ras association (RalGDS/AF-6) domain family (N-terminal) member 9
GO transporter activity	22	290	0.3368005	9481 solute carrier family 25, member 27
GO transporter activity	22	290	0.3368005	9962 solute carrier family 23 (nucleobase transporters), member 2
GO protein tyrosine/serine/threonine ph	3	30	0.3373522	11156 protein tyrosine phosphatase type IVA, member 3
GO protein tyrosine/serine/threonine ph	3	30	0.3373522	54961 slingshot homolog 3 (Drosophila)
GO protein tyrosine/serine/threonine ph	3	30	0.3373522	8556 CDC14 cell division cycle 14 homolog A (S. cerevisiae)
GO cell morphogenesis	3	30	0.3373522	134549 shroom family member 1
GO cell morphogenesis	3	30	0.3373522	57619 shroom family member 3
GO cell morphogenesis	3	30	0.3373522	604 B-cell CLL/lymphoma 6
GO gene silencing by RNA	3	30	0.3373522	143689 piwi-like 4 (Drosophila)
GO gene silencing by RNA	3	30	0.3373522	55124 piwi-like 2 (Drosophila)
GO gene silencing by RNA	3	30	0.3373522	9271 piwi-like 1 (Drosophila)
GO BMP signaling pathway	4	43	0.3384759	285704 RGM domain family, member B
GO BMP signaling pathway	4	43	0.3384759	64388 gremlin 2, cysteine knot superfamily, homolog (Xenopus laevis)
GO BMP signaling pathway	4	43	0.3384759	652 bone morphogenetic protein 4
GO BMP signaling pathway	4	43	0.3384759	7049 transforming growth factor, beta receptor III
GO cell-cell adhesion	6	70	0.3447352	10076 protein tyrosine phosphatase, receptor type, U
GO cell-cell adhesion	6	70	0.3447352	1009 cadherin 11, type 2, OB-cadherin (osteoblast)
GO cell-cell adhesion	6	70	0.3447352	4008 LIM domain 7
GO cell-cell adhesion	6	70	0.3447352	5318 plakophilin 2
GO cell-cell adhesion	6	70	0.3447352	79872 Cas-Br-M (murine) ecotropic retroviral transforming sequence-like 1
GO cell-cell adhesion	6	70	0.3447352	84059 G protein-coupled receptor 98
GO growth factor activity	12	152	0.3452406	1435 colony stimulating factor 1 (macrophage)
GO growth factor activity	12	152	0.3452406	183 angiotensinogen (serpin peptidase inhibitor, clade A, member 8)
GO growth factor activity	12	152	0.3452406	1839 heparin-binding EGF-like growth factor
GO growth factor activity	12	152	0.3452406	23529 cardiotrophin-like cytokine factor 1
GO growth factor activity	12	152	0.3452406	26281 fibroblast growth factor 20
GO growth factor activity	12	152	0.3452406	3479 insulin-like growth factor 1 (somatomedin C)
GO growth factor activity	12	152	0.3452406	3569 interleukin 6 (interferon, beta 2)
GO growth factor activity	12	152	0.3452406	4254 KIT ligand
GO growth factor activity	12	152	0.3452406	4856 nephroblastoma overexpressed gene

GO growth factor activity	12	152	0.3452406	627 brain-derived neurotrophic factor
GO growth factor activity	12	152	0.3452406	652 bone morphogenetic protein 4
GO growth factor activity	12	152	0.3452406	9518 growth differentiation factor 15
GO structural constituent of tooth enamel	1	6	0.3461221	10117 enamelin
GO alcohol dehydrogenase (NAD) activity	1	6	0.3461221	10170 dehydrogenase/reductase (SDR family) member 9
GO protein phosphatase 2B binding	1	6	0.3461221	10231 regulator of calcineurin 2
GO cellular phosphate ion homeostasis	1	6	0.3461221	10568 solute carrier family 34 (sodium phosphate), member 2
GO response to fructose stimulus	1	6	0.3461221	10568 solute carrier family 34 (sodium phosphate), member 2
GO bicarbonate transport	1	6	0.3461221	1080 cystic fibrosis transmembrane conductance regulator (ATP-binding cas
GO fatty acid oxidation	1	6	0.3461221	10891 peroxisome proliferator-activated receptor gamma, coactivator 1 alpha
GO acylglycerol lipase activity	1	6	0.3461221	11343 monoglyceride lipase
GO alcohol metabolic process	1	6	0.3461221	124 alcohol dehydrogenase 1A (class I), alpha polypeptide
GO positive regulation of translational in	1	6	0.3461221	127933 U2AF homology motif (UHM) kinase 1
GO response to dietary excess	1	6	0.3461221	130399 activin A receptor, type IC
GO glycogen catabolic process	1	6	0.3461221	1373 carbamoyl-phosphate synthetase 1, mitochondrial
GO response to glucagon stimulus	1	6	0.3461221	1373 carbamoyl-phosphate synthetase 1, mitochondrial
GO retinoic acid metabolic process	1	6	0.3461221	1382 cellular retinoic acid binding protein 2
GO activation of transmembrane receptc	1	6	0.3461221	154 adrenergic, beta-2-, receptor, surface
GO synaptic vesicle transport	1	6	0.3461221	1785 dynamin 2
GO negative regulation of synaptic transi	1	6	0.3461221	1813 dopamine receptor D2
GO positive regulation of growth hormor	1	6	0.3461221	1813 dopamine receptor D2
GO regulation of inhibitory postsynaptic	1	6	0.3461221	1815 dopamine receptor D4
GO positive regulation of epidermal grow	1	6	0.3461221	183 angiotensinogen (serpin peptidase inhibitor, clade A, member 8)
GO vasoconstriction	1	6	0.3461221	1906 endothelin 1
GO glycoprotein biosynthetic process	1	6	0.3461221	192134 UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 6 (core
GO glucocorticoid receptor binding	1	6	0.3461221	2033 E1A binding protein p300
GO neuromuscular process controlling pc	1	6	0.3461221	2055 ceroid-lipofuscinosis, neuronal 8 (epilepsy, progressive with mental ret
GO spinal cord motor neuron differentia	1	6	0.3461221	2055 ceroid-lipofuscinosis, neuronal 8 (epilepsy, progressive with mental ret
GO positive regulation of synaptic transn	1	6	0.3461221	2066 v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian)
GO germ cell migration	1	6	0.3461221	2296 forkhead box C1
GO actomyosin structure organization	1	6	0.3461221	22998 LIM and calponin homology domains 1
GO histone H3-K9 demethylation	1	6	0.3461221	23081 lysine (K)-specific demethylase 4C
GO histone H4-K5 acetylation	1	6	0.3461221	23338 PHD finger protein 15
GO histone H4-K8 acetylation	1	6	0.3461221	23338 PHD finger protein 15
GO high-density lipoprotein binding	1	6	0.3461221	23780 apolipoprotein L, 2
GO arachidonic acid metabolic process	1	6	0.3461221	240 arachidonate 5-lipoxygenase

GO nuclear envelope lumen	1	6	0.3461221	240 arachidonate 5-lipoxygenase
GO fucose metabolic process	1	6	0.3461221	2517 fucosidase, alpha-L- 1, tissue
GO extrinsic to external side of plasma m	1	6	0.3461221	255738 proprotein convertase subtilisin/kexin type 9
GO AP-2 adaptor complex	1	6	0.3461221	26119 low density lipoprotein receptor adaptor protein 1
GO glycoprotein catabolic process	1	6	0.3461221	26270 F-box protein 6
GO regulation of synaptic transmission, g	1	6	0.3461221	2911 glutamate receptor, metabotropic 1
GO transmembrane receptor protein tyros	1	6	0.3461221	29760 B-cell linker
GO phagocytic vesicle	1	6	0.3461221	311 annexin A11
GO negative regulation of survival gene p	1	6	0.3461221	3169 forkhead box A1
GO epithelial cell development	1	6	0.3461221	3175 one cut homeobox 1
GO hyaluronoglucosaminidase activity	1	6	0.3461221	3373 hyaluronoglucosaminidase 1
GO lung vasculature development	1	6	0.3461221	3479 insulin-like growth factor 1 (somatomedin C)
GO positive regulation of insulin-like gro	1	6	0.3461221	3479 insulin-like growth factor 1 (somatomedin C)
GO ammonia transmembrane transporte	1	6	0.3461221	358 aquaporin 1 (Colton blood group)
GO ammonium transport	1	6	0.3461221	358 aquaporin 1 (Colton blood group)
GO cellular response to hypoxia	1	6	0.3461221	358 aquaporin 1 (Colton blood group)
GO cellular response to UV	1	6	0.3461221	358 aquaporin 1 (Colton blood group)
GO activation of protein kinase B activity	1	6	0.3461221	3643 insulin receptor
GO lipoic acid binding	1	6	0.3461221	3643 insulin receptor
GO response to manganese ion	1	6	0.3461221	3643 insulin receptor
GO plasma membrane enriched fraction	1	6	0.3461221	3709 inositol 1,4,5-triphosphate receptor, type 2
GO striated muscle cell differentiation	1	6	0.3461221	3845 v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog
GO endothelial cell differentiation	1	6	0.3461221	3911 laminin, alpha 5
GO glutathione binding	1	6	0.3461221	4056 leukotriene C4 synthase
GO catecholamine metabolic process	1	6	0.3461221	4128 monoamine oxidase A
GO enucleate erythrocyte differentiation	1	6	0.3461221	4151 myoglobin
GO forebrain neuron differentiation	1	6	0.3461221	429 achaete-scute complex homolog 1 (Drosophila)
GO response to folic acid	1	6	0.3461221	429 achaete-scute complex homolog 1 (Drosophila)
GO cytoplasmic sequestering of NF-kapp	1	6	0.3461221	4792 nuclear factor of kappa light polypeptide gene enhancer in B-cells inhib
GO cadmium ion binding	1	6	0.3461221	4842 nitric oxide synthase 1 (neuronal)
GO negative regulation of glutamate secr	1	6	0.3461221	4889 neuropeptide Y receptor Y5
GO response to fluid shear stress	1	6	0.3461221	5025 purinergic receptor P2X, ligand-gated ion channel, 4
GO L-phenylalanine catabolic process	1	6	0.3461221	5053 phenylalanine hydroxylase
GO startle response	1	6	0.3461221	5071 Parkinson disease (autosomal recessive, juvenile) 2, parkin
GO peptide cross-linking via chondroitin	1	6	0.3461221	50859 sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican)
GO glycolipid transport	1	6	0.3461221	51228 glycolipid transfer protein

GO	rough endoplasmic reticulum membr	1	6	0.3461221	5351 procollagen-lysine 1, 2-oxoglutarate 5-dioxygenase 1
GO	antigen processing and presentation	1	6	0.3461221	55080 TAP binding protein-like
GO	meiotic prophase I	1	6	0.3461221	55124 piwi-like 2 (Drosophila)
GO	negative regulation of T cell activatio	1	6	0.3461221	55824 phosphoprotein associated with glycosphingolipid microdomains 1
GO	DNA packaging	1	6	0.3461221	55870 ash1 (absent, small, or homeotic)-like (Drosophila)
GO	complement activation, lectin pathw:	1	6	0.3461221	5648 mannan-binding lectin serine peptidase 1 (C4/C2 activating component
GO	parturition	1	6	0.3461221	5737 prostaglandin F receptor (FP)
GO	cytidine deaminase activity	1	6	0.3461221	57379 activation-induced cytidine deaminase
GO	apical junction complex	1	6	0.3461221	57619 shroom family member 3
GO	exocytic vesicle	1	6	0.3461221	5873 RAB27A, member RAS oncogene family
GO	erythrocyte development	1	6	0.3461221	604 B-cell CLL/lymphoma 6
GO	glycosphingolipid binding	1	6	0.3461221	6402 selectin L
GO	negative regulation of interleukin-2 p	1	6	0.3461221	64127 nucleotide-binding oligomerization domain containing 2
GO	sodium channel regulator activity	1	6	0.3461221	64699 transmembrane protease, serine 3
GO	negative regulation of striated muscl	1	6	0.3461221	652 bone morphogenetic protein 4
GO	ubiquitin-ubiquitin ligase activity	1	6	0.3461221	6563 solute carrier family 14 (urea transporter), member 1 (Kidd blood group)
GO	Hsp70 protein binding	1	6	0.3461221	6622 synuclein, alpha (non A4 component of amyloid precursor)
GO	amine metabolic process	1	6	0.3461221	6819 sulfotransferase family, cytosolic, 1C, member 2
GO	enzyme linked receptor protein signa	1	6	0.3461221	6850 spleen tyrosine kinase
GO	positive regulation of alpha-beta T ce	1	6	0.3461221	6850 spleen tyrosine kinase
GO	positive regulation of B cell differenti	1	6	0.3461221	6850 spleen tyrosine kinase
GO	macrophage activation	1	6	0.3461221	7099 toll-like receptor 4
GO	positive regulation of tumor necrosis	1	6	0.3461221	7099 toll-like receptor 4
GO	podosome	1	6	0.3461221	7170 tropomyosin 3
GO	store-operated calcium channel activ	1	6	0.3461221	7223 transient receptor potential cation channel, subfamily C, member 4
GO	C-X-C chemokine receptor activity	1	6	0.3461221	7852 chemokine (C-X-C motif) receptor 4
GO	DNA N-glycosylase activity	1	6	0.3461221	79661 nei endonuclease VIII-like 1 (E. coli)
GO	thyroid hormone receptor activity	1	6	0.3461221	8013 nuclear receptor subfamily 4, group A, member 3
GO	hyaluronan metabolic process	1	6	0.3461221	80760 inter-alpha (globulin) inhibitor H5
GO	juxtaparanode region of axon	1	6	0.3461221	8514 potassium voltage-gated channel, shaker-related subfamily, beta mem
GO	mammary gland epithelial cell prolife	1	6	0.3461221	8600 tumor necrosis factor (ligand) superfamily, member 11
GO	proton-transporting V-type ATPase, \	1	6	0.3461221	8992 ATPase, H+ transporting, lysosomal 9kDa, V0 subunit e1
GO	trophoblast giant cell differentiation	1	6	0.3461221	9021 suppressor of cytokine signaling 3
GO	phosphatidylinositol-3,5-bisphosphat	1	6	0.3461221	91404 SEC14 and spectrin domains 1
GO	positive regulation of BMP signaling p	1	6	0.3461221	94 activin A receptor type II-like 1
GO	phospholipid homeostasis	1	6	0.3461221	9619 ATP-binding cassette, sub-family G (WHITE), member 1



GO	bile acid binding	1	6	0.3461221	9971 nuclear receptor subfamily 1, group H, member 4
GO	locomotory behavior	5	57	0.3499555	1813 dopamine receptor D2
GO	locomotory behavior	5	57	0.3499555	2911 glutamate receptor, metabotropic 1
GO	locomotory behavior	5	57	0.3499555	4886 neuropeptide Y receptor Y1
GO	locomotory behavior	5	57	0.3499555	51168 myosin XVA
GO	locomotory behavior	5	57	0.3499555	56172 ankylosis, progressive homolog (mouse)
GO	neuron migration	5	57	0.3499555	429 achaete-scute complex homolog 1 (Drosophila)
GO	neuron migration	5	57	0.3499555	4692 necdin homolog (mouse)
GO	neuron migration	5	57	0.3499555	4929 nuclear receptor subfamily 4, group A, member 2
GO	neuron migration	5	57	0.3499555	7026 nuclear receptor subfamily 2, group F, member 2
GO	neuron migration	5	57	0.3499555	885 cholecystokinin
GO	DNA damage checkpoint	2	18	0.3511682	11200 CHK2 checkpoint homolog (S. pombe)
GO	DNA damage checkpoint	2	18	0.3511682	26270 F-box protein 6
GO	regulation of insulin secretion	2	18	0.3511682	143425 synaptotagmin IX
GO	regulation of insulin secretion	2	18	0.3511682	222546 regulatory factor X, 6
GO	embryonic placenta development	2	18	0.3511682	2624 GATA binding protein 2
GO	embryonic placenta development	2	18	0.3511682	6692 serine peptidase inhibitor, Kunitz type 1
GO	response to inorganic substance	2	18	0.3511682	4056 leukotriene C4 synthase
GO	response to inorganic substance	2	18	0.3511682	4929 nuclear receptor subfamily 4, group A, member 2
GO	pancreas development	2	18	0.3511682	4087 SMAD family member 2
GO	pancreas development	2	18	0.3511682	5122 proprotein convertase subtilisin/kexin type 1
GO	WW domain binding	2	18	0.3511682	4778 nuclear factor (erythroid-derived 2), 45kDa
GO	WW domain binding	2	18	0.3511682	55740 enabled homolog (Drosophila)
GO	protein import into nucleus, transloc	2	18	0.3511682	4792 nuclear factor of kappa light polypeptide gene enhancer in B-cells inhib
GO	protein import into nucleus, transloc	2	18	0.3511682	604 B-cell CLL/lymphoma 6
GO	ADP binding	2	18	0.3511682	498 ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subun
GO	ADP binding	2	18	0.3511682	9619 ATP-binding cassette, sub-family G (WHITE), member 1
GO	proton-transporting ATPase activity, i	2	18	0.3511682	498 ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subun
GO	proton-transporting ATPase activity, i	2	18	0.3511682	8992 ATPase, H+ transporting, lysosomal 9kDa, V0 subunit e1
GO	SNARE complex	2	18	0.3511682	51272 blocked early in transport 1 homolog (S. cerevisiae)-like
GO	SNARE complex	2	18	0.3511682	8673 vesicle-associated membrane protein 8 (endobrevin)
GO	anion transport	2	18	0.3511682	6521 solute carrier family 4, anion exchanger, member 1 (erythrocyte memb
GO	anion transport	2	18	0.3511682	8671 solute carrier family 4, sodium bicarbonate cotransporter, member 4
GO	cytolysis	2	18	0.3511682	731 complement component 8, alpha polypeptide
GO	cytolysis	2	18	0.3511682	8542 apolipoprotein L, 1
GO	recycling endosome	2	18	0.3511682	80223 RAB11 family interacting protein 1 (class I)

GO recycling endosome	2	18	0.3511682	9619 ATP-binding cassette, sub-family G (WHITE), member 1
GO pattern specification process	4	44	0.3543571	2737 GLI family zinc finger 3
GO pattern specification process	4	44	0.3543571	429 achaete-scute complex homolog 1 (Drosophila)
GO pattern specification process	4	44	0.3543571	57619 shroom family member 3
GO pattern specification process	4	44	0.3543571	8646 chordin
GO protein stabilization	3	31	0.3565002	10891 peroxisome proliferator-activated receptor gamma, coactivator 1 alpha
GO protein stabilization	3	31	0.3565002	4194 Mdm4 p53 binding protein homolog (mouse)
GO protein stabilization	3	31	0.3565002	5371 promyelocytic leukemia
GO cation binding	3	31	0.3565002	1117 chitinase 3-like 2
GO cation binding	3	31	0.3565002	2990 glucuronidase, beta
GO cation binding	3	31	0.3565002	5016 oviductal glycoprotein 1, 120kDa
GO phospholipid metabolic process	3	31	0.3565002	2055 ceroid-lipofuscinosis, neuronal 8 (epilepsy, progressive with mental ret
GO phospholipid metabolic process	3	31	0.3565002	255738 proprotein convertase subtilisin/kexin type 9
GO phospholipid metabolic process	3	31	0.3565002	6622 synuclein, alpha (non A4 component of amyloid precursor)
GO NADP or NADPH binding	3	31	0.3565002	27035 NADPH oxidase 1
GO NADP or NADPH binding	3	31	0.3565002	4842 nitric oxide synthase 1 (neuronal)
GO NADP or NADPH binding	3	31	0.3565002	9563 hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase)
GO embryonic digit morphogenesis	3	31	0.3565002	2737 GLI family zinc finger 3
GO embryonic digit morphogenesis	3	31	0.3565002	28982 feline leukemia virus subgroup C cellular receptor 1
GO embryonic digit morphogenesis	3	31	0.3565002	652 bone morphogenetic protein 4
GO ATPase activity, coupled to transmembrane transport	3	31	0.3565002	368 ATP-binding cassette, sub-family C (CFTR/MRP), member 6
GO ATPase activity, coupled to transmembrane transport	3	31	0.3565002	5243 ATP-binding cassette, sub-family B (MDR/TAP), member 1
GO ATPase activity, coupled to transmembrane transport	3	31	0.3565002	5244 ATP-binding cassette, sub-family B (MDR/TAP), member 4
GO early endosome	7	85	0.3618806	1080 cystic fibrosis transmembrane conductance regulator (ATP-binding cas
GO early endosome	7	85	0.3618806	11156 protein tyrosine phosphatase type IVA, member 3
GO early endosome	7	85	0.3618806	22906 trafficking protein, kinesin binding 1
GO early endosome	7	85	0.3618806	26119 low density lipoprotein receptor adaptor protein 1
GO early endosome	7	85	0.3618806	27035 NADPH oxidase 1
GO early endosome	7	85	0.3618806	8673 vesicle-associated membrane protein 8 (endobrevin)
GO early endosome	7	85	0.3618806	9595 cytohesin 1 interacting protein
GO intracellular signaling pathway	14	182	0.3629906	10156 RAS p21 protein activator 4
GO intracellular signaling pathway	14	182	0.3629906	1154 cytokine inducible SH2-containing protein
GO intracellular signaling pathway	14	182	0.3629906	118987 PDZ domain containing 8
GO intracellular signaling pathway	14	182	0.3629906	29760 B-cell linker
GO intracellular signaling pathway	14	182	0.3629906	4087 SMAD family member 2
GO intracellular signaling pathway	14	182	0.3629906	5577 protein kinase, cAMP-dependent, regulatory, type II, beta

GO intracellular signaling pathway	14	182	0.3629906	55824 phosphoprotein associated with glycosphingolipid microdomains 1
GO intracellular signaling pathway	14	182	0.3629906	57799 RAB40C, member RAS oncogene family
GO intracellular signaling pathway	14	182	0.3629906	6101 retinitis pigmentosa 1 (autosomal dominant)
GO intracellular signaling pathway	14	182	0.3629906	64127 nucleotide-binding oligomerization domain containing 2
GO intracellular signaling pathway	14	182	0.3629906	64798 DEP domain containing 6
GO intracellular signaling pathway	14	182	0.3629906	6494 signal-induced proliferation-associated 1
GO intracellular signaling pathway	14	182	0.3629906	7464 coronin, actin binding protein, 2A
GO intracellular signaling pathway	14	182	0.3629906	9021 suppressor of cytokine signaling 3
GO regulation of cell shape	5	58	0.3638013	10435 CDC42 effector protein (Rho GTPase binding) 2
GO regulation of cell shape	5	58	0.3638013	148170 CDC42 effector protein (Rho GTPase binding) 5
GO regulation of cell shape	5	58	0.3638013	152273 FYVE, RhoGEF and PH domain containing 5
GO regulation of cell shape	5	58	0.3638013	3689 integrin, beta 2 (complement component 3 receptor 3 and 4 subunit)
GO regulation of cell shape	5	58	0.3638013	57619 shroom family member 3
GO blood circulation	4	45	0.3702364	4223 mesenchyme homeobox 2
GO blood circulation	4	45	0.3702364	4524 5,10-methylenetetrahydrofolate reductase (NADPH)
GO blood circulation	4	45	0.3702364	4778 nuclear factor (erythroid-derived 2), 45kDa
GO blood circulation	4	45	0.3702364	94 activin A receptor type II-like 1
GO regulation of G-protein coupled receptor activity	3	32	0.3755707	10268 receptor (G protein-coupled) activity modifying protein 3
GO regulation of G-protein coupled receptor activity	3	32	0.3755707	6004 regulator of G-protein signaling 16
GO regulation of G-protein coupled receptor activity	3	32	0.3755707	8786 regulator of G-protein signaling 11
GO peptide binding	3	32	0.3755707	1508 cathepsin B
GO peptide binding	3	32	0.3755707	1803 dipeptidyl-peptidase 4
GO peptide binding	3	32	0.3755707	9971 nuclear receptor subfamily 1, group H, member 4
GO peptidyl-tyrosine phosphorylation	3	32	0.3755707	2066 v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian)
GO peptidyl-tyrosine phosphorylation	3	32	0.3755707	3643 insulin receptor
GO peptidyl-tyrosine phosphorylation	3	32	0.3755707	3815 v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog
GO G2/M transition of mitotic cell cycle	2	19	0.3764191	1785 dynamin 2
GO G2/M transition of mitotic cell cycle	2	19	0.3764191	5218 cyclin-dependent kinase 14
GO negative regulation of adenylate cyclase activity	2	19	0.3764191	1813 dopamine receptor D2
GO negative regulation of adenylate cyclase activity	2	19	0.3764191	1815 dopamine receptor D4
GO patterning of blood vessels	2	19	0.3764191	1906 endothelin 1
GO patterning of blood vessels	2	19	0.3764191	2303 forkhead box C2 (MFH-1, mesenchyme forkhead 1)
GO protein processing	2	19	0.3764191	2737 GLI family zinc finger 3
GO protein processing	2	19	0.3764191	834 caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, co)
GO heterophilic cell-cell adhesion	2	19	0.3764191	3678 integrin, alpha 5 (fibronectin receptor, alpha polypeptide)
GO heterophilic cell-cell adhesion	2	19	0.3764191	57863 cell adhesion molecule 3

GO collagen catabolic process	2	19	0.3764191	4316 matrix metallopeptidase 7 (matrilysin, uterine)
GO collagen catabolic process	2	19	0.3764191	56547 matrix metallopeptidase 26
GO cadherin binding	2	19	0.3764191	5025 purinergic receptor P2X, ligand-gated ion channel, 4
GO cadherin binding	2	19	0.3764191	53827 FXYP domain containing ion transport regulator 5
GO photoreceptor outer segment	2	19	0.3764191	5132 phosducin
GO photoreceptor outer segment	2	19	0.3764191	5873 RAB27A, member RAS oncogene family
GO regulation of synaptic plasticity	2	19	0.3764191	5327 plasminogen activator, tissue
GO regulation of synaptic plasticity	2	19	0.3764191	627 brain-derived neurotrophic factor
GO response to amino acid stimulus	2	19	0.3764191	6750 somatostatin
GO response to amino acid stimulus	2	19	0.3764191	8992 ATPase, H+ transporting, lysosomal 9kDa, V0 subunit e1
GO lipid transporter activity	2	19	0.3764191	80830 apolipoprotein L, 6
GO lipid transporter activity	2	19	0.3764191	80833 apolipoprotein L, 3
GO cell migration	5	59	0.3776571	27035 NADPH oxidase 1
GO cell migration	5	59	0.3776571	3911 laminin, alpha 5
GO cell migration	5	59	0.3776571	57147 SCY1-like 3 ( <i>S. cerevisiae</i> )
GO cell migration	5	59	0.3776571	7049 transforming growth factor, beta receptor III
GO cell migration	5	59	0.3776571	83666 poly (ADP-ribose) polymerase family, member 9
GO synaptic vesicle	4	46	0.3860879	4886 neuropeptide Y receptor Y1
GO synaptic vesicle	4	46	0.3860879	6857 synaptotagmin I
GO synaptic vesicle	4	46	0.3860879	9143 synaptogyrin 3
GO synaptic vesicle	4	46	0.3860879	9892 synaptosomal-associated protein, 91kDa homolog (mouse)
GO protein complex assembly	8	101	0.3862097	10891 peroxisome proliferator-activated receptor gamma, coactivator 1 alpha
GO protein complex assembly	8	101	0.3862097	4194 Mdm4 p53 binding protein homolog (mouse)
GO protein complex assembly	8	101	0.3862097	5371 promyelocytic leukemia
GO protein complex assembly	8	101	0.3862097	56288 par-3 partitioning defective 3 homolog ( <i>C. elegans</i> )
GO protein complex assembly	8	101	0.3862097	6850 spleen tyrosine kinase
GO protein complex assembly	8	101	0.3862097	7106 tetraspanin 4
GO protein complex assembly	8	101	0.3862097	8673 vesicle-associated membrane protein 8 (endobrevin)
GO protein complex assembly	8	101	0.3862097	9185 RALBP1 associated Eps domain containing 2
GO protein trimerization	1	7	0.3908275	10346 tripartite motif-containing 22
GO adenosine deaminase activity	1	7	0.3908275	104 adenosine deaminase, RNA-specific, B1 (RED1 homolog rat)
GO sodium:phosphate symporter activity	1	7	0.3908275	10568 solute carrier family 34 (sodium phosphate), member 2
GO folic acid transport	1	7	0.3908275	113235 solute carrier family 46 (folate transporter), member 1
GO long-chain fatty acid transport	1	7	0.3908275	123 perilipin 2
GO regulation of Cdc42 GTPase activity	1	7	0.3908275	152273 FYVE, RhoGEF and PH domain containing 5
GO adrenoceptor activity	1	7	0.3908275	154 adrenergic, beta-2-, receptor, surface

GO negative regulation of multicellular o	1	7	0.3908275	154 adrenergic, beta-2-, receptor, surface
GO steroid hydroxylase activity	1	7	0.3908275	1559 cytochrome P450, family 2, subfamily C, polypeptide 9
GO ear development	1	7	0.3908275	157506 retinol dehydrogenase 10 (all-trans)
GO adenohypophysis development	1	7	0.3908275	1813 dopamine receptor D2
GO positive regulation of cholesterol est	1	7	0.3908275	183 angiotensinogen (serpin peptidase inhibitor, clade A, member 8)
GO positive regulation of heart rate	1	7	0.3908275	1906 endothelin 1
GO ephrin receptor signaling pathway	1	7	0.3908275	1969 EPH receptor A2
GO positive regulation of proteolysis	1	7	0.3908275	2033 E1A binding protein p300
GO neurofilament cytoskeleton organiza	1	7	0.3908275	2055 ceroid-lipofuscinosis, neuronal 8 (epilepsy, progressive with mental ret
GO regulation of cell size	1	7	0.3908275	2055 ceroid-lipofuscinosis, neuronal 8 (epilepsy, progressive with mental ret
GO surfactant homeostasis	1	7	0.3908275	2066 v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian)
GO histone H4-K12 acetylation	1	7	0.3908275	23338 PHD finger protein 15
GO MOZ/MORF histone acetyltransferas	1	7	0.3908275	23774 bromodomain containing 1
GO alpha(1,3)-fucosyltransferase activity	1	7	0.3908275	2526 fucosyltransferase 4 (alpha (1,3) fucosyltransferase, myeloid-specific)
GO negative regulation of catalytic activi	1	7	0.3908275	255738 proprotein convertase subtilisin/kexin type 9
GO superoxide-generating NADPH oxidas	1	7	0.3908275	27035 NADPH oxidase 1
GO enteric nervous system development	1	7	0.3908275	3142 H2.0-like homeobox
GO regulation of cell-matrix adhesion	1	7	0.3908275	3175 one cut homeobox 1
GO prostate gland growth	1	7	0.3908275	3479 insulin-like growth factor 1 (somatomedin C)
GO protein heterotetramerization	1	7	0.3908275	3643 insulin receptor
GO receptor clustering	1	7	0.3908275	375790 agrin
GO LRR domain binding	1	7	0.3908275	3845 v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog
GO laminin-1 complex	1	7	0.3908275	3911 laminin, alpha 5
GO type I transforming growth factor bet	1	7	0.3908275	4087 SMAD family member 2
GO sympathetic nervous system develop	1	7	0.3908275	429 achaete-scute complex homolog 1 (Drosophila)
GO nucleosome disassembly	1	7	0.3908275	4778 nuclear factor (erythroid-derived 2), 45kDa
GO citrate metabolic process	1	7	0.3908275	48 aconitase 1, soluble
GO anagen	1	7	0.3908275	4851 Notch homolog 1, translocation-associated (Drosophila)
GO morphogenesis of an epithelial sheet	1	7	0.3908275	4853 Notch homolog 2 (Drosophila)
GO death	1	7	0.3908275	4929 nuclear receptor subfamily 4, group A, member 2
GO neuron maturation	1	7	0.3908275	4929 nuclear receptor subfamily 4, group A, member 2
GO extracellular ATP-gated cation chann	1	7	0.3908275	5025 purinergic receptor P2X, ligand-gated ion channel, 4
GO purinergic nucleotide receptor activit	1	7	0.3908275	5025 purinergic receptor P2X, ligand-gated ion channel, 4
GO glycoprotein metabolic process	1	7	0.3908275	5046 proprotein convertase subtilisin/kexin type 6
GO protein metabolic process	1	7	0.3908275	5071 Parkinson disease (autosomal recessive, juvenile) 2, parkin
GO peptide biosynthetic process	1	7	0.3908275	5122 proprotein convertase subtilisin/kexin type 1

GO	semaphorin receptor activity	1	7	0.3908275	5362	plexin A2
GO	DNA damage response, signal transduction	1	7	0.3908275	5371	promyelocytic leukemia
GO	protein K48-linked deubiquitination	1	7	0.3908275	55432	YOD1 OTU deubiquinating enzyme 1 homolog ( <i>S. cerevisiae</i> )
GO	negative regulation of cell-matrix adhesion	1	7	0.3908275	604	B-cell CLL/lymphoma 6
GO	nerve development	1	7	0.3908275	627	brain-derived neurotrophic factor
GO	negative regulation of cell size	1	7	0.3908275	64798	DEP domain containing 6
GO	glutamate binding	1	7	0.3908275	6505	solute carrier family 1 (neuronal/epithelial high affinity glutamate transporter)
GO	ankyrin binding	1	7	0.3908275	6521	solute carrier family 4, anion exchanger, member 1 (erythrocyte membrane)
GO	nuclear hormone receptor binding	1	7	0.3908275	6604	SWI/SNF related, matrix associated, actin dependent regulator of chromatin
GO	dynein binding	1	7	0.3908275	6622	synuclein, alpha (non A4 component of amyloid precursor)
GO	synaptic transmission, dopaminergic	1	7	0.3908275	6622	synuclein, alpha (non A4 component of amyloid precursor)
GO	synaptic vesicle endocytosis	1	7	0.3908275	6622	synuclein, alpha (non A4 component of amyloid precursor)
GO	response to mercury ion	1	7	0.3908275	682	basigin (Ok blood group)
GO	positive regulation of alpha-beta T cell	1	7	0.3908275	6850	spleen tyrosine kinase
GO	type II transforming growth factor beta	1	7	0.3908275	7049	transforming growth factor, beta receptor III
GO	erythrocyte maturation	1	7	0.3908275	7076	TIMP metalloproteinase inhibitor 1
GO	positive regulation of interleukin-10 production	1	7	0.3908275	7099	toll-like receptor 4
GO	positive regulation of interleukin-8 binding	1	7	0.3908275	7099	toll-like receptor 4
GO	positive regulation of MHC class II binding	1	7	0.3908275	7099	toll-like receptor 4
GO	response to molecule of bacterial origin	1	7	0.3908275	7100	toll-like receptor 5
GO	membrane attack complex	1	7	0.3908275	731	complement component 8, alpha polypeptide
GO	AU-rich element binding	1	7	0.3908275	7538	zinc finger protein 36, C3H type, homolog (mouse)
GO	developmental pigmentation	1	7	0.3908275	7546	Zic family member 2 (odd-paired homolog, <i>Drosophila</i> )
GO	secretion	1	7	0.3908275	760	carbonic anhydrase II
GO	adult behavior	1	7	0.3908275	8013	nuclear receptor subfamily 4, group A, member 3
GO	titin binding	1	7	0.3908275	84033	obscurin, cytoskeletal calmodulin and titin-interacting RhoGEF
GO	detection of mechanical stimulus involved in sensory perception of touch	1	7	0.3908275	84059	G protein-coupled receptor 98
GO	neurological system process	1	7	0.3908275	84059	G protein-coupled receptor 98
GO	pentose-phosphate shunt	1	7	0.3908275	9563	hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase)
GO	positive regulation of cell-cell adhesion	1	7	0.3908275	961	CD47 molecule
GO	response to lipid	1	7	0.3908275	9619	ATP-binding cassette, sub-family G (WHITE), member 1
GO	protein deacetylase activity	1	7	0.3908275	9734	histone deacetylase 9
GO	mitochondrial outer membrane transport	1	7	0.3908275	9804	translocase of outer mitochondrial membrane 20 homolog (yeast)
GO	clathrin coat assembly	1	7	0.3908275	9892	synaptosomal-associated protein, 91kDa homolog (mouse)
GO	sister chromatid cohesion	1	7	0.3908275	9985	REC8 homolog (yeast)
GO	specific RNA polymerase II transcription	3	33	0.3945231	2353	FBJ murine osteosarcoma viral oncogene homolog

GO specific RNA polymerase II transcripti	3	33	0.3945231	3665 interferon regulatory factor 7
GO specific RNA polymerase II transcripti	3	33	0.3945231	4212 Meis homeobox 2
GO endosome	16	215	0.3992926	112 adenylate cyclase 6
GO endosome	16	215	0.3992926	154 adrenergic, beta-2-, receptor, surface
GO endosome	16	215	0.3992926	25825 beta-site APP-cleaving enzyme 2
GO endosome	16	215	0.3992926	2642 glucagon receptor
GO endosome	16	215	0.3992926	3643 insulin receptor
GO endosome	16	215	0.3992926	3775 potassium channel, subfamily K, member 1
GO endosome	16	215	0.3992926	3949 low density lipoprotein receptor
GO endosome	16	215	0.3992926	412 steroid sulfatase (microsomal), isozyme S
GO endosome	16	215	0.3992926	50617 ATPase, H+ transporting, lysosomal V0 subunit a4
GO endosome	16	215	0.3992926	51272 blocked early in transport 1 homolog ( <i>S. cerevisiae</i> )-like
GO endosome	16	215	0.3992926	55275 vacuolar protein sorting 53 homolog ( <i>S. cerevisiae</i> )
GO endosome	16	215	0.3992926	57132 chromatin modifying protein 1B
GO endosome	16	215	0.3992926	64083 golgi phosphoprotein 3 (coat-protein)
GO endosome	16	215	0.3992926	7098 toll-like receptor 3
GO endosome	16	215	0.3992926	9182 Ras association (RalGDS/AF-6) domain family (N-terminal) member 9
GO endosome	16	215	0.3992926	9619 ATP-binding cassette, sub-family G (WHITE), member 1
GO desmosome	2	20	0.401252	11187 plakophilin 3
GO desmosome	2	20	0.401252	5318 plakophilin 2
GO dendrite development	2	20	0.401252	2182 acyl-CoA synthetase long-chain family member 4
GO dendrite development	2	20	0.401252	627 brain-derived neurotrophic factor
GO connexon complex	2	20	0.401252	2706 gap junction protein, beta 2, 26kDa
GO connexon complex	2	20	0.401252	2707 gap junction protein, beta 3, 31kDa
GO positive regulation of protein kinase I	2	20	0.401252	3643 insulin receptor
GO positive regulation of protein kinase I	2	20	0.401252	8600 tumor necrosis factor (ligand) superfamily, member 11
GO response to radiation	2	20	0.401252	3815 v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog
GO response to radiation	2	20	0.401252	8600 tumor necrosis factor (ligand) superfamily, member 11
GO neural crest cell migration	2	20	0.401252	3911 laminin, alpha 5
GO neural crest cell migration	2	20	0.401252	4254 KIT ligand
GO phosphate metabolic process	2	20	0.401252	5787 protein tyrosine phosphatase, receptor type, B
GO phosphate metabolic process	2	20	0.401252	5789 protein tyrosine phosphatase, receptor type, D
GO neuron differentiation	4	47	0.4018871	1969 EPH receptor A2
GO neuron differentiation	4	47	0.4018871	255738 proprotein convertase subtilisin/kexin type 9
GO neuron differentiation	4	47	0.4018871	2624 GATA binding protein 2
GO neuron differentiation	4	47	0.4018871	5801 protein tyrosine phosphatase, receptor type, R

GO exocytosis	4	47	0.4018871	2642 glucagon receptor
GO exocytosis	4	47	0.4018871	375056 melanoma inhibitory activity family, member 3
GO exocytosis	4	47	0.4018871	3993 lethal giant larvae homolog 2 (Drosophila)
GO exocytosis	4	47	0.4018871	5873 RAB27A, member RAS oncogene family
GO response to heat	4	47	0.4018871	4842 nitric oxide synthase 1 (neuronal)
GO response to heat	4	47	0.4018871	6750 somatostatin
GO response to heat	4	47	0.4018871	9021 suppressor of cytokine signaling 3
GO response to heat	4	47	0.4018871	929 CD14 molecule
GO protein domain specific binding	9	117	0.4068898	1822 atrophin 1
GO protein domain specific binding	9	117	0.4068898	399694 SHC (Src homology 2 domain containing) family, member 4
GO protein domain specific binding	9	117	0.4068898	4204 methyl CpG binding protein 2 (Rett syndrome)
GO protein domain specific binding	9	117	0.4068898	5465 peroxisome proliferator-activated receptor alpha
GO protein domain specific binding	9	117	0.4068898	5577 protein kinase, cAMP-dependent, regulatory, type II, beta
GO protein domain specific binding	9	117	0.4068898	57132 chromatin modifying protein 1B
GO protein domain specific binding	9	117	0.4068898	57524 CASK interacting protein 1
GO protein domain specific binding	9	117	0.4068898	6850 spleen tyrosine kinase
GO protein domain specific binding	9	117	0.4068898	8660 insulin receptor substrate 2
GO positive regulation of cell growth	3	34	0.4133202	1839 heparin-binding EGF-like growth factor
GO positive regulation of cell growth	3	34	0.4133202	3484 insulin-like growth factor binding protein 1
GO positive regulation of cell growth	3	34	0.4133202	952 CD38 molecule
GO platelet alpha granule lumen	3	34	0.4133202	2153 coagulation factor V (proaccelerin, labile factor)
GO platelet alpha granule lumen	3	34	0.4133202	22915 multimerin 1
GO platelet alpha granule lumen	3	34	0.4133202	3479 insulin-like growth factor 1 (somatomedin C)
GO receptor signaling protein activity	3	34	0.4133202	23767 fibronectin leucine rich transmembrane protein 3
GO receptor signaling protein activity	3	34	0.4133202	573 BCL2-associated athanogene
GO receptor signaling protein activity	3	34	0.4133202	8519 interferon induced transmembrane protein 1 (9-27)
GO presynaptic membrane	3	34	0.4133202	2911 glutamate receptor, metabotropic 1
GO presynaptic membrane	3	34	0.4133202	6857 synaptotagmin I
GO presynaptic membrane	3	34	0.4133202	9892 synaptosomal-associated protein, 91kDa homolog (mouse)
GO visual perception	14	189	0.417461	157506 retinol dehydrogenase 10 (all-trans)
GO visual perception	14	189	0.417461	23418 crumbs homolog 1 (Drosophila)
GO visual perception	14	189	0.417461	368 ATP-binding cassette, sub-family C (CFTR/MRP), member 6
GO visual perception	14	189	0.417461	3983 actin binding LIM protein 1
GO visual perception	14	189	0.417461	5132 phosducin
GO visual perception	14	189	0.417461	5158 phosphodiesterase 6B, cGMP-specific, rod, beta
GO visual perception	14	189	0.417461	6004 regulator of G-protein signaling 16



GO	visual perception	14	189	0.417461	6096 RAR-related orphan receptor B
GO	visual perception	14	189	0.417461	6101 retinitis pigmentosa 1 (autosomal dominant)
GO	visual perception	14	189	0.417461	783 calcium channel, voltage-dependent, beta 2 subunit
GO	visual perception	14	189	0.417461	83394 PTPN11 family member 3
GO	visual perception	14	189	0.417461	83872 hemicentin 1
GO	visual perception	14	189	0.417461	8842 prominin 1
GO	visual perception	14	189	0.417461	93589 calcium channel, voltage-dependent, alpha 2/delta subunit 4
GO	serine-type peptidase activity	4	48	0.4176107	10942 protease, serine, 21 (testisin)
GO	serine-type peptidase activity	4	48	0.4176107	1803 dipeptidyl-peptidase 4
GO	serine-type peptidase activity	4	48	0.4176107	5655 kallikrein-related peptidase 10
GO	serine-type peptidase activity	4	48	0.4176107	715 complement component 1, r subcomponent
GO	integrin binding	5	62	0.4191132	10085 EGF-like repeats and discoidin I-like domains 3
GO	integrin binding	5	62	0.4191132	10516 fibulin 5
GO	integrin binding	5	62	0.4191132	3678 integrin, alpha 5 (fibronectin receptor, alpha polypeptide)
GO	integrin binding	5	62	0.4191132	3911 laminin, alpha 5
GO	integrin binding	5	62	0.4191132	6850 spleen tyrosine kinase
GO	ATPase activity, coupled to transmembrane transport	2	21	0.4256062	148229 ATPase, class I, type 8B, member 3
GO	ATPase activity, coupled to transmembrane transport	2	21	0.4256062	79895 ATPase, class I, type 8B, member 4
GO	aromatase activity	2	21	0.4256062	1558 cytochrome P450, family 2, subfamily C, polypeptide 8
GO	aromatase activity	2	21	0.4256062	1577 cytochrome P450, family 3, subfamily A, polypeptide 5
GO	negative regulation of caspase activation	2	21	0.4256062	3164 nuclear receptor subfamily 4, group A, member 1
GO	negative regulation of caspase activation	2	21	0.4256062	6622 synuclein, alpha (non A4 component of amyloid precursor)
GO	regulation of multicellular organism growth	2	21	0.4256062	3479 insulin-like growth factor 1 (somatomedin C)
GO	regulation of multicellular organism growth	2	21	0.4256062	4886 neuropeptide Y receptor Y1
GO	defense response to virus	2	21	0.4256062	3569 interleukin 6 (interferon, beta 2)
GO	defense response to virus	2	21	0.4256062	7098 toll-like receptor 3
GO	release of cytochrome c from mitochondria	2	21	0.4256062	3725 jun oncogene
GO	release of cytochrome c from mitochondria	2	21	0.4256062	885 cholecystokinin
GO	positive regulation of mesenchymal cell proliferation	2	21	0.4256062	5396 paired related homeobox 1
GO	positive regulation of mesenchymal cell proliferation	2	21	0.4256062	8660 insulin receptor substrate 2
GO	sensory perception of sound	7	91	0.4301987	10253 sprouty homolog 2 (Drosophila)
GO	sensory perception of sound	7	91	0.4301987	2706 gap junction protein, beta 2, 26kDa
GO	sensory perception of sound	7	91	0.4301987	2707 gap junction protein, beta 3, 31kDa
GO	sensory perception of sound	7	91	0.4301987	50617 ATPase, H <sup>+</sup> transporting, lysosomal V0 subunit a4
GO	sensory perception of sound	7	91	0.4301987	51168 myosin XVA
GO	sensory perception of sound	7	91	0.4301987	53405 chloride intracellular channel 5

