

Term

positive regulation of signal transduction (GO:0009967)
positive regulation of JNK cascade (GO:0046330)
cell-cell junction assembly (GO:0007043)
positive regulation of stress-activated MAPK cascade (GO:0032874)
monoterpenoid metabolic process (GO:0016098)
positive regulation of myelination (GO:0031643)
mRNA 3'-splice site recognition (GO:0000389)
regulation of T cell tolerance induction (GO:0002664)
regulation of tooth mineralization (GO:0070170)
mesenchymal to epithelial transition involved in metanephros morphogenesis (GO:0003337)
regulation of glial cell apoptotic process (GO:0034350)
adherens junction assembly (GO:0034333)
forebrain neuron differentiation (GO:0021879)
melanocyte differentiation (GO:0030318)
terpenoid metabolic process (GO:0006721)
negative regulation of T cell mediated immunity (GO:0002710)
pituitary gland development (GO:0021983)
negative regulation of glial cell apoptotic process (GO:0034351)
kidney epithelium development (GO:0072073)
positive regulation of neurological system process (GO:0031646)
epithelial cell differentiation involved in kidney development (GO:0035850)
regulation of JNK cascade (GO:0046328)
positive regulation of macrophage differentiation (GO:0045651)
positive regulation of protein homodimerization activity (GO:0090073)
desmosome organization (GO:0002934)
central nervous system myelination (GO:0022010)
myelin maintenance (GO:0043217)
regulation of ERAD pathway (GO:1904292)
benzene-containing compound metabolic process (GO:0042537)
negative regulation of leukocyte mediated cytotoxicity (GO:0001911)
RNA destabilization (GO:0050779)
regulation of homotypic cell-cell adhesion (GO:0034110)
negative regulation of histone methylation (GO:0031061)
negative regulation of response to cytokine stimulus (GO:0060761)
adrenal gland development (GO:0030325)
cell differentiation involved in metanephros development (GO:0072202)
positive regulation of bone remodeling (GO:0046852)
mesenchymal to epithelial transition (GO:0060231)
positive regulation of bone resorption (GO:0045780)
insulin-like growth factor receptor signaling pathway (GO:0048009)
circulatory system development (GO:0072359)
regulation of hippo signaling (GO:0035330)
cellular response to interleukin-2 (GO:0071352)
interleukin-2-mediated signaling pathway (GO:0038110)
epithelial cell-cell adhesion (GO:0090136)

negative regulation of bone mineralization (GO:0030502)
positive regulation of kinase activity (GO:0033674)
epithelium development (GO:0060429)
regulation of antigen receptor-mediated signaling pathway (GO:0050854)
oligodendrocyte development (GO:0014003)
retinol metabolic process (GO:0042572)
regulation of macrophage differentiation (GO:0045649)
ribonucleoprotein complex disassembly (GO:0032988)
cranial nerve development (GO:0021545)
positive regulation of ERAD pathway (GO:1904294)
dephosphorylation (GO:0016311)
protein dephosphorylation (GO:0006470)
positive regulation of muscle hypertrophy (GO:0014742)
stem cell development (GO:0048864)
regulation of platelet aggregation (GO:0090330)
negative regulation of biomineral tissue development (GO:0070168)
oligodendrocyte differentiation (GO:0048709)
regulation of mRNA stability (GO:0043488)
substrate-dependent cell migration (GO:0006929)
regulation of T cell mediated cytotoxicity (GO:0001914)
regulation of protein homodimerization activity (GO:0043496)
positive regulation of antigen receptor-mediated signaling pathway (GO:0050857)
positive regulation of cardiac muscle hypertrophy (GO:0010613)
regulation of stem cell proliferation (GO:0072091)
positive regulation of response to endoplasmic reticulum stress (GO:1905898)
cardiac ventricle development (GO:0003231)
regulation of histone H3-K4 methylation (GO:0051569)
embryonic digit morphogenesis (GO:0042733)
regulation of myelination (GO:0031641)
positive regulation of stem cell proliferation (GO:2000648)
histone H2A monoubiquitination (GO:0035518)
ureteric bud development (GO:0001657)
mesonephric tubule development (GO:0072164)
histone H2A ubiquitination (GO:0033522)
positive regulation of response to biotic stimulus (GO:0002833)
regulation of lipopolysaccharide-mediated signaling pathway (GO:0031664)
mRNA destabilization (GO:0061157)
regulation of protein kinase activity (GO:0045859)
regulation of platelet activation (GO:0010543)
primary alcohol metabolic process (GO:0034308)
histone deubiquitination (GO:0016578)
macromolecule biosynthetic process (GO:0009059)
morphogenesis of an epithelium (GO:0002009)
heart development (GO:0007507)
glial cell development (GO:0021782)
inactivation of MAPK activity (GO:0000188)

