



SP_PIR_KEYWORDS:acetylation
 GOTERM_BP_FAT:G:0017053 transcriptional repressor complex
 GOTERM_BP_FAT:G:0045941 positive regulation of transcription
 GOTERM_BP_FAT:G:0010628 positive regulation of gene expression
 GOTERM_BP_FAT:G:0000169 nucleotide binding
 GOTERM_BP_FAT:G:0004529 positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process
 GOTERM_BP_FAT:G:0005173 positive regulation of nitrogen compound metabolic process
 GOTERM_BP_FAT:G:0010657 positive regulation of macromolecule biosynthetic process
 GOTERM_BP_FAT:G:0003132 positive regulation of cellular biosynthetic process
 GOTERM_BP_FAT:G:0006891 positive regulation of biosynthetic process
 SP_PIR_KEYWORDS:dna-binding
 SP_PIR_KEYWORDS:nucleotide-binding
 GOTERM_CC_FAT:G:0030529 ribonucleoprotein complex
 INTERPRO:IPRO00415 Ets
 SMART:SM00413 ETS
 INTERPRO:IPRO00504 RNA recognition motif, RNP-1
 GOTERM_BP_FAT:G:00051252 regulation of RNA metabolic process
 INTERPRO:IPRO1777 Nucleotide-binding, alpha-beta plat
 UP_SEQ_FEATURE:DNA-binding region:ETS
 SMART:SM00390 RRM
 GOTERM_BP_FAT:G:0010004 positive regulation of macromolecule metabolic process
 SP_PIR_KEYWORDS:ma-binding
 GOTERM_BP_FAT:G:0045934 negative regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process
 GOTERM_BP_FAT:G:00061172 negative regulation of nitrogen compound metabolic process
 GOTERM_MF_FAT:G:00030528 transcription regulator activity
 SP_PIR_KEYWORDS:transcription factor
 GOTERM_BP_FAT:G:0003977 DNA binding
 GOTERM_BP_FAT:G:0045893 positive regulation of transcription, DNA-dependent
 GOTERM_BP_FAT:G:00051254 positive regulation of RNA metabolic process
 GOTERM_MF_FAT:G:0003253 ribonucleotide binding
 GOTERM_BP_FAT:G:0006259 DNA metabolic process
 GOTERM_BP_FAT:G:0006357 regulation of transcription from RNA polymerase II promoter
 SP_PIR_KEYWORDS:transcription regulation
 GOTERM_BP_FAT:G:00031327 negative regulation of cellular biosynthetic process
 GOTERM_BP_FAT:G:0006890 negative regulation of biosynthetic process
 GOTERM_BP_FAT:G:0006357 regulation of transcription, DNA-dependent
 GOTERM_MF_FAT:G:0043565 sequence-specific DNA binding
 GOTERM_CC_FAT:G:0016581 NuRD complex
 GOTERM_MF_FAT:G:0016581 transcription repressor activity
 SP_PIR_KEYWORDS:methyltransferase
 GOTERM_BP_FAT:G:0045935 negative regulation of transcription, DNA-dependent
 GOTERM_BP_FAT:G:00051253 negative regulation of RNA metabolic process
 GOTERM_BP_FAT:G:0010005 negative regulation of macromolecule metabolic process
 GOTERM_BP_FAT:G:0010358 negative regulation of macromolecule biosynthetic process
 SP_PIR_KEYWORDS:Transcription
 GOTERM_BP_FAT:G:0045449 regulation of transcription
 SP_PIR_KEYWORDS:repressor
 GOTERM_BP_FAT:G:0006350 transcription
 GOTERM_BP_FAT:G:00016481 negative regulation of transcription
 GOTERM_BP_FAT:G:0010629 negative regulation of gene expression
 SP_PIR_KEYWORDS:activator