GO sensory perception of sound	7	91	0.4301987	84059 G protein-coupled receptor 98
GO induction of apoptosis by extracellular	7	91	0.4301987	1612 death-associated protein kinase 1
GO induction of apoptosis by extracellular	7	91	0.4301987	23263 MCF.2 cell line derived transforming sequence-like
GO induction of apoptosis by extracellular	7	91	0.4301987	23365 Rho guanine nucleotide exchange factor (GEF) 12
GO induction of apoptosis by extracellular	7	91	0.4301987	3429 interferon, alpha-inducible protein 27
GO induction of apoptosis by extracellular	7	91	0.4301987	84033 obscurin, cytoskeletal calmodulin and titin-interacting RhoGEF
GO induction of apoptosis by extracellular	7	91	0.4301987	9459 Rac/Cdc42 guanine nucleotide exchange factor (GEF) 6
GO induction of apoptosis by extracellular	7	91	0.4301987	952 CD38 molecule
GO negative regulation of transcription	11	148	0.431903	10076 protein tyrosine phosphatase, receptor type, U
GO negative regulation of transcription	11	148	0.431903	127343 diencephalon/mesencephalon homeobox 1
GO negative regulation of transcription	11	148	0.431903	2122 MDS1 and EVI1 complex locus
GO negative regulation of transcription	11	148	0.431903	2737 GLI family zinc finger 3
GO negative regulation of transcription	11	148	0.431903	3400 inhibitor of DNA binding 4, dominant negative helix-loop-helix protein
GO negative regulation of transcription	11	148	0.431903	4204 methyl CpG binding protein 2 (Rett syndrome)
GO negative regulation of transcription	11	148	0.431903	5187 period homolog 1 (Drosophila)
GO negative regulation of transcription	11	148	0.431903	5371 promyelocytic leukemia
GO negative regulation of transcription	11	148	0.431903	652 bone morphogenetic protein 4
GO negative regulation of transcription	11	148	0.431903	84911 zinc finger protein 382
GO negative regulation of transcription	11	148	0.431903	9734 histone deacetylase 9
GO transmembrane receptor protein tyrosine kinase	3	35	0.4319277	1969 EPH receptor A2
GO transmembrane receptor protein tyrosine kinase	3	35	0.4319277	2066 v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian)
GO transmembrane receptor protein tyrosine kinase	3	35	0.4319277	4915 neurotrophic tyrosine kinase, receptor, type 2
GO acute-phase response	3	35	0.4319277	23780 apolipoprotein L, 2
GO acute-phase response	3	35	0.4319277	3569 interleukin 6 (interferon, beta 2)
GO acute-phase response	3	35	0.4319277	3570 interleukin 6 receptor
GO excretion	3	35	0.4319277	50617 ATPase, H+ transporting, lysosomal V0 subunit a4
GO excretion	3	35	0.4319277	81693 amnionless homolog (mouse)
GO excretion	3	35	0.4319277	8645 potassium channel, subfamily K, member 5
GO U12-type spliceosomal complex	1	8	0.4324787	10081 programmed cell death 7
GO poly(A) RNA binding	1	8	0.4324787	11030 RNA binding protein with multiple splicing
GO creatine metabolic process	1	8	0.4324787	1152 creatine kinase, brain
GO triglyceride catabolic process	1	8	0.4324787	1373 carbamoyl-phosphate synthetase 1, mitochondrial
GO retinoid binding	1	8	0.4324787	1382 cellular retinoic acid binding protein 2
GO positive regulation of cell-matrix adhesion	1	8	0.4324787	1435 colony stimulating factor 1 (macrophage)
GO regulation of catalytic activity	1	8	0.4324787	1508 cathepsin B
GO small GTPase binding	1	8	0.4324787	152273 FYVE, RhoGEF and PH domain containing 5

GO sexual reproduction	1	8	0.4324787	158800 Rhox homeobox family, member 1
GO negative regulation of protein kinase	1	8	0.4324787	1813 dopamine receptor D2
GO prepulse inhibition	1	8	0.4324787	1813 dopamine receptor D2
GO dopamine receptor signaling pathway	1	8	0.4324787	1815 dopamine receptor D4
GO response to salt stress	1	8	0.4324787	183 angiotensinogen (serpin peptidase inhibitor, clade A, member 8)
GO non-membrane spanning protein tyrosine kinase activity	1	8	0.4324787	1843 dual specificity phosphatase 1
GO ephrin receptor binding	1	8	0.4324787	1948 ephrin-B2
GO tail morphogenesis	1	8	0.4324787	1969 EPH receptor A2
GO protein-DNA complex	1	8	0.4324787	2033 E1A binding protein p300
GO adenylate kinase activity	1	8	0.4324787	205 adenylate kinase 3-like 1
GO GABA receptor binding	1	8	0.4324787	22906 trafficking protein, kinesin binding 1
GO histone H4-K16 acetylation	1	8	0.4324787	23338 PHD finger protein 15
GO clathrin binding	1	8	0.4324787	26119 low density lipoprotein receptor adaptor protein 1
GO protein homotrimerization	1	8	0.4324787	286133 scavenger receptor class A, member 5 (putative)
GO tumor necrosis factor-mediated signaling pathway	1	8	0.4324787	29108 PYD and CARD domain containing
GO protein destabilization	1	8	0.4324787	29116 myosin regulatory light chain interacting protein
GO histidine catabolic process	1	8	0.4324787	3034 histidine ammonia-lyase
GO antigen processing and presentation	1	8	0.4324787	3134 major histocompatibility complex, class I, F
GO positive regulation of JAK-STAT cascade	1	8	0.4324787	3569 interleukin 6 (interferon, beta 2)
GO male sex determination	1	8	0.4324787	3643 insulin receptor
GO synapse organization	1	8	0.4324787	375790 agrin
GO epithelial cell proliferation	1	8	0.4324787	3815 v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog
GO intestinal cholesterol absorption	1	8	0.4324787	3949 low density lipoprotein receptor
GO embryonic hemopoiesis	1	8	0.4324787	4005 LIM domain only 2 (rhombotin-like 1)
GO co-SMAD binding	1	8	0.4324787	4087 SMAD family member 2
GO SMAD protein complex assembly	1	8	0.4324787	4087 SMAD family member 2
GO neurotransmitter catabolic process	1	8	0.4324787	4128 monoamine oxidase A
GO heterochromatin	1	8	0.4324787	4204 methyl CpG binding protein 2 (Rett syndrome)
GO response to lithium ion	1	8	0.4324787	429 achaete-scute complex homolog 1 (Drosophila)
GO hemostasis	1	8	0.4324787	4778 nuclear factor (erythroid-derived 2), 45kDa
GO nuclear localization sequence binding	1	8	0.4324787	4792 nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor 3
GO positive regulation of cholesterol efflux	1	8	0.4324787	4792 nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor 3
GO arginine catabolic process	1	8	0.4324787	4842 nitric oxide synthase 1 (neuronal)
GO central nervous system projection neuron development	1	8	0.4324787	4929 nuclear receptor subfamily 4, group A, member 2
GO hydrogen-exporting ATPase activity, lysosomal	1	8	0.4324787	50617 ATPase, H+ transporting, lysosomal V0 subunit a4
GO phospholipase inhibitor activity	1	8	0.4324787	5132 phosducin

GO response to sucrose stimulus	1	8	0.4324787	51703 acyl-CoA synthetase long-chain family member 5
GO cyclin binding	1	8	0.4324787	5218 cyclin-dependent kinase 14
GO pharyngeal system development	1	8	0.4324787	5362 plexin A2
GO RNA polymerase II transcription elongation factor 1	1	8	0.4324787	55140 elongation protein 3 homolog ( <i>S. cerevisiae</i> )
GO transferase activity, transferring nitrogen	1	8	0.4324787	55304 serine palmitoyltransferase, long chain base subunit 3
GO protein K63-linked deubiquitination	1	8	0.4324787	55432 YOD1 OTU deubiquinating enzyme 1 homolog ( <i>S. cerevisiae</i> )
GO sodium:dicarboxylate symporter activity	1	8	0.4324787	6505 solute carrier family 1 (neuronal/epithelial high affinity glutamate transporter)
GO hemopoietic progenitor cell differentiation	1	8	0.4324787	652 bone morphogenetic protein 4
GO membrane-bounded vesicle	1	8	0.4324787	652 bone morphogenetic protein 4
GO protein localization in nucleus	1	8	0.4324787	652 bone morphogenetic protein 4
GO SNARE binding	1	8	0.4324787	6812 syntaxin binding protein 1
GO antioxidant activity	1	8	0.4324787	7001 peroxiredoxin 2
GO immunoglobulin mediated immune response	1	8	0.4324787	7099 toll-like receptor 4
GO cellular protein localization	1	8	0.4324787	7474 wingless-type MMTV integration site family, member 5A
GO diacylglycerol binding	1	8	0.4324787	8527 diacylglycerol kinase, delta 130kDa
GO intrinsic to membrane	1	8	0.4324787	8542 apolipoprotein L, 1
GO transmembrane receptor protein serine/threonine kinase	1	8	0.4324787	91 activin A receptor, type IB
GO phosphatidylcholine binding	1	8	0.4324787	91404 SEC14 and spectrin domains 1
GO negative regulation of bone resorption	1	8	0.4324787	952 CD38 molecule
GO amyloid precursor protein catabolic process	1	8	0.4324787	9619 ATP-binding cassette, sub-family G (WHITE), member 1
GO actin monomer binding	1	8	0.4324787	9788 metastasis suppressor 1
GO cell redox homeostasis	5	63	0.432841	1193 chloride intracellular channel 2
GO cell redox homeostasis	5	63	0.432841	51314 thioredoxin domain containing 3 (spermatzoa)
GO cell redox homeostasis	5	63	0.432841	5768 quiescin Q6 sulfhydryl oxidase 1
GO cell redox homeostasis	5	63	0.432841	64359 nucleoredoxin
GO PDZ domain binding	4	49	0.4332369	7001 peroxiredoxin 2
GO PDZ domain binding	4	49	0.4332369	1080 cystic fibrosis transmembrane conductance regulator (ATP-binding cassette)
GO PDZ domain binding	4	49	0.4332369	5071 Parkinson disease (autosomal recessive, juvenile) 2, parkin
GO PDZ domain binding	4	49	0.4332369	7049 transforming growth factor, beta receptor III
GO caveola	4	49	0.4332369	9722 nitric oxide synthase 1 (neuronal) adaptor protein
GO caveola	4	49	0.4332369	1508 cathepsin B
GO caveola	4	49	0.4332369	2066 v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian)
GO caveola	4	49	0.4332369	3643 insulin receptor
GO response to unfolded protein	4	49	0.4332369	3949 low density lipoprotein receptor
GO response to unfolded protein	4	49	0.4332369	26270 F-box protein 6
GO response to unfolded protein	4	49	0.4332369	3306 heat shock 70kDa protein 2

GO	response to unfolded protein	4	49	0.4332369	55432 YOD1 OTU deubiquinating enzyme 1 homolog ( <i>S. cerevisiae</i> )
GO	response to unfolded protein	4	49	0.4332369	90993 cAMP responsive element binding protein 3-like 1
GO	protein serine/threonine kinase activ	24	335	0.4358063	10769 polo-like kinase 2 ( <i>Drosophila</i> )
GO	protein serine/threonine kinase activ	24	335	0.4358063	11200 CHK2 checkpoint homolog ( <i>S. pombe</i> )
GO	protein serine/threonine kinase activ	24	335	0.4358063	11213 interleukin-1 receptor-associated kinase 3
GO	protein serine/threonine kinase activ	24	335	0.4358063	127933 U2AF homology motif (UHM) kinase 1
GO	protein serine/threonine kinase activ	24	335	0.4358063	130399 activin A receptor, type IC
GO	protein serine/threonine kinase activ	24	335	0.4358063	140901 serine/threonine kinase 35
GO	protein serine/threonine kinase activ	24	335	0.4358063	150094 salt-inducible kinase 1
GO	protein serine/threonine kinase activ	24	335	0.4358063	1612 death-associated protein kinase 1
GO	protein serine/threonine kinase activ	24	335	0.4358063	23043 TRAF2 and NCK interacting kinase
GO	protein serine/threonine kinase activ	24	335	0.4358063	23387 SIK family kinase 3
GO	protein serine/threonine kinase activ	24	335	0.4358063	28996 homeodomain interacting protein kinase 2
GO	protein serine/threonine kinase activ	24	335	0.4358063	375449 microtubule associated serine/threonine kinase family member 4
GO	protein serine/threonine kinase activ	24	335	0.4358063	415116 pim-3 oncogene
GO	protein serine/threonine kinase activ	24	335	0.4358063	4293 mitogen-activated protein kinase kinase kinase 9
GO	protein serine/threonine kinase activ	24	335	0.4358063	5063 p21 protein (Cdc42/Rac)-activated kinase 3
GO	protein serine/threonine kinase activ	24	335	0.4358063	5129 cyclin-dependent kinase 18
GO	protein serine/threonine kinase activ	24	335	0.4358063	5608 mitogen-activated protein kinase kinase 6
GO	protein serine/threonine kinase activ	24	335	0.4358063	6446 serum/glucocorticoid regulated kinase 1
GO	protein serine/threonine kinase activ	24	335	0.4358063	81788 NUAK family, SNF1-like kinase, 2
GO	protein serine/threonine kinase activ	24	335	0.4358063	84033 obscurin, cytoskeletal calmodulin and titin-interacting RhoGEF
GO	protein serine/threonine kinase activ	24	335	0.4358063	9064 mitogen-activated protein kinase kinase kinase 6
GO	protein serine/threonine kinase activ	24	335	0.4358063	91 activin A receptor, type IB
GO	protein serine/threonine kinase activ	24	335	0.4358063	9263 serine/threonine kinase 17a
GO	protein serine/threonine kinase activ	24	335	0.4358063	94 activin A receptor type II-like 1
GO	nuclear envelope	7	92	0.4415374	240 arachidonate 5-lipoxygenase
GO	nuclear envelope	7	92	0.4415374	311 annexin A11
GO	nuclear envelope	7	92	0.4415374	4056 leukotriene C4 synthase
GO	nuclear envelope	7	92	0.4415374	412 steroid sulfatase (microsomal), isozyme S
GO	nuclear envelope	7	92	0.4415374	54894 ring finger protein 43
GO	nuclear envelope	7	92	0.4415374	5742 prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase a)
GO	nuclear envelope	7	92	0.4415374	93273 LEM domain containing 1
GO	protein tyrosine kinase activity	6	78	0.4440413	2263 fibroblast growth factor receptor 2
GO	protein tyrosine kinase activity	6	78	0.4440413	3643 insulin receptor
GO	protein tyrosine kinase activity	6	78	0.4440413	3815 v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog

GO	protein tyrosine kinase activity	6	78	0.4440413	5608	mitogen-activated protein kinase kinase 6
GO	protein tyrosine kinase activity	6	78	0.4440413	6850	spleen tyrosine kinase
GO	protein tyrosine kinase activity	6	78	0.4440413	84033	obscurin, cytoskeletal calmodulin and titin-interacting RhoGEF
GO	hormone-mediated signaling pathwa	4	50	0.4487451	112	adenylate cyclase 6
GO	hormone-mediated signaling pathwa	4	50	0.4487451	2642	glucagon receptor
GO	hormone-mediated signaling pathwa	4	50	0.4487451	5577	protein kinase, cAMP-dependent, regulatory, type II, beta
GO	hormone-mediated signaling pathwa	4	50	0.4487451	5972	renin
GO	small GTPase mediated signal transd	14	193	0.4487475	115273	RAB42, member RAS oncogene family
GO	small GTPase mediated signal transd	14	193	0.4487475	23179	ral guanine nucleotide dissociation stimulator-like 1
GO	small GTPase mediated signal transd	14	193	0.4487475	23682	RAB38, member RAS oncogene family
GO	small GTPase mediated signal transd	14	193	0.4487475	25837	RAB26, member RAS oncogene family
GO	small GTPase mediated signal transd	14	193	0.4487475	379	ADP-ribosylation factor-like 4D
GO	small GTPase mediated signal transd	14	193	0.4487475	3845	v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog
GO	small GTPase mediated signal transd	14	193	0.4487475	387496	RAS-like, family 11, member A
GO	small GTPase mediated signal transd	14	193	0.4487475	51285	RAS-like, family 12
GO	small GTPase mediated signal transd	14	193	0.4487475	51655	RAS, dexamethasone-induced 1
GO	small GTPase mediated signal transd	14	193	0.4487475	54769	DIRAS family, GTP-binding RAS-like 2
GO	small GTPase mediated signal transd	14	193	0.4487475	57799	RAB40C, member RAS oncogene family
GO	small GTPase mediated signal transd	14	193	0.4487475	5873	RAB27A, member RAS oncogene family
GO	small GTPase mediated signal transd	14	193	0.4487475	5900	ral guanine nucleotide dissociation stimulator
GO	small GTPase mediated signal transd	14	193	0.4487475	85004	RAS-like, estrogen-regulated, growth inhibitor
GO	microvillus	2	22	0.449431	1080	cystic fibrosis transmembrane conductance regulator (ATP-binding cas:
GO	microvillus	2	22	0.449431	760	carbonic anhydrase II
GO	calcium-independent cell-cell adhesio	2	22	0.449431	1364	claudin 4
GO	calcium-independent cell-cell adhesio	2	22	0.449431	9071	claudin 10
GO	photoreceptor cell maintenance	2	22	0.449431	2055	ceroid-lipofuscinosis, neuronal 8 (epilepsy, progressive with mental ret
GO	photoreceptor cell maintenance	2	22	0.449431	84059	G protein-coupled receptor 98
GO	placenta development	2	22	0.449431	2707	gap junction protein, beta 3, 31kDa
GO	placenta development	2	22	0.449431	6256	retinoid X receptor, alpha
GO	pigmentation	2	22	0.449431	4286	microphthalmia-associated transcription factor
GO	pigmentation	2	22	0.449431	5873	RAB27A, member RAS oncogene family
GO	eating behavior	2	22	0.449431	4889	neuropeptide Y receptor Y5
GO	eating behavior	2	22	0.449431	885	cholecystokinin
GO	histone-lysine N-methyltransferase a	2	22	0.449431	54904	Wolf-Hirschhorn syndrome candidate 1-like 1
GO	histone-lysine N-methyltransferase a	2	22	0.449431	55870	ash1 (absent, small, or homeotic)-like (Drosophila)
GO	transport	36	511	0.4498762	1080	cystic fibrosis transmembrane conductance regulator (ATP-binding cas:

GO transport	36	511	0.4498762	1193 chloride intracellular channel 2
GO transport	36	511	0.4498762	1382 cellular retinoic acid binding protein 2
GO transport	36	511	0.4498762	143425 synaptotagmin IX
GO transport	36	511	0.4498762	23208 synaptotagmin XI
GO transport	36	511	0.4498762	2564 gamma-aminobutyric acid (GABA) A receptor, epsilon
GO transport	36	511	0.4498762	26119 low density lipoprotein receptor adaptor protein 1
GO transport	36	511	0.4498762	2706 gap junction protein, beta 2, 26kDa
GO transport	36	511	0.4498762	28982 feline leukemia virus subgroup C cellular receptor 1
GO transport	36	511	0.4498762	368 ATP-binding cassette, sub-family C (CFTR/MRP), member 6
GO transport	36	511	0.4498762	3709 inositol 1,4,5-triphosphate receptor, type 2
GO transport	36	511	0.4498762	4151 myoglobin
GO transport	36	511	0.4498762	493 ATPase, Ca <sup>++</sup> transporting, plasma membrane 4
GO transport	36	511	0.4498762	5025 purinergic receptor P2X, ligand-gated ion channel, 4
GO transport	36	511	0.4498762	5243 ATP-binding cassette, sub-family B (MDR/TAP), member 1
GO transport	36	511	0.4498762	5244 ATP-binding cassette, sub-family B (MDR/TAP), member 4
GO transport	36	511	0.4498762	53405 chloride intracellular channel 5
GO transport	36	511	0.4498762	55068 ecto-NOX disulfide-thiol exchanger 1
GO transport	36	511	0.4498762	56172 ankylosis, progressive homolog (mouse)
GO transport	36	511	0.4498762	56605 ERO1-like beta ( <i>S. cerevisiae</i> )
GO transport	36	511	0.4498762	5950 retinol binding protein 4, plasma
GO transport	36	511	0.4498762	6505 solute carrier family 1 (neuronal/epithelial high affinity glutamate transp
GO transport	36	511	0.4498762	6535 solute carrier family 6 (neurotransmitter transporter, creatine), memb
GO transport	36	511	0.4498762	6542 solute carrier family 7 (cationic amino acid transporter, $\gamma$ + system), me
GO transport	36	511	0.4498762	6563 solute carrier family 14 (urea transporter), member 1 (Kidd blood group)
GO transport	36	511	0.4498762	6564 solute carrier family 15 (oligopeptide transporter), member 1
GO transport	36	511	0.4498762	6565 solute carrier family 15 (H <sup>+</sup> /peptide transporter), member 2
GO transport	36	511	0.4498762	6857 synaptotagmin I
GO transport	36	511	0.4498762	774 calcium channel, voltage-dependent, N type, alpha 1B subunit
GO transport	36	511	0.4498762	783 calcium channel, voltage-dependent, beta 2 subunit
GO transport	36	511	0.4498762	79152 fatty acid 2-hydroxylase
GO transport	36	511	0.4498762	83394 PITPNM family member 3
GO transport	36	511	0.4498762	8671 solute carrier family 4, sodium bicarbonate cotransporter, member 4
GO transport	36	511	0.4498762	8911 calcium channel, voltage-dependent, T type, alpha 1I subunit
GO transport	36	511	0.4498762	8912 calcium channel, voltage-dependent, T type, alpha 1H subunit
GO transport	36	511	0.4498762	8973 cholinergic receptor, nicotinic, alpha 6
GO cellular amino acid metabolic proces	3	36	0.4503147	27165 glutaminase 2 (liver, mitochondrial)

GO	cellular amino acid metabolic process	3	36	0.4503147	4524	5,10-methylenetetrahydrofolate reductase (NADPH)
GO	cellular amino acid metabolic process	3	36	0.4503147	6542	solute carrier family 7 (cationic amino acid transporter, y+ system), member 7
GO	I-kappaB kinase/NF-kappaB cascade	3	36	0.4503147	7097	toll-like receptor 2
GO	I-kappaB kinase/NF-kappaB cascade	3	36	0.4503147	7099	toll-like receptor 4
GO	I-kappaB kinase/NF-kappaB cascade	3	36	0.4503147	7100	toll-like receptor 5
GO	perinuclear region of cytoplasm	22	309	0.4530558	10335	murine retrovirus integration site 1 homolog
GO	perinuclear region of cytoplasm	22	309	0.4530558	11155	LIM domain binding 3
GO	perinuclear region of cytoplasm	22	309	0.4530558	114569	mal, T-cell differentiation protein 2
GO	perinuclear region of cytoplasm	22	309	0.4530558	1435	colony stimulating factor 1 (macrophage)
GO	perinuclear region of cytoplasm	22	309	0.4530558	1508	cathepsin B
GO	perinuclear region of cytoplasm	22	309	0.4530558	1540	cylindromatosis (turban tumor syndrome)
GO	perinuclear region of cytoplasm	22	309	0.4530558	255738	proprotein convertase subtilisin/kexin type 9
GO	perinuclear region of cytoplasm	22	309	0.4530558	2589	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyl transferase 1
GO	perinuclear region of cytoplasm	22	309	0.4530558	4645	myosin VB
GO	perinuclear region of cytoplasm	22	309	0.4530558	4794	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor 3
GO	perinuclear region of cytoplasm	22	309	0.4530558	4842	nitric oxide synthase 1 (neuronal)
GO	perinuclear region of cytoplasm	22	309	0.4530558	5025	purinergic receptor P2X, ligand-gated ion channel, 4
GO	perinuclear region of cytoplasm	22	309	0.4530558	5071	Parkinson disease (autosomal recessive, juvenile) 2, parkin
GO	perinuclear region of cytoplasm	22	309	0.4530558	5122	proprotein convertase subtilisin/kexin type 1
GO	perinuclear region of cytoplasm	22	309	0.4530558	5152	phosphodiesterase 9A
GO	perinuclear region of cytoplasm	22	309	0.4530558	51655	RAS, dexamethasone-induced 1
GO	perinuclear region of cytoplasm	22	309	0.4530558	5577	protein kinase, cAMP-dependent, regulatory, type II, beta
GO	perinuclear region of cytoplasm	22	309	0.4530558	57799	RAB40C, member RAS oncogene family
GO	perinuclear region of cytoplasm	22	309	0.4530558	5801	protein tyrosine phosphatase, receptor type, R
GO	perinuclear region of cytoplasm	22	309	0.4530558	6494	signal-induced proliferation-associated 1
GO	perinuclear region of cytoplasm	22	309	0.4530558	7099	toll-like receptor 4
GO	perinuclear region of cytoplasm	22	309	0.4530558	81544	glycerophosphodiester phosphodiesterase domain containing 5
GO	postsynaptic density	6	79	0.4563248	1785	dynamitin 2
GO	postsynaptic density	6	79	0.4563248	2066	v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian)
GO	postsynaptic density	6	79	0.4563248	22859	latrophilin 1
GO	postsynaptic density	6	79	0.4563248	2911	glutamate receptor, metabotropic 1
GO	postsynaptic density	6	79	0.4563248	5025	purinergic receptor P2X, ligand-gated ion channel, 4
GO	postsynaptic density	6	79	0.4563248	9892	synaptosomal-associated protein, 91kDa homolog (mouse)
GO	nervous system development	27	382	0.4569011	10439	olfactomedin 1
GO	nervous system development	27	382	0.4569011	10507	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) 1
GO	nervous system development	27	382	0.4569011	10752	cell adhesion molecule with homology to L1CAM (close homolog of L1)



GO nervous system development	27	382	0.4569011	1948 ephrin-B2
GO nervous system development	27	382	0.4569011	2033 E1A binding protein p300
GO nervous system development	27	382	0.4569011	2055 ceroid-lipofuscinosis, neuronal 8 (epilepsy, progressive with mental ret
GO nervous system development	27	382	0.4569011	223117 sema domain, immunoglobulin domain (Ig), short basic domain, secret
GO nervous system development	27	382	0.4569011	23092 Rho GTPase activating protein 26
GO nervous system development	27	382	0.4569011	2353 FBJ murine osteosarcoma viral oncogene homolog
GO nervous system development	27	382	0.4569011	26468 LIM homeobox 6
GO nervous system development	27	382	0.4569011	29116 myosin regulatory light chain interacting protein
GO nervous system development	27	382	0.4569011	342035 gliomedin
GO nervous system development	27	382	0.4569011	3479 insulin-like growth factor 1 (somatomedin C)
GO nervous system development	27	382	0.4569011	4209 myocyte enhancer factor 2D
GO nervous system development	27	382	0.4569011	4692 necdin homolog (mouse)
GO nervous system development	27	382	0.4569011	4853 Notch homolog 2 (Drosophila)
GO nervous system development	27	382	0.4569011	4915 neurotrophic tyrosine kinase, receptor, type 2
GO nervous system development	27	382	0.4569011	4929 nuclear receptor subfamily 4, group A, member 2
GO nervous system development	27	382	0.4569011	55816 docking protein 5
GO nervous system development	27	382	0.4569011	5801 protein tyrosine phosphatase, receptor type, R
GO nervous system development	27	382	0.4569011	627 brain-derived neurotrophic factor
GO nervous system development	27	382	0.4569011	6604 SWI/SNF related, matrix associated, actin dependent regulator of chrom
GO nervous system development	27	382	0.4569011	81544 glycerophosphodiester phosphodiesterase domain containing 5
GO nervous system development	27	382	0.4569011	84059 G protein-coupled receptor 98
GO nervous system development	27	382	0.4569011	85416 Zic family member 5 (odd-paired homolog, Drosophila)
GO nervous system development	27	382	0.4569011	9445 integral membrane protein 2B
GO nervous system development	27	382	0.4569011	9615 guanine deaminase
GO muscle organ development	7	94	0.4640939	1839 heparin-binding EGF-like growth factor
GO muscle organ development	7	94	0.4640939	1960 early growth response 3
GO muscle organ development	7	94	0.4640939	3479 insulin-like growth factor 1 (somatomedin C)
GO muscle organ development	7	94	0.4640939	3911 laminin, alpha 5
GO muscle organ development	7	94	0.4640939	4209 myocyte enhancer factor 2D
GO muscle organ development	7	94	0.4640939	5463 POU class 6 homeobox 1
GO muscle organ development	7	94	0.4640939	8912 calcium channel, voltage-dependent, T type, alpha 1H subunit
GO cell projection	7	94	0.4640939	2867 free fatty acid receptor 2
GO cell projection	7	94	0.4640939	4842 nitric oxide synthase 1 (neuronal)
GO cell projection	7	94	0.4640939	51168 myosin XVA
GO cell projection	7	94	0.4640939	5152 phosphodiesterase 9A
GO cell projection	7	94	0.4640939	729993 shisa homolog 9 (Xenopus laevis)

GO cell projection	7	94	0.4640939	81544 glycerophosphodiester phosphodiesterase domain containing 5
GO cell projection	7	94	0.4640939	8842 prominin 1
GO regulation of growth	4	51	0.4641161	10481 homeobox B13
GO regulation of growth	4	51	0.4641161	4692 necdin homolog (mouse)
GO regulation of growth	4	51	0.4641161	51754 transmembrane protein 8B
GO regulation of growth	4	51	0.4641161	9021 suppressor of cytokine signaling 3
GO secretory granule	4	51	0.4641161	1114 chromogranin B (secretogranin 1)
GO secretory granule	4	51	0.4641161	5066 peptidylglycine alpha-amidating monooxygenase
GO secretory granule	4	51	0.4641161	5122 proprotein convertase subtilisin/kexin type 1
GO secretory granule	4	51	0.4641161	5327 plasminogen activator, tissue
GO cartilage development	3	37	0.4684532	1906 endothelin 1
GO cartilage development	3	37	0.4684532	5307 paired-like homeodomain 1
GO cartilage development	3	37	0.4684532	5396 paired related homeobox 1
GO protein catabolic process	3	37	0.4684532	2055 ceroid-lipofuscinosis, neuronal 8 (epilepsy, progressive with mental ret
GO protein catabolic process	3	37	0.4684532	26232 F-box protein 2
GO protein catabolic process	3	37	0.4684532	26270 F-box protein 6
GO protein localization at cell surface	1	9	0.4712841	10076 protein tyrosine phosphatase, receptor type, U
GO androgen metabolic process	1	9	0.4712841	10170 dehydrogenase/reductase (SDR family) member 9
GO mitotic cell cycle	1	9	0.4712841	10769 polo-like kinase 2 (Drosophila)
GO pseudopodium	1	9	0.4712841	11155 LIM domain binding 3
GO adult feeding behavior	1	9	0.4712841	127343 diencephalon/mesencephalon homeobox 1
GO dendrite cytoplasm	1	9	0.4712841	127933 U2AF homology motif (UHM) kinase 1
GO macrophage differentiation	1	9	0.4712841	1435 colony stimulating factor 1 (macrophage)
GO histone monoubiquitination	1	9	0.4712841	151636 deltex 3-like (Drosophila)
GO gonad development	1	9	0.4712841	157506 retinol dehydrogenase 10 (all-trans)
GO lamellipodium membrane	1	9	0.4712841	1803 dipeptidyl-peptidase 4
GO positive regulation of JUN kinase acti	1	9	0.4712841	1906 endothelin 1
GO cellular response to reactive oxygen s	1	9	0.4712841	2353 FBJ murine osteosarcoma viral oncogene homolog
GO sleep	1	9	0.4712841	2353 FBJ murine osteosarcoma viral oncogene homolog
GO L-fucose catabolic process	1	9	0.4712841	2526 fucosyltransferase 4 (alpha (1,3) fucosyltransferase, myeloid-specific)
GO positive regulation of receptor-media	1	9	0.4712841	26119 low density lipoprotein receptor adaptor protein 1
GO DNA damage response, signal transdi	1	9	0.4712841	28996 homeodomain interacting protein kinase 2
GO specific granule	1	9	0.4712841	311 annexin A11
GO serotonin binding	1	9	0.4712841	3355 5-hydroxytryptamine (serotonin) receptor 1F
GO positive regulation of tyrosine phosph	1	9	0.4712841	3479 insulin-like growth factor 1 (somatomedin C)
GO proteoglycan biosynthetic process	1	9	0.4712841	3479 insulin-like growth factor 1 (somatomedin C)

GO	regulation of peptidyl-tyrosine phosphatase activity	1	9	0.4712841	3689 integrin, beta 2 (complement component 3 receptor 3 and 4 subunit)
GO	muscarinic acetylcholine receptor signaling pathway	1	9	0.4712841	375790 agrin
GO	positive regulation of nitric-oxide synthase activity	1	9	0.4712841	3845 v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog
GO	branching involved in salivary gland morphogenesis	1	9	0.4712841	3911 laminin, alpha 5
GO	organ growth	1	9	0.4712841	4087 SMAD family member 2
GO	axonal fasciculation	1	9	0.4712841	4692 necdin homolog (mouse)
GO	central nervous system neuron differentiation	1	9	0.4712841	4929 nuclear receptor subfamily 4, group A, member 2
GO	MHC class I protein binding	1	9	0.4712841	498 ATP synthase, H <sup>+</sup> transporting, mitochondrial F1 complex, alpha subunit
GO	vacuolar proton-transporting V-type ATPase activity	1	9	0.4712841	50617 ATPase, H <sup>+</sup> transporting, lysosomal V0 subunit a4
GO	insulin-like growth factor receptor signaling pathway	1	9	0.4712841	5295 phosphoinositide-3-kinase, regulatory subunit 1 (alpha)
GO	maintenance of protein location in nucleus	1	9	0.4712841	5371 promyelocytic leukemia
GO	female gonad development	1	9	0.4712841	54361 wingless-type MMTV integration site family, member 4
GO	organic anion transmembrane transporter activity	1	9	0.4712841	55867 solute carrier family 22 (organic anion/urate transporter), member 11
GO	grooming behavior	1	9	0.4712841	56923 neuromedin U receptor 2
GO	response to pain	1	9	0.4712841	56923 neuromedin U receptor 2
GO	apical protein localization	1	9	0.4712841	57619 shroom family member 3
GO	melanosome transport	1	9	0.4712841	5873 RAB27A, member RAS oncogene family
GO	negative regulation of S phase of mitotic cell cycle	1	9	0.4712841	604 B-cell CLL/lymphoma 6
GO	detection of bacterium	1	9	0.4712841	64127 nucleotide-binding oligomerization domain containing 2
GO	dicarboxylic acid transport	1	9	0.4712841	6505 solute carrier family 1 (neuronal/epithelial high affinity glutamate transporter)
GO	epithelial tube branching involved in morphogenesis	1	9	0.4712841	652 bone morphogenetic protein 4
GO	smooth muscle tissue development	1	9	0.4712841	652 bone morphogenetic protein 4
GO	muscle cell differentiation	1	9	0.4712841	6604 SWI/SNF related, matrix associated, actin dependent regulator of chromatin
GO	positive regulation of release of sequestered protein	1	9	0.4712841	6622 synuclein, alpha (non A4 component of amyloid precursor)
GO	spectrin	1	9	0.4712841	6710 spectrin, beta, erythrocytic
GO	T-helper 1 type immune response	1	9	0.4712841	7099 toll-like receptor 4
GO	cleavage furrow	1	9	0.4712841	7170 tropomyosin 3
GO	DNA-(apurinic or apyrimidinic site) lyase activity	1	9	0.4712841	79661 nei endonuclease VIII-like 1 (E. coli)
GO	quinone binding	1	9	0.4712841	79802 HHIP-like 2
GO	sensory perception of light stimulus	1	9	0.4712841	84059 G protein-coupled receptor 98
GO	ER overload response	1	9	0.4712841	84919 protein phosphatase 1, regulatory (inhibitor) subunit 15B
GO	hedgehog receptor activity	1	9	0.4712841	84976 dispatched homolog 1 (Drosophila)
GO	two-component signal transduction system	1	9	0.4712841	8622 phosphodiesterase 8B
GO	oligosaccharide biosynthetic process	1	9	0.4712841	8706 beta-1,3-N-acetylgalactosaminyltransferase 1 (globoside blood group)
GO	response to food	1	9	0.4712841	9021 suppressor of cytokine signaling 3
GO	ovulation from ovarian follicle	1	9	0.4712841	9510 ADAM metallopeptidase with thrombospondin type 1 motif, 1

GO phospholipid efflux	1	9	0.4712841	9619 ATP-binding cassette, sub-family G (WHITE), member 1
GO retinoid X receptor binding	1	9	0.4712841	9971 nuclear receptor subfamily 1, group H, member 4
GO condensed nuclear chromosome, cer	1	9	0.4712841	9985 REC8 homolog (yeast)
GO sarcoplasmic reticulum	2	23	0.4726851	10335 murine retrovirus integration site 1 homolog
GO sarcoplasmic reticulum	2	23	0.4726851	4842 nitric oxide synthase 1 (neuronal)
GO positive regulation of multicellular or	2	23	0.4726851	1435 colony stimulating factor 1 (macrophage)
GO positive regulation of multicellular or	2	23	0.4726851	183 angiotensinogen (serpin peptidase inhibitor, clade A, member 8)
GO protease binding	2	23	0.4726851	1471 cystatin C
GO protease binding	2	23	0.4726851	1803 dipeptidyl-peptidase 4
GO ER-associated protein catabolic proce	2	23	0.4726851	26270 F-box protein 6
GO ER-associated protein catabolic proce	2	23	0.4726851	55432 YOD1 OTU deubiquinating enzyme 1 homolog ( <i>S. cerevisiae</i> )
GO erythrocyte differentiation	2	23	0.4726851	28982 feline leukemia virus subgroup C cellular receptor 1
GO erythrocyte differentiation	2	23	0.4726851	652 bone morphogenetic protein 4
GO regulation of cell adhesion	2	23	0.4726851	3911 laminin, alpha 5
GO regulation of cell adhesion	2	23	0.4726851	9595 cytohesin 1 interacting protein
GO Golgi stack	2	23	0.4726851	53947 alpha 1,4-galactosyltransferase
GO Golgi stack	2	23	0.4726851	54947 lysophosphatidylcholine acyltransferase 2
GO nucleobase, nucleoside, nucleotide a	5	66	0.4735451	205 adenylate kinase 3-like 1
GO nucleobase, nucleoside, nucleotide a	5	66	0.4735451	4939 2'-5'-oligoadenylate synthetase 2, 69/71kDa
GO nucleobase, nucleoside, nucleotide a	5	66	0.4735451	54932 exonuclease 3'-5' domain containing 3
GO nucleobase, nucleoside, nucleotide a	5	66	0.4735451	9615 guanine deaminase
GO nucleobase, nucleoside, nucleotide a	5	66	0.4735451	9962 solute carrier family 23 (nucleobase transporters), member 2
GO DNA binding	96	1392	0.4787924	10838 zinc finger protein 275
GO DNA binding	96	1392	0.4787924	10891 peroxisome proliferator-activated receptor gamma, coactivator 1 alpha
GO DNA binding	96	1392	0.4787924	11279 Kruppel-like factor 8
GO DNA binding	96	1392	0.4787924	115196 zinc finger protein 554
GO DNA binding	96	1392	0.4787924	127343 diencephalon/mesencephalon homeobox 1
GO DNA binding	96	1392	0.4787924	147694 zinc finger protein 548
GO DNA binding	96	1392	0.4787924	147923 zinc finger protein 420
GO DNA binding	96	1392	0.4787924	158800 RhoX homeobox family, member 1
GO DNA binding	96	1392	0.4787924	162962 zinc finger protein 836
GO DNA binding	96	1392	0.4787924	163050 zinc finger protein 564
GO DNA binding	96	1392	0.4787924	163115 zinc finger protein 781
GO DNA binding	96	1392	0.4787924	1958 early growth response 1
GO DNA binding	96	1392	0.4787924	2033 E1A binding protein p300
GO DNA binding	96	1392	0.4787924	2114 v-ets erythroblastosis virus E26 oncogene homolog 2 (avian)

GO DNA binding	96	1392	0.4787924	2122 MDS1 and EVI1 complex locus
GO DNA binding	96	1392	0.4787924	220359 tigger transposable element derived 3
GO DNA binding	96	1392	0.4787924	222546 regulatory factor X, 6
GO DNA binding	96	1392	0.4787924	22807 IKAROS family zinc finger 2 (Helios)
GO DNA binding	96	1392	0.4787924	2290 forkhead box G1
GO DNA binding	96	1392	0.4787924	2296 forkhead box C1
GO DNA binding	96	1392	0.4787924	23099 zinc finger and BTB domain containing 43
GO DNA binding	96	1392	0.4787924	23119 hypermethylated in cancer 2
GO DNA binding	96	1392	0.4787924	23476 bromodomain containing 4
GO DNA binding	96	1392	0.4787924	2354 FBJ murine osteosarcoma viral oncogene homolog B
GO DNA binding	96	1392	0.4787924	23648 single stranded DNA binding protein 3
GO DNA binding	96	1392	0.4787924	2521 fused in sarcoma
GO DNA binding	96	1392	0.4787924	256051 zinc finger protein 549
GO DNA binding	96	1392	0.4787924	25946 zinc finger protein 385A
GO DNA binding	96	1392	0.4787924	27245 AT hook, DNA binding motif, containing 1
GO DNA binding	96	1392	0.4787924	27434 polymerase (DNA directed), mu
GO DNA binding	96	1392	0.4787924	284346 zinc finger protein 575
GO DNA binding	96	1392	0.4787924	3131 hepatic leukemia factor
GO DNA binding	96	1392	0.4787924	3164 nuclear receptor subfamily 4, group A, member 1
GO DNA binding	96	1392	0.4787924	3169 forkhead box A1
GO DNA binding	96	1392	0.4787924	3192 heterogeneous nuclear ribonucleoprotein U (scaffold attachment facto
GO DNA binding	96	1392	0.4787924	3428 interferon, gamma-inducible protein 16
GO DNA binding	96	1392	0.4787924	342908 zinc finger protein 404
GO DNA binding	96	1392	0.4787924	345462 zinc finger protein 879
GO DNA binding	96	1392	0.4787924	3725 jun oncogene
GO DNA binding	96	1392	0.4787924	3726 jun B proto-oncogene
GO DNA binding	96	1392	0.4787924	388536 zinc finger protein 790
GO DNA binding	96	1392	0.4787924	388558 zinc finger protein 808
GO DNA binding	96	1392	0.4787924	388567 zinc finger protein 749
GO DNA binding	96	1392	0.4787924	389058 Sp5 transcription factor
GO DNA binding	96	1392	0.4787924	4005 LIM domain only 2 (rhombotin-like 1)
GO DNA binding	96	1392	0.4787924	4087 SMAD family member 2
GO DNA binding	96	1392	0.4787924	4204 methyl CpG binding protein 2 (Rett syndrome)
GO DNA binding	96	1392	0.4787924	4613 v-myc myelocytomatosis viral related oncogene, neuroblastoma derive
GO DNA binding	96	1392	0.4787924	4692 necdin homolog (mouse)
GO DNA binding	96	1392	0.4787924	4783 nuclear factor, interleukin 3 regulated

