Functional Annotation Table

Help and Manual

Current Gene List: List_1
Current Background: Homo sapiens
32 DAVID IDs

32 record(s) Download File

ATP2B1	ATPase plasma membrane Ca2+ transporting 1(ATP2B1)	Related Genes	Homo sapiens
GOTERM_BP_DIRECT	negative regulation of cytokine production, regulation of vascular smooth muscle contraction, regulation of blood pressure, positive regulation of bone mineralization, ion transmembrane transport, regulation of cytosolic calcium ion concentration, negative regulation of cytosolic calcium ion concentration, positive regulation of calcium ion transport, transmembrane transport, regulation of cellular response to insulin stimulus, regulation of cardiac conduction, calcium ion export from cell,		
GOTERM_CC_DIRECT	immunological synapse, nucleoplasm, plasma membrane, membrane, basolateral plasma membrane, synaptic vesicle membrane, presynaptic membrane, cell projection, intracellular membrane-bounded organelle, extracellular exosome, photoreceptor ribbon synapse, glutamatergic synapse,		
GOTERM_MF_DIRECT	calcium-transporting ATPase activity, protein binding, calmodulin binding, ATP binding, calcium ion transmembrane transporter activity, ATPase activity, PDZ domain binding, metal ion binding,		
INTERPRO	P_typ_ATPase, ATPase_P-typ_cation-transptr_N, ATPase_P-typ_cation-transptr_C, P-type_ATPase_IIB, ATPase_P-typ_transduc_dom_A_sf, ATPase_P-typ_P_site, ATP_Ca_trans_C, HAD_sf, ATPase_P-typ_TM_dom_sf, ATPase_P-typ_cyto_dom_N, HAD-like_sf, P_typ_ATPase_HD_dom,		
KEGG_PATHWAY	Calcium signaling pathway, cGMP-PKG signaling pathway, cAMP signaling pathway, Adrenergic signaling in cardiomyocytes, Aldosterone synthesis and secretion, Endocrine and other factor-regulated calcium reabsorption, Salivary secretion, Pancreatic secretion, Mineral absorption,		
OMIM_DISEASE	Intellectual developmental disorder, autosomal dominant 66,		
SMART	Cation_ATPase_N,		
UP_KW_BIOLOGICAL_PROCESS	Calcium transport, Ion transport, Transport,		
UP_KW_CELLULAR_COMPONENT	Membrane, Synapse, Cell projection, Cytoplasmic vesicle, Cell membrane,		
UP_KW_DISEASE	Disease variant, Intellectual disability,		
UP_KW_DOMAIN	Transmembrane, Transmembrane helix,		
UP_KW_LIGAND	ATP-binding, Calcium, Magnesium, Metal-binding, Nucleotide-binding,		
UP_KW_MOLECULAR_FUNCTION	Calmodulin-binding, Translocase,		
UP_KW_PTM	Acetylation, Phosphoprotein,		
UP_SEQ_FEATURE	ACT_SITE:4-aspartylphosphate intermediate, COMPBIAS:Basic and acidic residues, COMPBIAS:Polar residues, DOMAIN:Cation-transporting P-type ATPase C-terminal, DOMAIN:Cation-transporting P-type ATPase N-terminal, DOMAIN:Plasma membrane calcium transporting P-type ATPase C-terminal, REGION:Calmodulin-binding subdomain A, REGION:Disordered, REGION:Required for basolateral membrane targeting, TOPO_DOM:Cytoplasmic, TOPO_DOM:Extracellular, TRANSMEM:Helical,		
CTR9	**CTR9 homolog, Paf1/RNA polymerase II complex component(CTR9)**	**Related Genes**	**Homo sapiens**
GOTERM_BP_DIRECT	negative regulation of transcription from RNA polymerase II promoter, endodermal cell fate commitment, inner cell mass cell differentiation, trophectodermal cell differentiation, blastocyst growth, blastocyst hatching, regulation of transcription, DNA-templated, transcription elongation from RNA polymerase II promoter, JAK-STAT cascade, Wnt signaling pathway, stem cell population maintenance, negative regulation of myeloid cell differentiation, negative regulation of gene expression, epigenetic, positive regulation of transcription from RNA polymerase II promoter, interleukin-6-mediated signaling pathway, cellular response to lipopolysaccharide,		
GOTERM_CC_DIRECT	euchromatin, nucleoplasm, Cdc73/Paf1 complex, nuclear speck, macromolecular complex, intracellular membrane-bounded organelle,		
GOTERM_MF_DIRECT	RNA polymerase II core binding, protein binding, SH2 domain binding,		
INTERPRO	TPR-like_helical_dom_sf, TPR_repeat, Ctr9,		
SMART	TPR,		
UP_KW_BIOLOGICAL_PROCESS	Transcription, Transcription regulation, Wnt signaling pathway,		
UP_KW_CELLULAR_COMPONENT	Nucleus,		
UP_KW_DOMAIN	Coiled coil, Repeat, TPR repeat,		
UP_KW_PTM	Phosphoprotein,		
UP_SEQ_FEATURE	COMPBIAS:Basic and acidic residues, COMPBIAS:Polar residues, REGION:Disordered, REPEAT:TPR, REPEAT:TPR 1, REPEAT:TPR 10, REPEAT:TPR 11, REPEAT:TPR 12, REPEAT:TPR 13, REPEAT:TPR 14, REPEAT:TPR 15, REPEAT:TPR 16, REPEAT:TPR 2, REPEAT:TPR 3, REPEAT:TPR 4, REPEAT:TPR 5, REPEAT:TPR 6, REPEAT:TPR 7, REPEAT:TPR 8, REPEAT:TPR 9,		
