

Ensembl ID	Name	Ensembl gene	GO - Biological Process	GO - Cellular Component	GO - Molecular Function	pval	qval	Ratio (knockdown / control)
ENSG00000169429	IL8	interleukin 8	activation of signaling prote	extracellular space (GO:0005	protein binding (GO:0005515	2.60E-43	9.45E-39	0.1084
ENSG00000145287	PLAC8	placenta-specific 8	response to cold (GO:0009409),	negative regulation of ap	chromatin binding (GO:00030	1.59E-29	2.89E-25	0.2441
ENSG00000164188	RANBP3L	RAN binding protein 3-like	intracellular transport (GO:0046907)			1.23E-13	1.48E-09	9.2353
ENSG00000149428	HYOU1	hypoxia up-regulated 1	activation of signaling prote	endocytic vesicle lumen (GO:	ATP binding (GO:0005524)	8.77E-11	7.95E-07	0.4513
ENSG00000113441	LNPEP	leucyl/cystinyl aminopeptidase	cell-cell signaling (GO:00072	lysosomal membrane (GO:00	aminopeptidase activity (GO:	2.05E-09	1.24E-05	0.4864
ENSG00000123989	CHPF	chondroitin polymerizing factor	chondroitin sulfate biosynt	Golgi cisterna membrane (GC	metal ion binding (GO:00468	1.78E-09	1.24E-05	2.4155
ENSG00000110092	CCND1	cyclin D1	mitotic cell cycle (GO:00002	cyclin-dependent protein kin	protein binding (GO:0005515	3.33E-09	1.72E-05	0.4785
ENSG00000079385	CEACAM1	carcinoembryonic antigen-related ce	cell migration (GO:0016477	plasma membrane (GO:0005	protein binding (GO:0005515	1.52E-08	6.29E-05	3.5252
ENSG00000170500	LONRF2	LON peptidase N-terminal domain a	proteolysis (GO:0006508)		ATP-dependent peptidase ac	1.56E-08	6.29E-05	0.5102
ENSG00000144959	NCEH1	neutral cholesterol ester hydrolase 1	lipid catabolic process (GO:0	integral to membrane (GO:00	carboxylesterase activity (GC	3.17E-08	0.00011487	0.5081
ENSG00000176153	GPX2	glutathione peroxidase 2 (gastrointe	temperature homeostasis (GO:	nucleolus (GO:0005730), cyto	electron carrier activity (GO:0	5.85E-08	0.00019312	3.4806
ENSG00000033867	SLC4A7	solute carrier family 4, sodium bicar	transmembrane transport (GO:	stereocilium (GO:0032420), a	inorganic anion exchanger ac	1.04E-07	0.00030247	0.5445
ENSG00000167552	TUBA1A	tubulin, alpha 1a	protein folding (GO:000645	cytosol (GO:0005829), cytopl	protein binding (GO:0005515	1.08E-07	0.00030247	2.1690
ENSG00000133321	RARRES3	retinoic acid receptor responder (ta	negative regulation of cell p	integral to membrane (GO:00	phospholipase A2 activity (GO:	1.17E-07	0.00030436	2.2777
ENSG00000116962	NID1	nidogen 1	positive regulation of cell-s	cell periphery (GO:0071944), collagen	binding (GO:000551	1.42E-07	0.00034371	2.0240
ENSG00000186081	KRT5	keratin 5	cell junction assembly (GO:0	cytosol (GO:0005829), mitoch	scaffold protein binding (GO:	1.81E-07	0.00041145	3.1269
ENSG00000110422	HIPK3	homeodomain interacting protein ki	mRNA transcription (GO:000	cytoplasm (GO:0005737), nu	protein kinase activity (GO:00	2.18E-07	0.00043933	1.9669
ENSG00000266037	RN7SL3	RN7SL3				2.15E-07	0.00043933	2.0371
ENSG00000100234	TIMP3	TIMP metallopeptidase inhibitor 3	cellular response to organic	extracellular matrix (GO:0031	metal ion binding (GO:00468	2.73E-07	0.00052057	1.9544
ENSG00000138829	FBN2	fibrillin 2	positive regulation of osteo	microfibril (GO:0001527), ext	extracellular matrix structura	2.99E-07	0.00054332	0.1239
ENSG00000168679	SLC16A4	solute carrier family 16, member 4	monocarboxylic acid transp	membrane (GO:0016020), int	monocarboxylic acid transme	4.64E-07	0.00080178	2.0323
ENSG00000156453	PCDH1	protocadherin 1	nervous system developme	plasma membrane (GO:0005	calcium ion binding (GO:000	5.30E-07	0.00087332	1.8992
ENSG00000185900	POMK	protein-O-mannose kinase				9.21E-07	0.0014522	0.5307
ENSG00000055732	MCOLN3	mucolipin 3	ion transport (GO:0006811)	plasma membrane (GO:0005886),	integral to membrane (GO:	1.31E-06	0.0019834	2.4836