 GOTERM_BP_FAT:G:00051276 chromosome organization
 UP_SEQ_FEATURE:domain:Leucine-zipper
 INTERPRO:IPRO11618 bZIP transcription factor, bZIP-1
 GOTERM_BP_FAT:G:0004594 positive regulation of transcription from RNA polymerase II promoter
 GOTERM_BP_FAT:G:0000122 negative regulation of transcription from RNA polymerase II promoter
 SP_PIR_KEYWORDS:chromatin regulator
 GOTERM_BP_FAT:G:00016568 histone modification
 GOTERM_CC_FAT:G:0000111 histone deacetylase complex
 GOTERM_MF_FAT:G:00003712 transcription cofactor activity
 GOTERM_BP_FAT:G:0006325 chromatin organization
 GOTERM_BP_FAT:G:0006964 chromosome
 GOTERM_CC_FAT:G:00034708 methyltransferase complex
 GOTERM_CC_FAT:G:00035097 histone methyltransferase complex
 INTERPRO:IPRO11697 Winged helix repressor DNA-binding
 INTERPRO:IPRO01766 Transcription factor, fork head
 INTERPRO:IPRO18122 Transcription factor, fork head, conserved site
 SMART:SM00390 FH
 UP_SEQ_FEATURE:DNA-binding region:Forkhead
 GOTERM_MF_FAT:G:0003982 chromatin binding
 GOTERM_BP_FAT:G:0003259 methylation
 GOTERM_CC_FAT:G:0000785 chromatin
 GOTERM_CC_FAT:G:0000792 heterochromatin
 GOTERM_CC_FAT:G:0003096 ESC/EC2 complex
 GOTERM_MF_FAT:G:00003729 mRNA binding
 KEGG_PATHWAY:mmu04012:Erk8 signaling pathway
 GOTERM_BP_FAT:G:00033554 cellular response to stress
 SP_PIR_KEYWORDS:phosphoprotein
 GOTERM_BP_FAT:G:00007267 cell-cell signaling
 KEGG_PATHWAY:mmu04610:Insulin signaling pathway
 GOTERM_BP_FAT:G:00031670 cellular response to nutrient
 KEGG_PATHWAY:mmu04662:Cell receptor signaling pathway
 INTERPRO:IPRO15737 Testis-specific serine/threonine kinase
 PIR_SUPERFAMILY:PIRSF038233 testis-specific serine/threonine-protein kinase
 SP_PIR_KEYWORDS:phosphoprotein
 KEGG_PATHWAY:mmu04643:Wnt signaling pathway
 BIOCARTA:m_il12Pathway:IL12 and Stat4 Dependent Signaling Pathway in Th1 Development
 BIOCARTA:m_gpcrPathway:Signaling Pathway from G-Protein Families
 SP_PIR_KEYWORDS:west signaling pathway
 GOTERM_MF_FAT:G:00019887 protein kinase regulator activity
 GOTERM_BP_FAT:G:0006966 negative regulation of signal transduction
 GOTERM_BP_FAT:G:0010546 negative regulation of cell communication
 GOTERM_MF_FAT:G:00019207 kinase regulator activity
 GOTERM_MF_FAT:G:00001002 pancreatic polypeptide receptor activity
 KEGG_PATHWAY:mmu04616:Metanogenesis
 SP_PIR_KEYWORDS:spermatogenesis
 GOTERM_BP_FAT:G:00032504 multicellular organism reproduction
 GOTERM_BP_FAT:G:0048906 reproductive process in a multicellular organism
 SP_PIR_KEYWORDS:developmental protein
 GOTERM_BP_FAT:G:0048592 eye morphogenesis
 GOTERM_BP_FAT:G:0001695 sexual reproduction
 GOTERM_BP_FAT:G:00007283 spermatogenesis
 GOTERM_BP_FAT:G:00048232 male gamete generation
 GOTERM_BP_FAT:G:00007276 gamete generation
 KEGG_PATHWAY:mmu05215:Prostate cancer
 KEGG_PATHWAY:mmu05200:Pathways in cancer
 KEGG_PATHWAY:mmu05211:Renal cell carcinoma
 SP_PIR_KEYWORDS:Proto-oncogene