GO DNA binding	96	1392	0.4787924	4802 nuclear transcription factor Y, gamma
GO DNA binding	96	1392	0.4787924	50809 heterochromatin protein 1, binding protein 3
GO DNA binding	96	1392	0.4787924	5083 paired box 9
GO DNA binding	96	1392	0.4787924	51085 MLX interacting protein-like
GO DNA binding	96	1392	0.4787924	51523 CXXC finger 5
GO DNA binding	96	1392	0.4787924	51621 Kruppel-like factor 13
GO DNA binding	96	1392	0.4787924	51710 zinc finger protein 44
GO DNA binding	96	1392	0.4787924	5325 pleiomorphic adenoma gene-like 1
GO DNA binding	96	1392	0.4787924	5371 promyelocytic leukemia
GO DNA binding	96	1392	0.4787924	5460 POU class 5 homeobox 1
GO DNA binding	96	1392	0.4787924	5465 peroxisome proliferator-activated receptor alpha
GO DNA binding	96	1392	0.4787924	55140 elongation protein 3 homolog ( <i>S. cerevisiae</i> )
GO DNA binding	96	1392	0.4787924	55657 zinc finger protein 692
GO DNA binding	96	1392	0.4787924	55762 zinc finger protein 701
GO DNA binding	96	1392	0.4787924	55870 ash1 (absent, small, or homeotic)-like ( <i>Drosophila</i> )
GO DNA binding	96	1392	0.4787924	55893 zinc finger protein 395
GO DNA binding	96	1392	0.4787924	56978 PR domain containing 8
GO DNA binding	96	1392	0.4787924	6097 RAR-related orphan receptor C
GO DNA binding	96	1392	0.4787924	6239 ras responsive element binding protein 1
GO DNA binding	96	1392	0.4787924	6256 retinoid X receptor, alpha
GO DNA binding	96	1392	0.4787924	64135 interferon induced with helicase C domain 1
GO DNA binding	96	1392	0.4787924	7022 transcription factor AP-2 gamma (activating enhancer binding protein 2)
GO DNA binding	96	1392	0.4787924	7538 zinc finger protein 36, C3H type, homolog (mouse)
GO DNA binding	96	1392	0.4787924	7546 Zic family member 2 (odd-paired homolog, <i>Drosophila</i> )
GO DNA binding	96	1392	0.4787924	7565 zinc finger protein 17
GO DNA binding	96	1392	0.4787924	7597 zinc finger and BTB domain containing 25
GO DNA binding	96	1392	0.4787924	7678 zinc finger protein 124
GO DNA binding	96	1392	0.4787924	79132 DEXH (Asp-Glu-X-His) box polypeptide 58
GO DNA binding	96	1392	0.4787924	79673 zinc finger protein 329
GO DNA binding	96	1392	0.4787924	79894 zinc finger protein 672
GO DNA binding	96	1392	0.4787924	8013 nuclear receptor subfamily 4, group A, member 3
GO DNA binding	96	1392	0.4787924	80169 chromosome 17 open reading frame 68
GO DNA binding	96	1392	0.4787924	84159 AT rich interactive domain 5B (MRF1-like)
GO DNA binding	96	1392	0.4787924	84911 zinc finger protein 382
GO DNA binding	96	1392	0.4787924	84969 TOX high mobility group box family member 2
GO DNA binding	96	1392	0.4787924	85416 Zic family member 5 (odd-paired homolog, <i>Drosophila</i> )

GO DNA binding	96	1392	0.4787924	85441 peroxisomal proliferator-activated receptor A interacting complex 285
GO DNA binding	96	1392	0.4787924	8653 DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, Y-linked
GO DNA binding	96	1392	0.4787924	90592 zinc finger protein 700
GO DNA binding	96	1392	0.4787924	91748 chromosome 14 open reading frame 43
GO DNA binding	96	1392	0.4787924	92283 zinc finger protein 461
GO DNA binding	96	1392	0.4787924	92822 zinc finger protein 276
GO DNA binding	96	1392	0.4787924	9324 high mobility group nucleosomal binding domain 3
GO DNA binding	96	1392	0.4787924	93349 SP140 nuclear body protein-like
GO DNA binding	96	1392	0.4787924	9422 zinc finger protein 264
GO DNA binding	96	1392	0.4787924	9496 T-box 4
GO signal transducer activity	20	285	0.4847925	10769 polo-like kinase 2 (Drosophila)
GO signal transducer activity	20	285	0.4847925	2769 guanine nucleotide binding protein (G protein), alpha 15 (Gq class)
GO signal transducer activity	20	285	0.4847925	3587 interleukin 10 receptor, alpha
GO signal transducer activity	20	285	0.4847925	3601 interleukin 15 receptor, alpha
GO signal transducer activity	20	285	0.4847925	5129 cyclin-dependent kinase 18
GO signal transducer activity	20	285	0.4847925	51523 CXXC finger 5
GO signal transducer activity	20	285	0.4847925	5187 period homolog 1 (Drosophila)
GO signal transducer activity	20	285	0.4847925	54361 wingless-type MMTV integration site family, member 4
GO signal transducer activity	20	285	0.4847925	6004 regulator of G-protein signaling 16
GO signal transducer activity	20	285	0.4847925	6778 signal transducer and activator of transcription 6, interleukin-4 inducer
GO signal transducer activity	20	285	0.4847925	684 bone marrow stromal cell antigen 2
GO signal transducer activity	20	285	0.4847925	7474 wingless-type MMTV integration site family, member 5A
GO signal transducer activity	20	285	0.4847925	7477 wingless-type MMTV integration site family, member 7B
GO signal transducer activity	20	285	0.4847925	79971 wntless homolog (Drosophila)
GO signal transducer activity	20	285	0.4847925	80833 apolipoprotein L, 3
GO signal transducer activity	20	285	0.4847925	8313 axin 2
GO signal transducer activity	20	285	0.4847925	8660 insulin receptor substrate 2
GO signal transducer activity	20	285	0.4847925	8786 regulator of G-protein signaling 11
GO signal transducer activity	20	285	0.4847925	8863 period homolog 3 (Drosophila)
GO signal transducer activity	20	285	0.4847925	8864 period homolog 2 (Drosophila)
GO carbohydrate metabolic process	14	198	0.4876563	1117 chitinase 3-like 2
GO carbohydrate metabolic process	14	198	0.4876563	2517 fucosidase, alpha-L- 1, tissue
GO carbohydrate metabolic process	14	198	0.4876563	2525 fucosyltransferase 3 (galactoside 3(4)-L-fucosyltransferase, Lewis blood
GO carbohydrate metabolic process	14	198	0.4876563	2526 fucosyltransferase 4 (alpha (1,3) fucosyltransferase, myeloid-specific)
GO carbohydrate metabolic process	14	198	0.4876563	2990 glucuronidase, beta
GO carbohydrate metabolic process	14	198	0.4876563	3373 hyaluronoglucosaminidase 1

GO carbohydrate metabolic process	14	198	0.4876563	3643 insulin receptor
GO carbohydrate metabolic process	14	198	0.4876563	5016 oviductal glycoprotein 1, 120kDa
GO carbohydrate metabolic process	14	198	0.4876563	5239 phosphoglucomutase 5
GO carbohydrate metabolic process	14	198	0.4876563	56261 glycerophosphocholine phosphodiesterase GDE1 homolog ( <i>S. cerevisia</i>
GO carbohydrate metabolic process	14	198	0.4876563	6489 ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 1
GO carbohydrate metabolic process	14	198	0.4876563	79802 HHIP-like 2
GO carbohydrate metabolic process	14	198	0.4876563	9435 carbohydrate (N-acetylglucosamine-6-O) sulfotransferase 2
GO carbohydrate metabolic process	14	198	0.4876563	9563 hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase)
GO microtubule cytoskeleton	4	53	0.4943761	10397 N-myc downstream regulated 1
GO microtubule cytoskeleton	4	53	0.4943761	51710 zinc finger protein 44
GO microtubule cytoskeleton	4	53	0.4943761	6819 sulfotransferase family, cytosolic, 1C, member 2
GO microtubule cytoskeleton	4	53	0.4943761	8900 cyclin A1
GO cellular membrane organization	4	53	0.4943761	1785 dynamin 2
GO cellular membrane organization	4	53	0.4943761	23418 crumbs homolog 1 ( <i>Drosophila</i> )
GO cellular membrane organization	4	53	0.4943761	54947 lysophosphatidylcholine acyltransferase 2
GO cellular membrane organization	4	53	0.4943761	8673 vesicle-associated membrane protein 8 (endobrevin)
GO activation of adenylate cyclase activit	2	24	0.4953352	154 adrenergic, beta-2-, receptor, surface
GO activation of adenylate cyclase activit	2	24	0.4953352	4915 neurotrophic tyrosine kinase, receptor, type 2
GO oxygen and reactive oxygen species r	2	24	0.4953352	183 angiotensinogen (serpin peptidase inhibitor, clade A, member 8)
GO oxygen and reactive oxygen species r	2	24	0.4953352	316 aldehyde oxidase 1
GO peripheral nervous system developm	2	24	0.4953352	1959 early growth response 2
GO peripheral nervous system developm	2	24	0.4953352	1960 early growth response 3
GO histone H3 acetylation	2	24	0.4953352	23338 PHD finger protein 15
GO histone H3 acetylation	2	24	0.4953352	23774 bromodomain containing 1
GO cilium assembly	2	24	0.4953352	3175 one cut homeobox 1
GO cilium assembly	2	24	0.4953352	3911 laminin, alpha 5
GO transmembrane transport	34	492	0.4993007	1080 cystic fibrosis transmembrane conductance regulator (ATP-binding cas:
GO transmembrane transport	34	492	0.4993007	113235 solute carrier family 46 (folate transporter), member 1
GO transmembrane transport	34	492	0.4993007	123096 solute carrier family 25, member 29
GO transmembrane transport	34	492	0.4993007	151473 solute carrier family 16, member 14 (monocarboxylic acid transporter :
GO transmembrane transport	34	492	0.4993007	157855 potassium channel, subfamily U, member 1
GO transmembrane transport	34	492	0.4993007	259232 sodium leak channel, non-selective
GO transmembrane transport	34	492	0.4993007	283537 solute carrier family 46, member 3
GO transmembrane transport	34	492	0.4993007	28982 feline leukemia virus subgroup C cellular receptor 1
GO transmembrane transport	34	492	0.4993007	29015 solute carrier family 43, member 3
GO transmembrane transport	34	492	0.4993007	368 ATP-binding cassette, sub-family C (CFTR/MRP), member 6



GO transmembrane transport	34	492	0.4993007	3709 inositol 1,4,5-triphosphate receptor, type 2
GO transmembrane transport	34	492	0.4993007	3786 potassium voltage-gated channel, KQT-like subfamily, member 3
GO transmembrane transport	34	492	0.4993007	3790 potassium voltage-gated channel, delayed-rectifier, subfamily S, memb
GO transmembrane transport	34	492	0.4993007	387923 stress-associated endoplasmic reticulum protein family member 2
GO transmembrane transport	34	492	0.4993007	5243 ATP-binding cassette, sub-family B (MDR/TAP), member 1
GO transmembrane transport	34	492	0.4993007	5244 ATP-binding cassette, sub-family B (MDR/TAP), member 4
GO transmembrane transport	34	492	0.4993007	53373 two pore segment channel 1
GO transmembrane transport	34	492	0.4993007	55867 solute carrier family 22 (organic anion/urate transporter), member 11
GO transmembrane transport	34	492	0.4993007	57210 solute carrier family 45, member 4
GO transmembrane transport	34	492	0.4993007	6006 Rh blood group, CcEe antigens
GO transmembrane transport	34	492	0.4993007	6238 ribosome binding protein 1 homolog 180kDa (dog)
GO transmembrane transport	34	492	0.4993007	63027 solute carrier family 22, member 23
GO transmembrane transport	34	492	0.4993007	64116 solute carrier family 39 (zinc transporter), member 8
GO transmembrane transport	34	492	0.4993007	6542 solute carrier family 7 (cationic amino acid transporter, y+ system), me
GO transmembrane transport	34	492	0.4993007	7223 transient receptor potential cation channel, subfamily C, member 4
GO transmembrane transport	34	492	0.4993007	774 calcium channel, voltage-dependent, N type, alpha 1B subunit
GO transmembrane transport	34	492	0.4993007	84561 solute carrier family 12 (potassium/chloride transporters), member 8
GO transmembrane transport	34	492	0.4993007	84879 major facilitator superfamily domain containing 2A
GO transmembrane transport	34	492	0.4993007	8514 potassium voltage-gated channel, shaker-related subfamily, beta mem
GO transmembrane transport	34	492	0.4993007	8911 calcium channel, voltage-dependent, T type, alpha 1I subunit
GO transmembrane transport	34	492	0.4993007	8912 calcium channel, voltage-dependent, T type, alpha 1H subunit
GO transmembrane transport	34	492	0.4993007	9194 solute carrier family 16, member 7 (monocarboxylic acid transporter 2)
GO transmembrane transport	34	492	0.4993007	9481 solute carrier family 25, member 27
GO transmembrane transport	34	492	0.4993007	9962 solute carrier family 23 (nucleobase transporters), member 2
GO beta-catenin binding	3	39	0.503887	10076 protein tyrosine phosphatase, receptor type, U
GO beta-catenin binding	3	39	0.503887	2737 GLI family zinc finger 3
GO beta-catenin binding	3	39	0.503887	8313 axin 2
GO insoluble fraction	3	39	0.503887	2026 enolase 2 (gamma, neuronal)
GO insoluble fraction	3	39	0.503887	53405 chloride intracellular channel 5
GO insoluble fraction	3	39	0.503887	5371 promyelocytic leukemia
GO G-protein signaling, coupled to cyclic	3	39	0.503887	3355 5-hydroxytryptamine (serotonin) receptor 1F
GO G-protein signaling, coupled to cyclic	3	39	0.503887	4886 neuropeptide Y receptor Y1
GO G-protein signaling, coupled to cyclic	3	39	0.503887	6751 somatostatin receptor 1
GO aging	6	83	0.5047025	10568 solute carrier family 34 (sodium phosphate), member 2
GO aging	6	83	0.5047025	2353 FBJ murine osteosarcoma viral oncogene homolog
GO aging	6	83	0.5047025	3725 jun oncogene

GO aging	6	83	0.5047025	5742 prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and
GO aging	6	83	0.5047025	6256 retinoid X receptor, alpha
GO aging	6	83	0.5047025	9021 suppressor of cytokine signaling 3
GO chromatin silencing	1	10	0.507438	10014 histone deacetylase 5
GO cellular respiration	1	10	0.507438	10891 peroxisome proliferator-activated receptor gamma, coactivator 1 alpha
GO acetylcholine binding	1	10	0.507438	1139 cholinergic receptor, nicotinic, alpha 7
GO cognition	1	10	0.507438	1139 cholinergic receptor, nicotinic, alpha 7
GO ribonucleoprotein binding	1	10	0.507438	127933 U2AF homology motif (UHM) kinase 1
GO urea cycle	1	10	0.507438	1373 carbamoyl-phosphate synthetase 1, mitochondrial
GO positive regulation of cytokine produ	1	10	0.507438	183 angiotensinogen (serpin peptidase inhibitor, clade A, member 8)
GO positive regulation of collagen biosyn	1	10	0.507438	2033 E1A binding protein p300
GO protein kinase B signaling cascade	1	10	0.507438	2033 E1A binding protein p300
GO carboxylic acid metabolic process	1	10	0.507438	2571 glutamate decarboxylase 1 (brain, 67kDa)
GO histone acetyltransferase binding	1	10	0.507438	2737 GLI family zinc finger 3
GO I kappaB kinase complex	1	10	0.507438	29108 PYD and CARD domain containing
GO MHC class I receptor activity	1	10	0.507438	3134 major histocompatibility complex, class I, F
GO positive regulation of smooth muscle	1	10	0.507438	3479 insulin-like growth factor 1 (somatomedin C)
GO acyl-CoA dehydrogenase activity	1	10	0.507438	35 acyl-Coenzyme A dehydrogenase, C-2 to C-3 short chain
GO water channel activity	1	10	0.507438	358 aquaporin 1 (Colton blood group)
GO morphogenesis of embryonic epithel	1	10	0.507438	3911 laminin, alpha 5
GO substrate adhesion-dependent cell sp	1	10	0.507438	3911 laminin, alpha 5
GO I-SMAD binding	1	10	0.507438	4087 SMAD family member 2
GO oxygen transporter activity	1	10	0.507438	4151 myoglobin
GO oxygen transport	1	10	0.507438	4151 myoglobin
GO lipopolysaccharide-mediated signalin	1	10	0.507438	4792 nuclear factor of kappa light polypeptide gene enhancer in B-cells inhib
GO stem cell maintenance	1	10	0.507438	4853 Notch homolog 2 (Drosophila)
GO Golgi lumen	1	10	0.507438	5046 proprotein convertase subtilisin/kexin type 6
GO CUL4 RING ubiquitin ligase complex	1	10	0.507438	54876 DDB1 and CUL4 associated factor 16
GO cAMP-dependent protein kinase com	1	10	0.507438	5577 protein kinase, cAMP-dependent, regulatory, type II, beta
GO transmission of nerve impulse	1	10	0.507438	56923 neuromedin U receptor 2
GO isotype switching	1	10	0.507438	57379 activation-induced cytidine deaminase
GO cardiac muscle tissue development	1	10	0.507438	5950 retinol binding protein 4, plasma
GO signalosome	1	10	0.507438	64127 nucleotide-binding oligomerization domain containing 2
GO L-glutamate transmembrane transpo	1	10	0.507438	6505 solute carrier family 1 (neuronal/epithelial high affinity glutamate trans
GO calcium ion homeostasis	1	10	0.507438	6622 synuclein, alpha (non A4 component of amyloid precursor)
GO platelet alpha granule membrane	1	10	0.507438	6622 synuclein, alpha (non A4 component of amyloid precursor)

GO platelet alpha granule	1	10	0.507438	6812 syntaxin binding protein 1
GO B cell receptor signaling pathway	1	10	0.507438	6850 spleen tyrosine kinase
GO interleukin-1 receptor binding	1	10	0.507438	7100 toll-like receptor 5
GO tumor necrosis factor receptor activit	1	10	0.507438	7133 tumor necrosis factor receptor superfamily, member 1B
GO complement activation	1	10	0.507438	731 complement component 8, alpha polypeptide
GO mRNA catabolic process	1	10	0.507438	7538 zinc finger protein 36, C3H type, homolog (mouse)
GO XY body	1	10	0.507438	80714 pre-B-cell leukemia homeobox 4
GO killing of cells of another organism	1	10	0.507438	8542 apolipoprotein L, 1
GO calcium ion-dependent exocytosis	1	10	0.507438	85477 scinderin
GO cytokine binding	1	10	0.507438	8646 chordin
GO embryonic digestive tract developme	1	10	0.507438	91461 protein kinase domain containing, cytoplasmic homolog (mouse)
GO mRNA cap binding complex	1	10	0.507438	9271 piwi-like 1 (Drosophila)
GO NAD metabolic process	1	10	0.507438	93100 nicotinate phosphoribosyltransferase domain containing 1
GO positive regulation of T cell activator	1	10	0.507438	961 CD47 molecule
GO cellular component movement	7	98	0.5084993	27076 LY6/PLAUR domain containing 3
GO cellular component movement	7	98	0.5084993	29116 myosin regulatory light chain interacting protein
GO cellular component movement	7	98	0.5084993	3479 insulin-like growth factor 1 (somatomedin C)
GO cellular component movement	7	98	0.5084993	4486 macrophage stimulating 1 receptor (c-met-related tyrosine kinase)
GO cellular component movement	7	98	0.5084993	7170 tropomyosin 3
GO cellular component movement	7	98	0.5084993	8875 vanin 2
GO dendrite	9	128	0.5146955	9788 metastasis suppressor 1
GO dendrite	9	128	0.5146955	154 adrenergic, beta-2-, receptor, surface
GO dendrite	9	128	0.5146955	1813 dopamine receptor D2
GO dendrite	9	128	0.5146955	240 arachidonate 5-lipoxygenase
GO dendrite	9	128	0.5146955	3759 potassium inwardly-rectifying channel, subfamily J, member 2
GO dendrite	9	128	0.5146955	4856 nephroblastoma overexpressed gene
GO dendrite	9	128	0.5146955	5122 proprotein convertase subtilisin/kexin type 1
GO dendrite	9	128	0.5146955	5873 RAB27A, member RAS oncogene family
GO dendrite	9	128	0.5146955	885 cholecystokinin
GO dendrite	9	128	0.5146955	8912 calcium channel, voltage-dependent, T type, alpha 1H subunit
GO melanosome	6	84	0.5165615	1508 cathepsin B
GO melanosome	6	84	0.5165615	2040 stomatin
GO melanosome	6	84	0.5165615	23682 RAB38, member RAS oncogene family
GO melanosome	6	84	0.5165615	311 annexin A11
GO melanosome	6	84	0.5165615	5873 RAB27A, member RAS oncogene family
GO melanosome	6	84	0.5165615	682 basigin (Ok blood group)

GO	mitochondrial intermembrane space	2	25	0.5173551	10628	thioredoxin interacting protein
GO	mitochondrial intermembrane space	2	25	0.5173551	64083	golgi phosphoprotein 3 (coat-protein)
GO	lipid biosynthetic process	2	25	0.5173551	2055	ceroid-lipofuscinosis, neuronal 8 (epilepsy, progressive with mental ret
GO	lipid biosynthetic process	2	25	0.5173551	53947	alpha 1,4-galactosyltransferase
GO	glycoprotein binding	2	25	0.5173551	26270	F-box protein 6
GO	glycoprotein binding	2	25	0.5173551	3689	integrin, beta 2 (complement component 3 receptor 3 and 4 subunit)
GO	heterotrimeric G-protein complex	2	25	0.5173551	2769	guanine nucleotide binding protein (G protein), alpha 15 (Gq class)
GO	heterotrimeric G-protein complex	2	25	0.5173551	8786	regulator of G-protein signaling 11
GO	fat cell differentiation	2	25	0.5173551	3643	insulin receptor
GO	fat cell differentiation	2	25	0.5173551	79689	STEAP family member 4
GO	osteoblast differentiation	2	25	0.5173551	3726	jun B proto-oncogene
GO	osteoblast differentiation	2	25	0.5173551	4209	myocyte enhancer factor 2D
GO	stress fiber	2	25	0.5173551	4486	macrophage stimulating 1 receptor (c-met-related tyrosine kinase)
GO	stress fiber	2	25	0.5173551	5239	phosphoglucomutase 5
GO	receptor-mediated endocytosis	3	40	0.5211403	10268	receptor (G protein-coupled) activity modifying protein 3
GO	receptor-mediated endocytosis	3	40	0.5211403	154	adrenergic, beta-2-, receptor, surface
GO	receptor-mediated endocytosis	3	40	0.5211403	6653	sortilin-related receptor, L(DLR class) A repeats-containing
GO	catalytic activity	8	114	0.5219419	157855	potassium channel, subfamily U, member 1
GO	catalytic activity	8	114	0.5219419	200150	phospholipase D family, member 5
GO	catalytic activity	8	114	0.5219419	284716	ribosomal modification protein rimK-like family member A
GO	catalytic activity	8	114	0.5219419	343450	potassium channel, subfamily T, member 2
GO	catalytic activity	8	114	0.5219419	5016	oviductal glycoprotein 1, 120kDa
GO	catalytic activity	8	114	0.5219419	57494	ribosomal modification protein rimK-like family member B
GO	catalytic activity	8	114	0.5219419	79802	HHIP-like 2
GO	catalytic activity	8	114	0.5219419	94059	leukocyte receptor cluster (LRC) member 9
GO	response to toxin	4	55	0.5238895	2353	FBJ murine osteosarcoma viral oncogene homolog
GO	response to toxin	4	55	0.5238895	4129	monoamine oxidase B
GO	response to toxin	4	55	0.5238895	7097	toll-like receptor 2
GO	response to toxin	4	55	0.5238895	7099	toll-like receptor 4
GO	cytoplasmic membrane-bounded ves	6	85	0.5283095	23048	formin binding protein 1
GO	cytoplasmic membrane-bounded ves	6	85	0.5283095	259173	ALS2 C-terminal like
GO	cytoplasmic membrane-bounded ves	6	85	0.5283095	55638	Golgi-localized protein
GO	cytoplasmic membrane-bounded ves	6	85	0.5283095	627	brain-derived neurotrophic factor
GO	cytoplasmic membrane-bounded ves	6	85	0.5283095	7852	chemokine (C-X-C motif) receptor 4
GO	cytoplasmic membrane-bounded ves	6	85	0.5283095	8527	diacylglycerol kinase, delta 130kDa
GO	voltage-gated potassium channel cor	6	85	0.5283095	27345	potassium large conductance calcium-activated channel, subfamily M,

GO voltage-gated potassium channel con	6	85	0.5283095	3773 potassium inwardly-rectifying channel, subfamily J, member 16
GO voltage-gated potassium channel con	6	85	0.5283095	3775 potassium channel, subfamily K, member 1
GO voltage-gated potassium channel con	6	85	0.5283095	3783 potassium intermediate/small conductance calcium-activated channel,
GO voltage-gated potassium channel con	6	85	0.5283095	3786 potassium voltage-gated channel, KQT-like subfamily, member 3
GO voltage-gated potassium channel con	6	85	0.5283095	3790 potassium voltage-gated channel, delayed-rectifier, subfamily S, memb
GO magnesium ion binding	11	159	0.5283259	11213 interleukin-1 receptor-associated kinase 3
GO magnesium ion binding	11	159	0.5283259	148229 ATPase, class I, type 8B, member 3
GO magnesium ion binding	11	159	0.5283259	150094 salt-inducible kinase 1
GO magnesium ion binding	11	159	0.5283259	2026 enolase 2 (gamma, neuronal)
GO magnesium ion binding	11	159	0.5283259	23387 SIK family kinase 3
GO magnesium ion binding	11	159	0.5283259	375449 microtubule associated serine/threonine kinase family member 4
GO magnesium ion binding	11	159	0.5283259	5239 phosphoglucomutase 5
GO magnesium ion binding	11	159	0.5283259	6622 synuclein, alpha (non A4 component of amyloid precursor)
GO magnesium ion binding	11	159	0.5283259	79895 ATPase, class I, type 8B, member 4
GO magnesium ion binding	11	159	0.5283259	81788 NUAKE family, SNF1-like kinase, 2
GO magnesium ion binding	11	159	0.5283259	9064 mitogen-activated protein kinase kinase kinase 6
GO negative regulation of cell cycle	3	41	0.5380605	23368 protein phosphatase 1, regulatory (inhibitor) subunit 13B
GO negative regulation of cell cycle	3	41	0.5380605	6494 signal-induced proliferation-associated 1
GO negative regulation of cell cycle	3	41	0.5380605	652 bone morphogenetic protein 4
GO protein import into nucleus	2	26	0.538725	10628 thioredoxin interacting protein
GO protein import into nucleus	2	26	0.538725	55705 importin 9
GO triglyceride metabolic process	2	26	0.538725	2182 acyl-CoA synthetase long-chain family member 4
GO triglyceride metabolic process	2	26	0.538725	255738 proprotein convertase subtilisin/kexin type 9
GO skin development	2	26	0.538725	2707 gap junction protein, beta 3, 31kDa
GO skin development	2	26	0.538725	412 steroid sulfatase (microsomal), isozyme S
GO terminal button	2	26	0.538725	5025 purinergic receptor P2X, ligand-gated ion channel, 4
GO terminal button	2	26	0.538725	885 cholecystokinin
GO embryo implantation	2	26	0.538725	682 basigin (Ok blood group)
GO embryo implantation	2	26	0.538725	687 Kruppel-like factor 9
GO lamellipodium	5	71	0.5390299	10252 sprouty homolog 1, antagonist of FGF signaling (Drosophila)
GO lamellipodium	5	71	0.5390299	152273 FYVE, RhoGEF and PH domain containing 5
GO lamellipodium	5	71	0.5390299	1803 dipeptidyl-peptidase 4
GO lamellipodium	5	71	0.5390299	55740 enabled homolog (Drosophila)
GO lamellipodium	5	71	0.5390299	57147 SCY1-like 3 (S. cerevisiae)
GO focal adhesion	6	86	0.5399386	23092 Rho GTPase activating protein 26
GO focal adhesion	6	86	0.5399386	23371 tensin like C1 domain containing phosphatase (tensin 2)

GO focal adhesion	6	86	0.5399386	3678 integrin, alpha 5 (fibronectin receptor, alpha polypeptide)
GO focal adhesion	6	86	0.5399386	5239 phosphoglucomutase 5
GO focal adhesion	6	86	0.5399386	55740 enabled homolog (Drosophila)
GO focal adhesion	6	86	0.5399386	7706 tripartite motif-containing 25
GO dipeptidyl-peptidase activity	1	11	0.5411214	1803 dipeptidyl-peptidase 4
GO motor axon guidance	1	11	0.5411214	1959 early growth response 2
GO positive regulation of axon extension	1	11	0.5411214	2033 E1A binding protein p300
GO negative regulation of JNK cascade	1	11	0.5411214	2122 MDS1 and EVI1 complex locus
GO fibroblast growth factor binding	1	11	0.5411214	2263 fibroblast growth factor receptor 2
GO DNA bending activity	1	11	0.5411214	2296 forkhead box C1
GO maternal process involved in female	1	11	0.5411214	23780 apolipoprotein L, 2
GO sodium channel activity	1	11	0.5411214	259232 sodium leak channel, non-selective
GO SCF ubiquitin ligase complex	1	11	0.5411214	26270 F-box protein 6
GO positive regulation of vascular endotl	1	11	0.5411214	3678 integrin, alpha 5 (fibronectin receptor, alpha polypeptide)
GO myelin sheath	1	11	0.5411214	3709 inositol 1,4,5-triphosphate receptor, type 2
GO trophoctodermal cell differentiation	1	11	0.5411214	3726 jun B proto-oncogene
GO delayed rectifier potassium channel α	1	11	0.5411214	3790 potassium voltage-gated channel, delayed-rectifier, subfamily S, memb
GO low-density lipoprotein receptor activ	1	11	0.5411214	3949 low density lipoprotein receptor
GO actin filament polymerization	1	11	0.5411214	395 Rho GTPase activating protein 6
GO positive regulation of epithelial to me	1	11	0.5411214	4087 SMAD family member 2
GO positive regulation of neurogenesis	1	11	0.5411214	429 achaete-scute complex homolog 1 (Drosophila)
GO methionine biosynthetic process	1	11	0.5411214	4524 5,10-methylenetetrahydrofolate reductase (NADPH)
GO gamma-tubulin binding	1	11	0.5411214	4692 necdin homolog (mouse)
GO FMN binding	1	11	0.5411214	4842 nitric oxide synthase 1 (neuronal)
GO nitric oxide biosynthetic process	1	11	0.5411214	4842 nitric oxide synthase 1 (neuronal)
GO oligodendrocyte differentiation	1	11	0.5411214	4851 Notch homolog 1, translocation-associated (Drosophila)
GO positive regulation of calcium ion tra	1	11	0.5411214	5025 purinergic receptor P2X, ligand-gated ion channel, 4
GO Ras GTPase binding	1	11	0.5411214	57139 ral guanine nucleotide dissociation stimulator-like 3
GO intermediate filament cytoskeleton	1	11	0.5411214	573 BCL2-associated athanogene
GO neuropeptide receptor activity	1	11	0.5411214	57537 sortilin-related VPS10 domain containing receptor 2
GO replication fork	1	11	0.5411214	604 B-cell CLL/lymphoma 6
GO npBAF complex	1	11	0.5411214	6604 SWI/SNF related, matrix associated, actin dependent regulator of chrom
GO cellular response to oxidative stress	1	11	0.5411214	6622 synuclein, alpha (non A4 component of amyloid precursor)
GO response to magnesium ion	1	11	0.5411214	6622 synuclein, alpha (non A4 component of amyloid precursor)
GO positive regulation of interferon-gam	1	11	0.5411214	7098 toll-like receptor 3
GO positive regulation of interferon-gam	1	11	0.5411214	7099 toll-like receptor 4

GO	initiation of viral infection	1	11	0.5411214	7852 chemokine (C-X-C motif) receptor 4
GO	positive regulation of erythrocyte dif	1	11	0.5411214	91 activin A receptor, type IB
GO	phosphatidylinositol-3,4-bisphosphat	1	11	0.5411214	91404 SEC14 and spectrin domains 1
GO	pyridine nucleotide biosynthetic proc	1	11	0.5411214	93100 nicotinate phosphoribosyltransferase domain containing 1
GO	P-P-bond-hydrolysis-driven protein tr	1	11	0.5411214	9804 translocase of outer mitochondrial membrane 20 homolog (yeast)
GO	bile acid metabolic process	1	11	0.5411214	9971 nuclear receptor subfamily 1, group H, member 4
GO	oocyte maturation	1	11	0.5411214	9985 REC8 homolog (yeast)
GO	transcription regulator activity	7	102	0.5515791	124 alcohol dehydrogenase 1A (class I), alpha polypeptide
GO	transcription regulator activity	7	102	0.5515791	23648 single stranded DNA binding protein 3
GO	transcription regulator activity	7	102	0.5515791	2624 GATA binding protein 2
GO	transcription regulator activity	7	102	0.5515791	4778 nuclear factor (erythroid-derived 2), 45kDa
GO	transcription regulator activity	7	102	0.5515791	4849 CCR4-NOT transcription complex, subunit 3
GO	transcription regulator activity	7	102	0.5515791	5371 promyelocytic leukemia
GO	transcription regulator activity	7	102	0.5515791	6604 SWI/SNF related, matrix associated, actin dependent regulator of chromatin
GO	synaptic vesicle membrane	3	42	0.5546329	143425 synaptotagmin IX
GO	synaptic vesicle membrane	3	42	0.5546329	23208 synaptotagmin XI
GO	synaptic vesicle membrane	3	42	0.5546329	6857 synaptotagmin I
GO	JAK-STAT cascade	2	27	0.5594311	23529 cardiotrophin-like cytokine factor 1
GO	JAK-STAT cascade	2	27	0.5594311	9021 suppressor of cytokine signaling 3
GO	negative regulation of Wnt receptor signaling pathway	2	27	0.5594311	27123 dickkopf homolog 2 (Xenopus laevis)
GO	negative regulation of Wnt receptor signaling pathway	2	27	0.5594311	8313 axin 2
GO	phagocytosis	2	27	0.5594311	311 annexin A11
GO	phagocytosis	2	27	0.5594311	929 CD14 molecule
GO	cell aging	2	27	0.5594311	3845 v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog
GO	cell aging	2	27	0.5594311	5371 promyelocytic leukemia
GO	meiosis	4	58	0.5665303	143689 piwi-like 4 (Drosophila)
GO	meiosis	4	58	0.5665303	55124 piwi-like 2 (Drosophila)
GO	meiosis	4	58	0.5665303	9271 piwi-like 1 (Drosophila)
GO	meiosis	4	58	0.5665303	9985 REC8 homolog (yeast)
GO	structural constituent of muscle	3	43	0.5708446	27295 PDZ and LIM domain 3
GO	structural constituent of muscle	3	43	0.5708446	84033 obscurin, cytoskeletal calmodulin and titin-interacting RhoGEF
GO	structural constituent of muscle	3	43	0.5708446	8736 myomesin 1, 185kDa
GO	ligand-dependent nuclear receptor binding activity	1	12	0.5725031	10891 peroxisome proliferator-activated receptor gamma, coactivator 1 alpha
GO	lysophospholipase activity	1	12	0.5725031	11343 monoglyceride lipase
GO	response to chemical stimulus	1	12	0.5725031	1139 cholinergic receptor, nicotinic, alpha 7
GO	endothelial cell migration	1	12	0.5725031	1803 dipeptidyl-peptidase 4

GO	release of sequestered calcium ion in	1	12	0.5725031	1813	dopamine receptor D2
GO	ephrin receptor activity	1	12	0.5725031	1969	EPH receptor A2
GO	acetyltransferase activity	1	12	0.5725031	2033	E1A binding protein p300
GO	arylsulfatase activity	1	12	0.5725031	22901	arylsulfatase G
GO	glutamate receptor activity	1	12	0.5725031	2911	glutamate receptor, metabotropic 1
GO	estradiol 17-beta-dehydrogenase act	1	12	0.5725031	3294	hydroxysteroid (17-beta) dehydrogenase 2
GO	male meiosis	1	12	0.5725031	3306	heat shock 70kDa protein 2
GO	positive regulation of peptidyl-serine	1	12	0.5725031	3569	interleukin 6 (interferon, beta 2)
GO	cGMP biosynthetic process	1	12	0.5725031	358	aquaporin 1 (Colton blood group)
GO	activation of protein kinase activity	1	12	0.5725031	3643	insulin receptor
GO	platelet-derived growth factor recept	1	12	0.5725031	3678	integrin, alpha 5 (fibronectin receptor, alpha polypeptide)
GO	smooth muscle contraction	1	12	0.5725031	3827	kininogen 1
GO	endochondral ossification	1	12	0.5725031	4209	myocyte enhancer factor 2D
GO	hydrolase activity, acting on carbon-r	1	12	0.5725031	4817	nitrilase 1
GO	mitochondrial ATP synthesis coupled	1	12	0.5725031	498	ATP synthase, H <sup>+</sup> transporting, mitochondrial F1 complex, alpha subun
GO	triglyceride homeostasis	1	12	0.5725031	51085	MLX interacting protein-like
GO	axon terminus	1	12	0.5725031	5122	proprotein convertase subtilisin/kexin type 1
GO	costamere	1	12	0.5725031	5239	phosphoglucomutase 5
GO	histone methylation	1	12	0.5725031	54904	Wolf-Hirschhorn syndrome candidate 1-like 1
GO	iron-sulfur cluster binding	1	12	0.5725031	55140	elongation protein 3 homolog ( <i>S. cerevisiae</i> )
GO	calcium channel regulator activity	1	12	0.5725031	57620	stromal interaction molecule 2
GO	positive regulation of cellular compo	1	12	0.5725031	604	B-cell CLL/lymphoma 6
GO	voltage-gated sodium channel compl	1	12	0.5725031	6330	sodium channel, voltage-gated, type IV, beta
GO	positive regulation of innate immune	1	12	0.5725031	64127	nucleotide-binding oligomerization domain containing 2
GO	dorsal/ventral neural tube patterning	1	12	0.5725031	652	bone morphogenetic protein 4
GO	nBAF complex	1	12	0.5725031	6604	SWI/SNF related, matrix associated, actin dependent regulator of chrom
GO	alpha-tubulin binding	1	12	0.5725031	6622	synuclein, alpha (non A4 component of amyloid precursor)
GO	ferrous iron binding	1	12	0.5725031	6622	synuclein, alpha (non A4 component of amyloid precursor)
GO	glutamate signaling pathway	1	12	0.5725031	6751	somatostatin receptor 1
GO	T cell receptor complex	1	12	0.5725031	6850	spleen tyrosine kinase
GO	negative regulation of cyclin-depend	1	12	0.5725031	7026	nuclear receptor subfamily 2, group F, member 2
GO	regulation of muscle contraction	1	12	0.5725031	7170	tropomyosin 3
GO	NLS-bearing substrate import into nu	1	12	0.5725031	7227	trichorhinophalangeal syndrome I
GO	mammary gland alveolus developme	1	12	0.5725031	8600	tumor necrosis factor (ligand) superfamily, member 11
GO	regulation of lipid metabolic process	1	12	0.5725031	8660	insulin receptor substrate 2
GO	cholesterol transporter activity	1	12	0.5725031	9619	ATP-binding cassette, sub-family G (WHITE), member 1



GO protein oligomerization	2	28	0.579464	10439 olfactomedin 1
GO protein oligomerization	2	28	0.579464	64127 nucleotide-binding oligomerization domain containing 2
GO activation of phospholipase C activity	2	28	0.579464	183 angiotensinogen (serpin peptidase inhibitor, clade A, member 8)
GO activation of phospholipase C activity	2	28	0.579464	56923 neuromedin U receptor 2
GO negative regulation of transforming g	2	28	0.579464	2122 MDS1 and EVI1 complex locus
GO negative regulation of transforming g	2	28	0.579464	3175 one cut homeobox 1
GO small GTPase regulator activity	2	28	0.579464	23043 TRAF2 and NCK interacting kinase
GO small GTPase regulator activity	2	28	0.579464	5900 ral guanine nucleotide dissociation stimulator
GO antigen processing and presentation	2	28	0.579464	3134 major histocompatibility complex, class I, F
GO antigen processing and presentation	2	28	0.579464	5698 proteasome (prosome, macropain) subunit, beta type, 9 (large multifur
GO regulation of cell migration	2	28	0.579464	3911 laminin, alpha 5
GO regulation of cell migration	2	28	0.579464	6750 somatostatin
GO ruffle membrane	2	29	0.5988191	3678 integrin, alpha 5 (fibronectin receptor, alpha polypeptide)
GO ruffle membrane	2	29	0.5988191	5152 phosphodiesterase 9A
GO chaperone binding	2	29	0.5988191	5071 Parkinson disease (autosomal recessive, juvenile) 2, parkin
GO chaperone binding	2	29	0.5988191	5122 proprotein convertase subtilisin/kexin type 1
GO cyclin-dependent protein kinase activ	2	29	0.5988191	5129 cyclin-dependent kinase 18
GO cyclin-dependent protein kinase activ	2	29	0.5988191	5218 cyclin-dependent kinase 14
GO phosphate binding	1	13	0.6017402	10568 solute carrier family 34 (sodium phosphate), member 2
GO cAMP biosynthetic process	1	13	0.6017402	112 adenylate cyclase 6
GO folic acid binding	1	13	0.6017402	113235 solute carrier family 46 (folate transporter), member 1
GO cell wall macromolecule catabolic pro	1	13	0.6017402	135112 nuclear receptor coactivator 7
GO regulation of cell differentiation	1	13	0.6017402	150094 salt-inducible kinase 1
GO bone resorption	1	13	0.6017402	154 adrenergic, beta-2-, receptor, surface
GO steroid hormone receptor signaling p	1	13	0.6017402	158800 RhoX homeobox family, member 1
GO epidermal growth factor receptor bin	1	13	0.6017402	1839 heparin-binding EGF-like growth factor
GO positive regulation of hormone secre	1	13	0.6017402	1906 endothelin 1
GO endosome organization	1	13	0.6017402	259173 ALS2 C-terminal like
GO receptor signaling complex scaffold a	1	13	0.6017402	26119 low density lipoprotein receptor adaptor protein 1
GO fibroblast growth factor receptor bin	1	13	0.6017402	26281 fibroblast growth factor 20
GO superoxide anion generation	1	13	0.6017402	27035 NADPH oxidase 1
GO serotonin receptor activity	1	13	0.6017402	3355 5-hydroxytryptamine (serotonin) receptor 1F
GO glial cell differentiation	1	13	0.6017402	3479 insulin-like growth factor 1 (somatomedin C)
GO myoblast differentiation	1	13	0.6017402	3479 insulin-like growth factor 1 (somatomedin C)
GO extracellular matrix binding	1	13	0.6017402	3491 cysteine-rich, angiogenic inducer, 61
GO oligodendrocyte development	1	13	0.6017402	429 achaete-scute complex homolog 1 (Drosophila)

GO hydrogen ion transporting ATP synthase	1	13	0.6017402	498 ATP synthase, H <sup>+</sup> transporting, mitochondrial F1 complex, alpha subunit
GO protein autoubiquitination	1	13	0.6017402	5071 Parkinson disease (autosomal recessive, juvenile) 2, parkin
GO retrograde transport, endosome to Golgi	1	13	0.6017402	51272 blocked early in transport 1 homolog ( <i>S. cerevisiae</i> )-like
GO transcription elongation factor complex	1	13	0.6017402	55140 elongation protein 3 homolog ( <i>S. cerevisiae</i> )
GO regulation of protein kinase activity	1	13	0.6017402	5577 protein kinase, cAMP-dependent, regulatory, type II, beta
GO organic anion transport	1	13	0.6017402	55867 solute carrier family 22 (organic anion/urate transporter), member 11
GO regulation of smooth muscle contraction	1	13	0.6017402	56923 neuromedin U receptor 2
GO hippo signaling pathway	1	13	0.6017402	60485 salvador homolog 1 ( <i>Drosophila</i> )
GO negative regulation of phosphorylation	1	13	0.6017402	652 bone morphogenetic protein 4
GO low-density lipoprotein binding	1	13	0.6017402	6653 sortilin-related receptor, L(DLR class) A repeats-containing
GO myosin binding	1	13	0.6017402	84059 G protein-coupled receptor 98
GO lipid homeostasis	1	13	0.6017402	8660 insulin receptor substrate 2
GO T cell homeostasis	1	13	0.6017402	8740 tumor necrosis factor (ligand) superfamily, member 14
GO response to bacterium	1	13	0.6017402	9021 suppressor of cytokine signaling 3
GO high-density lipoprotein particle removal	1	13	0.6017402	9619 ATP-binding cassette, sub-family G (WHITE), member 1
GO DNA-directed RNA polymerase II, core	1	14	0.6289792	10891 peroxisome proliferator-activated receptor gamma, coactivator 1 alpha
GO senescence	1	14	0.6289792	11200 CHK2 checkpoint homolog ( <i>S. pombe</i> )
GO dynein complex	1	14	0.6289792	144132 dynein heavy chain domain 1
GO nuclear heterochromatin	1	14	0.6289792	2296 forkhead box C1
GO DNA methylation	1	14	0.6289792	2353 FBJ murine osteosarcoma viral oncogene homolog
GO cellular response to starvation	1	14	0.6289792	255738 proprotein convertase subtilisin/kexin type 9
GO membrane protein ectodomain proteolysis	1	14	0.6289792	25825 beta-site APP-cleaving enzyme 2
GO regulation of action potential	1	14	0.6289792	27345 potassium large conductance calcium-activated channel, subfamily M,
GO anatomical structure formation involving	1	14	0.6289792	2737 GLI family zinc finger 3
GO positive regulation of transforming growth factor	1	14	0.6289792	28996 homeodomain interacting protein kinase 2
GO regulation of transforming growth factor	1	14	0.6289792	4087 SMAD family member 2
GO phosphoinositide phosphorylation	1	14	0.6289792	5295 phosphoinositide-3-kinase, regulatory subunit 1 (alpha)
GO 3'-5' exonuclease activity	1	14	0.6289792	54932 exonuclease 3'-5' domain containing 3
GO cytokine production	1	14	0.6289792	5724 platelet-activating factor receptor
GO microtubule-based flagellum	1	14	0.6289792	64064 3-oxoacid CoA transferase 2
GO response to interferon-gamma	1	14	0.6289792	6622 synuclein, alpha (non A4 component of amyloid precursor)
GO tropomyosin binding	1	14	0.6289792	7111 tropomodulin 1
GO filamentous actin	1	14	0.6289792	7170 tropomyosin 3
GO voltage-gated potassium channel activity	3	63	0.989	10008 potassium voltage-gated channel, Isk-related family, member 3
GO voltage-gated potassium channel activity	3	63	0.989	3786 potassium voltage-gated channel, KQT-like subfamily, member 3
GO voltage-gated potassium channel activity	3	63	0.989	8514 potassium voltage-gated channel, shaker-related subfamily, beta member