ENSG00000168214	RBPJ	recombination signal binding protei	endocardium morphogenes	nucleoplasm (GO:0005654), r	protein N-terminus binding (GO:	1.51E-06	0.0021899	0.5670
ENSG00000166145	SPINT1	serine peptidase inhibitor, Kunitz ty	placenta blood vessel devel	extracellular region (GO:000	serine-type endopeptidase in	2.47E-06	0.0034515	4.8897
ENSG00000186767	SPIN4	spindlin family, member 4	gamete generation (GO:0007276)			3.03E-06	0.0040665	0.5467
ENSG00000183778	B3GALT5	UDP-Gal:betaGlcNAc beta 1,3-galact	protein glycosylation (GO:00	Golgi apparatus (GO:000579	UDP-galactose:beta-N-acetyl	3.38E-06	0.0042293	0.5759
ENSG00000243927	MRPS6	mitochondrial ribosomal protein S6	translation (GO:0006412)	mitochondrion (GO:0005739)	rRNA binding (GO:0019843),	3.29E-06	0.0042293	1.9391
ENSG00000164120	HPGD	hydroxyprostaglandin dehydrogenas	lipoxygenase pathway (GO:0	nucleus (GO:0005634), cytos	15-hydroxyprostaglandin de	3.69E-06	0.0044582	1.8426
ENSG00000100033	PRODH	proline dehydrogenase (oxidase) 1	glutamate biosynthetic proc	mitochondrial inner membra	FAD binding (GO:0071949), p	3.97E-06	0.0046504	2.0201
ENSG00000254198	non-coding RN	RP11-598P20.3				4.99E-06	0.005654	0.5415
ENSG00000104327	CALB1	calbindin 1, 28kDa	metanephric distal convolut	nucleus (GO:0005634), axon	calcium ion binding (GO:000	5.32E-06	0.0056729	3.4565
ENSG00000119231	SENP5	SUMO1/sentrin specific peptidase 5	proteolysis (GO:0006508), c	nucleolus (GO:0005730), nuc	cysteine-type peptidase activ	5.23E-06	0.0056729	0.5702
ENSG00000060982	BCAT1	branched chain amino-acid transami	G1/S transition of mitotic ce	mitochondrion (GO:0005739)	L-valine transaminase activit	6.11E-06	0.0061939	0.5709
ENSG00000106069	CHN2	chimerin 2	small GTPase mediated sign	cytosol (GO:0005829), mem	SH3/SH2 adaptor activity (GC	6.49E-06	0.0061939	2.0514
ENSG00000189159	HN1	hematological and neurological expressed 1		nucleus (GO:0005634)		6.36E-06	0.0061939	0.5906
ENSG00000213853	EMP2	epithelial membrane protein 2	cell proliferation (GO:00082	integral to membrane (GO:00	integrin binding (GO:000517	6.29E-06	0.0061939	1.9720

ENSG00000133067	LGR6	leucine-rich repeat containing G protein-coupled receptor class 1 member	positive regulation of canonical trans-Golgi network membrane transmembrane signaling receptor activity	8.49E-06	0.0078983	2.9452
ENSG00000166546	BEAN1	brain expressed, associated with neuronal cell death	cell death (GO:0008219)	1.03E-05	0.0093375	2.9412
ENSG00000146250	PRSS35	protease, serine, 35	metabolic process (GO:0009991), extracellular region (GO:0005576), catalytic activity (GO:0003824)	1.13E-05	0.0099951	2.6038
ENSG00000111666	CHPT1	choline phosphotransferase 1	lipid metabolic process (GO:0006629), membrane (GO:0016020), intracellular diacylglycerol cholinephosphotransferase activity	1.16E-05	0.010034	0.5382
ENSG00000133519	ZDHC8P1	zinc finger, DHHC-type containing 8 pseudogene 1		1.25E-05	0.010441	2.1802
ENSG00000204070	SYS1	SYS1 Golgi-localized integral membrane protein	protein transport (GO:0015111), Golgi membrane (GO:0000139), integral to membrane (GO:0009986)	1.27E-05	0.010441	1.8070
ENSG00000090905	TNRC6A	trinucleotide repeat containing 6A	cellular response to starvation	1.44E-05	0.011625	1.7990
ENSG00000168386	FILIP1L	filamin A interacting protein 1-like	biological process (GO:0009989), myosin complex (GO:0016451), molecular function (GO:0003674)	1.55E-05	0.012263	2.4410
ENSG00000164284	GRPEL2	GrpE-like 2, mitochondrial (E. coli)	cellular protein metabolic process (GO:0005739), mitochondrion (GO:0005739), adenyl-nucleotide exchange factor activity	1.61E-05	0.012442	0.5781