embryonic digestive tract development (GO:0048566)
branching involved in ureteric bud morphogenesis (GO:0001658)
ureteric bud morphogenesis (GO:0060675)
regulation of regulatory T cell differentiation (GO:0045589)
organelle disassembly (GO:1903008)
Arp2/3 complex-mediated actin nucleation (GO:0034314)
regulation of cardiac muscle hypertrophy (GO:0010611)
epoxygenase P450 pathway (GO:0019373)
protein localization to cell surface (GO:0034394)
regulation of bone resorption (GO:0045124)
hematopoietic progenitor cell differentiation (GO:0002244)
exogenous drug catabolic process (GO:0042738)
lamellipodium assembly (GO:0030032)
histone monoubiquitination (GO:0010390)
negative regulation of sequestering of calcium ion (GO:0051283)
drug catabolic process (GO:0042737)
mRNA splice site selection (GO:0006376)
limb development (GO:0060173)
actin nucleation (GO:0045010)
ear morphogenesis (GO:0042471)

Genes	P-value
SALL1;PTPRC;PRKCA	0.00981884
DUSP22;TRAF4	0.01163539
PRKCA;VCL	0.01252749
DUSP22;TRAF4	0.01283134
CYP2E1	0.01283234
MYRF	0.01283234
ISY1	0.01283234
IL2RA	0.01283234
BCOR	0.01283234
SALL1	0.01283234
PRKCA	0.01283234
VCL	0.01495537
SALL1	0.01495537
USP13	0.01495537
CYP2E1	0.01495537
PTPRC	0.01495537
SALL1	0.01495537
PRKCA	0.01495537
SALL1	0.01495537
MYRF	0.01495537
SALL1	0.01495537
DUSP22;TRAF4	0.01604407
PRKCA	0.01707395
TRAF4	0.01707395
PRKCA	0.01707395
MYRF	0.01707395
MYRF	0.01707395
USP13	0.01707395
CYP2E1	0.01707395
PTPRC	0.01707395
GIGYF2	0.01918808
PRKCA	0.01918808
BCOR	0.01918808
PTPRC	0.02129777
SALL1	0.02129777
SALL1	0.02129777
PRKCA	0.02129777
SALL1	0.02129777
PRKCA	0.02129777
GIGYF2	0.02129777
SALL1;BCOR	0.0229825
NEK8	0.02340302
IL2RA	0.02340302
IL2RA	0.02340302
VCL	0.02340302

BCOR	0.02340302
PTPRC;TRAF4	0.02457554
SALL1;VCL	0.02538865
PTPRC	0.02550385
MYRF	0.02550385
LRAT	0.02550385
PRKCA	0.02760027
KLC1	0.02760027
SALL1	0.02760027
USP13	0.02760027
DUSP22;PTPRC	0.02918127
DUSP22;PTPRC	0.02961591
PRKCA	0.02969228
PTPRC	0.02969228
PRKCA	0.02969228
BCOR	0.02969228
MYRF	0.02969228
PRKCA;GIGYF2	0.0309354
PTPRC	0.0317799
PTPRC	0.0317799
TRAF4	0.03386312
PTPRC	0.03386312
PRKCA	0.03386312
PTPRC	0.03386312
USP13	0.03386312
SALL1	0.03386312
BCOR	0.03386312
SALL1	0.03386312
MYRF	0.03594198
PTPRC	0.03594198
BCOR	0.03594198
SALL1	0.03594198
SALL1	0.03594198
BCOR	0.03594198
PRKCA	0.03594198
PRKCA	0.03801646
GIGYF2	0.03801646
PTPRC;TRAF4	0.03981418
PRKCA	0.04008658
LRAT	0.04008658
USP3	0.04008658
PTPRC	0.04008658
VCL	0.04008658
SALL1;BCOR	0.0407992
MYRF	0.04215235
DUSP22	0.04215235