GO chromatin modification	11	204	0.989	10014 histone deacetylase 5
GO chromatin modification	11	204	0.989	151636 deltex 3-like (Drosophila)
GO chromatin modification	11	204	0.989	23081 lysine (K)-specific demethylase 4C
GO chromatin modification	11	204	0.989	23492 chromobox homolog 7
GO chromatin modification	11	204	0.989	23774 bromodomain containing 1
GO chromatin modification	11	204	0.989	54904 Wolf-Hirschhorn syndrome candidate 1-like 1
GO chromatin modification	11	204	0.989	55693 lysine (K)-specific demethylase 4D
GO chromatin modification	11	204	0.989	55870 ash1 (absent, small, or homeotic)-like (Drosophila)
GO chromatin modification	11	204	0.989	6604 SWI/SNF related, matrix associated, actin dependent regulator of chromatin
GO chromatin modification	11	204	0.989	7404 ubiquitously transcribed tetratricopeptide repeat gene, Y-linked
GO chromatin modification	11	204	0.989	9734 histone deacetylase 9
GO chromatin organization	1	19	0.989	10014 histone deacetylase 5
GO chromatin remodeling	2	46	0.989	10014 histone deacetylase 5
GO chromatin remodeling	2	46	0.989	3169 forkhead box A1
GO cytoplasm	293	4355	0.989	10014 histone deacetylase 5
GO cytoplasm	293	4355	0.989	10023 frequently rearranged in advanced T-cell lymphomas
GO cytoplasm	293	4355	0.989	1009 cadherin 11, type 2, OB-cadherin (osteoblast)
GO cytoplasm	293	4355	0.989	10116 fem-1 homolog b (C. elegans)
GO cytoplasm	293	4355	0.989	10156 RAS p21 protein activator 4
GO cytoplasm	293	4355	0.989	10221 tribbles homolog 1 (Drosophila)
GO cytoplasm	293	4355	0.989	10252 sprouty homolog 1, antagonist of FGF signaling (Drosophila)
GO cytoplasm	293	4355	0.989	10253 sprouty homolog 2 (Drosophila)
GO cytoplasm	293	4355	0.989	10335 murine retrovirus integration site 1 homolog
GO cytoplasm	293	4355	0.989	10346 tripartite motif-containing 22
GO cytoplasm	293	4355	0.989	10397 N-myc downstream regulated 1
GO cytoplasm	293	4355	0.989	10435 CDC42 effector protein (Rho GTPase binding) 2
GO cytoplasm	293	4355	0.989	10561 interferon-induced protein 44
GO cytoplasm	293	4355	0.989	10628 thioredoxin interacting protein
GO cytoplasm	293	4355	0.989	10766 transducer of ERBB2, 2
GO cytoplasm	293	4355	0.989	1080 cystic fibrosis transmembrane conductance regulator (ATP-binding cassette)
GO cytoplasm	293	4355	0.989	10811 NADPH oxidase activator 1
GO cytoplasm	293	4355	0.989	10942 protease, serine, 21 (testisin)
GO cytoplasm	293	4355	0.989	10964 interferon-induced protein 44-like
GO cytoplasm	293	4355	0.989	11030 RNA binding protein with multiple splicing
GO cytoplasm	293	4355	0.989	11043 midline 2
GO cytoplasm	293	4355	0.989	11074 tripartite motif-containing 31

GO cytoplasm	293	4355	0.989	11078 TRIO and F-actin binding protein
GO cytoplasm	293	4355	0.989	11155 LIM domain binding 3
GO cytoplasm	293	4355	0.989	11213 interleukin-1 receptor-associated kinase 3
GO cytoplasm	293	4355	0.989	113235 solute carrier family 46 (folate transporter), member 1
GO cytoplasm	293	4355	0.989	113263 glucocorticoid induced transcript 1
GO cytoplasm	293	4355	0.989	114569 mal, T-cell differentiation protein 2
GO cytoplasm	293	4355	0.989	1152 creatine kinase, brain
GO cytoplasm	293	4355	0.989	115265 DNA-damage-inducible transcript 4-like
GO cytoplasm	293	4355	0.989	116113 forkhead box P4
GO cytoplasm	293	4355	0.989	116984 ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 2
GO cytoplasm	293	4355	0.989	1193 chloride intracellular channel 2
GO cytoplasm	293	4355	0.989	123 perilipin 2
GO cytoplasm	293	4355	0.989	124 alcohol dehydrogenase 1A (class I), alpha polypeptide
GO cytoplasm	293	4355	0.989	125 alcohol dehydrogenase 1B (class I), beta polypeptide
GO cytoplasm	293	4355	0.989	127933 U2AF homology motif (UHM) kinase 1
GO cytoplasm	293	4355	0.989	134549 shroom family member 1
GO cytoplasm	293	4355	0.989	1373 carbamoyl-phosphate synthetase 1, mitochondrial
GO cytoplasm	293	4355	0.989	1382 cellular retinoic acid binding protein 2
GO cytoplasm	293	4355	0.989	140901 serine/threonine kinase 35
GO cytoplasm	293	4355	0.989	143689 piwi-like 4 (Drosophila)
GO cytoplasm	293	4355	0.989	148170 CDC42 effector protein (Rho GTPase binding) 5
GO cytoplasm	293	4355	0.989	150094 salt-inducible kinase 1
GO cytoplasm	293	4355	0.989	1508 cathepsin B
GO cytoplasm	293	4355	0.989	151636 deltex 3-like (Drosophila)
GO cytoplasm	293	4355	0.989	152273 FYVE, RhoGEF and PH domain containing 5
GO cytoplasm	293	4355	0.989	1540 cylindromatosis (turban tumor syndrome)
GO cytoplasm	293	4355	0.989	154043 CNKSR family member 3
GO cytoplasm	293	4355	0.989	154810 angiominin like 1
GO cytoplasm	293	4355	0.989	157506 retinol dehydrogenase 10 (all-trans)
GO cytoplasm	293	4355	0.989	157638 family with sequence similarity 84, member B
GO cytoplasm	293	4355	0.989	1612 death-associated protein kinase 1
GO cytoplasm	293	4355	0.989	1755 deleted in malignant brain tumors 1
GO cytoplasm	293	4355	0.989	1785 dynamin 2
GO cytoplasm	293	4355	0.989	1820 AT rich interactive domain 3A (BRIGHT-like)
GO cytoplasm	293	4355	0.989	1821 dystrophin related protein 2
GO cytoplasm	293	4355	0.989	1822 atrophin 1

GO cytoplasm	293	4355	0.989	1906 endothelin 1
GO cytoplasm	293	4355	0.989	1915 eukaryotic translation elongation factor 1 alpha 1
GO cytoplasm	293	4355	0.989	1958 early growth response 1
GO cytoplasm	293	4355	0.989	196383 Rab interacting lysosomal protein-like 2
GO cytoplasm	293	4355	0.989	1983 eukaryotic translation initiation factor 5
GO cytoplasm	293	4355	0.989	1999 E74-like factor 3 (ets domain transcription factor, epithelial-specific )
GO cytoplasm	293	4355	0.989	2026 enolase 2 (gamma, neuronal)
GO cytoplasm	293	4355	0.989	2033 E1A binding protein p300
GO cytoplasm	293	4355	0.989	2039 erythrocyte membrane protein band 4.9 (dematin)
GO cytoplasm	293	4355	0.989	2066 v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian)
GO cytoplasm	293	4355	0.989	2263 fibroblast growth factor receptor 2
GO cytoplasm	293	4355	0.989	22906 trafficking protein, kinesin binding 1
GO cytoplasm	293	4355	0.989	23035 PH domain and leucine rich repeat protein phosphatase 2
GO cytoplasm	293	4355	0.989	23043 TRAF2 and NCK interacting kinase
GO cytoplasm	293	4355	0.989	23048 formin binding protein 1
GO cytoplasm	293	4355	0.989	23092 Rho GTPase activating protein 26
GO cytoplasm	293	4355	0.989	23095 kinesin family member 1B
GO cytoplasm	293	4355	0.989	23263 MCF.2 cell line derived transforming sequence-like
GO cytoplasm	293	4355	0.989	23303 kinesin family member 13B
GO cytoplasm	293	4355	0.989	23365 Rho guanine nucleotide exchange factor (GEF) 12
GO cytoplasm	293	4355	0.989	23368 protein phosphatase 1, regulatory (inhibitor) subunit 13B
GO cytoplasm	293	4355	0.989	23373 CREB regulated transcription coactivator 1
GO cytoplasm	293	4355	0.989	23387 SIK family kinase 3
GO cytoplasm	293	4355	0.989	23476 bromodomain containing 4
GO cytoplasm	293	4355	0.989	23604 death-associated protein kinase 2
GO cytoplasm	293	4355	0.989	23650 tripartite motif-containing 29
GO cytoplasm	293	4355	0.989	23780 apolipoprotein L, 2
GO cytoplasm	293	4355	0.989	240 arachidonate 5-lipoxygenase
GO cytoplasm	293	4355	0.989	2517 fucosidase, alpha-L- 1, tissue
GO cytoplasm	293	4355	0.989	257019 FERM domain containing 3
GO cytoplasm	293	4355	0.989	2571 glutamate decarboxylase 1 (brain, 67kDa)
GO cytoplasm	293	4355	0.989	259173 ALS2 C-terminal like
GO cytoplasm	293	4355	0.989	25946 zinc finger protein 385A
GO cytoplasm	293	4355	0.989	25956 SEC31 homolog B (S. cerevisiae)
GO cytoplasm	293	4355	0.989	26119 low density lipoprotein receptor adaptor protein 1
GO cytoplasm	293	4355	0.989	26191 protein tyrosine phosphatase, non-receptor type 22 (lymphoid)

GO cytoplasm	293	4355	0.989	26270 F-box protein 6
GO cytoplasm	293	4355	0.989	27035 NADPH oxidase 1
GO cytoplasm	293	4355	0.989	27295 PDZ and LIM domain 3
GO cytoplasm	293	4355	0.989	2737 GLI family zinc finger 3
GO cytoplasm	293	4355	0.989	2752 glutamate-ammonia ligase (glutamine synthetase)
GO cytoplasm	293	4355	0.989	28951 tribbles homolog 2 (Drosophila)
GO cytoplasm	293	4355	0.989	28996 homeodomain interacting protein kinase 2
GO cytoplasm	293	4355	0.989	29108 PYD and CARD domain containing
GO cytoplasm	293	4355	0.989	29116 myosin regulatory light chain interacting protein
GO cytoplasm	293	4355	0.989	2947 glutathione S-transferase mu 3 (brain)
GO cytoplasm	293	4355	0.989	29760 B-cell linker
GO cytoplasm	293	4355	0.989	29943 peptidyl arginine deiminase, type I
GO cytoplasm	293	4355	0.989	3034 histidine ammonia-lyase
GO cytoplasm	293	4355	0.989	311 annexin A11
GO cytoplasm	293	4355	0.989	3142 H2.0-like homeobox
GO cytoplasm	293	4355	0.989	316 aldehyde oxidase 1
GO cytoplasm	293	4355	0.989	3192 heterogeneous nuclear ribonucleoprotein U (scaffold attachment facto
GO cytoplasm	293	4355	0.989	3428 interferon, gamma-inducible protein 16
GO cytoplasm	293	4355	0.989	345895 radial spoke head 4 homolog A (Chlamydomonas)
GO cytoplasm	293	4355	0.989	358 aquaporin 1 (Colton blood group)
GO cytoplasm	293	4355	0.989	3587 interleukin 10 receptor, alpha
GO cytoplasm	293	4355	0.989	3665 interferon regulatory factor 7
GO cytoplasm	293	4355	0.989	3709 inositol 1,4,5-triphosphate receptor, type 2
GO cytoplasm	293	4355	0.989	375449 microtubule associated serine/threonine kinase family member 4
GO cytoplasm	293	4355	0.989	3775 potassium channel, subfamily K, member 1
GO cytoplasm	293	4355	0.989	3790 potassium voltage-gated channel, delayed-rectifier, subfamily S, memb
GO cytoplasm	293	4355	0.989	3815 v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog
GO cytoplasm	293	4355	0.989	388743 calpain 8
GO cytoplasm	293	4355	0.989	389337 Rho guanine nucleotide exchange factor (GEF) 37
GO cytoplasm	293	4355	0.989	395 Rho GTPase activating protein 6
GO cytoplasm	293	4355	0.989	3958 lectin, galactoside-binding, soluble, 3
GO cytoplasm	293	4355	0.989	3983 actin binding LIM protein 1
GO cytoplasm	293	4355	0.989	3993 lethal giant larvae homolog 2 (Drosophila)
GO cytoplasm	293	4355	0.989	4008 LIM domain 7
GO cytoplasm	293	4355	0.989	4087 SMAD family member 2
GO cytoplasm	293	4355	0.989	4163 mutated in colorectal cancers

GO cytoplasm	293	4355	0.989	4170 myeloid cell leukemia sequence 1 (BCL2-related)
GO cytoplasm	293	4355	0.989	4209 myocyte enhancer factor 2D
GO cytoplasm	293	4355	0.989	4212 Meis homeobox 2
GO cytoplasm	293	4355	0.989	4223 mesenchyme homeobox 2
GO cytoplasm	293	4355	0.989	4254 KIT ligand
GO cytoplasm	293	4355	0.989	4306 nuclear receptor subfamily 3, group C, member 2
GO cytoplasm	293	4355	0.989	4582 mucin 1, cell surface associated
GO cytoplasm	293	4355	0.989	4599 myxovirus (influenza virus) resistance 1, interferon-inducible protein p.
GO cytoplasm	293	4355	0.989	4600 myxovirus (influenza virus) resistance 2 (mouse)
GO cytoplasm	293	4355	0.989	4692 necdin homolog (mouse)
GO cytoplasm	293	4355	0.989	4778 nuclear factor (erythroid-derived 2), 45kDa
GO cytoplasm	293	4355	0.989	4791 nuclear factor of kappa light polypeptide gene enhancer in B-cells 2 (p4
GO cytoplasm	293	4355	0.989	4792 nuclear factor of kappa light polypeptide gene enhancer in B-cells inhib
GO cytoplasm	293	4355	0.989	4794 nuclear factor of kappa light polypeptide gene enhancer in B-cells inhib
GO cytoplasm	293	4355	0.989	48 aconitase 1, soluble
GO cytoplasm	293	4355	0.989	4817 nitrilase 1
GO cytoplasm	293	4355	0.989	4842 nitric oxide synthase 1 (neuronal)
GO cytoplasm	293	4355	0.989	4849 CCR4-NOT transcription complex, subunit 3
GO cytoplasm	293	4355	0.989	4851 Notch homolog 1, translocation-associated (Drosophila)
GO cytoplasm	293	4355	0.989	4889 neuropeptide Y receptor Y5
GO cytoplasm	293	4355	0.989	4929 nuclear receptor subfamily 4, group A, member 2
GO cytoplasm	293	4355	0.989	5071 Parkinson disease (autosomal recessive, juvenile) 2, parkin
GO cytoplasm	293	4355	0.989	50865 heme binding protein 1
GO cytoplasm	293	4355	0.989	51085 MLX interacting protein-like
GO cytoplasm	293	4355	0.989	51168 myosin XVA
GO cytoplasm	293	4355	0.989	51228 glycolipid transfer protein
GO cytoplasm	293	4355	0.989	51314 thioredoxin domain containing 3 (spermatozoa)
GO cytoplasm	293	4355	0.989	5132 phosducin
GO cytoplasm	293	4355	0.989	5152 phosphodiesterase 9A
GO cytoplasm	293	4355	0.989	51523 CXXC finger 5
GO cytoplasm	293	4355	0.989	51655 RAS, dexamethasone-induced 1
GO cytoplasm	293	4355	0.989	51710 zinc finger protein 44
GO cytoplasm	293	4355	0.989	51754 transmembrane protein 8B
GO cytoplasm	293	4355	0.989	5187 period homolog 1 (Drosophila)
GO cytoplasm	293	4355	0.989	5218 cyclin-dependent kinase 14
GO cytoplasm	293	4355	0.989	5239 phosphoglucomutase 5

GO cytoplasm	293	4355	0.989	5327 plasminogen activator, tissue
GO cytoplasm	293	4355	0.989	53347 ubiquitin associated and SH3 domain containing, A
GO cytoplasm	293	4355	0.989	53405 chloride intracellular channel 5
GO cytoplasm	293	4355	0.989	5371 promyelocytic leukemia
GO cytoplasm	293	4355	0.989	5460 POU class 5 homeobox 1
GO cytoplasm	293	4355	0.989	54739 XIAP associated factor 1
GO cytoplasm	293	4355	0.989	54877 zinc finger, CCHC domain containing 2
GO cytoplasm	293	4355	0.989	54961 slingshot homolog 3 (Drosophila)
GO cytoplasm	293	4355	0.989	55124 piwi-like 2 (Drosophila)
GO cytoplasm	293	4355	0.989	55140 elongation protein 3 homolog ( <i>S. cerevisiae</i> )
GO cytoplasm	293	4355	0.989	55160 Rho guanine nucleotide exchange factor (GEF) 10-like
GO cytoplasm	293	4355	0.989	55200 pleckstrin homology domain containing, family G (with RhoGef domain
GO cytoplasm	293	4355	0.989	55249 YY1 associated protein 1
GO cytoplasm	293	4355	0.989	55616 ArfGAP with SH3 domain, ankyrin repeat and PH domain 3
GO cytoplasm	293	4355	0.989	55638 Golgi-localized protein
GO cytoplasm	293	4355	0.989	55705 importin 9
GO cytoplasm	293	4355	0.989	55740 enabled homolog (Drosophila)
GO cytoplasm	293	4355	0.989	5577 protein kinase, cAMP-dependent, regulatory, type II, beta
GO cytoplasm	293	4355	0.989	55893 zinc finger protein 395
GO cytoplasm	293	4355	0.989	55909 bridging integrator 3
GO cytoplasm	293	4355	0.989	56271 brain expressed, X-linked 4
GO cytoplasm	293	4355	0.989	56288 par-3 partitioning defective 3 homolog ( <i>C. elegans</i> )
GO cytoplasm	293	4355	0.989	5696 proteasome (prosome, macropain) subunit, beta type, 8 (large multifur
GO cytoplasm	293	4355	0.989	5698 proteasome (prosome, macropain) subunit, beta type, 9 (large multifur
GO cytoplasm	293	4355	0.989	5699 proteasome (prosome, macropain) subunit, beta type, 10
GO cytoplasm	293	4355	0.989	57118 calcium/calmodulin-dependent protein kinase ID
GO cytoplasm	293	4355	0.989	57132 chromatin modifying protein 1B
GO cytoplasm	293	4355	0.989	57147 SCY1-like 3 ( <i>S. cerevisiae</i> )
GO cytoplasm	293	4355	0.989	57186 Ral GTPase activating protein, alpha subunit 2 (catalytic)
GO cytoplasm	293	4355	0.989	57214 KIAA1199
GO cytoplasm	293	4355	0.989	573 BCL2-associated athanogene
GO cytoplasm	293	4355	0.989	57379 activation-induced cytidine deaminase
GO cytoplasm	293	4355	0.989	5742 prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase a
GO cytoplasm	293	4355	0.989	57524 CASK interacting protein 1
GO cytoplasm	293	4355	0.989	57619 shroom family member 3
GO cytoplasm	293	4355	0.989	5774 protein tyrosine phosphatase, non-receptor type 3



GO cytoplasm	293	4355	0.989	5791 protein tyrosine phosphatase, receptor type, E
GO cytoplasm	293	4355	0.989	5794 protein tyrosine phosphatase, receptor type, H
GO cytoplasm	293	4355	0.989	5801 protein tyrosine phosphatase, receptor type, R
GO cytoplasm	293	4355	0.989	60485 salvador homolog 1 (Drosophila)
GO cytoplasm	293	4355	0.989	6239 ras responsive element binding protein 1
GO cytoplasm	293	4355	0.989	64083 golgi phosphoprotein 3 (coat-protein)
GO cytoplasm	293	4355	0.989	64108 receptor (chemosensory) transporter protein 4
GO cytoplasm	293	4355	0.989	64127 nucleotide-binding oligomerization domain containing 2
GO cytoplasm	293	4355	0.989	64135 interferon induced with helicase C domain 1
GO cytoplasm	293	4355	0.989	642273 family with sequence similarity 110, member C
GO cytoplasm	293	4355	0.989	64359 nucleoredoxin
GO cytoplasm	293	4355	0.989	6446 serum/glucocorticoid regulated kinase 1
GO cytoplasm	293	4355	0.989	6494 signal-induced proliferation-associated 1
GO cytoplasm	293	4355	0.989	652 bone morphogenetic protein 4
GO cytoplasm	293	4355	0.989	6622 synuclein, alpha (non A4 component of amyloid precursor)
GO cytoplasm	293	4355	0.989	6706 small proline-rich protein 2G
GO cytoplasm	293	4355	0.989	6710 spectrin, beta, erythrocytic
GO cytoplasm	293	4355	0.989	6778 signal transducer and activator of transcription 6, interleukin-4 inducible
GO cytoplasm	293	4355	0.989	6812 syntaxin binding protein 1
GO cytoplasm	293	4355	0.989	6819 sulfotransferase family, cytosolic, 1C, member 2
GO cytoplasm	293	4355	0.989	6850 spleen tyrosine kinase
GO cytoplasm	293	4355	0.989	6857 synaptotagmin I
GO cytoplasm	293	4355	0.989	7001 peroxiredoxin 2
GO cytoplasm	293	4355	0.989	7097 toll-like receptor 2
GO cytoplasm	293	4355	0.989	7098 toll-like receptor 3
GO cytoplasm	293	4355	0.989	7099 toll-like receptor 4
GO cytoplasm	293	4355	0.989	7111 tropomodulin 1
GO cytoplasm	293	4355	0.989	7170 tropomyosin 3
GO cytoplasm	293	4355	0.989	7474 wingless-type MMTV integration site family, member 5A
GO cytoplasm	293	4355	0.989	7538 zinc finger protein 36, C3H type, homolog (mouse)
GO cytoplasm	293	4355	0.989	7597 zinc finger and BTB domain containing 25
GO cytoplasm	293	4355	0.989	760 carbonic anhydrase II
GO cytoplasm	293	4355	0.989	7706 tripartite motif-containing 25
GO cytoplasm	293	4355	0.989	7852 chemokine (C-X-C motif) receptor 4
GO cytoplasm	293	4355	0.989	79092 caspase recruitment domain family, member 14
GO cytoplasm	293	4355	0.989	79098 chromosome 1 open reading frame 116

GO cytoplasm	293	4355	0.989	79132 DEXH (Asp-Glu-X-His) box polypeptide 58
GO cytoplasm	293	4355	0.989	79444 baculoviral IAP repeat-containing 7
GO cytoplasm	293	4355	0.989	79661 nei endonuclease VIII-like 1 (E. coli)
GO cytoplasm	293	4355	0.989	79789 calmin (calponin-like, transmembrane)
GO cytoplasm	293	4355	0.989	79816 transducin-like enhancer of split 6 (E(sp1) homolog, Drosophila)
GO cytoplasm	293	4355	0.989	79987 sushi, von Willebrand factor type A, EGF and pentraxin domain contain
GO cytoplasm	293	4355	0.989	80830 apolipoprotein L, 6
GO cytoplasm	293	4355	0.989	80833 apolipoprotein L, 3
GO cytoplasm	293	4355	0.989	81544 glycerophosphodiester phosphodiesterase domain containing 5
GO cytoplasm	293	4355	0.989	8313 axin 2
GO cytoplasm	293	4355	0.989	834 caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, co
GO cytoplasm	293	4355	0.989	83593 Ras association (RalGDS/AF-6) domain family member 5
GO cytoplasm	293	4355	0.989	83595 SRY (sex determining region Y)-box 7
GO cytoplasm	293	4355	0.989	83666 poly (ADP-ribose) polymerase family, member 9
GO cytoplasm	293	4355	0.989	84033 obscurin, cytoskeletal calmodulin and titin-interacting RhoGEF
GO cytoplasm	293	4355	0.989	84059 G protein-coupled receptor 98
GO cytoplasm	293	4355	0.989	8418 cytidine monophosphate-N-acetylneuraminic acid hydroxylase (CMP-N
GO cytoplasm	293	4355	0.989	84875 poly (ADP-ribose) polymerase family, member 10
GO cytoplasm	293	4355	0.989	84941 hematopoietic SH2 domain containing
GO cytoplasm	293	4355	0.989	85004 RAS-like, estrogen-regulated, growth inhibitor
GO cytoplasm	293	4355	0.989	8514 potassium voltage-gated channel, shaker-related subfamily, beta mem
GO cytoplasm	293	4355	0.989	8527 diacylglycerol kinase, delta 130kDa
GO cytoplasm	293	4355	0.989	8531 cold shock domain protein A
GO cytoplasm	293	4355	0.989	85477 scinderin
GO cytoplasm	293	4355	0.989	8556 CDC14 cell division cycle 14 homolog A (S. cerevisiae)
GO cytoplasm	293	4355	0.989	8600 tumor necrosis factor (ligand) superfamily, member 11
GO cytoplasm	293	4355	0.989	8631 src kinase associated phosphoprotein 1
GO cytoplasm	293	4355	0.989	8653 DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, Y-linked
GO cytoplasm	293	4355	0.989	8660 insulin receptor substrate 2
GO cytoplasm	293	4355	0.989	8740 tumor necrosis factor (ligand) superfamily, member 14
GO cytoplasm	293	4355	0.989	8796 sciellin
GO cytoplasm	293	4355	0.989	8839 WNT1 inducible signaling pathway protein 2
GO cytoplasm	293	4355	0.989	8848 TSC22 domain family, member 1
GO cytoplasm	293	4355	0.989	8863 period homolog 3 (Drosophila)
GO cytoplasm	293	4355	0.989	8864 period homolog 2 (Drosophila)
GO cytoplasm	293	4355	0.989	8912 calcium channel, voltage-dependent, T type, alpha 1H subunit

GO cytoplasm	293	4355	0.989	89778 serpin peptidase inhibitor, clade B (ovalbumin), member 11 (gene/pse)
GO cytoplasm	293	4355	0.989	8996 nucleolar protein 3 (apoptosis repressor with CARD domain)
GO cytoplasm	293	4355	0.989	9021 suppressor of cytokine signaling 3
GO cytoplasm	293	4355	0.989	90362 family with sequence similarity 110, member B
GO cytoplasm	293	4355	0.989	9050 proline-serine-threonine phosphatase interacting protein 2
GO cytoplasm	293	4355	0.989	9087 thymosin beta 4, Y-linked
GO cytoplasm	293	4355	0.989	9185 RALBP1 associated Eps domain containing 2
GO cytoplasm	293	4355	0.989	9271 piwi-like 1 (Drosophila)
GO cytoplasm	293	4355	0.989	93100 nicotinate phosphoribosyltransferase domain containing 1
GO cytoplasm	293	4355	0.989	9414 tight junction protein 2 (zona occludens 2)
GO cytoplasm	293	4355	0.989	9592 immediate early response 2
GO cytoplasm	293	4355	0.989	9595 cytohesin 1 interacting protein
GO cytoplasm	293	4355	0.989	9633 metallothionein-like 5, testis-specific (tesmin)
GO cytoplasm	293	4355	0.989	9734 histone deacetylase 9
GO cytoplasm	293	4355	0.989	9764 KIAA0513
GO cytoplasm	293	4355	0.989	9788 metastasis suppressor 1
GO cytoplasm	293	4355	0.989	9904 RNA binding motif protein 19
GO cytoplasm	293	4355	0.989	9935 v-maf musculoaponeurotic fibrosarcoma oncogene homolog B (avian)
GO cytoplasm	293	4355	0.989	9962 solute carrier family 23 (nucleobase transporters), member 2
GO hydrolase activity	61	917	0.989	10014 histone deacetylase 5
GO hydrolase activity	61	917	0.989	10076 protein tyrosine phosphatase, receptor type, U
GO hydrolase activity	61	917	0.989	10106 CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) sma
GO hydrolase activity	61	917	0.989	104 adenosine deaminase, RNA-specific, B1 (RED1 homolog rat)
GO hydrolase activity	61	917	0.989	1080 cystic fibrosis transmembrane conductance regulator (ATP-binding cas:
GO hydrolase activity	61	917	0.989	11156 protein tyrosine phosphatase type IVA, member 3
GO hydrolase activity	61	917	0.989	1117 chitinase 3-like 2
GO hydrolase activity	61	917	0.989	11343 monoglyceride lipase
GO hydrolase activity	61	917	0.989	130367 sphingosine-1-phosphate phosphotase 2
GO hydrolase activity	61	917	0.989	148229 ATPase, class I, type 8B, member 3
GO hydrolase activity	61	917	0.989	1785 dynamin 2
GO hydrolase activity	61	917	0.989	1843 dual specificity phosphatase 1
GO hydrolase activity	61	917	0.989	1844 dual specificity phosphatase 2
GO hydrolase activity	61	917	0.989	1847 dual specificity phosphatase 5
GO hydrolase activity	61	917	0.989	22901 arylsulfatase G
GO hydrolase activity	61	917	0.989	23035 PH domain and leucine rich repeat protein phosphatase 2
GO hydrolase activity	61	917	0.989	23371 tensin like C1 domain containing phosphatase (tensin 2)

GO hydrolase activity	61	917	0.989	23382 adenosylhomocysteinase-like 2
GO hydrolase activity	61	917	0.989	26191 protein tyrosine phosphatase, non-receptor type 22 (lymphoid)
GO hydrolase activity	61	917	0.989	271 adenosine monophosphate deaminase 2
GO hydrolase activity	61	917	0.989	27165 glutaminase 2 (liver, mitochondrial)
GO hydrolase activity	61	917	0.989	29943 peptidyl arginine deiminase, type I
GO hydrolase activity	61	917	0.989	340654 lipase, family member M
GO hydrolase activity	61	917	0.989	412 steroid sulfatase (microsomal), isozyme S
GO hydrolase activity	61	917	0.989	493 ATPase, Ca <sup>++</sup> transporting, plasma membrane 4
GO hydrolase activity	61	917	0.989	5136 phosphodiesterase 1A, calmodulin-dependent
GO hydrolase activity	61	917	0.989	5152 phosphodiesterase 9A
GO hydrolase activity	61	917	0.989	5158 phosphodiesterase 6B, cGMP-specific, rod, beta
GO hydrolase activity	61	917	0.989	5243 ATP-binding cassette, sub-family B (MDR/TAP), member 1
GO hydrolase activity	61	917	0.989	5244 ATP-binding cassette, sub-family B (MDR/TAP), member 4
GO hydrolase activity	61	917	0.989	54932 exonuclease 3'-5' domain containing 3
GO hydrolase activity	61	917	0.989	54961 slingshot homolog 3 (Drosophila)
GO hydrolase activity	61	917	0.989	55601 DEAD (Asp-Glu-Ala-Asp) box polypeptide 60
GO hydrolase activity	61	917	0.989	56261 glycerophosphocholine phosphodiesterase GDE1 homolog (S. cerevisia
GO hydrolase activity	61	917	0.989	57104 patatin-like phospholipase domain containing 2
GO hydrolase activity	61	917	0.989	57379 activation-induced cytidine deaminase
GO hydrolase activity	61	917	0.989	5774 protein tyrosine phosphatase, non-receptor type 3
GO hydrolase activity	61	917	0.989	5787 protein tyrosine phosphatase, receptor type, B
GO hydrolase activity	61	917	0.989	5789 protein tyrosine phosphatase, receptor type, D
GO hydrolase activity	61	917	0.989	5791 protein tyrosine phosphatase, receptor type, E
GO hydrolase activity	61	917	0.989	5794 protein tyrosine phosphatase, receptor type, H
GO hydrolase activity	61	917	0.989	5799 protein tyrosine phosphatase, receptor type, N polypeptide 2
GO hydrolase activity	61	917	0.989	5801 protein tyrosine phosphatase, receptor type, R
GO hydrolase activity	61	917	0.989	58489 family with sequence similarity 108, member C1
GO hydrolase activity	61	917	0.989	64135 interferon induced with helicase C domain 1
GO hydrolase activity	61	917	0.989	79132 DEXH (Asp-Glu-X-His) box polypeptide 58
GO hydrolase activity	61	917	0.989	7941 phospholipase A2, group VII (platelet-activating factor acetylhydrolase,
GO hydrolase activity	61	917	0.989	79887 phospholipase B domain containing 1
GO hydrolase activity	61	917	0.989	79895 ATPase, class I, type 8B, member 4
GO hydrolase activity	61	917	0.989	81544 glycerophosphodiester phosphodiesterase domain containing 5
GO hydrolase activity	61	917	0.989	8509 N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 2
GO hydrolase activity	61	917	0.989	85441 peroxisomal proliferator-activated receptor A interacting complex 285
GO hydrolase activity	61	917	0.989	8556 CDC14 cell division cycle 14 homolog A (S. cerevisiae)

GO hydrolase activity	61	917	0.989	8622 phosphodiesterase 8B
GO hydrolase activity	61	917	0.989	8635 ribonuclease T2
GO hydrolase activity	61	917	0.989	8653 DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, Y-linked
GO hydrolase activity	61	917	0.989	8992 ATPase, H <sup>+</sup> transporting, lysosomal 9kDa, V0 subunit e1
GO hydrolase activity	61	917	0.989	9563 hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase)
GO hydrolase activity	61	917	0.989	9615 guanine deaminase
GO hydrolase activity	61	917	0.989	9734 histone deacetylase 9
GO hydrolase activity	61	917	0.989	9914 ATPase, Ca <sup>++</sup> transporting, type 2C, member 2
GO nucleus	305	4735	0.989	10014 histone deacetylase 5
GO nucleus	305	4735	0.989	10081 programmed cell death 7
GO nucleus	305	4735	0.989	10106 CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) sma
GO nucleus	305	4735	0.989	10221 tribbles homolog 1 (Drosophila)
GO nucleus	305	4735	0.989	10346 tripartite motif-containing 22
GO nucleus	305	4735	0.989	10397 N-myc downstream regulated 1
GO nucleus	305	4735	0.989	104 adenosine deaminase, RNA-specific, B1 (RED1 homolog rat)
GO nucleus	305	4735	0.989	10481 homeobox B13
GO nucleus	305	4735	0.989	10628 thioredoxin interacting protein
GO nucleus	305	4735	0.989	10766 transducer of ERBB2, 2
GO nucleus	305	4735	0.989	10838 zinc finger protein 275
GO nucleus	305	4735	0.989	10891 peroxisome proliferator-activated receptor gamma, coactivator 1 alpha
GO nucleus	305	4735	0.989	10957 proline-rich nuclear receptor coactivator 1
GO nucleus	305	4735	0.989	11030 RNA binding protein with multiple splicing
GO nucleus	305	4735	0.989	11078 TRIO and F-actin binding protein
GO nucleus	305	4735	0.989	11187 plakophilin 3
GO nucleus	305	4735	0.989	11200 CHK2 checkpoint homolog (S. pombe)
GO nucleus	305	4735	0.989	11213 interleukin-1 receptor-associated kinase 3
GO nucleus	305	4735	0.989	11279 Kruppel-like factor 8
GO nucleus	305	4735	0.989	115196 zinc finger protein 554
GO nucleus	305	4735	0.989	116071 basic leucine zipper transcription factor, ATF-like 2
GO nucleus	305	4735	0.989	116113 forkhead box P4
GO nucleus	305	4735	0.989	116844 leucine-rich alpha-2-glycoprotein 1
GO nucleus	305	4735	0.989	1193 chloride intracellular channel 2
GO nucleus	305	4735	0.989	123 perilipin 2
GO nucleus	305	4735	0.989	123036 tandem C2 domains, nuclear
GO nucleus	305	4735	0.989	127343 diencephalon/mesencephalon homeobox 1
GO nucleus	305	4735	0.989	127933 U2AF homology motif (UHM) kinase 1

GO nucleus	305	4735	0.989	135112 nuclear receptor coactivator 7
GO nucleus	305	4735	0.989	1382 cellular retinoic acid binding protein 2
GO nucleus	305	4735	0.989	140901 serine/threonine kinase 35
GO nucleus	305	4735	0.989	143689 piwi-like 4 (Drosophila)
GO nucleus	305	4735	0.989	147694 zinc finger protein 548
GO nucleus	305	4735	0.989	147923 zinc finger protein 420
GO nucleus	305	4735	0.989	148398 sterile alpha motif domain containing 11
GO nucleus	305	4735	0.989	150094 salt-inducible kinase 1
GO nucleus	305	4735	0.989	151636 deltex 3-like (Drosophila)
GO nucleus	305	4735	0.989	154 adrenergic, beta-2-, receptor, surface
GO nucleus	305	4735	0.989	157506 retinol dehydrogenase 10 (all-trans)
GO nucleus	305	4735	0.989	158800 RhoX homeobox family, member 1
GO nucleus	305	4735	0.989	1628 D site of albumin promoter (albumin D-box) binding protein
GO nucleus	305	4735	0.989	162962 zinc finger protein 836
GO nucleus	305	4735	0.989	163050 zinc finger protein 564
GO nucleus	305	4735	0.989	163115 zinc finger protein 781
GO nucleus	305	4735	0.989	171483 family with sequence similarity 9, member B
GO nucleus	305	4735	0.989	1820 AT rich interactive domain 3A (BRIGHT-like)
GO nucleus	305	4735	0.989	1822 atrophin 1
GO nucleus	305	4735	0.989	1843 dual specificity phosphatase 1
GO nucleus	305	4735	0.989	1844 dual specificity phosphatase 2
GO nucleus	305	4735	0.989	1847 dual specificity phosphatase 5
GO nucleus	305	4735	0.989	1958 early growth response 1
GO nucleus	305	4735	0.989	1959 early growth response 2
GO nucleus	305	4735	0.989	1960 early growth response 3
GO nucleus	305	4735	0.989	1999 E74-like factor 3 (ets domain transcription factor, epithelial-specific )
GO nucleus	305	4735	0.989	2033 E1A binding protein p300
GO nucleus	305	4735	0.989	2066 v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian)
GO nucleus	305	4735	0.989	2114 v-ets erythroblastosis virus E26 oncogene homolog 2 (avian)
GO nucleus	305	4735	0.989	2115 ets variant 1
GO nucleus	305	4735	0.989	2117 ets variant 3
GO nucleus	305	4735	0.989	2122 MDS1 and EVI1 complex locus
GO nucleus	305	4735	0.989	219539 yippee-like 4 (Drosophila)
GO nucleus	305	4735	0.989	220359 tigger transposable element derived 3
GO nucleus	305	4735	0.989	222546 regulatory factor X, 6
GO nucleus	305	4735	0.989	2263 fibroblast growth factor receptor 2

GO nucleus	305	4735	0.989	22807 IKAROS family zinc finger 2 (Helios)
GO nucleus	305	4735	0.989	2290 forkhead box G1
GO nucleus	305	4735	0.989	22906 trafficking protein, kinesin binding 1
GO nucleus	305	4735	0.989	2296 forkhead box C1
GO nucleus	305	4735	0.989	2303 forkhead box C2 (MFH-1, mesenchyme forkhead 1)
GO nucleus	305	4735	0.989	23035 PH domain and leucine rich repeat protein phosphatase 2
GO nucleus	305	4735	0.989	23043 TRAF2 and NCK interacting kinase
GO nucleus	305	4735	0.989	2306 forkhead box D2
GO nucleus	305	4735	0.989	23081 lysine (K)-specific demethylase 4C
GO nucleus	305	4735	0.989	23099 zinc finger and BTB domain containing 43
GO nucleus	305	4735	0.989	23119 hypermethylated in cancer 2
GO nucleus	305	4735	0.989	23368 protein phosphatase 1, regulatory (inhibitor) subunit 13B
GO nucleus	305	4735	0.989	23373 CREB regulated transcription coactivator 1
GO nucleus	305	4735	0.989	23476 bromodomain containing 4
GO nucleus	305	4735	0.989	23492 chromobox homolog 7
GO nucleus	305	4735	0.989	2353 FBJ murine osteosarcoma viral oncogene homolog
GO nucleus	305	4735	0.989	2354 FBJ murine osteosarcoma viral oncogene homolog B
GO nucleus	305	4735	0.989	23648 single stranded DNA binding protein 3
GO nucleus	305	4735	0.989	23774 bromodomain containing 1
GO nucleus	305	4735	0.989	240 arachidonate 5-lipoxygenase
GO nucleus	305	4735	0.989	2521 fused in sarcoma
GO nucleus	305	4735	0.989	256051 zinc finger protein 549
GO nucleus	305	4735	0.989	25946 zinc finger protein 385A
GO nucleus	305	4735	0.989	2624 GATA binding protein 2
GO nucleus	305	4735	0.989	26240 family with sequence similarity 50, member B
GO nucleus	305	4735	0.989	26468 LIM homeobox 6
GO nucleus	305	4735	0.989	27090 ST6 (alpha-N-acetyl-neuraminy-2,3-beta-galactosyl-1,3)-N-acetylgalact
GO nucleus	305	4735	0.989	27295 PDZ and LIM domain 3
GO nucleus	305	4735	0.989	2737 GLI family zinc finger 3
GO nucleus	305	4735	0.989	27434 polymerase (DNA directed), mu
GO nucleus	305	4735	0.989	284346 zinc finger protein 575
GO nucleus	305	4735	0.989	28959 transmembrane protein 176B
GO nucleus	305	4735	0.989	28996 homeodomain interacting protein kinase 2
GO nucleus	305	4735	0.989	2911 glutamate receptor, metabotropic 1
GO nucleus	305	4735	0.989	29123 ankyrin repeat domain 11
GO nucleus	305	4735	0.989	311 annexin A11

GO nucleus	305	4735	0.989	3131 hepatic leukemia factor
GO nucleus	305	4735	0.989	3142 H2.0-like homeobox
GO nucleus	305	4735	0.989	3164 nuclear receptor subfamily 4, group A, member 1
GO nucleus	305	4735	0.989	3169 forkhead box A1
GO nucleus	305	4735	0.989	3175 one cut homeobox 1
GO nucleus	305	4735	0.989	3192 heterogeneous nuclear ribonucleoprotein U (scaffold attachment facto
GO nucleus	305	4735	0.989	3400 inhibitor of DNA binding 4, dominant negative helix-loop-helix protein
GO nucleus	305	4735	0.989	3428 interferon, gamma-inducible protein 16
GO nucleus	305	4735	0.989	342908 zinc finger protein 404
GO nucleus	305	4735	0.989	345462 zinc finger protein 879
GO nucleus	305	4735	0.989	3486 insulin-like growth factor binding protein 3
GO nucleus	305	4735	0.989	358 aquaporin 1 (Colton blood group)
GO nucleus	305	4735	0.989	3601 interleukin 15 receptor, alpha
GO nucleus	305	4735	0.989	3643 insulin receptor
GO nucleus	305	4735	0.989	3659 interferon regulatory factor 1
GO nucleus	305	4735	0.989	3665 interferon regulatory factor 7
GO nucleus	305	4735	0.989	3725 jun oncogene
GO nucleus	305	4735	0.989	3726 jun B proto-oncogene
GO nucleus	305	4735	0.989	379 ADP-ribosylation factor-like 4D
GO nucleus	305	4735	0.989	387496 RAS-like, family 11, member A
GO nucleus	305	4735	0.989	388536 zinc finger protein 790
GO nucleus	305	4735	0.989	388558 zinc finger protein 808
GO nucleus	305	4735	0.989	388567 zinc finger protein 749
GO nucleus	305	4735	0.989	389058 Sp5 transcription factor
GO nucleus	305	4735	0.989	3958 lectin, galactoside-binding, soluble, 3
GO nucleus	305	4735	0.989	3959 lectin, galactoside-binding, soluble, 3 binding protein
GO nucleus	305	4735	0.989	4005 LIM domain only 2 (rhombotin-like 1)
GO nucleus	305	4735	0.989	4008 LIM domain 7
GO nucleus	305	4735	0.989	4015 lysyl oxidase
GO nucleus	305	4735	0.989	4056 leukotriene C4 synthase
GO nucleus	305	4735	0.989	4087 SMAD family member 2
GO nucleus	305	4735	0.989	4163 mutated in colorectal cancers
GO nucleus	305	4735	0.989	4170 myeloid cell leukemia sequence 1 (BCL2-related)
GO nucleus	305	4735	0.989	4194 Mdm4 p53 binding protein homolog (mouse)
GO nucleus	305	4735	0.989	4204 methyl CpG binding protein 2 (Rett syndrome)
GO nucleus	305	4735	0.989	4209 myocyte enhancer factor 2D