 KEGG_PATHWAY:mmu05220:Chronic myeloid leukemia
 KEGG_PATHWAY:mmu05210:Colorectal cancer
 KEGG_PATHWAY:mmu05219:Bladder cancer
 KEGG_PATHWAY:mmu05213:Endometrial cancer
 GOTERM_BP_FAT:G:00051728 regulation of cell cycle
 GOTERM_BP_FAT:G:00008285 negative regulation of cell proliferation
 GOTERM_BP_FAT:G:00045789 negative regulation of cell cycle
 GOTERM_BP_FAT:G:00042127 regulation of cell proliferation
 KEGG_PATHWAY:mmu04110:Cell cycle
 GOTERM_BP_FAT:G:00006270 DNA replication initiation
 SP_PIR_KEYWORDS:nucleus
 GOTERM_BP_FAT:G:00006111 protein export from nucleus
 GOTERM_BP_FAT:G:00006027 regulation of vesicle-mediated transport
 GOTERM_BP_FAT:G:00006969 intracellular protein transport
 GOTERM_BP_FAT:G:00034612 cellular protein localization
 GOTERM_BP_FAT:G:00070727 cellular macromolecule localization
 GOTERM_CC_FAT:G:00005920 cytosol
 GOTERM_BP_FAT:G:0046907 intracellular transport
 GOTERM_BP_FAT:G:00051169 nuclear export
 GOTERM_CC_FAT:G:0000594 nucleoplasm
 GOTERM_CC_FAT:G:0004461 nucleoplasm part
 GOTERM_CC_FAT:G:00031981 nuclear lumen
 GOTERM_BP_FAT:G:0006341 regulation of cellular localization
 GOTERM_BP_FAT:G:0006913 nucleocytoplasmic transport
 GOTERM_BP_FAT:G:00051169 nuclear transport
 SP_PIR_KEYWORDS:cytoplasm
 GOTERM_CC_FAT:G:00070013 intracellular organelle lumen
 GOTERM_CC_FAT:G:0043233 organelle lumen
 GOTERM_CC_FAT:G:0003124 membrane-enclosed lumen
 VUIRVM_CC_FAT:G:00004427 chromosomal part
 GOTERM_BP_FAT:G:00051187 cofactor catabolic process
 GOTERM_MF_FAT:G:00019417 S-acyltransferase activity
 GOTERM_CC_FAT:G:00005739 mitochondrion
 GOTERM_BP_FAT:G:00008084 acetyl-CoA metabolic process
 KEGG_PATHWAY:mmu03801:Tryptophan metabolism
 GOTERM_BP_FAT:G:00044265 cellular macromolecule catabolic process
 GOTERM_BP_FAT:G:00043414 biopolymer methylation
 GOTERM_BP_FAT:G:00051693 proteolysis involved in cellular protein catabolic process
 GOTERM_BP_FAT:G:00044257 cellular protein catabolic process
 GOTERM_BP_FAT:G:00006057 macromolecule catabolic process
 GOTERM_BP_FAT:G:00030163 protein catabolic process
 SP_PIR_KEYWORDS:transferase
 SP_PIR_KEYWORDS:zfp-binding
 INTERPRO:IPRO17465 Zinc finger, FYVE-related
 UP_SEQ_FEATURE:nucleotide phosphate-binding region:ATP
 SP_PIR_KEYWORDS:ubi conjugation
 UP_SEQ_FEATURE:zinc finger region:FYVE-type
 GOTERM_MF_FAT:G:00005624 ATP binding
 GOTERM_MF_FAT:G:00032555 guanine ribonucleotide binding
 GOTERM_MF_FAT:G:00032555 adenylyl ribonucleotide binding
 SP_PIR_KEYWORDS:methylation
 GOTERM_MF_FAT:G:00004396 helicase activity
 SP_PIR_KEYWORDS:zinc-finger
 SP_PIR_KEYWORDS:prenylation
 SP_PIR_KEYWORDS:metal-binding
 UP_SEQ_FEATURE:region of interest:S-adenosyl-L-methionine binding
 SP_PIR_KEYWORDS:isopeptide bond
 SP_PIR_KEYWORDS:helicase
 SP_PIR_KEYWORDS:S-adenosyl-L-methionine
 GOTERM_BP_FAT:G:00017157 regulation of exocytosis
 GOTERM_BP_FAT:G:00045920 negative regulation of exocytosis

Supp. Fig. S6