SALL1	0.04215235
SALL1	0.04215235
SALL1	0.04215235
IL2RA	0.04215235
KLC1	0.04215235
ARPC3	0.04215235
PRKCA	0.04421378
CYP2E1	0.04421378
VCL	0.04627087
PRKCA	0.04627087
PTPRC	0.04627087
CYP2E1	0.04832364
VCL	0.04832364
BCOR	0.0503721
PTPRC	0.0503721
CYP2E1	0.0503721
ISY1	0.0503721
SALL1	0.0503721
ARPC3	0.0503721
SALL1	0.0503721

Term

ubiquitin-like protein-specific protease activity (GO:0019783)

thiol-dependent ubiquitin-specific protease activity (GO:0004843)

histone threonine kinase activity (GO:0035184)

thiol-dependent ubiquitinyl hydrolase activity (GO:0036459)

protein kinase C activity (GO:0004697)

ubiquitin protein ligase binding (GO:0031625)

calcium-dependent protein serine/threonine kinase activity (GO:0009931)

tumor necrosis factor receptor binding (GO:0005164)

thioesterase binding (GO:0031996)

ubiquitin-like protein ligase binding (GO:0044389)

acid-amino acid ligase activity (GO:0016881)

transmembrane receptor protein tyrosine phosphatase activity (GO:0005001)

transmembrane receptor protein phosphatase activity (GO:0019198)

phosphoprotein phosphatase activity (GO:0004721)

arachidonic acid epoxygenase activity (GO:0008392)

arachidonic acid monooxygenase activity (GO:0008391)

proteasome binding (GO:0070628)

oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, re

tumor necrosis factor receptor superfamily binding (GO:0032813)

Genes	P-value
USP13;USP3	0.01105699
USP13;USP3	0.01163539
PRKCA	0.01495537
USP13;USP3	0.01672391
PRKCA	0.02129777
USP13;TRAF4;VCL	0.0230209
PRKCA	0.02340302
TRAF4	0.02340302
TRAF4	0.02340302
USP13;TRAF4;VCL	0.02584205
TLL8	0.02969228
PTPRC	0.0317799
PTPRC	0.0317799
DUSP22;PTPRC	0.03456591
CYP2E1	0.03594198
CYP2E1	0.03594198
USP13	0.04215235
CYP2E1	0.04421378
TRAF4	0.0544561

Term	Genes
post-mRNA release spliceosomal complex (GO:0071014)	ISY1
NuRD complex (GO:0016581)	SALL1
CHD-type complex (GO:0090545)	SALL1
focal adhesion (GO:0005925)	PTPRC;ARPC3;VC
cytoplasmic ribonucleoprotein granule (GO:0036464)	USP3;GIGYF2

P-value

0.0191880788

0.0338631248

0.0338631248

0.0408809795

0.051681926

Term

Fc gamma R-mediated phagocytosis
Pathogenic Escherichia coli infection
Shigellosis
Bacterial invasion of epithelial cells
Salmonella infection
Amoebiasis
Leukocyte transendothelial migration
Spliceosome
Vitamin digestion and absorption

Genes

PTPRC;ARPC3;PRKC
ARPC3;PRKCA
ARPC3;VCL
ARPC3;VCL
ARPC3;KLC1
PRKCA;VCL
PRKCA;VCL
ISY1;ISY1-RAB43
LRAT

P-value

9.86E-04

0.0062377586

0.0086193089

0.0110569897

0.0147213489

0.0181199662

0.0241731105

0.0336432495

0.0503720993

Term

NME2 (human)

CBFB (human)

RELB (human)

Genes

CSMD2;C1ORF94

ISY1;ISY1-RAB43;IL2RA;BCOR;LBX1

ISY1;DUSP22;BCOR;KLC1;CSMD2;ELFN1;C1ORF94

P-value

0.0042154

0.02448793

0.03572633