ENSG00000111907	TPD52L1	tumor protein D52-like 1	positive regulation of MAP kinase activity (GO:0005737), peroxisome (GO:0005737), protein binding (GO:0005515)	1.71E-05	0.012941	2.0116
ENSG00000152104	PTPN14	protein tyrosine phosphatase, non-receptor type 14	transcription, DNA-dependent cytoplasm (GO:0005737), cytoplasmic protein tyrosine phosphatase activity	2.14E-05	0.015853	0.6093
ENSG00000214049	UCA1	urothelial cancer associated 1 (non-protein coding)		2.23E-05	0.016172	2.0152
ENSG00000143324	XPR1	xenotropic and polytropic retrovirus G-protein coupled receptor	integral to plasma membrane transmembrane signaling receptor activity	2.46E-05	0.0175	1.7339
ENSG00000152291	TGOLN2	trans-golgi network protein 2	nucleus (GO:0005634), transmembrane protein binding (GO:0005515)	2.68E-05	0.018708	0.6132
ENSG00000118503	TNFAIP3	tumor necrosis factor, alpha-inducible protein 3	response to molecule of bacterial origin (GO:0005737), lysosomal protein binding (GO:0005515)	2.78E-05	0.018999	0.5203
ENSG00000103811	CTSH	cathepsin H	positive regulation of peptidase activity (GO:0008203)	2.93E-05	0.019683	1.7381
ENSG00000205413	SAMD9	sterile alpha motif domain containing 9	intracellular membrane-bounded protein binding (GO:0005515)	3.00E-05	0.019792	1.9011
ENSG00000135535	CD164	CD164 molecule, sialomucin	multicellular organismal development (GO:0009989), extracellular region (GO:0005576), protein binding (GO:0005515)	3.63E-05	0.023299	0.6389
ENSG00000149403	GRIK4	glutamate receptor, ionotropic, kainate type 4	glutamate receptor signaling pathway (GO:0007258), kainate selective glutamate receptor activity (GO:0005515)	3.66E-05	0.023299	27.0285
ENSG00000171658	RP11-443P15.2	non-coding RNA		3.87E-05	0.023951	0.3875
ENSG00000198455	ZXDB	zinc finger, X-linked, duplicated B domain containing 1	regulation of transcription, nuclear (GO:0005634)	3.89E-05	0.023951	0.5961
ENSG00000250920	RP11-297P16.4	non-coding RNA		4.07E-05	0.02459	2.1688
ENSG00000128872	TMOD2	tropomodulin 2 (neuronal)	neuron-neuron synaptic transmission (GO:0005856), cytoskeleton (GO:0005856), actin binding (GO:0003779), regulation of protein ubiquitination	4.20E-05	0.024964	2.2189
ENSG00000116661	FBXO2	F-box protein 2	regulation of protein ubiquitination (GO:0006960), organelle membrane (GO:0009986), ubiquitin-protein ligase activity	4.52E-05	0.026473	2.7429
ENSG00000122557	HERPUD2	HERPUD family member 2	response to unfolded protein (GO:0009989), integral to membrane (GO:0009986), protein binding (GO:0005515)	4.69E-05	0.026586	1.7695
ENSG00000171045	TSNARE1	t-SNARE domain containing 1	synaptic vesicle exocytosis (GO:0007155), integral to membrane (GO:0009986), SNARE binding (GO:0000149)	4.67E-05	0.026586	2.6814
ENSG00000181104	F2R	coagulation factor II (thrombin) receptor type 2	tyrosine phosphorylation of platelet dense tubular network (GO:0007258), G-protein alpha-subunit binding	5.23E-05	0.02921	1.7066
ENSG00000204789	ZNF204P	zinc finger protein 204, pseudogene		5.31E-05	0.029212	2.2487
ENSG00000196754	S100A2	S100 calcium binding protein A2	endothelial cell migration (GO:0009989), cellular component (GO:0009989), identical protein binding (GO:0005515)	5.64E-05	0.030516	2.2208
ENSG00000116095	PLEKHA3	pleckstrin homology domain containing 3	biological process (GO:0009989), membrane (GO:0016020), G-protein phospholipid binding (GO:0005515)	5.75E-05	0.030699	0.6178
ENSG00000039560	RAI14	retinoic acid induced 14	vesicle-mediated transport (GO:0005739), mitochondrion (GO:0005739), protein binding (GO:0005515)	5.95E-05	0.031216	0.6196