GO nucleus	305	4735	0.989	4212 Meis homeobox 2
GO nucleus	305	4735	0.989	4223 mesenchyme homeobox 2
GO nucleus	305	4735	0.989	4286 microphthalmia-associated transcription factor
GO nucleus	305	4735	0.989	429 achaete-scute complex homolog 1 (Drosophila)
GO nucleus	305	4735	0.989	4306 nuclear receptor subfamily 3, group C, member 2
GO nucleus	305	4735	0.989	440603 BCL2-like 15
GO nucleus	305	4735	0.989	4582 mucin 1, cell surface associated
GO nucleus	305	4735	0.989	4600 myxovirus (influenza virus) resistance 2 (mouse)
GO nucleus	305	4735	0.989	4613 v-myc myelocytomatosis viral related oncogene, neuroblastoma derive
GO nucleus	305	4735	0.989	467 activating transcription factor 3
GO nucleus	305	4735	0.989	4692 necdin homolog (mouse)
GO nucleus	305	4735	0.989	4778 nuclear factor (erythroid-derived 2), 45kDa
GO nucleus	305	4735	0.989	4783 nuclear factor, interleukin 3 regulated
GO nucleus	305	4735	0.989	4784 nuclear factor I/X (CCAAT-binding transcription factor)
GO nucleus	305	4735	0.989	4791 nuclear factor of kappa light polypeptide gene enhancer in B-cells 2 (p4
GO nucleus	305	4735	0.989	4792 nuclear factor of kappa light polypeptide gene enhancer in B-cells inhib
GO nucleus	305	4735	0.989	4794 nuclear factor of kappa light polypeptide gene enhancer in B-cells inhib
GO nucleus	305	4735	0.989	4802 nuclear transcription factor Y, gamma
GO nucleus	305	4735	0.989	4849 CCR4-NOT transcription complex, subunit 3
GO nucleus	305	4735	0.989	4851 Notch homolog 1, translocation-associated (Drosophila)
GO nucleus	305	4735	0.989	4853 Notch homolog 2 (Drosophila)
GO nucleus	305	4735	0.989	4929 nuclear receptor subfamily 4, group A, member 2
GO nucleus	305	4735	0.989	4939 2'-5'-oligoadenylate synthetase 2, 69/71kDa
GO nucleus	305	4735	0.989	5071 Parkinson disease (autosomal recessive, juvenile) 2, parkin
GO nucleus	305	4735	0.989	50809 heterochromatin protein 1, binding protein 3
GO nucleus	305	4735	0.989	5083 paired box 9
GO nucleus	305	4735	0.989	51085 MLX interacting protein-like
GO nucleus	305	4735	0.989	51274 Kruppel-like factor 3 (basic)
GO nucleus	305	4735	0.989	51523 CXXC finger 5
GO nucleus	305	4735	0.989	51621 Kruppel-like factor 13
GO nucleus	305	4735	0.989	51655 RAS, dexamethasone-induced 1
GO nucleus	305	4735	0.989	51710 zinc finger protein 44
GO nucleus	305	4735	0.989	51754 transmembrane protein 8B
GO nucleus	305	4735	0.989	5187 period homolog 1 (Drosophila)
GO nucleus	305	4735	0.989	5218 cyclin-dependent kinase 14
GO nucleus	305	4735	0.989	5307 paired-like homeodomain 1

GO nucleus	305	4735	0.989	5308 paired-like homeodomain 2
GO nucleus	305	4735	0.989	5318 plakophilin 2
GO nucleus	305	4735	0.989	5325 pleiomorphic adenoma gene-like 1
GO nucleus	305	4735	0.989	53347 ubiquitin associated and SH3 domain containing, A
GO nucleus	305	4735	0.989	5367 pro-melanin-concentrating hormone
GO nucleus	305	4735	0.989	5371 promyelocytic leukemia
GO nucleus	305	4735	0.989	5396 paired related homeobox 1
GO nucleus	305	4735	0.989	5460 POU class 5 homeobox 1
GO nucleus	305	4735	0.989	5463 POU class 6 homeobox 1
GO nucleus	305	4735	0.989	5465 peroxisome proliferator-activated receptor alpha
GO nucleus	305	4735	0.989	54739 XIAP associated factor 1
GO nucleus	305	4735	0.989	54894 ring finger protein 43
GO nucleus	305	4735	0.989	54904 Wolf-Hirschhorn syndrome candidate 1-like 1
GO nucleus	305	4735	0.989	54961 slingshot homolog 3 (Drosophila)
GO nucleus	305	4735	0.989	55140 elongation protein 3 homolog (S. cerevisiae)
GO nucleus	305	4735	0.989	55249 YY1 associated protein 1
GO nucleus	305	4735	0.989	55657 zinc finger protein 692
GO nucleus	305	4735	0.989	55693 lysine (K)-specific demethylase 4D
GO nucleus	305	4735	0.989	55705 importin 9
GO nucleus	305	4735	0.989	55762 zinc finger protein 701
GO nucleus	305	4735	0.989	55769 zinc finger protein 83
GO nucleus	305	4735	0.989	55810 forkhead box J2
GO nucleus	305	4735	0.989	55870 ash1 (absent, small, or homeotic)-like (Drosophila)
GO nucleus	305	4735	0.989	55893 zinc finger protein 395
GO nucleus	305	4735	0.989	56271 brain expressed, X-linked 4
GO nucleus	305	4735	0.989	5696 proteasome (prosome, macropain) subunit, beta type, 8 (large multifur
GO nucleus	305	4735	0.989	56978 PR domain containing 8
GO nucleus	305	4735	0.989	5698 proteasome (prosome, macropain) subunit, beta type, 9 (large multifur
GO nucleus	305	4735	0.989	5699 proteasome (prosome, macropain) subunit, beta type, 10
GO nucleus	305	4735	0.989	57018 cyclin L1
GO nucleus	305	4735	0.989	57118 calcium/calmodulin-dependent protein kinase ID
GO nucleus	305	4735	0.989	573 BCL2-associated athanogene
GO nucleus	305	4735	0.989	5742 prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase a
GO nucleus	305	4735	0.989	57459 GATA zinc finger domain containing 2B
GO nucleus	305	4735	0.989	57594 homeobox and leucine zipper encoding
GO nucleus	305	4735	0.989	5791 protein tyrosine phosphatase, receptor type, E

GO nucleus	305	4735	0.989	5801 protein tyrosine phosphatase, receptor type, R
GO nucleus	305	4735	0.989	604 B-cell CLL/lymphoma 6
GO nucleus	305	4735	0.989	60485 salvador homolog 1 (Drosophila)
GO nucleus	305	4735	0.989	6096 RAR-related orphan receptor B
GO nucleus	305	4735	0.989	6097 RAR-related orphan receptor C
GO nucleus	305	4735	0.989	6239 ras responsive element binding protein 1
GO nucleus	305	4735	0.989	6256 retinoid X receptor, alpha
GO nucleus	305	4735	0.989	64135 interferon induced with helicase C domain 1
GO nucleus	305	4735	0.989	64332 nuclear factor of kappa light polypeptide gene enhancer in B-cells inhib
GO nucleus	305	4735	0.989	64359 nucleoredoxin
GO nucleus	305	4735	0.989	6446 serum/glucocorticoid regulated kinase 1
GO nucleus	305	4735	0.989	64651 cysteine-serine-rich nuclear protein 1
GO nucleus	305	4735	0.989	6604 SWI/SNF related, matrix associated, actin dependent regulator of chrom
GO nucleus	305	4735	0.989	6622 synuclein, alpha (non A4 component of amyloid precursor)
GO nucleus	305	4735	0.989	6778 signal transducer and activator of transcription 6, interleukin-4 induc
GO nucleus	305	4735	0.989	687 Kruppel-like factor 9
GO nucleus	305	4735	0.989	6921 transcription elongation factor B (SIII), polypeptide 1 (15kDa, elongin C
GO nucleus	305	4735	0.989	6941 transcription factor 19
GO nucleus	305	4735	0.989	7008 thyrotrophic embryonic factor
GO nucleus	305	4735	0.989	7022 transcription factor AP-2 gamma (activating enhancer binding protein 2
GO nucleus	305	4735	0.989	7026 nuclear receptor subfamily 2, group F, member 2
GO nucleus	305	4735	0.989	7069 thyroid hormone responsive (SPOT14 homolog, rat)
GO nucleus	305	4735	0.989	7071 Kruppel-like factor 10
GO nucleus	305	4735	0.989	7089 transducin-like enhancer of split 2 (E(sp1) homolog, Drosophila)
GO nucleus	305	4735	0.989	7090 transducin-like enhancer of split 3 (E(sp1) homolog, Drosophila)
GO nucleus	305	4735	0.989	7111 tropomodulin 1
GO nucleus	305	4735	0.989	7227 trichorhinophalangeal syndrome I
GO nucleus	305	4735	0.989	7404 ubiquitously transcribed tetratricopeptide repeat gene, Y-linked
GO nucleus	305	4735	0.989	7538 zinc finger protein 36, C3H type, homolog (mouse)
GO nucleus	305	4735	0.989	7546 Zic family member 2 (odd-paired homolog, Drosophila)
GO nucleus	305	4735	0.989	7565 zinc finger protein 17
GO nucleus	305	4735	0.989	7597 zinc finger and BTB domain containing 25
GO nucleus	305	4735	0.989	760 carbonic anhydrase II
GO nucleus	305	4735	0.989	7678 zinc finger protein 124
GO nucleus	305	4735	0.989	7706 tripartite motif-containing 25
GO nucleus	305	4735	0.989	79444 baculoviral IAP repeat-containing 7

GO nucleus	305	4735	0.989	79661 nei endonuclease VIII-like 1 (E. coli)
GO nucleus	305	4735	0.989	79673 zinc finger protein 329
GO nucleus	305	4735	0.989	79816 transducin-like enhancer of split 6 (E(sp1) homolog, Drosophila)
GO nucleus	305	4735	0.989	79894 zinc finger protein 672
GO nucleus	305	4735	0.989	8013 nuclear receptor subfamily 4, group A, member 3
GO nucleus	305	4735	0.989	80169 chromosome 17 open reading frame 68
GO nucleus	305	4735	0.989	80714 pre-B-cell leukemia homeobox 4
GO nucleus	305	4735	0.989	80763 chromosome 12 open reading frame 39
GO nucleus	305	4735	0.989	81603 tripartite motif-containing 8
GO nucleus	305	4735	0.989	8313 axin 2
GO nucleus	305	4735	0.989	834 caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, co
GO nucleus	305	4735	0.989	83595 SRY (sex determining region Y)-box 7
GO nucleus	305	4735	0.989	83666 poly (ADP-ribose) polymerase family, member 9
GO nucleus	305	4735	0.989	83719 yippee-like 3 (Drosophila)
GO nucleus	305	4735	0.989	84124 zinc finger protein 394
GO nucleus	305	4735	0.989	84159 AT rich interactive domain 5B (MRF1-like)
GO nucleus	305	4735	0.989	84366 prostate cancer susceptibility candidate
GO nucleus	305	4735	0.989	8462 Kruppel-like factor 11
GO nucleus	305	4735	0.989	84858 zinc finger protein 503
GO nucleus	305	4735	0.989	84875 poly (ADP-ribose) polymerase family, member 10
GO nucleus	305	4735	0.989	84911 zinc finger protein 382
GO nucleus	305	4735	0.989	84941 hematopoietic SH2 domain containing
GO nucleus	305	4735	0.989	84969 TOX high mobility group box family member 2
GO nucleus	305	4735	0.989	85004 RAS-like, estrogen-regulated, growth inhibitor
GO nucleus	305	4735	0.989	8531 cold shock domain protein A
GO nucleus	305	4735	0.989	85416 Zic family member 5 (odd-paired homolog, Drosophila)
GO nucleus	305	4735	0.989	85441 peroxisomal proliferator-activated receptor A interacting complex 285
GO nucleus	305	4735	0.989	8553 basic helix-loop-helix family, member e40
GO nucleus	305	4735	0.989	8556 CDC14 cell division cycle 14 homolog A (S. cerevisiae)
GO nucleus	305	4735	0.989	862 runt-related transcription factor 1; translocated to, 1 (cyclin D-related)
GO nucleus	305	4735	0.989	8631 src kinase associated phosphoprotein 1
GO nucleus	305	4735	0.989	8653 DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, Y-linked
GO nucleus	305	4735	0.989	8848 TSC22 domain family, member 1
GO nucleus	305	4735	0.989	8863 period homolog 3 (Drosophila)
GO nucleus	305	4735	0.989	8864 period homolog 2 (Drosophila)
GO nucleus	305	4735	0.989	8900 cyclin A1

GO nucleus	305	4735	0.989	8912 calcium channel, voltage-dependent, T type, alpha 1H subunit
GO nucleus	305	4735	0.989	8996 nucleolar protein 3 (apoptosis repressor with CARD domain)
GO nucleus	305	4735	0.989	90592 zinc finger protein 700
GO nucleus	305	4735	0.989	90993 cAMP responsive element binding protein 3-like 1
GO nucleus	305	4735	0.989	91607 schlafen family member 11
GO nucleus	305	4735	0.989	91748 chromosome 14 open reading frame 43
GO nucleus	305	4735	0.989	92283 zinc finger protein 461
GO nucleus	305	4735	0.989	9263 serine/threonine kinase 17a
GO nucleus	305	4735	0.989	92822 zinc finger protein 276
GO nucleus	305	4735	0.989	9314 Kruppel-like factor 4 (gut)
GO nucleus	305	4735	0.989	9324 high mobility group nucleosomal binding domain 3
GO nucleus	305	4735	0.989	93349 SP140 nuclear body protein-like
GO nucleus	305	4735	0.989	9414 tight junction protein 2 (zona occludens 2)
GO nucleus	305	4735	0.989	9422 zinc finger protein 264
GO nucleus	305	4735	0.989	9496 T-box 4
GO nucleus	305	4735	0.989	952 CD38 molecule
GO nucleus	305	4735	0.989	9572 nuclear receptor subfamily 1, group D, member 1
GO nucleus	305	4735	0.989	9633 metallothionein-like 5, testis-specific (tesmin)
GO nucleus	305	4735	0.989	9734 histone deacetylase 9
GO nucleus	305	4735	0.989	9764 KIAA0513
GO nucleus	305	4735	0.989	9875 URB1 ribosome biogenesis 1 homolog ( <i>S. cerevisiae</i> )
GO nucleus	305	4735	0.989	9904 RNA binding motif protein 19
GO nucleus	305	4735	0.989	9935 v-maf musculoaponeurotic fibrosarcoma oncogene homolog B (avian)
GO nucleus	305	4735	0.989	9971 nuclear receptor subfamily 1, group H, member 4
GO nucleus	305	4735	0.989	9985 REC8 homolog (yeast)
GO regulation of transcription	64	956	0.989	10014 histone deacetylase 5
GO regulation of transcription	64	956	0.989	10628 thioredoxin interacting protein
GO regulation of transcription	64	956	0.989	10957 proline-rich nuclear receptor coactivator 1
GO regulation of transcription	64	956	0.989	11030 RNA binding protein with multiple splicing
GO regulation of transcription	64	956	0.989	11279 Kruppel-like factor 8
GO regulation of transcription	64	956	0.989	135112 nuclear receptor coactivator 7
GO regulation of transcription	64	956	0.989	163115 zinc finger protein 781
GO regulation of transcription	64	956	0.989	1785 dynamin 2
GO regulation of transcription	64	956	0.989	1960 early growth response 3
GO regulation of transcription	64	956	0.989	2033 E1A binding protein p300
GO regulation of transcription	64	956	0.989	2066 v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian)

GO	regulation of transcription	64	956	0.989	220359 tigger transposable element derived 3
GO	regulation of transcription	64	956	0.989	22807 IKAROS family zinc finger 2 (Helios)
GO	regulation of transcription	64	956	0.989	22904 strawberry notch homolog 2 (Drosophila)
GO	regulation of transcription	64	956	0.989	23081 lysine (K)-specific demethylase 4C
GO	regulation of transcription	64	956	0.989	23099 zinc finger and BTB domain containing 43
GO	regulation of transcription	64	956	0.989	23119 hypermethylated in cancer 2
GO	regulation of transcription	64	956	0.989	23373 CREB regulated transcription coactivator 1
GO	regulation of transcription	64	956	0.989	23492 chromobox homolog 7
GO	regulation of transcription	64	956	0.989	23648 single stranded DNA binding protein 3
GO	regulation of transcription	64	956	0.989	25946 zinc finger protein 385A
GO	regulation of transcription	64	956	0.989	284346 zinc finger protein 575
GO	regulation of transcription	64	956	0.989	28996 homeodomain interacting protein kinase 2
GO	regulation of transcription	64	956	0.989	387496 RAS-like, family 11, member A
GO	regulation of transcription	64	956	0.989	388567 zinc finger protein 749
GO	regulation of transcription	64	956	0.989	389058 Sp5 transcription factor
GO	regulation of transcription	64	956	0.989	429 achaete-scute complex homolog 1 (Drosophila)
GO	regulation of transcription	64	956	0.989	4849 CCR4-NOT transcription complex, subunit 3
GO	regulation of transcription	64	956	0.989	4851 Notch homolog 1, translocation-associated (Drosophila)
GO	regulation of transcription	64	956	0.989	51274 Kruppel-like factor 3 (basic)
GO	regulation of transcription	64	956	0.989	51621 Kruppel-like factor 13
GO	regulation of transcription	64	956	0.989	5325 pleiomorphic adenoma gene-like 1
GO	regulation of transcription	64	956	0.989	54904 Wolf-Hirschhorn syndrome candidate 1-like 1
GO	regulation of transcription	64	956	0.989	55140 elongation protein 3 homolog (S. cerevisiae)
GO	regulation of transcription	64	956	0.989	55657 zinc finger protein 692
GO	regulation of transcription	64	956	0.989	55693 lysine (K)-specific demethylase 4D
GO	regulation of transcription	64	956	0.989	55870 ash1 (absent, small, or homeotic)-like (Drosophila)
GO	regulation of transcription	64	956	0.989	56978 PR domain containing 8
GO	regulation of transcription	64	956	0.989	57018 cyclin L1
GO	regulation of transcription	64	956	0.989	604 B-cell CLL/lymphoma 6
GO	regulation of transcription	64	956	0.989	64332 nuclear factor of kappa light polypeptide gene enhancer in B-cells inhib
GO	regulation of transcription	64	956	0.989	687 Kruppel-like factor 9
GO	regulation of transcription	64	956	0.989	6921 transcription elongation factor B (SIII), polypeptide 1 (15kDa, elongin C
GO	regulation of transcription	64	956	0.989	6941 transcription factor 19
GO	regulation of transcription	64	956	0.989	7071 Kruppel-like factor 10
GO	regulation of transcription	64	956	0.989	7089 transducin-like enhancer of split 2 (E(sp1) homolog, Drosophila)
GO	regulation of transcription	64	956	0.989	7597 zinc finger and BTB domain containing 25

GO	regulation of transcription	64	956	0.989	79673 zinc finger protein 329
GO	regulation of transcription	64	956	0.989	79816 transducin-like enhancer of split 6 (E(sp1) homolog, Drosophila)
GO	regulation of transcription	64	956	0.989	79894 zinc finger protein 672
GO	regulation of transcription	64	956	0.989	83595 SRY (sex determining region Y)-box 7
GO	regulation of transcription	64	956	0.989	84159 AT rich interactive domain 5B (MRF1-like)
GO	regulation of transcription	64	956	0.989	8462 Kruppel-like factor 11
GO	regulation of transcription	64	956	0.989	84858 zinc finger protein 503
GO	regulation of transcription	64	956	0.989	84969 TOX high mobility group box family member 2
GO	regulation of transcription	64	956	0.989	8543 LIM domain only 4
GO	regulation of transcription	64	956	0.989	85441 peroxisomal proliferator-activated receptor A interacting complex 285
GO	regulation of transcription	64	956	0.989	91 activin A receptor, type IB
GO	regulation of transcription	64	956	0.989	91748 chromosome 14 open reading frame 43
GO	regulation of transcription	64	956	0.989	92822 zinc finger protein 276
GO	regulation of transcription	64	956	0.989	9314 Kruppel-like factor 4 (gut)
GO	regulation of transcription	64	956	0.989	94 activin A receptor type II-like 1
GO	regulation of transcription	64	956	0.989	9619 ATP-binding cassette, sub-family G (WHITE), member 1
GO	regulation of transcription	64	956	0.989	9734 histone deacetylase 9
GO	specific transcriptional repressor activity	2	38	0.989	10014 histone deacetylase 5
GO	specific transcriptional repressor activity	2	38	0.989	9734 histone deacetylase 9
GO	homophilic cell adhesion	8	135	0.989	1004 cadherin 6, type 2, K-cadherin (fetal kidney)
GO	homophilic cell adhesion	8	135	0.989	1009 cadherin 11, type 2, OB-cadherin (osteoblast)
GO	homophilic cell adhesion	8	135	0.989	1014 cadherin 16, KSP-cadherin
GO	homophilic cell adhesion	8	135	0.989	1016 cadherin 18, type 2
GO	homophilic cell adhesion	8	135	0.989	10205 myelin protein zero-like 2
GO	homophilic cell adhesion	8	135	0.989	5099 protocadherin 7
GO	homophilic cell adhesion	8	135	0.989	57453 Down syndrome cell adhesion molecule like 1
GO	homophilic cell adhesion	8	135	0.989	57863 cell adhesion molecule 3
GO	Wnt receptor signaling pathway through G-protein	1	23	0.989	10076 protein tyrosine phosphatase, receptor type, U
GO	RNA splicing	5	251	0.989	10081 programmed cell death 7
GO	RNA splicing	5	251	0.989	10891 peroxisome proliferator-activated receptor gamma, coactivator 1 alpha
GO	RNA splicing	5	251	0.989	2521 fused in sarcoma
GO	RNA splicing	5	251	0.989	3192 heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor 1)
GO	RNA splicing	5	251	0.989	8996 nucleolar protein 3 (apoptosis repressor with CARD domain)
GO	carbohydrate biosynthetic process	1	17	0.989	10090 uronyl-2-sulfotransferase
GO	transferase activity	57	1127	0.989	10090 uronyl-2-sulfotransferase
GO	transferase activity	57	1127	0.989	10162 lysophosphatidylcholine acyltransferase 3

GO transferase activity	57	1127	0.989	10769 polo-like kinase 2 (Drosophila)
GO transferase activity	57	1127	0.989	11200 CHK2 checkpoint homolog (S. pombe)
GO transferase activity	57	1127	0.989	11213 interleukin-1 receptor-associated kinase 3
GO transferase activity	57	1127	0.989	127933 U2AF homology motif (UHM) kinase 1
GO transferase activity	57	1127	0.989	130399 activin A receptor, type IC
GO transferase activity	57	1127	0.989	140901 serine/threonine kinase 35
GO transferase activity	57	1127	0.989	150094 salt-inducible kinase 1
GO transferase activity	57	1127	0.989	154141 membrane bound O-acyltransferase domain containing 1
GO transferase activity	57	1127	0.989	1612 death-associated protein kinase 1
GO transferase activity	57	1127	0.989	166929 sphingomyelin synthase 2
GO transferase activity	57	1127	0.989	1969 EPH receptor A2
GO transferase activity	57	1127	0.989	2033 E1A binding protein p300
GO transferase activity	57	1127	0.989	2044 EPH receptor A5
GO transferase activity	57	1127	0.989	205 adenylate kinase 3-like 1
GO transferase activity	57	1127	0.989	2066 v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian)
GO transferase activity	57	1127	0.989	2263 fibroblast growth factor receptor 2
GO transferase activity	57	1127	0.989	23043 TRAF2 and NCK interacting kinase
GO transferase activity	57	1127	0.989	23387 SIK family kinase 3
GO transferase activity	57	1127	0.989	23604 death-associated protein kinase 2
GO transferase activity	57	1127	0.989	27434 polymerase (DNA directed), mu
GO transferase activity	57	1127	0.989	28996 homeodomain interacting protein kinase 2
GO transferase activity	57	1127	0.989	2947 glutathione S-transferase mu 3 (brain)
GO transferase activity	57	1127	0.989	3643 insulin receptor
GO transferase activity	57	1127	0.989	375449 microtubule associated serine/threonine kinase family member 4
GO transferase activity	57	1127	0.989	3815 v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog
GO transferase activity	57	1127	0.989	415116 pim-3 oncogene
GO transferase activity	57	1127	0.989	4293 mitogen-activated protein kinase kinase kinase 9
GO transferase activity	57	1127	0.989	4486 macrophage stimulating 1 receptor (c-met-related tyrosine kinase)
GO transferase activity	57	1127	0.989	4638 myosin light chain kinase
GO transferase activity	57	1127	0.989	4915 neurotrophic tyrosine kinase, receptor, type 2
GO transferase activity	57	1127	0.989	4939 2'-5'-oligoadenylate synthetase 2, 69/71kDa
GO transferase activity	57	1127	0.989	5063 p21 protein (Cdc42/Rac)-activated kinase 3
GO transferase activity	57	1127	0.989	5129 cyclin-dependent kinase 18
GO transferase activity	57	1127	0.989	5218 cyclin-dependent kinase 14
GO transferase activity	57	1127	0.989	54904 Wolf-Hirschhorn syndrome candidate 1-like 1
GO transferase activity	57	1127	0.989	54947 lysophosphatidylcholine acyltransferase 2



GO transferase activity	57	1127	0.989	55140 elongation protein 3 homolog ( <i>S. cerevisiae</i> )
GO transferase activity	57	1127	0.989	55870 ash1 (absent, small, or homeotic)-like ( <i>Drosophila</i> )
GO transferase activity	57	1127	0.989	5608 mitogen-activated protein kinase kinase 6
GO transferase activity	57	1127	0.989	57118 calcium/calmodulin-dependent protein kinase ID
GO transferase activity	57	1127	0.989	64064 3-oxoacid CoA transferase 2
GO transferase activity	57	1127	0.989	6446 serum/glucocorticoid regulated kinase 1
GO transferase activity	57	1127	0.989	6819 sulfotransferase family, cytosolic, 1C, member 2
GO transferase activity	57	1127	0.989	6850 spleen tyrosine kinase
GO transferase activity	57	1127	0.989	81788 NUAKE family, SNF1-like kinase, 2
GO transferase activity	57	1127	0.989	83666 poly (ADP-ribose) polymerase family, member 9
GO transferase activity	57	1127	0.989	84033 obscurin, cytoskeletal calmodulin and titin-interacting RhoGEF
GO transferase activity	57	1127	0.989	8509 N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 2
GO transferase activity	57	1127	0.989	8527 diacylglycerol kinase, delta 130kDa
GO transferase activity	57	1127	0.989	9064 mitogen-activated protein kinase kinase kinase 6
GO transferase activity	57	1127	0.989	91 activin A receptor, type IB
GO transferase activity	57	1127	0.989	91461 protein kinase domain containing, cytoplasmic homolog (mouse)
GO transferase activity	57	1127	0.989	9263 serine/threonine kinase 17a
GO transferase activity	57	1127	0.989	94 activin A receptor type II-like 1
GO transferase activity	57	1127	0.989	9435 carbohydrate (N-acetylglucosamine-6-O) sulfotransferase 2
GO lysosomal membrane	2	83	0.989	10103 tetraspanin 1
GO lysosomal membrane	2	83	0.989	55332 DNA-damage regulated autophagy modulator 1
GO soluble fraction	20	315	0.989	10106 CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) sma
GO soluble fraction	20	315	0.989	10516 fibulin 5
GO soluble fraction	20	315	0.989	1508 cathepsin B
GO soluble fraction	20	315	0.989	1604 CD55 molecule, decay accelerating factor for complement (Cromer blo
GO soluble fraction	20	315	0.989	1803 dipeptidyl-peptidase 4
GO soluble fraction	20	315	0.989	183 angiotensinogen (serpin peptidase inhibitor, clade A, member 8)
GO soluble fraction	20	315	0.989	1843 dual specificity phosphatase 1
GO soluble fraction	20	315	0.989	2026 enolase 2 (gamma, neuronal)
GO soluble fraction	20	315	0.989	240 arachidonate 5-lipoxygenase
GO soluble fraction	20	315	0.989	2517 fucosidase, alpha-L- 1, tissue
GO soluble fraction	20	315	0.989	26281 fibroblast growth factor 20
GO soluble fraction	20	315	0.989	27090 ST6 (alpha-N-acetyl-neuraminy-2,3-beta-galactosyl-1,3)-N-acetylgalact
GO soluble fraction	20	315	0.989	2947 glutathione S-transferase mu 3 (brain)
GO soluble fraction	20	315	0.989	3034 histidine ammonia-lyase
GO soluble fraction	20	315	0.989	3643 insulin receptor

GO	soluble fraction	20	315	0.989	5046 proprotein convertase subtilisin/kexin type 6
GO	soluble fraction	20	315	0.989	51655 RAS, dexamethasone-induced 1
GO	soluble fraction	20	315	0.989	5577 protein kinase, cAMP-dependent, regulatory, type II, beta
GO	soluble fraction	20	315	0.989	8839 WNT1 inducible signaling pathway protein 2
GO	soluble fraction	20	315	0.989	9633 metallothionein-like 5, testis-specific (tesmin)
GO	cellular_component	34	528	0.989	10116 fem-1 homolog b (C. elegans)
GO	cellular_component	34	528	0.989	10231 regulator of calcineurin 2
GO	cellular_component	34	528	0.989	1154 cytokine inducible SH2-containing protein
GO	cellular_component	34	528	0.989	117157 SH2 domain containing 1B
GO	cellular_component	34	528	0.989	1953 multiple EGF-like-domains 6
GO	cellular_component	34	528	0.989	202 absent in melanoma 1
GO	cellular_component	34	528	0.989	22904 strawberry notch homolog 2 (Drosophila)
GO	cellular_component	34	528	0.989	23092 Rho GTPase activating protein 26
GO	cellular_component	34	528	0.989	23179 ral guanine nucleotide dissociation stimulator-like 1
GO	cellular_component	34	528	0.989	23348 dedicator of cytokinesis 9
GO	cellular_component	34	528	0.989	23682 RAB38, member RAS oncogene family
GO	cellular_component	34	528	0.989	25837 RAB26, member RAS oncogene family
GO	cellular_component	34	528	0.989	26053 autism susceptibility candidate 2
GO	cellular_component	34	528	0.989	271 adenosine monophosphate deaminase 2
GO	cellular_component	34	528	0.989	27202 G protein-coupled receptor 77
GO	cellular_component	34	528	0.989	3268 ArfGAP with FG repeats 2
GO	cellular_component	34	528	0.989	3437 interferon-induced protein with tetratricopeptide repeats 3
GO	cellular_component	34	528	0.989	345275 hydroxysteroid (17-beta) dehydrogenase 13
GO	cellular_component	34	528	0.989	376940 zinc finger CCCH-type containing 6
GO	cellular_component	34	528	0.989	4007 prickly homolog 3 (Drosophila)
GO	cellular_component	34	528	0.989	4038 low density lipoprotein receptor-related protein 4
GO	cellular_component	34	528	0.989	4246 secretoglobin, family 2A, member 1
GO	cellular_component	34	528	0.989	4293 mitogen-activated protein kinase kinase kinase 9
GO	cellular_component	34	528	0.989	50486 G0/G1switch 2
GO	cellular_component	34	528	0.989	5129 cyclin-dependent kinase 18
GO	cellular_component	34	528	0.989	54436 SH3 domain and tetratricopeptide repeats 1
GO	cellular_component	34	528	0.989	54664 transmembrane protein 106B
GO	cellular_component	34	528	0.989	57464 family with sequence similarity 40, member B
GO	cellular_component	34	528	0.989	57535 KIAA1324
GO	cellular_component	34	528	0.989	6343 secretin
GO	cellular_component	34	528	0.989	64651 cysteine-serine-rich nuclear protein 1

GO cellular_component	34	528	0.989	80833 apolipoprotein L, 3
GO cellular_component	34	528	0.989	8382 non-metastatic cells 5, protein expressed in (nucleoside-diphosphate k
GO cellular_component	34	528	0.989	8622 phosphodiesterase 8B
GO cytosol	59	1230	0.989	10156 RAS p21 protein activator 4
GO cytosol	59	1230	0.989	10252 sprouty homolog 1, antagonist of FGF signaling (Drosophila)
GO cytosol	59	1230	0.989	10253 sprouty homolog 2 (Drosophila)
GO cytosol	59	1230	0.989	10891 peroxisome proliferator-activated receptor gamma, coactivator 1 alpha
GO cytosol	59	1230	0.989	1152 creatine kinase, brain
GO cytosol	59	1230	0.989	150094 salt-inducible kinase 1
GO cytosol	59	1230	0.989	1915 eukaryotic translation elongation factor 1 alpha 1
GO cytosol	59	1230	0.989	196383 Rab interacting lysosomal protein-like 2
GO cytosol	59	1230	0.989	1983 eukaryotic translation initiation factor 5
GO cytosol	59	1230	0.989	23263 MCF.2 cell line derived transforming sequence-like
GO cytosol	59	1230	0.989	23365 Rho guanine nucleotide exchange factor (GEF) 12
GO cytosol	59	1230	0.989	240 arachidonate 5-lipoxygenase
GO cytosol	59	1230	0.989	26119 low density lipoprotein receptor adaptor protein 1
GO cytosol	59	1230	0.989	2737 GLI family zinc finger 3
GO cytosol	59	1230	0.989	2752 glutamate-ammonia ligase (glutamine synthetase)
GO cytosol	59	1230	0.989	3034 histidine ammonia-lyase
GO cytosol	59	1230	0.989	3643 insulin receptor
GO cytosol	59	1230	0.989	3665 interferon regulatory factor 7
GO cytosol	59	1230	0.989	3725 jun oncogene
GO cytosol	59	1230	0.989	4087 SMAD family member 2
GO cytosol	59	1230	0.989	440603 BCL2-like 15
GO cytosol	59	1230	0.989	4524 5,10-methylenetetrahydrofolate reductase (NADPH)
GO cytosol	59	1230	0.989	4599 myxovirus (influenza virus) resistance 1, interferon-inducible protein p
GO cytosol	59	1230	0.989	4638 myosin light chain kinase
GO cytosol	59	1230	0.989	4792 nuclear factor of kappa light polypeptide gene enhancer in B-cells inhib
GO cytosol	59	1230	0.989	48 aconitase 1, soluble
GO cytosol	59	1230	0.989	4886 neuropeptide Y receptor Y1
GO cytosol	59	1230	0.989	5071 Parkinson disease (autosomal recessive, juvenile) 2, parkin
GO cytosol	59	1230	0.989	50865 heme binding protein 1
GO cytosol	59	1230	0.989	5132 phosducin
GO cytosol	59	1230	0.989	5136 phosphodiesterase 1A, calmodulin-dependent
GO cytosol	59	1230	0.989	5152 phosphodiesterase 9A
GO cytosol	59	1230	0.989	5218 cyclin-dependent kinase 14

GO cytosol	59	1230	0.989	5295 phosphoinositide-3-kinase, regulatory subunit 1 (alpha)
GO cytosol	59	1230	0.989	53347 ubiquitin associated and SH3 domain containing, A
GO cytosol	59	1230	0.989	5460 POU class 5 homeobox 1
GO cytosol	59	1230	0.989	55740 enabled homolog (Drosophila)
GO cytosol	59	1230	0.989	5577 protein kinase, cAMP-dependent, regulatory, type II, beta
GO cytosol	59	1230	0.989	57104 patatin-like phospholipase domain containing 2
GO cytosol	59	1230	0.989	57132 chromatin modifying protein 1B
GO cytosol	59	1230	0.989	57161 pellino homolog 2 (Drosophila)
GO cytosol	59	1230	0.989	5900 ral guanine nucleotide dissociation stimulator
GO cytosol	59	1230	0.989	64083 golgi phosphoprotein 3 (coat-protein)
GO cytosol	59	1230	0.989	64127 nucleotide-binding oligomerization domain containing 2
GO cytosol	59	1230	0.989	64359 nucleoredoxin
GO cytosol	59	1230	0.989	6622 synuclein, alpha (non A4 component of amyloid precursor)
GO cytosol	59	1230	0.989	6710 spectrin, beta, erythrocytic
GO cytosol	59	1230	0.989	6921 transcription elongation factor B (SIII), polypeptide 1 (15kDa, elongin C)
GO cytosol	59	1230	0.989	7538 zinc finger protein 36, C3H type, homolog (mouse)
GO cytosol	59	1230	0.989	760 carbonic anhydrase II
GO cytosol	59	1230	0.989	84033 obscurin, cytoskeletal calmodulin and titin-interacting RhoGEF
GO cytosol	59	1230	0.989	85004 RAS-like, estrogen-regulated, growth inhibitor
GO cytosol	59	1230	0.989	8660 insulin receptor substrate 2
GO cytosol	59	1230	0.989	8900 cyclin A1
GO cytosol	59	1230	0.989	8996 nucleolar protein 3 (apoptosis repressor with CARD domain)
GO cytosol	59	1230	0.989	9050 proline-serine-threonine phosphatase interacting protein 2
GO cytosol	59	1230	0.989	9182 Ras association (RalGDS/AF-6) domain family (N-terminal) member 9
GO cytosol	59	1230	0.989	93100 nicotinate phosphoribosyltransferase domain containing 1
GO cytosol	59	1230	0.989	9459 Rac/Cdc42 guanine nucleotide exchange factor (GEF) 6
GO acyltransferase activity	5	133	0.989	10162 lysophosphatidylcholine acyltransferase 3
GO acyltransferase activity	5	133	0.989	154141 membrane bound O-acyltransferase domain containing 1
GO acyltransferase activity	5	133	0.989	54947 lysophosphatidylcholine acyltransferase 2
GO acyltransferase activity	5	133	0.989	55140 elongation protein 3 homolog ( <i>S. cerevisiae</i> )
GO acyltransferase activity	5	133	0.989	55304 serine palmitoyltransferase, long chain base subunit 3
GO integral to endoplasmic reticulum me	2	46	0.989	10170 dehydrogenase/reductase (SDR family) member 9
GO integral to endoplasmic reticulum me	2	46	0.989	6238 ribosome binding protein 1 homolog 180kDa (dog)
GO cytoskeleton	39	635	0.989	10205 myelin protein zero-like 2
GO cytoskeleton	39	635	0.989	10435 CDC42 effector protein (Rho GTPase binding) 2
GO cytoskeleton	39	635	0.989	11043 midline 2

GO cytoskeleton	39	635	0.989	11155 LIM domain binding 3
GO cytoskeleton	39	635	0.989	134549 shroom family member 1
GO cytoskeleton	39	635	0.989	148170 CDC42 effector protein (Rho GTPase binding) 5
GO cytoskeleton	39	635	0.989	152273 FYVE, RhoGEF and PH domain containing 5
GO cytoskeleton	39	635	0.989	1540 cylindromatosis (turban tumor syndrome)
GO cytoskeleton	39	635	0.989	1785 dynamin 2
GO cytoskeleton	39	635	0.989	1821 dystrophin related protein 2
GO cytoskeleton	39	635	0.989	2040 stomatin
GO cytoskeleton	39	635	0.989	23048 formin binding protein 1
GO cytoskeleton	39	635	0.989	23092 Rho GTPase activating protein 26
GO cytoskeleton	39	635	0.989	23095 kinesin family member 1B
GO cytoskeleton	39	635	0.989	23303 kinesin family member 13B
GO cytoskeleton	39	635	0.989	257019 FERM domain containing 3
GO cytoskeleton	39	635	0.989	28951 tribbles homolog 2 (Drosophila)
GO cytoskeleton	39	635	0.989	29116 myosin regulatory light chain interacting protein
GO cytoskeleton	39	635	0.989	311 annexin A11
GO cytoskeleton	39	635	0.989	345895 radial spoke head 4 homolog A (Chlamydomonas)
GO cytoskeleton	39	635	0.989	4254 KIT ligand
GO cytoskeleton	39	635	0.989	4842 nitric oxide synthase 1 (neuronal)
GO cytoskeleton	39	635	0.989	51168 myosin XVA
GO cytoskeleton	39	635	0.989	5239 phosphoglucomutase 5
GO cytoskeleton	39	635	0.989	54961 slingshot homolog 3 (Drosophila)
GO cytoskeleton	39	635	0.989	55200 pleckstrin homology domain containing, family G (with RhoGef domain
GO cytoskeleton	39	635	0.989	55638 Golgi-localized protein
GO cytoskeleton	39	635	0.989	55740 enabled homolog (Drosophila)
GO cytoskeleton	39	635	0.989	55909 bridging integrator 3
GO cytoskeleton	39	635	0.989	56288 par-3 partitioning defective 3 homolog (C. elegans)
GO cytoskeleton	39	635	0.989	57619 shroom family member 3
GO cytoskeleton	39	635	0.989	5774 protein tyrosine phosphatase, non-receptor type 3
GO cytoskeleton	39	635	0.989	642273 family with sequence similarity 110, member C
GO cytoskeleton	39	635	0.989	7170 tropomyosin 3
GO cytoskeleton	39	635	0.989	85477 scinderin
GO cytoskeleton	39	635	0.989	8556 CDC14 cell division cycle 14 homolog A (S. cerevisiae)
GO cytoskeleton	39	635	0.989	90362 family with sequence similarity 110, member B
GO cytoskeleton	39	635	0.989	9050 proline-serine-threonine phosphatase interacting protein 2
GO cytoskeleton	39	635	0.989	9087 thymosin beta 4, Y-linked

GO	ATP binding	87	1426	0.989	10221 tribbles homolog 1 (Drosophila)
GO	ATP binding	87	1426	0.989	10769 polo-like kinase 2 (Drosophila)
GO	ATP binding	87	1426	0.989	1080 cystic fibrosis transmembrane conductance regulator (ATP-binding cas
GO	ATP binding	87	1426	0.989	112 adenylate cyclase 6
GO	ATP binding	87	1426	0.989	11200 CHK2 checkpoint homolog (S. pombe)
GO	ATP binding	87	1426	0.989	11213 interleukin-1 receptor-associated kinase 3
GO	ATP binding	87	1426	0.989	1152 creatine kinase, brain
GO	ATP binding	87	1426	0.989	127933 U2AF homology motif (UHM) kinase 1
GO	ATP binding	87	1426	0.989	130399 activin A receptor, type IC
GO	ATP binding	87	1426	0.989	134111 ubiquitin-conjugating enzyme E2Q family-like 1
GO	ATP binding	87	1426	0.989	1373 carbamoyl-phosphate synthetase 1, mitochondrial
GO	ATP binding	87	1426	0.989	140901 serine/threonine kinase 35
GO	ATP binding	87	1426	0.989	147945 NLR family, pyrin domain containing 4
GO	ATP binding	87	1426	0.989	148229 ATPase, class I, type 8B, member 3
GO	ATP binding	87	1426	0.989	150094 salt-inducible kinase 1
GO	ATP binding	87	1426	0.989	1612 death-associated protein kinase 1
GO	ATP binding	87	1426	0.989	1969 EPH receptor A2
GO	ATP binding	87	1426	0.989	197259 mixed lineage kinase domain-like
GO	ATP binding	87	1426	0.989	2044 EPH receptor A5
GO	ATP binding	87	1426	0.989	205 adenylate kinase 3-like 1
GO	ATP binding	87	1426	0.989	2066 v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian)
GO	ATP binding	87	1426	0.989	2182 acyl-CoA synthetase long-chain family member 4
GO	ATP binding	87	1426	0.989	2263 fibroblast growth factor receptor 2
GO	ATP binding	87	1426	0.989	23043 TRAF2 and NCK interacting kinase
GO	ATP binding	87	1426	0.989	23095 kinesin family member 1B
GO	ATP binding	87	1426	0.989	23303 kinesin family member 13B
GO	ATP binding	87	1426	0.989	23387 SIK family kinase 3
GO	ATP binding	87	1426	0.989	23604 death-associated protein kinase 2
GO	ATP binding	87	1426	0.989	2752 glutamate-ammonia ligase (glutamine synthetase)
GO	ATP binding	87	1426	0.989	284716 ribosomal modification protein rimK-like family member A
GO	ATP binding	87	1426	0.989	28951 tribbles homolog 2 (Drosophila)
GO	ATP binding	87	1426	0.989	28996 homeodomain interacting protein kinase 2
GO	ATP binding	87	1426	0.989	3192 heterogeneous nuclear ribonucleoprotein U (scaffold attachment facto
GO	ATP binding	87	1426	0.989	3306 heat shock 70kDa protein 2
GO	ATP binding	87	1426	0.989	343450 potassium channel, subfamily T, member 2
GO	ATP binding	87	1426	0.989	3643 insulin receptor