DHX9	**DExH-box helicase 9(DHX9)**	**Related Genes**	**Homo sapiens**
GOTERM_BP_DIRECT	alternative mRNA splicing, via spliceosome, osteoblast differentiation, DNA replication, DNA-templated transcription, termination, regulation of transcription from RNA polymerase II promoter, inflammatory response, RNA secondary structure unwinding, DNA duplex unwinding, positive regulation of interferon-alpha production, positive regulation of interferon-beta production, positive regulation of interleukin-18 production, positive regulation of interleukin-6 production, positive regulation of tumor necrosis factor production, gene silencing by miRNA, DNA-templated viral transcription, G-quadruplex DNA unwinding, innate immune response, positive regulation of innate immune response, positive regulation of DNA repair, positive regulation of DNA replication, positive regulation of transcription from RNA polymerase II promoter, positive regulation of RNA export from nucleus, positive regulation of fibroblast proliferation, rhythmic process, positive regulation of viral transcription, regulation of mRNA processing, regulation of defense response to virus by host, positive regulation of inflammatory response, mRNA transport, positive regulation of NF-kappaB transcription factor activity, positive regulation of response to cytokine stimulus, macromolecular complex assembly, pyroptosis, small RNA loading onto RISC, CRD-mediated mRNA stabilization, cellular response to tumor necrosis factor, cellular response to exogenous dsRNA, negative regulation of nuclear-transcribed mRNA catabolic process, deadenylation-dependent decay, protein localization to cytoplasmic stress granule, positive regulation of viral translation, positive regulation of polysome binding, positive regulation of DNA topoisomerase (ATP-hydrolyzing) activity, regulation of cytoplasmic translation, positive regulation of cytoplasmic translation,		
GOTERM_CC_DIRECT	intracellular, nucleus, nucleoplasm, perichromatin fibrils, nucleolus, cytoplasm, centrosome, cytosol, polysome, actin cytoskeleton, membrane, RISC complex, nuclear body, macromolecular complex, cytoplasmic ribonucleoprotein granule, polysomal ribosome, RISC-loading complex, CRD-mediated mRNA stability complex, nuclear stress granule, ribonucleoprotein complex,		
GOTERM_MF_DIRECT	RNA polymerase II core promoter proximal region sequence-specific DNA binding, RNA polymerase II core binding, regulatory region RNA binding, DNA binding, DNA helicase activity, DNA replication origin binding, double-stranded DNA binding, single-stranded DNA binding, transcription cofactor activity, transcription coactivator activity, RNA binding, RNA helicase activity, double-stranded RNA binding, single-stranded RNA binding, mRNA binding, helicase activity, protein binding, ATP binding, hydrolase activity, ATPase activity, nucleoside-triphosphatase activity, chromatin DNA binding, 3'-5' DNA/RNA helicase activity, 3'-5' RNA helicase activity, siRNA binding, RNA stem-loop binding, ribosome binding, 3'-5' DNA helicase activity, triplex DNA binding, metal ion binding, nucleoside-triphosphate diphosphatase activity, RNA polymerase II sequence-specific DNA binding transcription factor binding, importin-alpha family protein binding, RNA polymerase binding, RISC complex binding, polysome binding, single-stranded DNA-dependent ATP-dependent 3'-5' DNA helicase activity, sequence-specific mRNA binding, promoter-specific chromatin binding,		
INTERPRO	Helicase_C, DNA/RNA_helicase_DEAH_CS, Helicase-assoc_dom, DEAD/DEAH_box_helicase_dom, DEAD-box_helicase_OB_fold, Helicase_ATP-bd, dsRBD_dom, P-loop_NTPase, DHX9_DSRM_1, DHX9_DSRM_2, DHX9_DEXHc, HA2_WH,		
SMART	DSRM, DEXDc, HELICc, HA2,		
UP_KW_BIOLOGICAL_PROCESS	Biological rhythms, DNA replication, Immunity, Inflammatory response, Innate immunity, mRNA processing, mRNA splicing, mRNA transport, Transcription, Transcription regulation, Transcription termination, Translation regulation, Transport, RNA-mediated gene silencing, Host-virus interaction,		
UP_KW_CELLULAR_COMPONENT	Cytoskeleton, Nucleus, Cytoplasm,		
UP_KW_DOMAIN	Repeat,		
UP_KW_LIGAND	ATP-binding, Manganese, Metal-binding, Nucleotide-binding,		
UP_KW_MOLECULAR_FUNCTION	Activator, DNA-binding, Helicase, Hydrolase, RNA-binding,		
UP_KW_PTM	Acetylation, Methylation, Phosphoprotein, Ubl conjugation, Isopeptide bond,		