ENSG00000047634	SCML1	sex comb on midleg-like 1 (Drosophila)	anatomical structure morphogenesis (GO:0005634), DNA binding (GO:0003677), response to hypoxia	6.02E-05	0.031216	0.5835
ENSG00000108342	CSF3	colony stimulating factor 3 (granulocyte colony-stimulating factor)	positive regulation of protein expression (GO:0005974), extracellular space (GO:0005576), growth factor activity (GO:0005200)	6.46E-05	0.031694	0.0000
ENSG00000111696	NT5DC3	5'-nucleotidase domain containing 3	mitochondrion (GO:0005739), metal ion binding (GO:0046814)	6.46E-05	0.031694	0.5761
ENSG00000164164	OTUD4	OTU domain containing 4	proteolysis (GO:0006508), cellular component (GO:0009989), ubiquitin-specific protease activity	6.42E-05	0.031694	0.6156
ENSG00000268205	lncRNA	lncRNA		6.33E-05	0.031694	0.5840
ENSG00000051341	POLQ	polymerase (DNA directed), theta	DNA repair (GO:0006281), nucleoplasm (GO:0005654), single-stranded DNA-dependent DNA replication	6.84E-05	0.03264	0.6184
ENSG00000158966	CACHD1	cache domain containing 1	calcium ion transport (GO:0006812), integral to membrane (GO:0016021)	6.75E-05	0.03264	1.7988
ENSG00000164023	SGMS2	sphingomyelin synthase 2	sphingolipid biosynthetic process (GO:0006974), plasma membrane (GO:0005576), kinase activity (GO:0016301)	7.68E-05	0.036196	0.6354
ENSG00000148411	NACC2	NACC family member 2, BEN and BT domain containing 2	positive regulation of cell proliferation (GO:0000122), nuclear chromatin (GO:0000122), histone deacetylase activity (GO:0004402)	7.81E-05	0.036333	0.6066
ENSG00000081041	CXCL2	chemokine (C-X-C motif) ligand 2	chemotaxis (GO:0006935), extracellular region (GO:0005576), chemokine activity (GO:0005515)	8.07E-05	0.037073	0.4227

ENSG00000005893	LAMP2	lysosomal-associated membrane protein	platelet degranulation (GO:0006621), integral to membrane (GO:0016021), platelet dense granule organization (GO:0070272)	8.36E-05	0.037642	1.6526
ENSG00000137726	FXYP6	FXYP domain containing ion transport	biological process (GO:0009987), integral to membrane (GO:0016021), molecular function (GO:0005506)	8.40E-05	0.037642	2.1477
ENSG00000070159	PTPN3	protein tyrosine phosphatase, non-receptor type 3	peptidyl-tyrosine dephosphorylation (GO:0005737), intracellular phosphotyrosine binding (GO:0005506)	8.61E-05	0.03765	1.7065
ENSG00000111816	FRK	fyn-related kinase	protein phosphorylation (GO:0006462), intracellular (GO:0005622), non-membrane spanning protein (GO:0005622)	8.57E-05	0.03765	0.6444
ENSG00000071575	TRIB2	tribbles pseudokinase 2	negative regulation of protein synthesis (GO:0005634), cytoplasmic nucleotide binding (GO:0005506)	9.92E-05	0.042828	1.8759
ENSG00000126524	SBDS	Shwachman-Bodian-Diamond syndrome protein	cell proliferation (GO:0008283), spindle pole body organization (GO:0009222), rRNA binding (GO:0019843), non-coding RNA (GO:0003812)	0.00010439	0.04456	0.6279
ENSG00000250072	CTC-529P8.1	non-coding RNA		0.0001082	0.045648	2.3237
ENSG00000163898	LIPH	lipase, member H	lipid catabolic process (GO:0006621), plasma membrane (GO:0005586), heparin binding (GO:0008203)	0.00011013	0.04593	1.6898
ENSG00000115107	STEAP3	STEAP family member 3, metalloreductase	transmembrane transport (GO:0006878), plasma membrane (GO:0005586), protein binding (GO:0005515)	0.00011294	0.046568	1.7855
ENSG00000168411	RFWD3	ring finger and WD repeat domain 3	protein ubiquitination (GO:0016605), PML body (GO:0016605), nuclear ubiquitin-protein ligase activity (GO:0004714)	0.00011946	0.048463	0.6259
ENSG00000176853	FAM91A1	family with sequence similarity 91, member A1		0.00012201	0.048463	0.6442
ENSG00000225648	SBDSP1	Shwachman-Bodian-Diamond syndrome pseudogene 1		0.00012288	0.048463	0.5985
ENSG00000236548	RP11-510H23.1	non-coding RNA		0.0001211	0.048463	2.4435