GO	ATP binding	87	1426	0.989	368 ATP-binding cassette, sub-family C (CFTR/MRP), member 6
GO	ATP binding	87	1426	0.989	375449 microtubule associated serine/threonine kinase family member 4
GO	ATP binding	87	1426	0.989	3815 v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog
GO	ATP binding	87	1426	0.989	415116 pim-3 oncogene
GO	ATP binding	87	1426	0.989	4293 mitogen-activated protein kinase kinase kinase 9
GO	ATP binding	87	1426	0.989	4486 macrophage stimulating 1 receptor (c-met-related tyrosine kinase)
GO	ATP binding	87	1426	0.989	4638 myosin light chain kinase
GO	ATP binding	87	1426	0.989	4645 myosin VB
GO	ATP binding	87	1426	0.989	4915 neurotrophic tyrosine kinase, receptor, type 2
GO	ATP binding	87	1426	0.989	493 ATPase, Ca <sup>++</sup> transporting, plasma membrane 4
GO	ATP binding	87	1426	0.989	4939 2'-5'-oligoadenylate synthetase 2, 69/71kDa
GO	ATP binding	87	1426	0.989	498 ATP synthase, H <sup>+</sup> transporting, mitochondrial F1 complex, alpha subun
GO	ATP binding	87	1426	0.989	5025 purinergic receptor P2X, ligand-gated ion channel, 4
GO	ATP binding	87	1426	0.989	5063 p21 protein (Cdc42/Rac)-activated kinase 3
GO	ATP binding	87	1426	0.989	51168 myosin XVA
GO	ATP binding	87	1426	0.989	5129 cyclin-dependent kinase 18
GO	ATP binding	87	1426	0.989	51314 thioredoxin domain containing 3 (spermatzoa)
GO	ATP binding	87	1426	0.989	51703 acyl-CoA synthetase long-chain family member 5
GO	ATP binding	87	1426	0.989	5218 cyclin-dependent kinase 14
GO	ATP binding	87	1426	0.989	5243 ATP-binding cassette, sub-family B (MDR/TAP), member 1
GO	ATP binding	87	1426	0.989	5244 ATP-binding cassette, sub-family B (MDR/TAP), member 4
GO	ATP binding	87	1426	0.989	55601 DEAD (Asp-Glu-Ala-Asp) box polypeptide 60
GO	ATP binding	87	1426	0.989	5608 mitogen-activated protein kinase kinase 6
GO	ATP binding	87	1426	0.989	57118 calcium/calmodulin-dependent protein kinase ID
GO	ATP binding	87	1426	0.989	57147 SCY1-like 3 (S. cerevisiae)
GO	ATP binding	87	1426	0.989	57494 ribosomal modification protein rimK-like family member B
GO	ATP binding	87	1426	0.989	64127 nucleotide-binding oligomerization domain containing 2
GO	ATP binding	87	1426	0.989	64135 interferon induced with helicase C domain 1
GO	ATP binding	87	1426	0.989	6446 serum/glucocorticoid regulated kinase 1
GO	ATP binding	87	1426	0.989	6850 spleen tyrosine kinase
GO	ATP binding	87	1426	0.989	774 calcium channel, voltage-dependent, N type, alpha 1B subunit
GO	ATP binding	87	1426	0.989	79132 DEXH (Asp-Glu-X-His) box polypeptide 58
GO	ATP binding	87	1426	0.989	79611 acyl-CoA synthetase short-chain family member 3
GO	ATP binding	87	1426	0.989	79895 ATPase, class I, type 8B, member 4
GO	ATP binding	87	1426	0.989	81788 NUAK family, SNF1-like kinase, 2
GO	ATP binding	87	1426	0.989	8382 non-metastatic cells 5, protein expressed in (nucleoside-diphosphate k

GO	ATP binding	87	1426	0.989	83858 ATPase family, AAA domain containing 3B
GO	ATP binding	87	1426	0.989	84033 obscurin, cytoskeletal calmodulin and titin-interacting RhoGEF
GO	ATP binding	87	1426	0.989	8527 diacylglycerol kinase, delta 130kDa
GO	ATP binding	87	1426	0.989	85441 peroxisomal proliferator-activated receptor A interacting complex 285
GO	ATP binding	87	1426	0.989	8653 DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, Y-linked
GO	ATP binding	87	1426	0.989	9060 3'-phosphoadenosine 5'-phosphosulfate synthase 2
GO	ATP binding	87	1426	0.989	9064 mitogen-activated protein kinase kinase kinase 6
GO	ATP binding	87	1426	0.989	91 activin A receptor, type IB
GO	ATP binding	87	1426	0.989	91461 protein kinase domain containing, cytoplasmic homolog (mouse)
GO	ATP binding	87	1426	0.989	91607 schlafen family member 11
GO	ATP binding	87	1426	0.989	9263 serine/threonine kinase 17a
GO	ATP binding	87	1426	0.989	94 activin A receptor type II-like 1
GO	ATP binding	87	1426	0.989	9445 integral membrane protein 2B
GO	ATP binding	87	1426	0.989	9619 ATP-binding cassette, sub-family G (WHITE), member 1
GO	ATP binding	87	1426	0.989	9914 ATPase, Ca <sup>++</sup> transporting, type 2C, member 2
GO	negative regulation of transcription f	1	30	0.989	10221 tribbles homolog 1 (Drosophila)
GO	protein kinase activity	7	170	0.989	10221 tribbles homolog 1 (Drosophila)
GO	protein kinase activity	7	170	0.989	197259 mixed lineage kinase domain-like
GO	protein kinase activity	7	170	0.989	28951 tribbles homolog 2 (Drosophila)
GO	protein kinase activity	7	170	0.989	28996 homeodomain interacting protein kinase 2
GO	protein kinase activity	7	170	0.989	57147 SCY1-like 3 (S. cerevisiae)
GO	protein kinase activity	7	170	0.989	6850 spleen tyrosine kinase
GO	protein kinase activity	7	170	0.989	91461 protein kinase domain containing, cytoplasmic homolog (mouse)
GO	microtubule	9	233	0.989	10253 sprouty homolog 2 (Drosophila)
GO	microtubule	9	233	0.989	11043 midline 2
GO	microtubule	9	233	0.989	134549 shroom family member 1
GO	microtubule	9	233	0.989	1785 dynamin 2
GO	microtubule	9	233	0.989	23095 kinesin family member 1B
GO	microtubule	9	233	0.989	23303 kinesin family member 13B
GO	microtubule	9	233	0.989	57619 shroom family member 3
GO	microtubule	9	233	0.989	642273 family with sequence similarity 110, member C
GO	microtubule	9	233	0.989	83593 Ras association (RalGDS/AF-6) domain family member 5
GO	intracellular protein transport	2	174	0.989	10268 receptor (G protein-coupled) activity modifying protein 3
GO	intracellular protein transport	2	174	0.989	55705 importin 9
GO	protein transporter activity	2	69	0.989	10268 receptor (G protein-coupled) activity modifying protein 3
GO	protein transporter activity	2	69	0.989	55705 importin 9



GO protein transport	25	388	0.989	10268 receptor (G protein-coupled) activity modifying protein 3
GO protein transport	25	388	0.989	10282 blocked early in transport 1 homolog ( <i>S. cerevisiae</i> )
GO protein transport	25	388	0.989	112574 sorting nexin 18
GO protein transport	25	388	0.989	127845 golgi transport 1 homolog A ( <i>S. cerevisiae</i> )
GO protein transport	25	388	0.989	1755 deleted in malignant brain tumors 1
GO protein transport	25	388	0.989	23682 RAB38, member RAS oncogene family
GO protein transport	25	388	0.989	25837 RAB26, member RAS oncogene family
GO protein transport	25	388	0.989	25956 SEC31 homolog B ( <i>S. cerevisiae</i> )
GO protein transport	25	388	0.989	375056 melanoma inhibitory activity family, member 3
GO protein transport	25	388	0.989	387923 stress-associated endoplasmic reticulum protein family member 2
GO protein transport	25	388	0.989	405753 dual oxidase maturation factor 2
GO protein transport	25	388	0.989	4645 myosin VB
GO protein transport	25	388	0.989	51272 blocked early in transport 1 homolog ( <i>S. cerevisiae</i> )-like
GO protein transport	25	388	0.989	55275 vacuolar protein sorting 53 homolog ( <i>S. cerevisiae</i> )
GO protein transport	25	388	0.989	57132 chromatin modifying protein 1B
GO protein transport	25	388	0.989	57799 RAB40C, member RAS oncogene family
GO protein transport	25	388	0.989	5873 RAB27A, member RAS oncogene family
GO protein transport	25	388	0.989	6238 ribosome binding protein 1 homolog 180kDa (dog)
GO protein transport	25	388	0.989	6564 solute carrier family 15 (oligopeptide transporter), member 1
GO protein transport	25	388	0.989	6565 solute carrier family 15 (H <sup>+</sup> /peptide transporter), member 2
GO protein transport	25	388	0.989	6812 syntaxin binding protein 1
GO protein transport	25	388	0.989	80223 RAB11 family interacting protein 1 (class I)
GO protein transport	25	388	0.989	8527 diacylglycerol kinase, delta 130kDa
GO protein transport	25	388	0.989	89866 SEC16 homolog B ( <i>S. cerevisiae</i> )
GO protein transport	25	388	0.989	91461 protein kinase domain containing, cytoplasmic homolog (mouse)
GO ER to Golgi vesicle-mediated transport	1	41	0.989	10282 blocked early in transport 1 homolog ( <i>S. cerevisiae</i> )
GO vesicle-mediated transport	6	165	0.989	10282 blocked early in transport 1 homolog ( <i>S. cerevisiae</i> )
GO vesicle-mediated transport	6	165	0.989	127845 golgi transport 1 homolog A ( <i>S. cerevisiae</i> )
GO vesicle-mediated transport	6	165	0.989	25956 SEC31 homolog B ( <i>S. cerevisiae</i> )
GO vesicle-mediated transport	6	165	0.989	6812 syntaxin binding protein 1
GO vesicle-mediated transport	6	165	0.989	8673 vesicle-associated membrane protein 8 (endobrevin)
GO vesicle-mediated transport	6	165	0.989	89866 SEC16 homolog B ( <i>S. cerevisiae</i> )
GO membrane fraction	31	472	0.989	10288 leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM)
GO membrane fraction	31	472	0.989	10942 protease, serine, 21 (testisin)
GO membrane fraction	31	472	0.989	112 adenylate cyclase 6
GO membrane fraction	31	472	0.989	154 adrenergic, beta-2-, receptor, surface

GO membrane fraction	31	472	0.989	157506 retinol dehydrogenase 10 (all-trans)
GO membrane fraction	31	472	0.989	1803 dipeptidyl-peptidase 4
GO membrane fraction	31	472	0.989	2525 fucosyltransferase 3 (galactoside 3(4)-L-fucosyltransferase, Lewis blood
GO membrane fraction	31	472	0.989	2526 fucosyltransferase 4 (alpha (1,3) fucosyltransferase, myeloid-specific)
GO membrane fraction	31	472	0.989	368 ATP-binding cassette, sub-family C (CFTR/MRP), member 6
GO membrane fraction	31	472	0.989	3845 v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog
GO membrane fraction	31	472	0.989	412 steroid sulfatase (microsomal), isozyme S
GO membrane fraction	31	472	0.989	4121 mannosidase, alpha, class 1A, member 1
GO membrane fraction	31	472	0.989	5243 ATP-binding cassette, sub-family B (MDR/TAP), member 1
GO membrane fraction	31	472	0.989	5244 ATP-binding cassette, sub-family B (MDR/TAP), member 4
GO membrane fraction	31	472	0.989	53947 alpha 1,4-galactosyltransferase
GO membrane fraction	31	472	0.989	5577 protein kinase, cAMP-dependent, regulatory, type II, beta
GO membrane fraction	31	472	0.989	6004 regulator of G-protein signaling 16
GO membrane fraction	31	472	0.989	6505 solute carrier family 1 (neuronal/epithelial high affinity glutamate transp
GO membrane fraction	31	472	0.989	6542 solute carrier family 7 (cationic amino acid transporter, gamma system), me
GO membrane fraction	31	472	0.989	6564 solute carrier family 15 (oligopeptide transporter), member 1
GO membrane fraction	31	472	0.989	6565 solute carrier family 15 (H+/peptide transporter), member 2
GO membrane fraction	31	472	0.989	6692 serine peptidase inhibitor, Kunitz type 1
GO membrane fraction	31	472	0.989	6751 somatostatin receptor 1
GO membrane fraction	31	472	0.989	7133 tumor necrosis factor receptor superfamily, member 1B
GO membrane fraction	31	472	0.989	8434 reversion-inducing-cysteine-rich protein with kazal motifs
GO membrane fraction	31	472	0.989	8673 vesicle-associated membrane protein 8 (endobrevin)
GO membrane fraction	31	472	0.989	8992 ATPase, H+ transporting, lysosomal 9kDa, V0 subunit e1
GO membrane fraction	31	472	0.989	9050 proline-serine-threonine phosphatase interacting protein 2
GO membrane fraction	31	472	0.989	9194 solute carrier family 16, member 7 (monocarboxylic acid transporter 2)
GO membrane fraction	31	472	0.989	952 CD38 molecule
GO membrane fraction	31	472	0.989	9962 solute carrier family 23 (nucleobase transporters), member 2
GO hydrogen ion transmembrane transp	1	20	0.989	10312 T-cell, immune regulator 1, ATPase, H+ transporting, lysosomal V0 subu
GO mitochondrion	51	1193	0.989	10312 T-cell, immune regulator 1, ATPase, H+ transporting, lysosomal V0 subu
GO mitochondrion	51	1193	0.989	11067 chromosome 10 open reading frame 10
GO mitochondrion	51	1193	0.989	11074 tripartite motif-containing 31
GO mitochondrion	51	1193	0.989	11199 annexin A10
GO mitochondrion	51	1193	0.989	11238 carbonic anhydrase VB, mitochondrial
GO mitochondrion	51	1193	0.989	112724 retinol dehydrogenase 13 (all-trans/9-cis)
GO mitochondrion	51	1193	0.989	1152 creatine kinase, brain
GO mitochondrion	51	1193	0.989	123096 solute carrier family 25, member 29

GO	mitochondrion	51	1193	0.989	1373 carbamoyl-phosphate synthetase 1, mitochondrial
GO	mitochondrion	51	1193	0.989	137994 leucine zipper-EF-hand containing transmembrane protein 2
GO	mitochondrion	51	1193	0.989	1508 cathepsin B
GO	mitochondrion	51	1193	0.989	1571 cytochrome P450, family 2, subfamily E, polypeptide 1
GO	mitochondrion	51	1193	0.989	205 adenylate kinase 3-like 1
GO	mitochondrion	51	1193	0.989	2182 acyl-CoA synthetase long-chain family member 4
GO	mitochondrion	51	1193	0.989	22906 trafficking protein, kinesin binding 1
GO	mitochondrion	51	1193	0.989	23095 kinesin family member 1B
GO	mitochondrion	51	1193	0.989	23151 GRAM domain containing 4
GO	mitochondrion	51	1193	0.989	23263 MCF.2 cell line derived transforming sequence-like
GO	mitochondrion	51	1193	0.989	2571 glutamate decarboxylase 1 (brain, 67kDa)
GO	mitochondrion	51	1193	0.989	27165 glutaminase 2 (liver, mitochondrial)
GO	mitochondrion	51	1193	0.989	2752 glutamate-ammonia ligase (glutamine synthetase)
GO	mitochondrion	51	1193	0.989	29103 DnaJ (Hsp40) homolog, subfamily C, member 15
GO	mitochondrion	51	1193	0.989	3306 heat shock 70kDa protein 2
GO	mitochondrion	51	1193	0.989	3429 interferon, alpha-inducible protein 27
GO	mitochondrion	51	1193	0.989	35 acyl-Coenzyme A dehydrogenase, C-2 to C-3 short chain
GO	mitochondrion	51	1193	0.989	3845 v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog
GO	mitochondrion	51	1193	0.989	4128 monoamine oxidase A
GO	mitochondrion	51	1193	0.989	4129 monoamine oxidase B
GO	mitochondrion	51	1193	0.989	4170 myeloid cell leukemia sequence 1 (BCL2-related)
GO	mitochondrion	51	1193	0.989	4817 nitrilase 1
GO	mitochondrion	51	1193	0.989	4939 2'-5'-oligoadenylate synthetase 2, 69/71kDa
GO	mitochondrion	51	1193	0.989	498 ATP synthase, H <sup>+</sup> transporting, mitochondrial F1 complex, alpha subun
GO	mitochondrion	51	1193	0.989	50865 heme binding protein 1
GO	mitochondrion	51	1193	0.989	51703 acyl-CoA synthetase long-chain family member 5
GO	mitochondrion	51	1193	0.989	51754 transmembrane protein 8B
GO	mitochondrion	51	1193	0.989	54739 XIAP associated factor 1
GO	mitochondrion	51	1193	0.989	55268 enoyl Coenzyme A hydratase domain containing 2
GO	mitochondrion	51	1193	0.989	622 3-hydroxybutyrate dehydrogenase, type 1
GO	mitochondrion	51	1193	0.989	64064 3-oxoacid CoA transferase 2
GO	mitochondrion	51	1193	0.989	64083 golgi phosphoprotein 3 (coat-protein)
GO	mitochondrion	51	1193	0.989	6812 syntaxin binding protein 1
GO	mitochondrion	51	1193	0.989	682 basigin (Ok blood group)
GO	mitochondrion	51	1193	0.989	7001 peroxiredoxin 2
GO	mitochondrion	51	1193	0.989	79611 acyl-CoA synthetase short-chain family member 3

GO mitochondrion	51	1193	0.989	79899 proline rich 5 like
GO mitochondrion	51	1193	0.989	83857 transmembrane and tetratricopeptide repeat containing 1
GO mitochondrion	51	1193	0.989	84277 DnaJ (Hsp40) homolog, subfamily C, member 30
GO mitochondrion	51	1193	0.989	8673 vesicle-associated membrane protein 8 (endobrevin)
GO mitochondrion	51	1193	0.989	90362 family with sequence similarity 110, member B
GO mitochondrion	51	1193	0.989	9481 solute carrier family 25, member 27
GO mitochondrion	51	1193	0.989	9804 translocase of outer mitochondrial membrane 20 homolog (yeast)
GO Cajal body	1	38	0.989	10346 tripartite motif-containing 22
GO ligase activity	16	303	0.989	10346 tripartite motif-containing 22
GO ligase activity	16	303	0.989	11074 tripartite motif-containing 31
GO ligase activity	16	303	0.989	134111 ubiquitin-conjugating enzyme E2Q family-like 1
GO ligase activity	16	303	0.989	1373 carbamoyl-phosphate synthetase 1, mitochondrial
GO ligase activity	16	303	0.989	151636 deltex 3-like (Drosophila)
GO ligase activity	16	303	0.989	154214 ring finger protein 217
GO ligase activity	16	303	0.989	2182 acyl-CoA synthetase long-chain family member 4
GO ligase activity	16	303	0.989	255488 ring finger protein 144B
GO ligase activity	16	303	0.989	2752 glutamate-ammonia ligase (glutamine synthetase)
GO ligase activity	16	303	0.989	29116 myosin regulatory light chain interacting protein
GO ligase activity	16	303	0.989	5071 Parkinson disease (autosomal recessive, juvenile) 2, parkin
GO ligase activity	16	303	0.989	51703 acyl-CoA synthetase long-chain family member 5
GO ligase activity	16	303	0.989	54894 ring finger protein 43
GO ligase activity	16	303	0.989	7706 tripartite motif-containing 25
GO ligase activity	16	303	0.989	79611 acyl-CoA synthetase short-chain family member 3
GO ligase activity	16	303	0.989	79872 Cas-Br-M (murine) ecotropic retroviral transforming sequence-like 1
GO nuclear speck	4	111	0.989	10346 tripartite motif-containing 22
GO nuclear speck	4	111	0.989	2122 MDS1 and EVI1 complex locus
GO nuclear speck	4	111	0.989	57018 cyclin L1
GO nuclear speck	4	111	0.989	6239 ras responsive element binding protein 1
GO double-stranded RNA binding	2	31	0.989	104 adenosine deaminase, RNA-specific, B1 (RED1 homolog rat)
GO double-stranded RNA binding	2	31	0.989	7098 toll-like receptor 3
GO mRNA processing	5	231	0.989	104 adenosine deaminase, RNA-specific, B1 (RED1 homolog rat)
GO mRNA processing	5	231	0.989	10891 peroxisome proliferator-activated receptor gamma, coactivator 1 alpha
GO mRNA processing	5	231	0.989	3192 heterogeneous nuclear ribonucleoprotein U (scaffold attachment facto
GO mRNA processing	5	231	0.989	57379 activation-induced cytidine deaminase
GO mRNA processing	5	231	0.989	8996 nucleolar protein 3 (apoptosis repressor with CARD domain)
GO nucleolus	41	692	0.989	104 adenosine deaminase, RNA-specific, B1 (RED1 homolog rat)

GO nucleolus	41	692	0.989	10838 zinc finger protein 275
GO nucleolus	41	692	0.989	116113 forkhead box P4
GO nucleolus	41	692	0.989	140901 serine/threonine kinase 35
GO nucleolus	41	692	0.989	2033 E1A binding protein p300
GO nucleolus	41	692	0.989	219539 yippee-like 4 (Drosophila)
GO nucleolus	41	692	0.989	23043 TRAF2 and NCK interacting kinase
GO nucleolus	41	692	0.989	23099 zinc finger and BTB domain containing 43
GO nucleolus	41	692	0.989	23476 bromodomain containing 4
GO nucleolus	41	692	0.989	2353 FBJ murine osteosarcoma viral oncogene homolog
GO nucleolus	41	692	0.989	2521 fused in sarcoma
GO nucleolus	41	692	0.989	25946 zinc finger protein 385A
GO nucleolus	41	692	0.989	2624 GATA binding protein 2
GO nucleolus	41	692	0.989	27295 PDZ and LIM domain 3
GO nucleolus	41	692	0.989	3142 H2.0-like homeobox
GO nucleolus	41	692	0.989	3428 interferon, gamma-inducible protein 16
GO nucleolus	41	692	0.989	3726 jun B proto-oncogene
GO nucleolus	41	692	0.989	379 ADP-ribosylation factor-like 4D
GO nucleolus	41	692	0.989	387496 RAS-like, family 11, member A
GO nucleolus	41	692	0.989	4209 myocyte enhancer factor 2D
GO nucleolus	41	692	0.989	4212 Meis homeobox 2
GO nucleolus	41	692	0.989	467 activating transcription factor 3
GO nucleolus	41	692	0.989	4778 nuclear factor (erythroid-derived 2), 45kDa
GO nucleolus	41	692	0.989	4794 nuclear factor of kappa light polypeptide gene enhancer in B-cells inhib
GO nucleolus	41	692	0.989	5307 paired-like homeodomain 1
GO nucleolus	41	692	0.989	5371 promyelocytic leukemia
GO nucleolus	41	692	0.989	55140 elongation protein 3 homolog (S. cerevisiae)
GO nucleolus	41	692	0.989	55762 zinc finger protein 701
GO nucleolus	41	692	0.989	57459 GATA zinc finger domain containing 2B
GO nucleolus	41	692	0.989	604 B-cell CLL/lymphoma 6
GO nucleolus	41	692	0.989	6778 signal transducer and activator of transcription 6, interleukin-4 induc
GO nucleolus	41	692	0.989	7404 ubiquitously transcribed tetratricopeptide repeat gene, Y-linked
GO nucleolus	41	692	0.989	7706 tripartite motif-containing 25
GO nucleolus	41	692	0.989	80763 chromosome 12 open reading frame 39
GO nucleolus	41	692	0.989	83719 yippee-like 3 (Drosophila)
GO nucleolus	41	692	0.989	84875 poly (ADP-ribose) polymerase family, member 10
GO nucleolus	41	692	0.989	8996 nucleolar protein 3 (apoptosis repressor with CARD domain)

GO	nucleolus	41	692	0.989	91748 chromosome 14 open reading frame 43
GO	nucleolus	41	692	0.989	9314 Kruppel-like factor 4 (gut)
GO	nucleolus	41	692	0.989	9875 URB1 ribosome biogenesis 1 homolog ( <i>S. cerevisiae</i> )
GO	nucleolus	41	692	0.989	9904 RNA binding motif protein 19
GO	nucleoplasm	12	455	0.989	104 adenosine deaminase, RNA-specific, B1 (RED1 homolog rat)
GO	nucleoplasm	12	455	0.989	311 annexin A11
GO	nucleoplasm	12	455	0.989	3164 nuclear receptor subfamily 4, group A, member 1
GO	nucleoplasm	12	455	0.989	3428 interferon, gamma-inducible protein 16
GO	nucleoplasm	12	455	0.989	3665 interferon regulatory factor 7
GO	nucleoplasm	12	455	0.989	3725 jun oncogene
GO	nucleoplasm	12	455	0.989	4087 SMAD family member 2
GO	nucleoplasm	12	455	0.989	4170 myeloid cell leukemia sequence 1 (BCL2-related)
GO	nucleoplasm	12	455	0.989	5371 promyelocytic leukemia
GO	nucleoplasm	12	455	0.989	6604 SWI/SNF related, matrix associated, actin dependent regulator of chromatin
GO	nucleoplasm	12	455	0.989	6921 transcription elongation factor B (SIII), polypeptide 1 (15kDa, elongin C)
GO	nucleoplasm	12	455	0.989	9904 RNA binding motif protein 19
GO	RNA binding	17	562	0.989	104 adenosine deaminase, RNA-specific, B1 (RED1 homolog rat)
GO	RNA binding	17	562	0.989	10891 peroxisome proliferator-activated receptor gamma, coactivator 1 alpha
GO	RNA binding	17	562	0.989	11030 RNA binding protein with multiple splicing
GO	RNA binding	17	562	0.989	127933 U2AF homology motif (UHM) kinase 1
GO	RNA binding	17	562	0.989	2521 fused in sarcoma
GO	RNA binding	17	562	0.989	3192 heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor)
GO	RNA binding	17	562	0.989	48 aconitase 1, soluble
GO	RNA binding	17	562	0.989	4939 2'-5'-oligoadenylate synthetase 2, 69/71kDa
GO	RNA binding	17	562	0.989	55601 DEAD (Asp-Glu-Ala-Asp) box polypeptide 60
GO	RNA binding	17	562	0.989	64135 interferon induced with helicase C domain 1
GO	RNA binding	17	562	0.989	79132 DEXH (Asp-Glu-X-His) box polypeptide 58
GO	RNA binding	17	562	0.989	80315 cytoplasmic polyadenylation element binding protein 4
GO	RNA binding	17	562	0.989	85441 peroxisomal proliferator-activated receptor A interacting complex 285
GO	RNA binding	17	562	0.989	8635 ribonuclease T2
GO	RNA binding	17	562	0.989	8653 DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, Y-linked
GO	RNA binding	17	562	0.989	8996 nucleolar protein 3 (apoptosis repressor with CARD domain)
GO	RNA binding	17	562	0.989	9904 RNA binding motif protein 19
GO	RNA processing	3	80	0.989	104 adenosine deaminase, RNA-specific, B1 (RED1 homolog rat)
GO	RNA processing	3	80	0.989	11030 RNA binding protein with multiple splicing
GO	RNA processing	3	80	0.989	3192 heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor)

GO axon guidance	4	71	0.989	10417 spondin 2, extracellular matrix protein
GO axon guidance	4	71	0.989	2737 GLI family zinc finger 3
GO axon guidance	4	71	0.989	627 brain-derived neurotrophic factor
GO axon guidance	4	71	0.989	7869 sema domain, immunoglobulin domain (Ig), short basic domain, secret
GO endoplasmic reticulum lumen	3	68	0.989	10439 olfactomedin 1
GO endoplasmic reticulum lumen	3	68	0.989	121506 endoplasmic reticulum protein 27
GO endoplasmic reticulum lumen	3	68	0.989	9563 hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase)
GO biological_process	36	547	0.989	10447 family with sequence similarity 3, member C
GO biological_process	36	547	0.989	11043 midline 2
GO biological_process	36	547	0.989	11273 ataxin 2-like
GO biological_process	36	547	0.989	116844 leucine-rich alpha-2-glycoprotein 1
GO biological_process	36	547	0.989	117157 SH2 domain containing 1B
GO biological_process	36	547	0.989	125476 INO80 complex subunit C
GO biological_process	36	547	0.989	1953 multiple EGF-like-domains 6
GO biological_process	36	547	0.989	202 absent in melanoma 1
GO biological_process	36	547	0.989	2117 ets variant 3
GO biological_process	36	547	0.989	22807 IKAROS family zinc finger 2 (Helios)
GO biological_process	36	547	0.989	23348 dedicator of cytokinesis 9
GO biological_process	36	547	0.989	23767 fibronectin leucine rich transmembrane protein 3
GO biological_process	36	547	0.989	25837 RAB26, member RAS oncogene family
GO biological_process	36	547	0.989	26053 autism susceptibility candidate 2
GO biological_process	36	547	0.989	266675 bestrophin 4
GO biological_process	36	547	0.989	26998 fetuin B
GO biological_process	36	547	0.989	27202 G protein-coupled receptor 77
GO biological_process	36	547	0.989	3268 ArfGAP with FG repeats 2
GO biological_process	36	547	0.989	3437 interferon-induced protein with tetratricopeptide repeats 3
GO biological_process	36	547	0.989	345275 hydroxysteroid (17-beta) dehydrogenase 13
GO biological_process	36	547	0.989	376940 zinc finger CCCH-type containing 6
GO biological_process	36	547	0.989	4007 prickle homolog 3 (Drosophila)
GO biological_process	36	547	0.989	4038 low density lipoprotein receptor-related protein 4
GO biological_process	36	547	0.989	4246 secretoglobin, family 2A, member 1
GO biological_process	36	547	0.989	4817 nitrilase 1
GO biological_process	36	547	0.989	5239 phosphoglucomutase 5
GO biological_process	36	547	0.989	5304 prolactin-induced protein
GO biological_process	36	547	0.989	54436 SH3 domain and tetratricopeptide repeats 1
GO biological_process	36	547	0.989	54664 transmembrane protein 106B

GO biological_process	36	547	0.989	57464 family with sequence similarity 40, member B
GO biological_process	36	547	0.989	57535 KIAA1324
GO biological_process	36	547	0.989	8013 nuclear receptor subfamily 4, group A, member 3
GO biological_process	36	547	0.989	81603 tripartite motif-containing 8
GO biological_process	36	547	0.989	8418 cytidine monophosphate-N-acetylneuraminic acid hydroxylase (CMP-N
GO biological_process	36	547	0.989	9324 high mobility group nucleosomal binding domain 3
GO biological_process	36	547	0.989	9875 URB1 ribosome biogenesis 1 homolog ( <i>S. cerevisiae</i> )
GO sodium ion transport	7	129	0.989	10568 solute carrier family 34 (sodium phosphate), member 2
GO sodium ion transport	7	129	0.989	259232 sodium leak channel, non-selective
GO sodium ion transport	7	129	0.989	6330 sodium channel, voltage-gated, type IV, beta
GO sodium ion transport	7	129	0.989	6446 serum/glucocorticoid regulated kinase 1
GO sodium ion transport	7	129	0.989	6535 solute carrier family 6 (neurotransmitter transporter, creatine), memb
GO sodium ion transport	7	129	0.989	8671 solute carrier family 4, sodium bicarbonate cotransporter, member 4
GO sodium ion transport	7	129	0.989	9962 solute carrier family 23 (nucleobase transporters), member 2
GO cell cycle	19	458	0.989	10628 thioredoxin interacting protein
GO cell cycle	19	458	0.989	11200 CHK2 checkpoint homolog ( <i>S. pombe</i> )
GO cell cycle	19	458	0.989	150094 salt-inducible kinase 1
GO cell cycle	19	458	0.989	1540 cylindromatosis (turban tumor syndrome)
GO cell cycle	19	458	0.989	1843 dual specificity phosphatase 1
GO cell cycle	19	458	0.989	2033 E1A binding protein p300
GO cell cycle	19	458	0.989	311 annexin A11
GO cell cycle	19	458	0.989	3993 lethal giant larvae homolog 2 ( <i>Drosophila</i> )
GO cell cycle	19	458	0.989	415116 pim-3 oncogene
GO cell cycle	19	458	0.989	50486 G0/G1switch 2
GO cell cycle	19	458	0.989	5218 cyclin-dependent kinase 14
GO cell cycle	19	458	0.989	55909 bridging integrator 3
GO cell cycle	19	458	0.989	56288 par-3 partitioning defective 3 homolog ( <i>C. elegans</i> )
GO cell cycle	19	458	0.989	5655 kallikrein-related peptidase 10
GO cell cycle	19	458	0.989	57132 chromatin modifying protein 1B
GO cell cycle	19	458	0.989	60370 arginine vasopressin-induced 1
GO cell cycle	19	458	0.989	83937 Ras association (RalGDS/AF-6) domain family member 4
GO cell cycle	19	458	0.989	8556 CDC14 cell division cycle 14 homolog A ( <i>S. cerevisiae</i> )
GO cell cycle	19	458	0.989	8900 cyclin A1
GO female gamete generation	1	15	0.989	10766 transducer of ERBB2, 2
GO regulation of gene expression	2	32	0.989	10766 transducer of ERBB2, 2
GO regulation of gene expression	2	32	0.989	5460 POU class 5 homeobox 1



GO	nucleotide binding	110	1859	0.989	10769 polo-like kinase 2 (Drosophila)
GO	nucleotide binding	110	1859	0.989	1080 cystic fibrosis transmembrane conductance regulator (ATP-binding cas:
GO	nucleotide binding	110	1859	0.989	10891 peroxisome proliferator-activated receptor gamma, coactivator 1 alpha
GO	nucleotide binding	110	1859	0.989	11030 RNA binding protein with multiple splicing
GO	nucleotide binding	110	1859	0.989	112 adenylate cyclase 6
GO	nucleotide binding	110	1859	0.989	11200 CHK2 checkpoint homolog (S. pombe)
GO	nucleotide binding	110	1859	0.989	11213 interleukin-1 receptor-associated kinase 3
GO	nucleotide binding	110	1859	0.989	1152 creatine kinase, brain
GO	nucleotide binding	110	1859	0.989	115273 RAB42, member RAS oncogene family
GO	nucleotide binding	110	1859	0.989	127933 U2AF homology motif (UHM) kinase 1
GO	nucleotide binding	110	1859	0.989	130399 activin A receptor, type IC
GO	nucleotide binding	110	1859	0.989	134111 ubiquitin-conjugating enzyme E2Q family-like 1
GO	nucleotide binding	110	1859	0.989	1373 carbamoyl-phosphate synthetase 1, mitochondrial
GO	nucleotide binding	110	1859	0.989	140901 serine/threonine kinase 35
GO	nucleotide binding	110	1859	0.989	147945 NLR family, pyrin domain containing 4
GO	nucleotide binding	110	1859	0.989	148229 ATPase, class I, type 8B, member 3
GO	nucleotide binding	110	1859	0.989	150094 salt-inducible kinase 1
GO	nucleotide binding	110	1859	0.989	1612 death-associated protein kinase 1
GO	nucleotide binding	110	1859	0.989	1785 dynamin 2
GO	nucleotide binding	110	1859	0.989	1915 eukaryotic translation elongation factor 1 alpha 1
GO	nucleotide binding	110	1859	0.989	1969 EPH receptor A2
GO	nucleotide binding	110	1859	0.989	1983 eukaryotic translation initiation factor 5
GO	nucleotide binding	110	1859	0.989	2044 EPH receptor A5
GO	nucleotide binding	110	1859	0.989	205 adenylate kinase 3-like 1
GO	nucleotide binding	110	1859	0.989	2066 v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian)
GO	nucleotide binding	110	1859	0.989	2182 acyl-CoA synthetase long-chain family member 4
GO	nucleotide binding	110	1859	0.989	2263 fibroblast growth factor receptor 2
GO	nucleotide binding	110	1859	0.989	23043 TRAF2 and NCK interacting kinase
GO	nucleotide binding	110	1859	0.989	23095 kinesin family member 1B
GO	nucleotide binding	110	1859	0.989	23303 kinesin family member 13B
GO	nucleotide binding	110	1859	0.989	23387 SIK family kinase 3
GO	nucleotide binding	110	1859	0.989	23604 death-associated protein kinase 2
GO	nucleotide binding	110	1859	0.989	23682 RAB38, member RAS oncogene family
GO	nucleotide binding	110	1859	0.989	25837 RAB26, member RAS oncogene family
GO	nucleotide binding	110	1859	0.989	26157 GTPase, IMAP family member 2
GO	nucleotide binding	110	1859	0.989	2633 guanylate binding protein 1, interferon-inducible, 67kDa

GO	nucleotide binding	110	1859	0.989	2634 guanylate binding protein 2, interferon-inducible
GO	nucleotide binding	110	1859	0.989	2635 guanylate binding protein 3
GO	nucleotide binding	110	1859	0.989	2752 glutamate-ammonia ligase (glutamine synthetase)
GO	nucleotide binding	110	1859	0.989	2769 guanine nucleotide binding protein (G protein), alpha 15 (Gq class)
GO	nucleotide binding	110	1859	0.989	284716 ribosomal modification protein rimK-like family member A
GO	nucleotide binding	110	1859	0.989	28951 tribbles homolog 2 (Drosophila)
GO	nucleotide binding	110	1859	0.989	28996 homeodomain interacting protein kinase 2
GO	nucleotide binding	110	1859	0.989	3192 heterogeneous nuclear ribonucleoprotein U (scaffold attachment facto
GO	nucleotide binding	110	1859	0.989	3306 heat shock 70kDa protein 2
GO	nucleotide binding	110	1859	0.989	343450 potassium channel, subfamily T, member 2
GO	nucleotide binding	110	1859	0.989	3643 insulin receptor
GO	nucleotide binding	110	1859	0.989	368 ATP-binding cassette, sub-family C (CFTR/MRP), member 6
GO	nucleotide binding	110	1859	0.989	375449 microtubule associated serine/threonine kinase family member 4
GO	nucleotide binding	110	1859	0.989	379 ADP-ribosylation factor-like 4D
GO	nucleotide binding	110	1859	0.989	3815 v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog
GO	nucleotide binding	110	1859	0.989	3845 v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog
GO	nucleotide binding	110	1859	0.989	387496 RAS-like, family 11, member A
GO	nucleotide binding	110	1859	0.989	392509 ADP-ribosylation factor-like 13A
GO	nucleotide binding	110	1859	0.989	415116 pim-3 oncogene
GO	nucleotide binding	110	1859	0.989	4293 mitogen-activated protein kinase kinase kinase 9
GO	nucleotide binding	110	1859	0.989	4486 macrophage stimulating 1 receptor (c-met-related tyrosine kinase)
GO	nucleotide binding	110	1859	0.989	4599 myxovirus (influenza virus) resistance 1, interferon-inducible protein p
GO	nucleotide binding	110	1859	0.989	4600 myxovirus (influenza virus) resistance 2 (mouse)
GO	nucleotide binding	110	1859	0.989	4638 myosin light chain kinase
GO	nucleotide binding	110	1859	0.989	4645 myosin VB
GO	nucleotide binding	110	1859	0.989	4915 neurotrophic tyrosine kinase, receptor, type 2
GO	nucleotide binding	110	1859	0.989	493 ATPase, Ca <sup>++</sup> transporting, plasma membrane 4
GO	nucleotide binding	110	1859	0.989	4939 2'-5'-oligoadenylate synthetase 2, 69/71kDa
GO	nucleotide binding	110	1859	0.989	498 ATP synthase, H <sup>+</sup> transporting, mitochondrial F1 complex, alpha subun
GO	nucleotide binding	110	1859	0.989	5063 p21 protein (Cdc42/Rac)-activated kinase 3
GO	nucleotide binding	110	1859	0.989	51168 myosin XVA
GO	nucleotide binding	110	1859	0.989	51285 RAS-like, family 12
GO	nucleotide binding	110	1859	0.989	5129 cyclin-dependent kinase 18
GO	nucleotide binding	110	1859	0.989	51655 RAS, dexamethasone-induced 1
GO	nucleotide binding	110	1859	0.989	51703 acyl-CoA synthetase long-chain family member 5
GO	nucleotide binding	110	1859	0.989	5218 cyclin-dependent kinase 14

GO	nucleotide binding	110	1859	0.989	5243 ATP-binding cassette, sub-family B (MDR/TAP), member 1
GO	nucleotide binding	110	1859	0.989	5244 ATP-binding cassette, sub-family B (MDR/TAP), member 4
GO	nucleotide binding	110	1859	0.989	54769 DIRAS family, GTP-binding RAS-like 2
GO	nucleotide binding	110	1859	0.989	55068 ecto-NOX disulfide-thiol exchanger 1
GO	nucleotide binding	110	1859	0.989	55601 DEAD (Asp-Glu-Ala-Asp) box polypeptide 60
GO	nucleotide binding	110	1859	0.989	5577 protein kinase, cAMP-dependent, regulatory, type II, beta
GO	nucleotide binding	110	1859	0.989	5608 mitogen-activated protein kinase kinase 6
GO	nucleotide binding	110	1859	0.989	57118 calcium/calmodulin-dependent protein kinase ID
GO	nucleotide binding	110	1859	0.989	57494 ribosomal modification protein rimK-like family member B
GO	nucleotide binding	110	1859	0.989	57799 RAB40C, member RAS oncogene family
GO	nucleotide binding	110	1859	0.989	5873 RAB27A, member RAS oncogene family
GO	nucleotide binding	110	1859	0.989	64127 nucleotide-binding oligomerization domain containing 2
GO	nucleotide binding	110	1859	0.989	64135 interferon induced with helicase C domain 1
GO	nucleotide binding	110	1859	0.989	6446 serum/glucocorticoid regulated kinase 1
GO	nucleotide binding	110	1859	0.989	6850 spleen tyrosine kinase
GO	nucleotide binding	110	1859	0.989	774 calcium channel, voltage-dependent, N type, alpha 1B subunit
GO	nucleotide binding	110	1859	0.989	79132 DEXH (Asp-Glu-X-His) box polypeptide 58
GO	nucleotide binding	110	1859	0.989	79611 acyl-CoA synthetase short-chain family member 3
GO	nucleotide binding	110	1859	0.989	79895 ATPase, class I, type 8B, member 4
GO	nucleotide binding	110	1859	0.989	80315 cytoplasmic polyadenylation element binding protein 4
GO	nucleotide binding	110	1859	0.989	81788 NUAKE family, SNF1-like kinase, 2
GO	nucleotide binding	110	1859	0.989	83858 ATPase family, AAA domain containing 3B
GO	nucleotide binding	110	1859	0.989	84033 obscurin, cytoskeletal calmodulin and titin-interacting RhoGEF
GO	nucleotide binding	110	1859	0.989	85004 RAS-like, estrogen-regulated, growth inhibitor
GO	nucleotide binding	110	1859	0.989	8527 diacylglycerol kinase, delta 130kDa
GO	nucleotide binding	110	1859	0.989	85441 peroxisomal proliferator-activated receptor A interacting complex 285
GO	nucleotide binding	110	1859	0.989	8653 DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, Y-linked
GO	nucleotide binding	110	1859	0.989	9060 3'-phosphoadenosine 5'-phosphosulfate synthase 2
GO	nucleotide binding	110	1859	0.989	9064 mitogen-activated protein kinase kinase kinase 6
GO	nucleotide binding	110	1859	0.989	91 activin A receptor, type IB
GO	nucleotide binding	110	1859	0.989	91461 protein kinase domain containing, cytoplasmic homolog (mouse)
GO	nucleotide binding	110	1859	0.989	91607 schlafen family member 11
GO	nucleotide binding	110	1859	0.989	9263 serine/threonine kinase 17a
GO	nucleotide binding	110	1859	0.989	94 activin A receptor type II-like 1
GO	nucleotide binding	110	1859	0.989	9567 GTP binding protein 1
GO	nucleotide binding	110	1859	0.989	9619 ATP-binding cassette, sub-family G (WHITE), member 1

GO	nucleotide binding	110	1859	0.989	9904 RNA binding motif protein 19
GO	nucleotide binding	110	1859	0.989	9914 ATPase, Ca <sup>++</sup> transporting, type 2C, member 2
GO	ATPase activity	8	128	0.989	1080 cystic fibrosis transmembrane conductance regulator (ATP-binding cas
GO	ATPase activity	8	128	0.989	148229 ATPase, class I, type 8B, member 3
GO	ATPase activity	8	128	0.989	23095 kinesin family member 1B
GO	ATPase activity	8	128	0.989	368 ATP-binding cassette, sub-family C (CFTR/MRP), member 6
GO	ATPase activity	8	128	0.989	498 ATP synthase, H <sup>+</sup> transporting, mitochondrial F1 complex, alpha subun
GO	ATPase activity	8	128	0.989	5243 ATP-binding cassette, sub-family B (MDR/TAP), member 1
GO	ATPase activity	8	128	0.989	5244 ATP-binding cassette, sub-family B (MDR/TAP), member 4
GO	ATPase activity	8	128	0.989	9619 ATP-binding cassette, sub-family G (WHITE), member 1
GO	cholesterol biosynthetic process	1	25	0.989	1080 cystic fibrosis transmembrane conductance regulator (ATP-binding cas
GO	cytoplasmic vesicle membrane	4	61	0.989	1080 cystic fibrosis transmembrane conductance regulator (ATP-binding cas
GO	cytoplasmic vesicle membrane	4	61	0.989	23095 kinesin family member 1B
GO	cytoplasmic vesicle membrane	4	61	0.989	3601 interleukin 15 receptor, alpha
GO	cytoplasmic vesicle membrane	4	61	0.989	79971 wntless homolog (Drosophila)
GO	early endosome membrane	1	37	0.989	1080 cystic fibrosis transmembrane conductance regulator (ATP-binding cas
GO	enzyme binding	7	114	0.989	1080 cystic fibrosis transmembrane conductance regulator (ATP-binding cas
GO	enzyme binding	7	114	0.989	10811 NADPH oxidase activator 1
GO	enzyme binding	7	114	0.989	1571 cytochrome P450, family 2, subfamily E, polypeptide 1
GO	enzyme binding	7	114	0.989	1785 dynamin 2
GO	enzyme binding	7	114	0.989	3570 interleukin 6 receptor
GO	enzyme binding	7	114	0.989	64127 nucleotide-binding oligomerization domain containing 2
GO	enzyme binding	7	114	0.989	79444 baculoviral IAP repeat-containing 7
GO	androgen receptor binding	1	29	0.989	10891 peroxisome proliferator-activated receptor gamma, coactivator 1 alpha
GO	androgen receptor signaling pathway	1	39	0.989	10891 peroxisome proliferator-activated receptor gamma, coactivator 1 alpha
GO	ligand-dependent nuclear receptor tr	1	31	0.989	10891 peroxisome proliferator-activated receptor gamma, coactivator 1 alpha
GO	mitochondrion organization	1	25	0.989	10891 peroxisome proliferator-activated receptor gamma, coactivator 1 alpha
GO	RNA polymerase II transcription med	1	28	0.989	10891 peroxisome proliferator-activated receptor gamma, coactivator 1 alpha
GO	transcription initiation from RNA pol	1	64	0.989	10891 peroxisome proliferator-activated receptor gamma, coactivator 1 alpha
GO	DNA repair	2	182	0.989	10912 growth arrest and DNA-damage-inducible, gamma
GO	DNA repair	2	182	0.989	26270 F-box protein 6
GO	molecular_function	27	577	0.989	11043 midline 2
GO	molecular_function	27	577	0.989	11273 ataxin 2-like
GO	molecular_function	27	577	0.989	1154 cytokine inducible SH2-containing protein
GO	molecular_function	27	577	0.989	116844 leucine-rich alpha-2-glycoprotein 1
GO	molecular_function	27	577	0.989	117157 SH2 domain containing 1B

GO	molecular_function	27	577	0.989	125476 INO80 complex subunit C
GO	molecular_function	27	577	0.989	134218 DnaJ (Hsp40) homolog, subfamily C, member 21
GO	molecular_function	27	577	0.989	202 absent in melanoma 1
GO	molecular_function	27	577	0.989	2117 ets variant 3
GO	molecular_function	27	577	0.989	22807 IKAROS family zinc finger 2 (Helios)
GO	molecular_function	27	577	0.989	26053 autism susceptibility candidate 2
GO	molecular_function	27	577	0.989	266675 bestrophin 4
GO	molecular_function	27	577	0.989	26998 fetuin B
GO	molecular_function	27	577	0.989	3268 ArfGAP with FG repeats 2
GO	molecular_function	27	577	0.989	3429 interferon, alpha-inducible protein 27
GO	molecular_function	27	577	0.989	3437 interferon-induced protein with tetratricopeptide repeats 3
GO	molecular_function	27	577	0.989	345275 hydroxysteroid (17-beta) dehydrogenase 13
GO	molecular_function	27	577	0.989	345895 radial spoke head 4 homolog A (Chlamydomonas)
GO	molecular_function	27	577	0.989	376940 zinc finger CCCH-type containing 6
GO	molecular_function	27	577	0.989	50486 G0/G1switch 2
GO	molecular_function	27	577	0.989	5318 plakophilin 2
GO	molecular_function	27	577	0.989	54664 transmembrane protein 106B
GO	molecular_function	27	577	0.989	57464 family with sequence similarity 40, member B
GO	molecular_function	27	577	0.989	57535 KIAA1324
GO	molecular_function	27	577	0.989	64651 cysteine-serine-rich nuclear protein 1
GO	molecular_function	27	577	0.989	7170 tropomyosin 3
GO	molecular_function	27	577	0.989	9875 URB1 ribosome biogenesis 1 homolog (S. cerevisiae)
GO	identical protein binding	22	338	0.989	11156 protein tyrosine phosphatase type IVA, member 3
GO	identical protein binding	22	338	0.989	11213 interleukin-1 receptor-associated kinase 3
GO	identical protein binding	22	338	0.989	1364 claudin 4
GO	identical protein binding	22	338	0.989	154810 angiominin like 1
GO	identical protein binding	22	338	0.989	196383 Rab interacting lysosomal protein-like 2
GO	identical protein binding	22	338	0.989	23048 formin binding protein 1
GO	identical protein binding	22	338	0.989	23604 death-associated protein kinase 2
GO	identical protein binding	22	338	0.989	255738 proprotein convertase subtilisin/kexin type 9
GO	identical protein binding	22	338	0.989	259173 ALS2 C-terminal like
GO	identical protein binding	22	338	0.989	2752 glutamate-ammonia ligase (glutamine synthetase)
GO	identical protein binding	22	338	0.989	285704 RGM domain family, member B
GO	identical protein binding	22	338	0.989	2947 glutathione S-transferase mu 3 (brain)
GO	identical protein binding	22	338	0.989	4254 KIT ligand
GO	identical protein binding	22	338	0.989	467 activating transcription factor 3

GO identical protein binding	22	338	0.989	4792 nuclear factor of kappa light polypeptide gene enhancer in B-cells inhib
GO identical protein binding	22	338	0.989	60485 salvador homolog 1 (Drosophila)
GO identical protein binding	22	338	0.989	6622 synuclein, alpha (non A4 component of amyloid precursor)
GO identical protein binding	22	338	0.989	6812 syntaxin binding protein 1
GO identical protein binding	22	338	0.989	6857 synaptotagmin I
GO identical protein binding	22	338	0.989	83593 Ras association (RalGDS/AF-6) domain family member 5
GO identical protein binding	22	338	0.989	8996 nucleolar protein 3 (apoptosis repressor with CARD domain)
GO identical protein binding	22	338	0.989	9071 claudin 10
GO inhibition of adenylate cyclase activit	2	30	0.989	112 adenylate cyclase 6
GO inhibition of adenylate cyclase activit	2	30	0.989	4886 neuropeptide Y receptor Y1
GO chromosome, telomeric region	1	23	0.989	11200 CHK2 checkpoint homolog (S. pombe)
GO response to DNA damage stimulus	3	78	0.989	11200 CHK2 checkpoint homolog (S. pombe)
GO response to DNA damage stimulus	3	78	0.989	151636 deltex 3-like (Drosophila)
GO response to DNA damage stimulus	3	78	0.989	604 B-cell CLL/lymphoma 6
GO neuron projection morphogenesis	1	17	0.989	11202 kallikrein-related peptidase 8
GO cell communication	5	90	0.989	112574 sorting nexin 18
GO cell communication	5	90	0.989	2707 gap junction protein, beta 3, 31kDa
GO cell communication	5	90	0.989	3691 integrin, beta 4
GO cell communication	5	90	0.989	54877 zinc finger, CCHC domain containing 2
GO cell communication	5	90	0.989	84059 G protein-coupled receptor 98
GO phosphoinositide binding	3	56	0.989	112574 sorting nexin 18
GO phosphoinositide binding	3	56	0.989	3709 inositol 1,4,5-triphosphate receptor, type 2
GO phosphoinositide binding	3	56	0.989	54877 zinc finger, CCHC domain containing 2
GO cellular calcium ion homeostasis	4	60	0.989	1139 cholinergic receptor, nicotinic, alpha 7
GO cellular calcium ion homeostasis	4	60	0.989	1813 dopamine receptor D2
GO cellular calcium ion homeostasis	4	60	0.989	1815 dopamine receptor D4
GO cellular calcium ion homeostasis	4	60	0.989	57620 stromal interaction molecule 2
GO extracellular ligand-gated ion channe	3	46	0.989	1139 cholinergic receptor, nicotinic, alpha 7
GO extracellular ligand-gated ion channe	3	46	0.989	2564 gamma-aminobutyric acid (GABA) A receptor, epsilon
GO extracellular ligand-gated ion channe	3	46	0.989	8973 cholinergic receptor, nicotinic, alpha 6
GO postsynaptic membrane	7	149	0.989	1139 cholinergic receptor, nicotinic, alpha 7
GO postsynaptic membrane	7	149	0.989	1785 dynamin 2
GO postsynaptic membrane	7	149	0.989	2564 gamma-aminobutyric acid (GABA) A receptor, epsilon
GO postsynaptic membrane	7	149	0.989	399694 SHC (Src homology 2 domain containing) family, member 4
GO postsynaptic membrane	7	149	0.989	8082 sarcospan (Kras oncogene-associated gene)
GO postsynaptic membrane	7	149	0.989	8973 cholinergic receptor, nicotinic, alpha 6

GO postsynaptic membrane	7	149	0.989	9892 synaptosomal-associated protein, 91kDa homolog (mouse)
GO synapse	16	255	0.989	1139 cholinergic receptor, nicotinic, alpha 7
GO synapse	16	255	0.989	143425 synaptotagmin IX
GO synapse	16	255	0.989	1785 dynamin 2
GO synapse	16	255	0.989	23208 synaptotagmin XI
GO synapse	16	255	0.989	2564 gamma-aminobutyric acid (GABA) A receptor, epsilon
GO synapse	16	255	0.989	2571 glutamate decarboxylase 1 (brain, 67kDa)
GO synapse	16	255	0.989	3643 insulin receptor
GO synapse	16	255	0.989	375790 agrin
GO synapse	16	255	0.989	399694 SHC (Src homology 2 domain containing) family, member 4
GO synapse	16	255	0.989	5025 purinergic receptor P2X, ligand-gated ion channel, 4
GO synapse	16	255	0.989	5327 plasminogen activator, tissue
GO synapse	16	255	0.989	55740 enabled homolog (Drosophila)
GO synapse	16	255	0.989	6857 synaptotagmin I
GO synapse	16	255	0.989	729993 shisa homolog 9 (Xenopus laevis)
GO synapse	16	255	0.989	8082 sarcospan (Kras oncogene-associated gene)
GO synapse	16	255	0.989	8973 cholinergic receptor, nicotinic, alpha 6
GO G-protein coupled receptor protein s	43	725	0.989	115330 G protein-coupled receptor 146
GO G-protein coupled receptor protein s	43	725	0.989	121130 olfactory receptor, family 10, subfamily P, member 1
GO G-protein coupled receptor protein s	43	725	0.989	143503 olfactory receptor, family 51, subfamily E, member 1
GO G-protein coupled receptor protein s	43	725	0.989	154 adrenergic, beta-2-, receptor, surface
GO G-protein coupled receptor protein s	43	725	0.989	1813 dopamine receptor D2
GO G-protein coupled receptor protein s	43	725	0.989	183 angiotensinogen (serpin peptidase inhibitor, clade A, member 8)
GO G-protein coupled receptor protein s	43	725	0.989	1901 sphingosine-1-phosphate receptor 1
GO G-protein coupled receptor protein s	43	725	0.989	1902 lysophosphatidic acid receptor 1
GO G-protein coupled receptor protein s	43	725	0.989	1906 endothelin 1
GO G-protein coupled receptor protein s	43	725	0.989	2015 egf-like module containing, mucin-like, hormone receptor-like 1
GO G-protein coupled receptor protein s	43	725	0.989	222545 G protein-coupled receptor, family C, group 6, member A
GO G-protein coupled receptor protein s	43	725	0.989	22859 latrophilin 1
GO G-protein coupled receptor protein s	43	725	0.989	23266 latrophilin 2
GO G-protein coupled receptor protein s	43	725	0.989	23284 latrophilin 3
GO G-protein coupled receptor protein s	43	725	0.989	23365 Rho guanine nucleotide exchange factor (GEF) 12
GO G-protein coupled receptor protein s	43	725	0.989	2642 glucagon receptor
GO G-protein coupled receptor protein s	43	725	0.989	27202 G protein-coupled receptor 77
GO G-protein coupled receptor protein s	43	725	0.989	283383 G protein-coupled receptor 133
GO G-protein coupled receptor protein s	43	725	0.989	2861 G protein-coupled receptor 37 (endothelin receptor type B-like)

GO	G-protein coupled receptor protein s	43	725	0.989	2865 free fatty acid receptor 3
GO	G-protein coupled receptor protein s	43	725	0.989	2867 free fatty acid receptor 2
GO	G-protein coupled receptor protein s	43	725	0.989	2911 glutamate receptor, metabotropic 1
GO	G-protein coupled receptor protein s	43	725	0.989	338557 G protein-coupled receptor 120
GO	G-protein coupled receptor protein s	43	725	0.989	353345 G protein-coupled receptor 141
GO	G-protein coupled receptor protein s	43	725	0.989	3643 insulin receptor
GO	G-protein coupled receptor protein s	43	725	0.989	387509 G protein-coupled receptor 153
GO	G-protein coupled receptor protein s	43	725	0.989	392392 olfactory receptor, family 1, subfamily K, member 1
GO	G-protein coupled receptor protein s	43	725	0.989	4889 neuropeptide Y receptor Y5
GO	G-protein coupled receptor protein s	43	725	0.989	5132 phosducin
GO	G-protein coupled receptor protein s	43	725	0.989	51655 RAS, dexamethasone-induced 1
GO	G-protein coupled receptor protein s	43	725	0.989	5724 platelet-activating factor receptor
GO	G-protein coupled receptor protein s	43	725	0.989	5732 prostaglandin E receptor 2 (subtype EP2), 53kDa
GO	G-protein coupled receptor protein s	43	725	0.989	5734 prostaglandin E receptor 4 (subtype EP4)
GO	G-protein coupled receptor protein s	43	725	0.989	5737 prostaglandin F receptor (FP)
GO	G-protein coupled receptor protein s	43	725	0.989	57512 G protein-coupled receptor 158
GO	G-protein coupled receptor protein s	43	725	0.989	6750 somatostatin
GO	G-protein coupled receptor protein s	43	725	0.989	718 complement component 3
GO	G-protein coupled receptor protein s	43	725	0.989	7852 chemokine (C-X-C motif) receptor 4
GO	G-protein coupled receptor protein s	43	725	0.989	799 calcitonin receptor
GO	G-protein coupled receptor protein s	43	725	0.989	81285 olfactory receptor, family 51, subfamily E, member 2
GO	G-protein coupled receptor protein s	43	725	0.989	81470 olfactory receptor, family 2, subfamily G, member 2
GO	G-protein coupled receptor protein s	43	725	0.989	84059 G protein-coupled receptor 98
GO	G-protein coupled receptor protein s	43	725	0.989	8938 BAI1-associated protein 3
GO	electron carrier activity	10	149	0.989	1193 chloride intracellular channel 2
GO	electron carrier activity	10	149	0.989	1558 cytochrome P450, family 2, subfamily C, polypeptide 8
GO	electron carrier activity	10	149	0.989	1559 cytochrome P450, family 2, subfamily C, polypeptide 9
GO	electron carrier activity	10	149	0.989	1571 cytochrome P450, family 2, subfamily E, polypeptide 1
GO	electron carrier activity	10	149	0.989	1577 cytochrome P450, family 3, subfamily A, polypeptide 5
GO	electron carrier activity	10	149	0.989	27035 NADPH oxidase 1
GO	electron carrier activity	10	149	0.989	316 aldehyde oxidase 1
GO	electron carrier activity	10	149	0.989	4129 monoamine oxidase B
GO	electron carrier activity	10	149	0.989	6916 thromboxane A synthase 1 (platelet)
GO	electron carrier activity	10	149	0.989	79689 STEAP family member 4
GO	protein disulfide oxidoreductase acti	1	15	0.989	1193 chloride intracellular channel 2
GO	olfactory receptor activity	5	290	0.989	121130 olfactory receptor, family 10, subfamily P, member 1



GO olfactory receptor activity	5	290	0.989	143503 olfactory receptor, family 51, subfamily E, member 1
GO olfactory receptor activity	5	290	0.989	392392 olfactory receptor, family 1, subfamily K, member 1
GO olfactory receptor activity	5	290	0.989	81285 olfactory receptor, family 51, subfamily E, member 2
GO olfactory receptor activity	5	290	0.989	81470 olfactory receptor, family 2, subfamily G, member 2
GO response to stimulus	17	477	0.989	121130 olfactory receptor, family 10, subfamily P, member 1
GO response to stimulus	17	477	0.989	143503 olfactory receptor, family 51, subfamily E, member 1
GO response to stimulus	17	477	0.989	23418 crumbs homolog 1 (Drosophila)
GO response to stimulus	17	477	0.989	368 ATP-binding cassette, sub-family C (CFTR/MRP), member 6
GO response to stimulus	17	477	0.989	392392 olfactory receptor, family 1, subfamily K, member 1
GO response to stimulus	17	477	0.989	5132 phosducin
GO response to stimulus	17	477	0.989	5158 phosphodiesterase 6B, cGMP-specific, rod, beta
GO response to stimulus	17	477	0.989	5950 retinol binding protein 4, plasma
GO response to stimulus	17	477	0.989	6096 RAR-related orphan receptor B
GO response to stimulus	17	477	0.989	6101 retinitis pigmentosa 1 (autosomal dominant)
GO response to stimulus	17	477	0.989	81285 olfactory receptor, family 51, subfamily E, member 2
GO response to stimulus	17	477	0.989	81470 olfactory receptor, family 2, subfamily G, member 2
GO response to stimulus	17	477	0.989	83394 PITPNM family member 3
GO response to stimulus	17	477	0.989	83872 hemicentin 1
GO response to stimulus	17	477	0.989	84059 G protein-coupled receptor 98
GO response to stimulus	17	477	0.989	8842 prominin 1
GO response to stimulus	17	477	0.989	93589 calcium channel, voltage-dependent, alpha 2/delta subunit 4
GO sensory perception of smell	6	305	0.989	121130 olfactory receptor, family 10, subfamily P, member 1
GO sensory perception of smell	6	305	0.989	143503 olfactory receptor, family 51, subfamily E, member 1
GO sensory perception of smell	6	305	0.989	1813 dopamine receptor D2
GO sensory perception of smell	6	305	0.989	392392 olfactory receptor, family 1, subfamily K, member 1
GO sensory perception of smell	6	305	0.989	81285 olfactory receptor, family 51, subfamily E, member 2
GO sensory perception of smell	6	305	0.989	81470 olfactory receptor, family 2, subfamily G, member 2
GO mitochondrial inner membrane	10	231	0.989	123096 solute carrier family 25, member 29
GO mitochondrial inner membrane	10	231	0.989	1373 carbamoyl-phosphate synthetase 1, mitochondrial
GO mitochondrial inner membrane	10	231	0.989	137994 leucine zipper-EF-hand containing transmembrane protein 2
GO mitochondrial inner membrane	10	231	0.989	3958 lectin, galactoside-binding, soluble, 3
GO mitochondrial inner membrane	10	231	0.989	4129 monoamine oxidase B
GO mitochondrial inner membrane	10	231	0.989	498 ATP synthase, H <sup>+</sup> transporting, mitochondrial F1 complex, alpha subun
GO mitochondrial inner membrane	10	231	0.989	51703 acyl-CoA synthetase long-chain family member 5
GO mitochondrial inner membrane	10	231	0.989	5577 protein kinase, cAMP-dependent, regulatory, type II, beta
GO mitochondrial inner membrane	10	231	0.989	622 3-hydroxybutyrate dehydrogenase, type 1

GO	mitochondrial inner membrane	10	231	0.989	9481 solute carrier family 25, member 27
GO	MLL1 complex	1	26	0.989	125476 INO80 complex subunit C
GO	cell cycle arrest	5	108	0.989	127933 U2AF homology motif (UHM) kinase 1
GO	cell cycle arrest	5	108	0.989	4853 Notch homolog 2 (Drosophila)
GO	cell cycle arrest	5	108	0.989	5325 pleiomorphic adenoma gene-like 1
GO	cell cycle arrest	5	108	0.989	5371 promyelocytic leukemia
GO	cell cycle arrest	5	108	0.989	5608 mitogen-activated protein kinase kinase 6
GO	neuron projection development	2	41	0.989	127933 U2AF homology motif (UHM) kinase 1
GO	neuron projection development	2	41	0.989	3569 interleukin 6 (interferon, beta 2)
GO	peptidyl-serine phosphorylation	1	26	0.989	127933 U2AF homology motif (UHM) kinase 1
GO	Rab GTPase activator activity	2	44	0.989	129049 small G protein signaling modulator 1
GO	Rab GTPase activator activity	2	44	0.989	55357 TBC1 domain family, member 2
GO	regulation of Rab GTPase activity	2	44	0.989	129049 small G protein signaling modulator 1
GO	regulation of Rab GTPase activity	2	44	0.989	55357 TBC1 domain family, member 2
GO	post-translational protein modificati	1	27	0.989	134111 ubiquitin-conjugating enzyme E2Q family-like 1
GO	regulation of protein metabolic proce	2	42	0.989	134111 ubiquitin-conjugating enzyme E2Q family-like 1
GO	regulation of protein metabolic proce	2	42	0.989	3479 insulin-like growth factor 1 (somatomedin C)
GO	heat shock protein binding	4	62	0.989	134218 DnaJ (Hsp40) homolog, subfamily C, member 21
GO	heat shock protein binding	4	62	0.989	29103 DnaJ (Hsp40) homolog, subfamily C, member 15
GO	heat shock protein binding	4	62	0.989	4792 nuclear factor of kappa light polypeptide gene enhancer in B-cells inhib
GO	heat shock protein binding	4	62	0.989	84277 DnaJ (Hsp40) homolog, subfamily C, member 30
GO	nucleic acid binding	9	254	0.989	134218 DnaJ (Hsp40) homolog, subfamily C, member 21
GO	nucleic acid binding	9	254	0.989	201501 zinc finger and BTB domain containing 7C
GO	nucleic acid binding	9	254	0.989	23081 lysine (K)-specific demethylase 4C
GO	nucleic acid binding	9	254	0.989	376940 zinc finger CCCH-type containing 6
GO	nucleic acid binding	9	254	0.989	400713 zinc finger protein 880
GO	nucleic acid binding	9	254	0.989	54877 zinc finger, CCHC domain containing 2
GO	nucleic acid binding	9	254	0.989	54932 exonuclease 3'-5' domain containing 3
GO	nucleic acid binding	9	254	0.989	55068 ecto-NOX disulfide-thiol exchanger 1
GO	nucleic acid binding	9	254	0.989	94059 leukocyte receptor cluster (LRC) member 9
GO	protein folding	5	139	0.989	134218 DnaJ (Hsp40) homolog, subfamily C, member 21
GO	protein folding	5	139	0.989	4802 nuclear transcription factor Y, gamma
GO	protein folding	5	139	0.989	51303 FK506 binding protein 11, 19 kDa
GO	protein folding	5	139	0.989	56605 ERO1-like beta (S. cerevisiae)
GO	protein folding	5	139	0.989	84277 DnaJ (Hsp40) homolog, subfamily C, member 30
GO	ribosome	3	172	0.989	134218 DnaJ (Hsp40) homolog, subfamily C, member 21

GO	ribosome	3	172	0.989	1540 cylindromatosis (turban tumor syndrome)
GO	ribosome	3	172	0.989	6238 ribosome binding protein 1 homolog 180kDa (dog)
GO	actin filament binding	3	50	0.989	134549 shroom family member 1
GO	actin filament binding	3	50	0.989	6710 spectrin, beta, erythrocytic
GO	actin filament binding	3	50	0.989	85477 scinderin
GO	metabolic process	31	455	0.989	1363 carboxypeptidase E
GO	metabolic process	31	455	0.989	148229 ATPase, class I, type 8B, member 3
GO	metabolic process	31	455	0.989	157855 potassium channel, subfamily U, member 1
GO	metabolic process	31	455	0.989	200150 phospholipase D family, member 5
GO	metabolic process	31	455	0.989	2182 acyl-CoA synthetase long-chain family member 4
GO	metabolic process	31	455	0.989	22901 arylsulfatase G
GO	metabolic process	31	455	0.989	23382 adenosylhomocysteinase-like 2
GO	metabolic process	31	455	0.989	2517 fucosidase, alpha-L- 1, tissue
GO	metabolic process	31	455	0.989	2947 glutathione S-transferase mu 3 (brain)
GO	metabolic process	31	455	0.989	2990 glucuronidase, beta
GO	metabolic process	31	455	0.989	3373 hyaluronoglucosaminidase 1
GO	metabolic process	31	455	0.989	343450 potassium channel, subfamily T, member 2
GO	metabolic process	31	455	0.989	412 steroid sulfatase (microsomal), isozyme S
GO	metabolic process	31	455	0.989	4121 mannosidase, alpha, class 1A, member 1
GO	metabolic process	31	455	0.989	4316 matrix metalloproteinase 7 (matrilysin, uterine)
GO	metabolic process	31	455	0.989	48 aconitase 1, soluble
GO	metabolic process	31	455	0.989	493 ATPase, Ca <sup>++</sup> transporting, plasma membrane 4
GO	metabolic process	31	455	0.989	5122 proprotein convertase subtilisin/kexin type 1
GO	metabolic process	31	455	0.989	51703 acyl-CoA synthetase long-chain family member 5
GO	metabolic process	31	455	0.989	54511 3-hydroxymethyl-3-methylglutaryl-Coenzyme A lyase-like 1
GO	metabolic process	31	455	0.989	54947 lysophosphatidylcholine acyltransferase 2
GO	metabolic process	31	455	0.989	55140 elongation protein 3 homolog ( <i>S. cerevisiae</i> )
GO	metabolic process	31	455	0.989	55268 enoyl Coenzyme A hydratase domain containing 2
GO	metabolic process	31	455	0.989	57104 patatin-like phospholipase domain containing 2
GO	metabolic process	31	455	0.989	57134 mannosidase, alpha, class 1C, member 1
GO	metabolic process	31	455	0.989	622 3-hydroxybutyrate dehydrogenase, type 1
GO	metabolic process	31	455	0.989	64064 3-oxoacid CoA transferase 2
GO	metabolic process	31	455	0.989	79611 acyl-CoA synthetase short-chain family member 3
GO	metabolic process	31	455	0.989	79661 nei endonuclease VIII-like 1 ( <i>E. coli</i> )
GO	metabolic process	31	455	0.989	952 CD38 molecule
GO	metabolic process	31	455	0.989	9914 ATPase, Ca <sup>++</sup> transporting, type 2C, member 2

GO metallopeptidase activity	6	88	0.989	1363 carboxypeptidase E
GO metallopeptidase activity	6	88	0.989	1368 carboxypeptidase M
GO metallopeptidase activity	6	88	0.989	57094 carboxypeptidase A6
GO metallopeptidase activity	6	88	0.989	79956 endoplasmic reticulum metallopeptidase 1
GO metallopeptidase activity	6	88	0.989	8751 ADAM metallopeptidase domain 15
GO metallopeptidase activity	6	88	0.989	9510 ADAM metallopeptidase with thrombospondin type 1 motif, 1
GO protein modification process	9	145	0.989	1363 carboxypeptidase E
GO protein modification process	9	145	0.989	26232 F-box protein 2
GO protein modification process	9	145	0.989	284716 ribosomal modification protein rimK-like family member A
GO protein modification process	9	145	0.989	29943 peptidyl arginine deiminase, type I
GO protein modification process	9	145	0.989	4015 lysyl oxidase
GO protein modification process	9	145	0.989	5066 peptidylglycine alpha-amidating monooxygenase
GO protein modification process	9	145	0.989	5327 plasminogen activator, tissue
GO protein modification process	9	145	0.989	5351 procollagen-lysine 1, 2-oxoglutarate 5-dioxygenase 1
GO protein modification process	9	145	0.989	57494 ribosomal modification protein rimK-like family member B
GO structural molecule activity	8	196	0.989	1364 claudin 4
GO structural molecule activity	8	196	0.989	3911 laminin, alpha 5
GO structural molecule activity	8	196	0.989	3913 laminin, beta 2 (laminin S)
GO structural molecule activity	8	196	0.989	3914 laminin, beta 3
GO structural molecule activity	8	196	0.989	4359 myelin protein zero
GO structural molecule activity	8	196	0.989	5239 phosphoglucomutase 5
GO structural molecule activity	8	196	0.989	9019 myelin protein zero-like 1
GO structural molecule activity	8	196	0.989	9071 claudin 10
GO mitochondrial matrix	5	147	0.989	1373 carbamoyl-phosphate synthetase 1, mitochondrial
GO mitochondrial matrix	5	147	0.989	205 adenylate kinase 3-like 1
GO mitochondrial matrix	5	147	0.989	35 acyl-Coenzyme A dehydrogenase, C-2 to C-3 short chain
GO mitochondrial matrix	5	147	0.989	498 ATP synthase, H <sup>+</sup> transporting, mitochondrial F1 complex, alpha subun
GO mitochondrial matrix	5	147	0.989	622 3-hydroxybutyrate dehydrogenase, type 1
GO mitochondrial nucleoid	1	31	0.989	1373 carbamoyl-phosphate synthetase 1, mitochondrial
GO protein complex	8	153	0.989	1373 carbamoyl-phosphate synthetase 1, mitochondrial
GO protein complex	8	153	0.989	4005 LIM domain only 2 (rhombotin-like 1)
GO protein complex	8	153	0.989	5071 Parkinson disease (autosomal recessive, juvenile) 2, parkin
GO protein complex	8	153	0.989	57161 pellino homolog 2 (Drosophila)
GO protein complex	8	153	0.989	6494 signal-induced proliferation-associated 1
GO protein complex	8	153	0.989	6710 spectrin, beta, erythrocytic
GO protein complex	8	153	0.989	6812 syntaxin binding protein 1

GO protein complex	8	153	0.989	85477 scinderin
GO cytoplasmic vesicle	14	229	0.989	143425 synaptotagmin IX
GO cytoplasmic vesicle	14	229	0.989	23208 synaptotagmin XI
GO cytoplasmic vesicle	14	229	0.989	25956 SEC31 homolog B ( <i>S. cerevisiae</i> )
GO cytoplasmic vesicle	14	229	0.989	3601 interleukin 15 receptor, alpha
GO cytoplasmic vesicle	14	229	0.989	4179 CD46 molecule, complement regulatory protein
GO cytoplasmic vesicle	14	229	0.989	5016 oviductal glycoprotein 1, 120kDa
GO cytoplasmic vesicle	14	229	0.989	5122 proprotein convertase subtilisin/kexin type 1
GO cytoplasmic vesicle	14	229	0.989	6857 synaptotagmin I
GO cytoplasmic vesicle	14	229	0.989	7852 chemokine (C-X-C motif) receptor 4
GO cytoplasmic vesicle	14	229	0.989	79971 wntless homolog ( <i>Drosophila</i> )
GO cytoplasmic vesicle	14	229	0.989	80223 RAB11 family interacting protein 1 (class I)
GO cytoplasmic vesicle	14	229	0.989	80763 chromosome 12 open reading frame 39
GO cytoplasmic vesicle	14	229	0.989	9143 synaptogyrin 3
GO cytoplasmic vesicle	14	229	0.989	9510 ADAM metallopeptidase with thrombospondin type 1 motif, 1
GO homeostasis of number of cells within	1	15	0.989	1435 colony stimulating factor 1 (macrophage)
GO positive regulation of protein kinase ;	1	16	0.989	1435 colony stimulating factor 1 (macrophage)
GO regulation of translation	3	61	0.989	143689 piwi-like 4 ( <i>Drosophila</i> )
GO regulation of translation	3	61	0.989	84919 protein phosphatase 1, regulatory (inhibitor) subunit 15B
GO regulation of translation	3	61	0.989	9271 piwi-like 1 ( <i>Drosophila</i> )
GO spermatogenesis	16	261	0.989	143689 piwi-like 4 ( <i>Drosophila</i> )
GO spermatogenesis	16	261	0.989	3815 v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog
GO spermatogenesis	16	261	0.989	4851 Notch homolog 1, translocation-associated ( <i>Drosophila</i> )
GO spermatogenesis	16	261	0.989	51314 thioredoxin domain containing 3 (spermatzoa)
GO spermatogenesis	16	261	0.989	5367 pro-melanin-concentrating hormone
GO spermatogenesis	16	261	0.989	55124 piwi-like 2 ( <i>Drosophila</i> )
GO spermatogenesis	16	261	0.989	5950 retinol binding protein 4, plasma
GO spermatogenesis	16	261	0.989	604 B-cell CLL/lymphoma 6
GO spermatogenesis	16	261	0.989	79820 cation channel, sperm-associated, beta
GO spermatogenesis	16	261	0.989	8382 non-metastatic cells 5, protein expressed in (nucleoside-diphosphate k
GO spermatogenesis	16	261	0.989	83890 spermatogenesis associated 9
GO spermatogenesis	16	261	0.989	8531 cold shock domain protein A
GO spermatogenesis	16	261	0.989	8900 cyclin A1
GO spermatogenesis	16	261	0.989	9271 piwi-like 1 ( <i>Drosophila</i> )
GO spermatogenesis	16	261	0.989	9633 metallothionein-like 5, testis-specific (tesmin)
GO spermatogenesis	16	261	0.989	9985 REC8 homolog (yeast)

GO	microtubule motor activity	3	76	0.989	144132 dynein heavy chain domain 1
GO	microtubule motor activity	3	76	0.989	23095 kinesin family member 1B
GO	microtubule motor activity	3	76	0.989	23303 kinesin family member 13B
GO	microtubule-based movement	3	84	0.989	144132 dynein heavy chain domain 1
GO	microtubule-based movement	3	84	0.989	23095 kinesin family member 1B
GO	microtubule-based movement	3	84	0.989	23303 kinesin family member 13B
GO	hyaluronic acid binding	1	19	0.989	1462 versican
GO	Rho protein signal transduction	2	36	0.989	148170 CDC42 effector protein (Rho GTPase binding) 5
GO	Rho protein signal transduction	2	36	0.989	395 Rho GTPase activating protein 6
GO	binding of sperm to zona pellucida	1	15	0.989	148229 ATPase, class I, type 8B, member 3
GO	autophagy	2	36	0.989	1508 cathepsin B
GO	autophagy	2	36	0.989	55332 DNA-damage regulated autophagy modulator 1
GO	histone binding	3	44	0.989	151636 deltex 3-like (Drosophila)
GO	histone binding	3	44	0.989	55705 importin 9
GO	histone binding	3	44	0.989	6622 synuclein, alpha (non A4 component of amyloid precursor)
GO	ruffle	3	53	0.989	152273 FYVE, RhoGEF and PH domain containing 5
GO	ruffle	3	53	0.989	3678 integrin, alpha 5 (fibronectin receptor, alpha polypeptide)
GO	ruffle	3	53	0.989	9788 metastasis suppressor 1
GO	cysteine-type peptidase activity	3	76	0.989	1540 cylindromatosis (turban tumor syndrome)
GO	cysteine-type peptidase activity	3	76	0.989	25862 ubiquitin specific peptidase 49
GO	cysteine-type peptidase activity	3	76	0.989	55432 YOD1 OTU deubiquinating enzyme 1 homolog (S. cerevisiae)
GO	structural constituent of ribosome	1	146	0.989	1540 cylindromatosis (turban tumor syndrome)
GO	translation	2	197	0.989	1540 cylindromatosis (turban tumor syndrome)
GO	translation	2	197	0.989	6238 ribosome binding protein 1 homolog 180kDa (dog)
GO	ubiquitin thiolesterase activity	3	68	0.989	1540 cylindromatosis (turban tumor syndrome)
GO	ubiquitin thiolesterase activity	3	68	0.989	159195 ubiquitin specific peptidase 54
GO	ubiquitin thiolesterase activity	3	68	0.989	25862 ubiquitin specific peptidase 49
GO	ubiquitin-dependent protein cataboli	5	139	0.989	1540 cylindromatosis (turban tumor syndrome)
GO	ubiquitin-dependent protein cataboli	5	139	0.989	159195 ubiquitin specific peptidase 54
GO	ubiquitin-dependent protein cataboli	5	139	0.989	25862 ubiquitin specific peptidase 49
GO	ubiquitin-dependent protein cataboli	5	139	0.989	5071 Parkinson disease (autosomal recessive, juvenile) 2, parkin
GO	ubiquitin-dependent protein cataboli	5	139	0.989	6921 transcription elongation factor B (SIII), polypeptide 1 (15kDa, elongin C
GO	intrinsic to endoplasmic reticulum m	1	16	0.989	1571 cytochrome P450, family 2, subfamily E, polypeptide 1
GO	RNA polymerase II transcription factc	8	126	0.989	1628 D site of albumin promoter (albumin D-box) binding protein
GO	RNA polymerase II transcription factc	8	126	0.989	3725 jun oncogene
GO	RNA polymerase II transcription factc	8	126	0.989	3726 jun B proto-oncogene

GO	RNA polymerase II transcription factc	8	126	0.989	4802 nuclear transcription factor Y, gamma
GO	RNA polymerase II transcription factc	8	126	0.989	51621 Kruppel-like factor 13
GO	RNA polymerase II transcription factc	8	126	0.989	55870 ash1 (absent, small, or homeotic)-like (Drosophila)
GO	RNA polymerase II transcription factc	8	126	0.989	7008 thyrotrophic embryonic factor
GO	RNA polymerase II transcription factc	8	126	0.989	8531 cold shock domain protein A
GO	kinase activity	2	117	0.989	166929 sphingomyelin synthase 2
GO	kinase activity	2	117	0.989	57147 SCY1-like 3 (S. cerevisiae)
GO	metalloendopeptidase activity	6	102	0.989	170692 ADAM metallopeptidase with thrombospondin type 1 motif, 18
GO	metalloendopeptidase activity	6	102	0.989	4316 matrix metallopeptidase 7 (matrilysin, uterine)
GO	metalloendopeptidase activity	6	102	0.989	56547 matrix metallopeptidase 26
GO	metalloendopeptidase activity	6	102	0.989	7092 tolloid-like 1
GO	metalloendopeptidase activity	6	102	0.989	8751 ADAM metallopeptidase domain 15
GO	metalloendopeptidase activity	6	102	0.989	9510 ADAM metallopeptidase with thrombospondin type 1 motif, 1
GO	microtubule binding	1	58	0.989	1785 dynamin 2
GO	motor activity	3	64	0.989	1785 dynamin 2
GO	motor activity	3	64	0.989	4645 myosin VB
GO	motor activity	3	64	0.989	51168 myosin XVA
GO	post-Golgi vesicle-mediated transpor	2	37	0.989	1785 dynamin 2
GO	post-Golgi vesicle-mediated transpor	2	37	0.989	8673 vesicle-associated membrane protein 8 (endobrevin)
GO	aminopeptidase activity	1	28	0.989	1803 dipeptidyl-peptidase 4
GO	collagen binding	2	34	0.989	1803 dipeptidyl-peptidase 4
GO	collagen binding	2	34	0.989	22795 nidogen 2 (osteonidogen)
GO	response to cocaine	1	16	0.989	1813 dopamine receptor D2
GO	synapse assembly	2	33	0.989	1813 dopamine receptor D2
GO	synapse assembly	2	33	0.989	375790 agrin
GO	regulation of neuron differentiation	1	19	0.989	1822 atrophin 1
GO	regulation of heart contraction	2	32	0.989	1839 heparin-binding EGF-like growth factor
GO	regulation of heart contraction	2	32	0.989	8912 calcium channel, voltage-dependent, T type, alpha 1H subunit
GO	inactivation of MAPK activity	1	20	0.989	1844 dual specificity phosphatase 2
GO	glucose transport	1	22	0.989	1906 endothelin 1
GO	translation elongation factor activity	1	20	0.989	1915 eukaryotic translation elongation factor 1 alpha 1
GO	translational elongation	1	87	0.989	1915 eukaryotic translation elongation factor 1 alpha 1
GO	T cell differentiation	1	19	0.989	1958 early growth response 1
GO	myelination	1	29	0.989	1959 early growth response 2
GO	vasculogenesis	2	42	0.989	1969 EPH receptor A2
GO	vasculogenesis	2	42	0.989	3726 jun B proto-oncogene

GO	regulation of translational initiation	1	24	0.989	1983 eukaryotic translation initiation factor 5
GO	translation factor activity, nucleic aci	1	21	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	glycolysis	1	41	0.989	2026 enolase 2 (gamma, neuronal)
GO	synaptosome	5	91	0.989	2026 enolase 2 (gamma, neuronal)
GO	synaptosome	5	91	0.989	2353 FBJ murine osteosarcoma viral oncogene homolog
GO	synaptosome	5	91	0.989	3678 integrin, alpha 5 (fibronectin receptor, alpha polypeptide)
GO	synaptosome	5	91	0.989	4645 myosin VB
GO	synaptosome	5	91	0.989	6622 synuclein, alpha (non A4 component of amyloid precursor)
GO	histone acetyltransferase activity	2	38	0.989	2033 E1A binding protein p300
GO	histone acetyltransferase activity	2	38	0.989	55140 elongation protein 3 homolog ( <i>S. cerevisiae</i> )
GO	histone H4 acetylation	1	15	0.989	2033 E1A binding protein p300
GO	ceramide metabolic process	1	16	0.989	2055 ceroid-lipofuscinosis, neuronal 8 (epilepsy, progressive with mental ret
GO	ER-Golgi intermediate compartment	1	17	0.989	2055 ceroid-lipofuscinosis, neuronal 8 (epilepsy, progressive with mental ret
GO	lysosome organization	1	22	0.989	2055 ceroid-lipofuscinosis, neuronal 8 (epilepsy, progressive with mental ret
GO	positive regulation of epithelial cell p	2	34	0.989	2066 v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian)
GO	positive regulation of epithelial cell p	2	34	0.989	3479 insulin-like growth factor 1 (somatomedin C)
GO	mitochondrial outer membrane	5	81	0.989	2182 acyl-CoA synthetase long-chain family member 4
GO	mitochondrial outer membrane	5	81	0.989	4128 monoamine oxidase A
GO	mitochondrial outer membrane	5	81	0.989	4129 monoamine oxidase B
GO	mitochondrial outer membrane	5	81	0.989	4170 myeloid cell leukemia sequence 1 (BCL2-related)
GO	mitochondrial outer membrane	5	81	0.989	51703 acyl-CoA synthetase long-chain family member 5
GO	neuronal cell body	10	148	0.989	2182 acyl-CoA synthetase long-chain family member 4
GO	neuronal cell body	10	148	0.989	3759 potassium inwardly-rectifying channel, subfamily J, member 2
GO	neuronal cell body	10	148	0.989	429 achaete-scute complex homolog 1 ( <i>Drosophila</i> )
GO	neuronal cell body	10	148	0.989	4645 myosin VB
GO	neuronal cell body	10	148	0.989	4684 neural cell adhesion molecule 1
GO	neuronal cell body	10	148	0.989	4856 nephroblastoma overexpressed gene
GO	neuronal cell body	10	148	0.989	5025 purinergic receptor P2X, ligand-gated ion channel, 4
GO	neuronal cell body	10	148	0.989	5122 proprotein convertase subtilisin/kexin type 1
GO	neuronal cell body	10	148	0.989	6750 somatostatin
GO	neuronal cell body	10	148	0.989	799 calcitonin receptor
GO	peroxisomal membrane	1	41	0.989	2182 acyl-CoA synthetase long-chain family member 4
GO	peroxisome	1	92	0.989	2182 acyl-CoA synthetase long-chain family member 4
GO	chromosome, centromeric region	1	47	0.989	220359 tigger transposable element derived 3



GO	fibroblast growth factor receptor sigr	2	33	0.989	2263 fibroblast growth factor receptor 2
GO	fibroblast growth factor receptor sigr	2	33	0.989	26281 fibroblast growth factor 20
GO	positive regulation of cell cycle	1	15	0.989	2290 forkhead box G1
GO	cell development	1	15	0.989	2303 forkhead box C2 (MFH-1, mesenchyme forkhead 1)
GO	mesoderm development	1	27	0.989	2303 forkhead box C2 (MFH-1, mesenchyme forkhead 1)
GO	microtubule associated complex	1	25	0.989	23095 kinesin family member 1B
GO	protein C-terminus binding	9	146	0.989	23119 hypermethylated in cancer 2
GO	protein C-terminus binding	9	146	0.989	26119 low density lipoprotein receptor adaptor protein 1
GO	protein C-terminus binding	9	146	0.989	4692 necdin homolog (mouse)
GO	protein C-terminus binding	9	146	0.989	6494 signal-induced proliferation-associated 1
GO	protein C-terminus binding	9	146	0.989	6521 solute carrier family 4, anion exchanger, member 1 (erythrocyte memb
GO	protein C-terminus binding	9	146	0.989	774 calcium channel, voltage-dependent, N type, alpha 1B subunit
GO	protein C-terminus binding	9	146	0.989	79661 nei endonuclease VIII-like 1 (E. coli)
GO	protein C-terminus binding	9	146	0.989	8938 BAI1-associated protein 3
GO	protein C-terminus binding	9	146	0.989	9414 tight junction protein 2 (zona occludens 2)
GO	mitochondrial membrane	1	51	0.989	23151 GRAM domain containing 4
GO	protein kinase binding	7	113	0.989	23303 kinesin family member 13B
GO	protein kinase binding	7	113	0.989	3689 integrin, beta 2 (complement component 3 receptor 3 and 4 subunit)
GO	protein kinase binding	7	113	0.989	5801 protein tyrosine phosphatase, receptor type, R
GO	protein kinase binding	7	113	0.989	64127 nucleotide-binding oligomerization domain containing 2
GO	protein kinase binding	7	113	0.989	8313 axin 2
GO	protein kinase binding	7	113	0.989	8631 src kinase associated phosphoprotein 1
GO	protein kinase binding	7	113	0.989	8660 insulin receptor substrate 2
GO	GTPase binding	1	15	0.989	23348 dedicator of cytokinesis 9
GO	G-protein-coupled receptor binding	1	24	0.989	23365 Rho guanine nucleotide exchange factor (GEF) 12
GO	chromatin assembly or disassembly	1	36	0.989	23492 chromobox homolog 7
GO	chromatin binding	7	156	0.989	23492 chromobox homolog 7
GO	chromatin binding	7	156	0.989	2737 GLI family zinc finger 3
GO	chromatin binding	7	156	0.989	4087 SMAD family member 2
GO	chromatin binding	7	156	0.989	4286 microphthalmia-associated transcription factor
GO	chromatin binding	7	156	0.989	604 B-cell CLL/lymphoma 6
GO	chromatin binding	7	156	0.989	79987 sushi, von Willebrand factor type A, EGF and pentraxin domain contain
GO	chromatin binding	7	156	0.989	9324 high mobility group nucleosomal binding domain 3
GO	chromatin	4	81	0.989	23492 chromobox homolog 7
GO	chromatin	4	81	0.989	3726 jun B proto-oncogene
GO	chromatin	4	81	0.989	4613 v-myc myelocytomatosis viral related oncogene, neuroblastoma derive

GO chromatin	4	81	0.989	9324 high mobility group nucleosomal binding domain 3
GO single-stranded DNA binding	3	49	0.989	23648 single stranded DNA binding protein 3
GO single-stranded DNA binding	3	49	0.989	80169 chromosome 17 open reading frame 68
GO single-stranded DNA binding	3	49	0.989	8531 cold shock domain protein A
GO protein binding, bridging	2	44	0.989	23767 fibronectin leucine rich transmembrane protein 3
GO protein binding, bridging	2	44	0.989	26119 low density lipoprotein receptor adaptor protein 1
GO nuclear matrix	2	62	0.989	240 arachidonate 5-lipoxygenase
GO nuclear matrix	2	62	0.989	5371 promyelocytic leukemia
GO nuclear membrane	5	87	0.989	240 arachidonate 5-lipoxygenase
GO nuclear membrane	5	87	0.989	28959 transmembrane protein 176B
GO nuclear membrane	5	87	0.989	358 aquaporin 1 (Colton blood group)
GO nuclear membrane	5	87	0.989	3601 interleukin 15 receptor, alpha
GO nuclear membrane	5	87	0.989	5371 promyelocytic leukemia
GO ubiquitin ligase complex	3	54	0.989	255488 ring finger protein 144B
GO ubiquitin ligase complex	3	54	0.989	4008 LIM domain 7
GO ubiquitin ligase complex	3	54	0.989	79872 Cas-Br-M (murine) ecotropic retroviral transforming sequence-like 1
GO late endosome	2	43	0.989	255738 proprotein convertase subtilisin/kexin type 9
GO late endosome	2	43	0.989	5873 RAB27A, member RAS oncogene family
GO GABA-A receptor activity	1	19	0.989	2564 gamma-aminobutyric acid (GABA) A receptor, epsilon
GO gamma-aminobutyric acid signaling p	1	20	0.989	2564 gamma-aminobutyric acid (GABA) A receptor, epsilon
GO pyridoxal phosphate binding	2	51	0.989	2571 glutamate decarboxylase 1 (brain, 67kDa)
GO pyridoxal phosphate binding	2	51	0.989	55304 serine palmitoyltransferase, long chain base subunit 3
GO vesicle membrane	1	15	0.989	2571 glutamate decarboxylase 1 (brain, 67kDa)
GO manganese ion binding	1	32	0.989	2589 UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosami
GO Rab GTPase binding	2	33	0.989	259173 ALS2 C-terminal like
GO Rab GTPase binding	2	33	0.989	4645 myosin VB
GO isomerase activity	4	99	0.989	26035 glucuronic acid epimerase
GO isomerase activity	4	99	0.989	51303 FK506 binding protein 11, 19 kDa
GO isomerase activity	4	99	0.989	6916 thromboxane A synthase 1 (platelet)
GO isomerase activity	4	99	0.989	81888 hydroxypyruvate isomerase homolog (E. coli)
GO generation of precursor metabolites	3	55	0.989	2642 glucagon receptor
GO generation of precursor metabolites	3	55	0.989	862 runt-related transcription factor 1; translocated to, 1 (cyclin D-related)
GO generation of precursor metabolites	3	55	0.989	9481 solute carrier family 25, member 27
GO peptide hormone binding	1	22	0.989	2642 glucagon receptor
GO electron transport chain	4	86	0.989	27035 NADPH oxidase 1
GO electron transport chain	4	86	0.989	55068 ecto-NOX disulfide-thiol exchanger 1

GO	electron transport chain	4	86	0.989	56605 ERO1-like beta ( <i>S. cerevisiae</i> )
GO	electron transport chain	4	86	0.989	79152 fatty acid 2-hydroxylase
GO	male genitalia development	1	17	0.989	2706 gap junction protein, beta 2, 26kDa
GO	purine ribonucleoside monophospha	1	17	0.989	271 adenosine monophosphate deaminase 2
GO	chemotaxis	7	117	0.989	27202 G protein-coupled receptor 77
GO	chemotaxis	7	117	0.989	2921 chemokine (C-X-C motif) ligand 3
GO	chemotaxis	7	117	0.989	3491 cysteine-rich, angiogenic inducer, 61
GO	chemotaxis	7	117	0.989	56477 chemokine (C-C motif) ligand 28
GO	chemotaxis	7	117	0.989	5724 platelet-activating factor receptor
GO	chemotaxis	7	117	0.989	6372 chemokine (C-X-C motif) ligand 6 (granulocyte chemotactic protein 2)
GO	chemotaxis	7	117	0.989	6374 chemokine (C-X-C motif) ligand 5
GO	neuron apoptosis	1	16	0.989	27242 tumor necrosis factor receptor superfamily, member 21
GO	anterior/posterior pattern formation	4	81	0.989	2737 GLI family zinc finger 3
GO	anterior/posterior pattern formation	4	81	0.989	28996 homeodomain interacting protein kinase 2
GO	anterior/posterior pattern formation	4	81	0.989	4087 SMAD family member 2
GO	anterior/posterior pattern formation	4	81	0.989	7026 nuclear receptor subfamily 2, group F, member 2
GO	cilium	2	90	0.989	2737 GLI family zinc finger 3
GO	cilium	2	90	0.989	5132 phosducin
GO	embryonic skeletal system morphoge	2	36	0.989	2737 GLI family zinc finger 3
GO	embryonic skeletal system morphoge	2	36	0.989	57453 Down syndrome cell adhesion molecule like 1
GO	histone deacetylase binding	2	39	0.989	2737 GLI family zinc finger 3
GO	histone deacetylase binding	2	39	0.989	9734 histone deacetylase 9
GO	mediator complex	1	31	0.989	2737 GLI family zinc finger 3
GO	proximal/distal pattern formation	1	22	0.989	2737 GLI family zinc finger 3
GO	DNA replication	3	146	0.989	27434 polymerase (DNA directed), mu
GO	DNA replication	3	146	0.989	3479 insulin-like growth factor 1 (somatomedin C)
GO	DNA replication	3	146	0.989	4784 nuclear factor I/X (CCAAT-binding transcription factor)
GO	DNA-directed DNA polymerase activi	1	30	0.989	27434 polymerase (DNA directed), mu
GO	guanyl nucleotide binding	1	17	0.989	2769 guanine nucleotide binding protein (G protein), alpha 15 (Gq class)
GO	protein amino acid ADP-ribosylation	1	22	0.989	2769 guanine nucleotide binding protein (G protein), alpha 15 (Gq class)
GO	cellular iron ion homeostasis	1	24	0.989	286133 scavenger receptor class A, member 5 (putative)
GO	induction of apoptosis by intracellula	1	15	0.989	28996 homeodomain interacting protein kinase 2
GO	protein ubiquitination	4	85	0.989	29116 myosin regulatory light chain interacting protein
GO	protein ubiquitination	4	85	0.989	4008 LIM domain 7
GO	protein ubiquitination	4	85	0.989	54876 DDB1 and CUL4 associated factor 16
GO	protein ubiquitination	4	85	0.989	79872 Cas-Br-M (murine) ecotropic retroviral transforming sequence-like 1

GO	negative regulation of T cell proliferation	1	18	0.989	29126 CD274 molecule
GO	glutathione transferase activity	1	17	0.989	2947 glutathione S-transferase mu 3 (brain)
GO	biosynthetic process	2	49	0.989	3034 histidine ammonia-lyase
GO	biosynthetic process	2	49	0.989	55304 serine palmitoyltransferase, long chain base subunit 3
GO	cell division	6	246	0.989	311 annexin A11
GO	cell division	6	246	0.989	3993 lethal giant larvae homolog 2 (Drosophila)
GO	cell division	6	246	0.989	5218 cyclin-dependent kinase 14
GO	cell division	6	246	0.989	57132 chromatin modifying protein 1B
GO	cell division	6	246	0.989	8556 CDC14 cell division cycle 14 homolog A (S. cerevisiae)
GO	cell division	6	246	0.989	8900 cyclin A1
GO	midbody	1	25	0.989	311 annexin A11
GO	spindle	3	90	0.989	311 annexin A11
GO	spindle	3	90	0.989	56288 par-3 partitioning defective 3 homolog (C. elegans)
GO	spindle	3	90	0.989	8556 CDC14 cell division cycle 14 homolog A (S. cerevisiae)
GO	MHC class I protein complex	1	18	0.989	3134 major histocompatibility complex, class I, F
GO	NAD or NADH binding	1	37	0.989	316 aldehyde oxidase 1
GO	positive regulation of mitotic cell cycle	1	16	0.989	3169 forkhead box A1
GO	heterogeneous nuclear ribonucleoprotein complex	1	15	0.989	3192 heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor 1)
GO	ribonucleoprotein complex	1	95	0.989	3192 heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor 1)
GO	spliceosomal complex	1	118	0.989	3192 heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor 1)
GO	steroid biosynthetic process	1	30	0.989	3294 hydroxysteroid (17-beta) dehydrogenase 2
GO	unfolded protein binding	4	103	0.989	3306 heat shock 70kDa protein 2
GO	unfolded protein binding	4	103	0.989	56605 ERO1-like beta (S. cerevisiae)
GO	unfolded protein binding	4	103	0.989	84277 DnaJ (Hsp40) homolog, subfamily C, member 30
GO	unfolded protein binding	4	103	0.989	9804 translocase of outer mitochondrial membrane 20 homolog (yeast)
GO	G1/S transition of mitotic cell cycle	2	42	0.989	3400 inhibitor of DNA binding 4, dominant negative helix-loop-helix protein
GO	G1/S transition of mitotic cell cycle	2	42	0.989	91 activin A receptor, type IB
GO	hippocampus development	1	20	0.989	3400 inhibitor of DNA binding 4, dominant negative helix-loop-helix protein
GO	lipid catabolic process	5	90	0.989	340654 lipase, family member M
GO	lipid catabolic process	5	90	0.989	5346 perilipin 1
GO	lipid catabolic process	5	90	0.989	57104 patatin-like phospholipase domain containing 2
GO	lipid catabolic process	5	90	0.989	7941 phospholipase A2, group VII (platelet-activating factor acetylhydrolase, cytosolic)
GO	lipid catabolic process	5	90	0.989	79887 phospholipase B domain containing 1
GO	activation of pro-apoptotic gene expression	1	22	0.989	3429 interferon, alpha-inducible protein 27
GO	cilium axoneme	1	26	0.989	345895 radial spoke head 4 homolog A (Chlamydomonas)
GO	phosphoinositide-mediated signaling	2	33	0.989	3479 insulin-like growth factor 1 (somatomedin C)

GO phosphoinositide-mediated signaling	2	33	0.989	5724 platelet-activating factor receptor
GO Ras protein signal transduction	4	64	0.989	3479 insulin-like growth factor 1 (somatomedin C)
GO Ras protein signal transduction	4	64	0.989	3845 v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog
GO Ras protein signal transduction	4	64	0.989	5900 ral guanine nucleotide dissociation stimulator
GO Ras protein signal transduction	4	64	0.989	6239 ras responsive element binding protein 1
GO negative regulation of translation	1	18	0.989	3488 insulin-like growth factor binding protein 5
GO acyl-CoA binding	1	15	0.989	35 acyl-Coenzyme A dehydrogenase, C-2 to C-3 short chain
GO fatty acid beta-oxidation	1	21	0.989	35 acyl-Coenzyme A dehydrogenase, C-2 to C-3 short chain
GO platelet activation	1	24	0.989	3569 interleukin 6 (interferon, beta 2)
GO positive regulation of T cell proliferat	1	27	0.989	3569 interleukin 6 (interferon, beta 2)
GO brush border	1	22	0.989	358 aquaporin 1 (Colton blood group)
GO cytokine receptor activity	1	17	0.989	3601 interleukin 15 receptor, alpha
GO endosome membrane	5	92	0.989	3643 insulin receptor
GO endosome membrane	5	92	0.989	3665 interferon regulatory factor 7
GO endosome membrane	5	92	0.989	3949 low density lipoprotein receptor
GO endosome membrane	5	92	0.989	55275 vacuolar protein sorting 53 homolog ( <i>S. cerevisiae</i> )
GO endosome membrane	5	92	0.989	7098 toll-like receptor 3
GO negative regulation of gene expressic	1	23	0.989	3643 insulin receptor
GO response to activity	1	18	0.989	3643 insulin receptor
GO response to tumor necrosis factor	1	17	0.989	3643 insulin receptor
GO sarcoplasmic reticulum membrane	1	17	0.989	3709 inositol 1,4,5-triphosphate receptor, type 2
GO nuclear chromatin	1	16	0.989	3725 jun oncogene
GO nuclear chromosome	1	23	0.989	3725 jun oncogene
GO structural constituent of cytoskeleton	2	73	0.989	375790 agrin
GO structural constituent of cytoskeleton	2	73	0.989	6710 spectrin, beta, erythrocytic
GO protein secretion	1	16	0.989	379 ADP-ribosylation factor-like 4D
GO intracellular membrane-bounded org	8	127	0.989	3790 potassium voltage-gated channel, delayed-rectifier, subfamily S, memb
GO intracellular membrane-bounded org	8	127	0.989	3959 lectin, galactoside-binding, soluble, 3 binding protein
GO intracellular membrane-bounded org	8	127	0.989	4209 myocyte enhancer factor 2D
GO intracellular membrane-bounded org	8	127	0.989	4582 mucin 1, cell surface associated
GO intracellular membrane-bounded org	8	127	0.989	4794 nuclear factor of kappa light polypeptide gene enhancer in B-cells inhib
GO intracellular membrane-bounded org	8	127	0.989	54947 lysophosphatidylcholine acyltransferase 2
GO intracellular membrane-bounded org	8	127	0.989	7049 transforming growth factor, beta receptor III
GO intracellular membrane-bounded org	8	127	0.989	80763 chromosome 12 open reading frame 39
GO transcription	1	69	0.989	388558 zinc finger protein 808
GO focal adhesion assembly	1	15	0.989	3911 laminin, alpha 5

GO	coated pit	2	41	0.989	3949 low density lipoprotein receptor
GO	coated pit	2	41	0.989	9892 synaptosomal-associated protein, 91kDa homolog (mouse)
GO	actin filament	1	28	0.989	395 Rho GTPase activating protein 6
GO	regulation of GTPase activity	1	16	0.989	395 Rho GTPase activating protein 6
GO	collagen	1	22	0.989	4015 lysyl oxidase
GO	enzyme activator activity	1	40	0.989	4056 leukotriene C4 synthase
GO	nuclear outer membrane	1	20	0.989	4056 leukotriene C4 synthase
GO	gastrulation	1	15	0.989	4087 SMAD family member 2
GO	insulin secretion	1	23	0.989	4087 SMAD family member 2
GO	protein N-terminus binding	3	72	0.989	4204 methyl CpG binding protein 2 (Rett syndrome)
GO	protein N-terminus binding	3	72	0.989	4778 nuclear factor (erythroid-derived 2), 45kDa
GO	protein N-terminus binding	3	72	0.989	9143 synaptogyrin 3
GO	cerebral cortex development	1	16	0.989	429 achaete-scute complex homolog 1 (Drosophila)
GO	muscle contraction	6	97	0.989	4638 myosin light chain kinase
GO	muscle contraction	6	97	0.989	6535 solute carrier family 6 (neurotransmitter transporter, creatine), member 1
GO	muscle contraction	6	97	0.989	7170 tropomyosin 3
GO	muscle contraction	6	97	0.989	8082 sarcospan (Kras oncogene-associated gene)
GO	muscle contraction	6	97	0.989	8736 myomesin 1, 185kDa
GO	muscle contraction	6	97	0.989	8912 calcium channel, voltage-dependent, T type, alpha 1H subunit
GO	myosin complex	2	41	0.989	4645 myosin VB
GO	myosin complex	2	41	0.989	51168 myosin XVA
GO	regulation of protein localization	1	18	0.989	4645 myosin VB
GO	centrosome	2	117	0.989	4692 necdin homolog (mouse)
GO	centrosome	2	117	0.989	55762 zinc finger protein 701
GO	neuron development	1	27	0.989	4692 necdin homolog (mouse)
GO	4 iron, 4 sulfur cluster binding	1	25	0.989	48 aconitase 1, soluble
GO	tricarboxylic acid cycle	1	21	0.989	48 aconitase 1, soluble
GO	hair follicle morphogenesis	1	16	0.989	4851 Notch homolog 1, translocation-associated (Drosophila)
GO	cation transport	2	65	0.989	493 ATPase, Ca <sup>++</sup> transporting, plasma membrane 4
GO	cation transport	2	65	0.989	9914 ATPase, Ca <sup>++</sup> transporting, type 2C, member 2
GO	nucleotidyltransferase activity	2	71	0.989	4939 2'-5'-oligoadenylate synthetase 2, 69/71kDa
GO	nucleotidyltransferase activity	2	71	0.989	9060 3'-phosphoadenosine 5'-phosphosulfate synthase 2
GO	mitochondrial proton-transporting A <sup>+</sup>	1	16	0.989	498 ATP synthase, H <sup>+</sup> transporting, mitochondrial F1 complex, alpha subunit
GO	endopeptidase activity	1	15	0.989	5046 proprotein convertase subtilisin/kexin type 6
GO	amino acid binding	1	15	0.989	5053 phenylalanine hydroxylase
GO	cellular amino acid biosynthetic process	1	24	0.989	5053 phenylalanine hydroxylase

GO cofactor binding	1	19	0.989	5053 phenylalanine hydroxylase
GO acid-amino acid ligase activity	2	34	0.989	5071 Parkinson disease (autosomal recessive, juvenile) 2, parkin
GO acid-amino acid ligase activity	2	34	0.989	7706 tripartite motif-containing 25
GO kinase binding	1	27	0.989	5071 Parkinson disease (autosomal recessive, juvenile) 2, parkin
GO neuron projection	2	60	0.989	5071 Parkinson disease (autosomal recessive, juvenile) 2, parkin
GO neuron projection	2	60	0.989	6857 synaptotagmin I
GO protein polyubiquitination	1	25	0.989	5071 Parkinson disease (autosomal recessive, juvenile) 2, parkin
GO chromosome	2	135	0.989	50809 heterochromatin protein 1, binding protein 3
GO chromosome	2	135	0.989	80169 chromosome 17 open reading frame 68
GO nucleosome assembly	1	65	0.989	50809 heterochromatin protein 1, binding protein 3
GO nucleosome	1	52	0.989	50809 heterochromatin protein 1, binding protein 3
GO trans-Golgi network	3	51	0.989	5122 proprotein convertase subtilisin/kexin type 1
GO trans-Golgi network	3	51	0.989	64083 golgi phosphoprotein 3 (coat-protein)
GO trans-Golgi network	3	51	0.989	9435 carbohydrate (N-acetylglucosamine-6-O) sulfotransferase 2
GO SNAP receptor activity	1	20	0.989	51272 blocked early in transport 1 homolog ( <i>S. cerevisiae</i> )-like
GO peptidyl-prolyl cis-trans isomerase ac	1	32	0.989	51303 FK506 binding protein 11, 19 kDa
GO phototransduction	1	21	0.989	5132 phosducin
GO calcium channel activity	3	44	0.989	53373 two pore segment channel 1
GO calcium channel activity	3	44	0.989	783 calcium channel, voltage-dependent, beta 2 subunit
GO calcium channel activity	3	44	0.989	93589 calcium channel, voltage-dependent, alpha 2/delta subunit 4
GO microtubule organizing center	4	96	0.989	53405 chloride intracellular channel 5
GO microtubule organizing center	4	96	0.989	642273 family with sequence similarity 110, member C
GO microtubule organizing center	4	96	0.989	8556 CDC14 cell division cycle 14 homolog A ( <i>S. cerevisiae</i> )
GO microtubule organizing center	4	96	0.989	90362 family with sequence similarity 110, member B
GO lactation	1	28	0.989	5367 pro-melanin-concentrating hormone
GO negative regulation of angiogenesis	1	28	0.989	5371 promyelocytic leukemia
GO response to UV	1	30	0.989	5371 promyelocytic leukemia
GO sex differentiation	1	23	0.989	54361 wingless-type MMTV integration site family, member 4
GO cis-Golgi network	1	17	0.989	54463 family with sequence similarity 134, member B
GO methyltransferase activity	2	106	0.989	54904 Wolf-Hirschhorn syndrome candidate 1-like 1
GO methyltransferase activity	2	106	0.989	55870 ash1 (absent, small, or homeotic)-like ( <i>Drosophila</i> )
GO N-acetyltransferase activity	1	20	0.989	55140 elongation protein 3 homolog ( <i>S. cerevisiae</i> )
GO spindle pole	2	50	0.989	55200 pleckstrin homology domain containing, family G (with RhoGef domain)
GO spindle pole	2	50	0.989	642273 family with sequence similarity 110, member C
GO endoplasmic reticulum unfolded prot	1	20	0.989	55432 YOD1 OTU deubiquinating enzyme 1 homolog ( <i>S. cerevisiae</i> )
GO ubiquitin-specific protease activity	1	28	0.989	55432 YOD1 OTU deubiquinating enzyme 1 homolog ( <i>S. cerevisiae</i> )

GO	ATP-dependent helicase activity	2	61	0.989	55601 DEAD (Asp-Glu-Ala-Asp) box polypeptide 60
GO	ATP-dependent helicase activity	2	61	0.989	8653 DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, Y-linked
GO	helicase activity	5	107	0.989	55601 DEAD (Asp-Glu-Ala-Asp) box polypeptide 60
GO	helicase activity	5	107	0.989	64135 interferon induced with helicase C domain 1
GO	helicase activity	5	107	0.989	79132 DEXH (Asp-Glu-X-His) box polypeptide 58
GO	helicase activity	5	107	0.989	85441 peroxisomal proliferator-activated receptor A interacting complex 285
GO	helicase activity	5	107	0.989	8653 DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, Y-linked
GO	filopodium	1	25	0.989	55740 enabled homolog (Drosophila)
GO	intracellular transport	1	17	0.989	55740 enabled homolog (Drosophila)
GO	cAMP binding	1	17	0.989	5577 protein kinase, cAMP-dependent, regulatory, type II, beta
GO	cAMP-dependent protein kinase regu	1	16	0.989	5577 protein kinase, cAMP-dependent, regulatory, type II, beta
GO	MAPKKK cascade	1	31	0.989	55816 docking protein 5
GO	cytokinesis	1	34	0.989	55909 bridging integrator 3
GO	cardiac muscle contraction	1	17	0.989	5608 mitogen-activated protein kinase kinase 6
GO	anaphase-promoting complex-depen	3	63	0.989	5696 proteasome (prosome, macropain) subunit, beta type, 8 (large multifur
GO	anaphase-promoting complex-depen	3	63	0.989	5698 proteasome (prosome, macropain) subunit, beta type, 9 (large multifur
GO	anaphase-promoting complex-depen	3	63	0.989	5699 proteasome (prosome, macropain) subunit, beta type, 10
GO	negative regulation of ubiquitin-prote	3	62	0.989	5696 proteasome (prosome, macropain) subunit, beta type, 8 (large multifur
GO	negative regulation of ubiquitin-prote	3	62	0.989	5698 proteasome (prosome, macropain) subunit, beta type, 9 (large multifur
GO	negative regulation of ubiquitin-prote	3	62	0.989	5699 proteasome (prosome, macropain) subunit, beta type, 10
GO	positive regulation of ubiquitin-prote	3	65	0.989	5696 proteasome (prosome, macropain) subunit, beta type, 8 (large multifur
GO	positive regulation of ubiquitin-prote	3	65	0.989	5698 proteasome (prosome, macropain) subunit, beta type, 9 (large multifur
GO	positive regulation of ubiquitin-prote	3	65	0.989	5699 proteasome (prosome, macropain) subunit, beta type, 10
GO	proteasome complex	3	56	0.989	5696 proteasome (prosome, macropain) subunit, beta type, 8 (large multifur
GO	proteasome complex	3	56	0.989	5698 proteasome (prosome, macropain) subunit, beta type, 9 (large multifur
GO	proteasome complex	3	56	0.989	5699 proteasome (prosome, macropain) subunit, beta type, 10
GO	triglyceride lipase activity	1	16	0.989	57104 patatin-like phospholipase domain containing 2
GO	late endosome membrane	1	51	0.989	57132 chromatin modifying protein 1B
GO	protein amino acid N-linked glycosyla	1	15	0.989	57134 mannosidase, alpha, class 1C, member 1
GO	ARF guanyl-nucleotide exchange fact	1	17	0.989	57221 KIAA1244
GO	regulation of ARF protein signal trans	1	16	0.989	57221 KIAA1244
GO	peroxidase activity	1	17	0.989	5742 prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase a
GO	dephosphorylation	1	21	0.989	5787 protein tyrosine phosphatase, receptor type, B
GO	embryonic skeletal system developm	1	23	0.989	5950 retinol binding protein 4, plasma
GO	voltage-gated sodium channel activit	1	15	0.989	6330 sodium channel, voltage-gated, type IV, beta
GO	metal ion transmembrane transporte	1	16	0.989	64116 solute carrier family 39 (zinc transporter), member 8



GO metal ion transport	1	20	0.989	64116 solute carrier family 39 (zinc transporter), member 8
GO zinc ion transport	1	24	0.989	64116 solute carrier family 39 (zinc transporter), member 8
GO defense response to bacterium	4	75	0.989	64127 nucleotide-binding oligomerization domain containing 2
GO defense response to bacterium	4	75	0.989	7098 toll-like receptor 3
GO defense response to bacterium	4	75	0.989	7099 toll-like receptor 4
GO defense response to bacterium	4	75	0.989	7100 toll-like receptor 5
GO positive regulation of protein ubiquit	1	25	0.989	64127 nucleotide-binding oligomerization domain containing 2
GO vesicle	1	17	0.989	64127 nucleotide-binding oligomerization domain containing 2
GO chemoattractant activity	1	15	0.989	652 bone morphogenetic protein 4
GO germ cell development	1	22	0.989	652 bone morphogenetic protein 4
GO growth	1	29	0.989	652 bone morphogenetic protein 4
GO positive regulation of endothelial cell	2	31	0.989	652 bone morphogenetic protein 4
GO positive regulation of endothelial cell	2	31	0.989	7474 wingless-type MMTV integration site family, member 5A
GO neurotransmitter transport	1	40	0.989	6535 solute carrier family 6 (neurotransmitter transporter, creatine), membe
GO amino acid transport	1	46	0.989	6542 solute carrier family 7 (cationic amino acid transporter, $\gamma^+$ system), me
GO SWI/SNF complex	1	15	0.989	6604 SWI/SNF related, matrix associated, actin dependent regulator of chrom
GO growth cone	3	58	0.989	6622 synuclein, alpha (non A4 component of amyloid precursor)
GO growth cone	3	58	0.989	7170 tropomyosin 3
GO growth cone	3	58	0.989	81544 glycerophosphodiester phosphodiesterase domain containing 5
GO keratinization	1	31	0.989	6706 small proline-rich protein 2G
GO vesicle docking involved in exocytosis	1	19	0.989	6812 syntaxin binding protein 1
GO mannose binding	1	16	0.989	682 basigin (Ok blood group)
GO non-membrane spanning protein tyros	1	40	0.989	6850 spleen tyrosine kinase
GO endocytic vesicle membrane	1	22	0.989	6857 synaptotagmin I
GO hydrogen peroxide catabolic process	1	16	0.989	7001 peroxiredoxin 2
GO thymus development	1	23	0.989	7001 peroxiredoxin 2
GO response to zinc ion	1	18	0.989	760 carbonic anhydrase II
GO C-C chemokine receptor activity	1	16	0.989	7852 chemokine (C-X-C motif) receptor 4
GO cell leading edge	1	17	0.989	7852 chemokine (C-X-C motif) receptor 4
GO DNA fragmentation involved in apopt	1	18	0.989	79444 baculoviral IAP repeat-containing 7
GO base-excision repair	1	19	0.989	79661 nei endonuclease VIII-like 1 (E. coli)
GO damaged DNA binding	1	44	0.989	79661 nei endonuclease VIII-like 1 (E. coli)
GO nucleotide-excision repair	1	26	0.989	79661 nei endonuclease VIII-like 1 (E. coli)
GO iron ion transport	1	22	0.989	79689 STEAP family member 4
GO flagellum	1	19	0.989	79820 cation channel, sperm-associated, beta
GO phospholipid transport	1	18	0.989	79895 ATPase, class I, type 8B, member 4

GO nuclear chromosome, telomeric region	1	16	0.989	80169 chromosome 17 open reading frame 68
GO telomere maintenance	1	19	0.989	80169 chromosome 17 open reading frame 68
GO cell adhesion molecule binding	1	15	0.989	819 calcium modulating ligand
GO nucleoside metabolic process	1	16	0.989	8382 non-metastatic cells 5, protein expressed in (nucleoside-diphosphate kinase)
GO nucleoside-triphosphatase activity	1	59	0.989	83858 ATPase family, AAA domain containing 3B
GO protein serine/threonine phosphatase activity	1	37	0.989	84919 protein phosphatase 1, regulatory (inhibitor) subunit 15B
GO estrogen receptor binding	1	15	0.989	85004 RAS-like, estrogen-regulated, growth inhibitor
GO diacylglycerol kinase activity	1	15	0.989	8527 diacylglycerol kinase, delta 130kDa
GO fertilization	1	17	0.989	8531 cold shock domain protein A
GO mRNA 3'-UTR binding	1	17	0.989	8531 cold shock domain protein A
GO high-density lipoprotein particle	1	19	0.989	8542 apolipoprotein L, 1
GO very-low-density lipoprotein particle	1	19	0.989	8542 apolipoprotein L, 1
GO T cell receptor signaling pathway	1	22	0.989	8631 src kinase associated phosphoprotein 1
GO endonuclease activity	1	57	0.989	8635 ribonuclease T2
GO gastrulation with mouth forming secondary palate	1	21	0.989	8646 chordin
GO positive regulation of cell adhesion	1	20	0.989	8646 chordin
GO cellular membrane fusion	1	22	0.989	8673 vesicle-associated membrane protein 8 (endobrevin)
GO neuropeptide hormone activity	1	21	0.989	885 cholecystokinin
GO mitosis	1	199	0.989	8900 cyclin A1
GO MAP kinase kinase kinase activity	1	15	0.989	9064 mitogen-activated protein kinase kinase kinase 6
GO growth factor binding	1	23	0.989	91 activin A receptor, type IB
GO peptidyl-threonine phosphorylation	1	18	0.989	91 activin A receptor, type IB
GO neuromuscular junction	1	24	0.989	9143 synaptogyrin 3
GO endosome transport	1	21	0.989	9182 Ras association (RalGDS/AF-6) domain family (N-terminal) member 9
GO thyroid hormone receptor binding	1	25	0.989	9324 high mobility group nucleosomal binding domain 3
GO RNA metabolic process	1	19	0.989	94059 leukocyte receptor cluster (LRC) member 9
GO N-acetylglucosamine metabolic process	1	15	0.989	9435 carbohydrate (N-acetylglucosamine-6-O) sulfotransferase 2
GO cholesterol binding	1	18	0.989	9619 ATP-binding cassette, sub-family G (WHITE), member 1
GO cholesterol efflux	1	19	0.989	9619 ATP-binding cassette, sub-family G (WHITE), member 1
GO reverse cholesterol transport	1	15	0.989	9619 ATP-binding cassette, sub-family G (WHITE), member 1
GO histone methyltransferase complex	1	17	0.989	9734 histone deacetylase 9
GO phosphoprotein phosphatase inhibitor activity	1	18	0.989	9749 phosphatase and actin regulator 2
GO protein targeting to mitochondrion	1	25	0.989	9804 translocase of outer mitochondrial membrane 20 homolog (yeast)
GO regulation of endocytosis	1	15	0.989	9892 synaptosomal-associated protein, 91kDa homolog (mouse)
GO male germ cell nucleus	1	15	0.989	9985 REC8 homolog (yeast)
GO reciprocal meiotic recombination	1	22	0.989	9985 REC8 homolog (yeast)



ed, (semaphorin) 3D

nyltransferase 1 (GalNAc-T1)

a and mu polypeptides

er A1

) 3

t of Ra-reactive factor)

ed, (semaphorin) 3B  
, plasma)

ing 1

invertase)

1 domains), member 2  
unit A3

od group)



beta member 4

ific cross reacting antigen)

porter, system Xag), member 1  
brane protein band 3, Diego blood group)  
er 8  
mber 2  
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ut an intracellular domain

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t of Ra-reactive factor)

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sette sub-family C, member 7)

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ed, (semaphorin) 3D

l group)

nyltransferase 1 (GalNAc-T1)

:osaminide alpha-2,6-sialyltransferase 4

beta member 4

nyltransferase-like 4

. subfamily N, member 4





:osaminide alpha-2,6-sialyltransferase 1

transferase, 1

porter, system Xag), member 1  
brane protein band 3, Diego blood group)  
er 8  
mber 2

ed, (semaphorin) 3B

nyltransferase 12 (GalNAc-T12)

ing 1

truncated death domain

od group)

i) member 3

i) member 7

i) member 6

M) and short cytoplasmic domain, (semaphorin 4D

sette sub-family C, member 7)

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3 synthase)

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nyltransferase 1 (GalNAc-T1)

:osaminide alpha-2,6-sialyltransferase 4

nyltransferase-like 4

. subfamily N, member 3

. subfamily N, member 4



:osaminide alpha-2,6-sialyltransferase 1

transferase, 1



nyltransferase 12 (GalNAc-T12)

ber 2

runcated death domain









itor, alpha





78 (mouse)  
fic cross reacting antigen)  
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truncated death domain  
with an intracellular domain

Unit A3

sette sub-family C, member 7)

beta member 4



. subfamily N, member 3

. subfamily N, member 4

er 3

it 1, cardiac muscle

er 8

ber 2

i) member 3

ii) member 7

iii) member 6

√ domains), member 2  
unit A3

TM) and short cytoplasmic domain, (semaphorin) 4D

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od group)



. subfamily N, member 3  
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fic cross reacting antigen)

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ut an intracellular domain

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ific cross reacting antigen)

ut an intracellular domain

unit A3

ette sub-family C, member 7)

1 domains), member 2

TM) and short cytoplasmic domain, (semaphorin) 4D

α and μ polypeptides

sette sub-family C, member 7)

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3



TM) and short cytoplasmic domain, (semaphorin) 4D

ed, (semaphorin) 3D

transferase, 1

ed, (semaphorin) 3B

inase)



M) and short cytoplasmic domain, (semaphorin) 4D

ing 1



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sette sub-family C, member 7)

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itor, alpha

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itor, alpha

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nd cyclooxygenase)

nd cyclooxygenase)

II phosphatase 2







transferase, 1

nd cyclooxygenase)







1 domains), member 2

ic cross reacting antigen)

2 gamma)

ed, (semaphorin) 3B

sette sub-family C, member 7)

invertase)









Il phosphatase 2





transferase, 1

unit A3



beta member 4

. subfamily N, member 4

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:osaminide alpha-2,6-sialyltransferase 4

:osaminide alpha-2,6-sialyltransferase 1

2 gamma)

78 (mouse)

invertase)

sette sub-family C, member 7)







ardation)

nd cyclooxygenase)



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invertase)

matin, subfamily d, member 3





ardation)

i) member 3



i) member 7

i) member 6

invertase)



sette sub-family C, member 7)

itor, alpha  
itor, epsilon  
itor-like 1

nd cyclooxygenase)

l-acetylneuraminate monooxygenase) pseudogene

ber 2

nd cyclooxygenase)



sette sub-family C, member 7)

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Unit A3

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subfamily N, member 4

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itor, alpha

itor, alpha

nd cyclooxygenase)

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78 (mouse)

t of Ra-reactive factor)

nctional peptidase 7)

nctional peptidase 2)

nvertase)

nyltransferase 1 (GalNAc-T1)  
nyltransferase-like 4

nyltransferase 12 (GalNAc-T12)

sette sub-family C, member 7)

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beta member 4

or A)

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78 (mouse)  
:d (avian)

19/p100)  
)itor, alpha  
)itor, epsilon  
)itor-like 1

it 1, cardiac muscle

t of Ra-reactive factor)  
nctional peptidase 7)

porter, system Xag), member 1

brane protein band 3, Diego blood group)

matin, subfamily d, member 3

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runcated death domain



itor, alpha

invertase)

uncated death domain  
ut an intracellular domain

nd cyclooxygenase)

brane protein band 3, Diego blood group)

3 synthase)  
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:osaminide alpha-2,6-sialyltransferase 4

:osaminide alpha-2,6-sialyltransferase 1

truncated death domain  
with an intracellular domain

itor, alpha

invertase)





t of Ra-reactive factor)



t of Ra-reactive factor)

transferrin receptor protein band 3, Diego blood group)

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transferrin receptor, alpha

transferrin receptor, subfamily d, member 3

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itor, alpha

3 synthase)

:osaminide alpha-2,6-sialyltransferase 4

nyltransferase-like 4

:osaminide alpha-2,6-sialyltransferase 1

nyltransferase 12 (GalNAc-T12)

1 domains), member 2

M) and short cytoplasmic domain, (semaphorin) 4D

ed, (semaphorin) 3D





ed, (semaphorin) 3B

od group)



t of Ra-reactive factor)

invertase)

prane protein band 3, Diego blood group)

it 1, cardiac muscle

matin, subfamily d, member 3

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Director, alpha





TM) and short cytoplasmic domain, (semaphorin) 4D

ceptor, alpha

inase)  
runcated death domain

inase)

3

beta member 4

. subfamily N, member 4

:osaminide alpha-2,6-sialyltransferase 4

:osaminide alpha-2,6-sialyltransferase 1

invertase)  
nctional peptidase 7)  
nctional peptidase 2)

3 synthase)

sette sub-family C, member 7)

sette sub-family C, member 7)

3 synthase)

:osaminide alpha-2,6-sialyltransferase 4





:osaminide alpha-2,6-sialyltransferase 1

t of Ra-reactive factor)  
transferase, 1

sporter, system Xag), member 1

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er 8

er 8



l-acetylneuraminate monooxygenase) pseudogene

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it 1, cardiac muscle

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nd cyclooxygenase)

, plasma)

sette sub-family C, member 7)

nd cyclooxygenase)

l-acetylneuraminate monooxygenase) pseudogene

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itor, alpha







sette sub-family C, member 7)

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ardation)

78 (mouse)



a and mu polypeptides

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it 1, cardiac muscle

sette sub-family C, member 7)

beta member 4

. subfamily N, member 3

. subfamily N, member 4



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TM) and short cytoplasmic domain, (semaphorin) 4D

ed, (semaphorin) 3D

transferase, 1

sette sub-family C, member 7)

sette sub-family C, member 7)

nd cyclooxygenase)

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nd cyclooxygenase)



ed, (semaphorin) 3B

ardation)

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invertase)

nyltransferase 1 (GalNAc-T1)  
nyltransferase-like 4  
nyltransferase 12 (GalNAc-T12)

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beta member 4

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3 synthase)  
d group)

nyltransferase 1 (GalNAc-T1)

:osaminide alpha-2,6-sialyltransferase 4

nyltransferase-like 4  
er 3

itor, epsilon



:osaminide alpha-2,6-sialyltransferase 1

nd cyclooxygenase)

nyltransferase 12 (GalNAc-T12)

sette sub-family C, member 7)  
sette sub-family C, member 7)

3



3 synthase)

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:ardation)

:osaminide alpha-2,6-sialyltransferase 4



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itor, alpha  
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nd cyclooxygenase)  
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invertase)



sette sub-family C, member 7)

nyltransferase 1 (GalNAc-T1)

19/p100)

. subfamily N, member 4

78 (mouse)

1 domains), member 2

prane protein band 3, Diego blood group)

nd cyclooxygenase)

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beta member 4

. subfamily N, member 3  
. subfamily N, member 4

er 3

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78 (mouse)

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.subfamily N, member 3

.subfamily N, member 4

invertase)



transferase, 1

beta member 4

porter, system Xag), member 1

nd cyclooxygenase)

nctional peptidase 7)  
nctional peptidase 2)

ardation)

beta member 4

subfamily N, member 4

itor, alpha

d (avian)

matin, subfamily d, member 3

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nyltransferase 1 (GalNAc-T1)  
nyltransferase 1 (GalNAc-T1)

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›itor, alpha  
›itor, alpha

nd cyclooxygenase)

porter, system Xag), member 1

brane protein band 3, Diego blood group)  
mber 2

invertase)

M) and short cytoplasmic domain, (semaphorin) 4D

matin, subfamily d, member 3

sette sub-family C, member 7)

brane protein band 3, Diego blood group)

prane protein band 3, Diego blood group)

ardation)





matin, subfamily d, member 3

it 1, cardiac muscle

nd cyclooxygenase)

3 synthase)  
l group)

nyltransferase 1 (GalNAc-T1)  
nyltransferase-like 4

transferase, 1

nyltransferase 12 (GalNAc-T12)

nd cyclooxygenase)  
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nctional peptidase 7)  
nctional peptidase 2)

nd cyclooxygenase)

II phosphatase 2



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porter, system Xag), member 1  
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II phosphatase 2

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. subfamily N, member 4

itor, alpha  
itor, alpha

it 1, cardiac muscle  
it 1, cardiac muscle

porter, system Xag), member 1

brane protein band 3, Diego blood group)  
p)



beta member 4

it 1, cardiac muscle

it 1, cardiac muscle

nd cyclooxygenase)

brane protein band 3, Diego blood group)

l group)

nyltransferase 1 (GalNAc-T1)

itor, alpha



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nctional peptidase 7)  
nctional peptidase 2)

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it 1, cardiac muscle

sette sub-family C, member 7)

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brane protein band 3, Diego blood group)  
brane protein band 3, Diego blood group)

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TM) and short cytoplasmic domain, (semaphorin) 4D



it 1, cardiac muscle

1 domains), member 2  
unit A3

unit A3

it 1, cardiac muscle

sette sub-family C, member 7)

brane protein band 3, Diego blood group)



spouter, system Xag), member 1

itor, alpha

invertase)

l-acetylneuraminate monooxygenase) pseudogene

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19/p100)

matin, subfamily d, member 3

unit A3

brane protein band 3, Diego blood group)



ette sub-family C, member 7)

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3 synthase)

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ardation)



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t of Ra-reactive factor)

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Myoglobin, alpha

Myoglobin, cardiac muscle

Myoglobin, cardiac muscle

Myoglobin (transmembrane protein band 3, Diego blood group)

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ardation)

ette sub-family C, member 7)

invertase)



ardation)

ardation)

porter, system Xag), member 1  
brane protein band 3, Diego blood group)  
matin, subfamily d, member 3











itor, alpha  
itor, alpha

sporter, system Xag), member 1

sette sub-family C, member 7)

nd cyclooxygenase)

sette sub-family C, member 7)

ardation)

sette sub-family C, member 7)



porter, system Xag), member 1  
er 8  
mber 2  
p)

mber 2

nyltransferase 1 (GalNAc-T1)

itor, epsilon

TM) and short cytoplasmic domain, (semaphorin) 4D

ardation)  
ed, (semaphorin) 3D

matin, subfamily d, member 3

ardation)

it 1, cardiac muscle

porter, system Xag), member 1

matin, subfamily d, member 3



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