ATP2B1	ATPase plasma membrane Ca2+ transporting 1(ATP2B1)	Related Genes	Homo sapiens
UP_SEQ_FEATURE	CROSSLNK:Glycyl lysine isopeptide (Lys-Gly) (interchain with G-Cter in SUMO2), DOMAIN:DRBM, DOMAIN:DRBM 1, DOMAIN:DRBM 2, DOMAIN:Helicase ATP-binding, DOMAIN:Helicase C-terminal, DOMAIN:Helicase-associated, MOTIF:DEIH box, MOTIF:Nuclear localization signal (NLS1), MOTIF:Nuclear localization signal (NLS2), MUTAGEN:D->A: Does not inhibit binding to origins of DNA replication; when associated with A-512., MUTAGEN:E->A: Does not inhibit binding to origins of DNA replication; when associated with A-511., MUTAGEN:H->A: Reduces siRNA-binding and interaction with AGO2., MUTAGEN:I->A: Reduces NUP98-induced mRNA transcription and alternative splicing activities., MUTAGEN:K->A: Inhibits siRNA-binding and decreases interaction with AGO2; when associated with A-53 and A-54., MUTAGEN:K->A: Inhibits siRNA-binding and decreases interaction with AGO2; when associated with A-53 and A-55., MUTAGEN:K->A: Inhibits siRNA-binding and interaction with AGO2; when associated with A-234 and A-235., MUTAGEN:K->A: Inhibits siRNA-binding and interaction with AGO2; when associated with A-234 and A-236., MUTAGEN:K->A: Localizes in the cytoplasm and does not interact with the importin complex., MUTAGEN:K->A: Reduces siRNA-binding and interaction with AGO2., MUTAGEN:K->A: Reduces siRNA-binding and interaction with AGO2; when associated with A-6., MUTAGEN:K->R,N: Inhibits interaction with AGO2, DICER1 and TARBP2. Abrogates helicase activity and transcriptional activation. Does not inhibit binding to origins of DNA replication., MUTAGEN:K->R: Reduces NUP98-induced mRNA transcription and alternative splicing activities., MUTAGEN:Missing: Abolishes nuclear localization., MUTAGEN:N->A: Does not reduce siRNA-binding and interaction with AGO2., MUTAGEN:N->A: Inhibits siRNA-binding and decreases interaction with AGO2; when associated with A-54 and A-55., MUTAGEN:N->A: Inhibits siRNA-binding and interaction with AGO2; when associated with A-235 and A-236., MUTAGEN:N->A: Reduces siRNA-binding and interaction with AGO2; when associated with A-187., MUTAGEN:N->A: Reduces siRNA-binding; when associated with A-5., MUTAGEN:Q->A: Reduces siRNA-binding and interaction with AGO2; when associated with A-186., MUTAGEN:R->A: Localizes in the nucleus and interacts with the importin complex., MUTAGEN:R->A: Localizes in the nucleus and the cytoplasm and interacts weakly with the importin complex., MUTAGEN:R->L: Abolishes nuclear localization., MUTAGEN:S->L: Does not inhibit binding to origins of DNA replication., MUTAGEN:W->A: Abrogates transcriptional activation and RNA polymerase II binding by the MTAD region. No change in ATP binding and ATPase activities., MUTAGEN:W->A: Abrogates transcriptional activation by the MTAD region. No change in RNA polymerase II holoenzyme binding., MUTAGEN:Y->A: Inhibits siRNA-binding and interaction with AGO2., REGION:Core helicase, REGION:Disordered, REGION:HA2, REGION:Interaction with BRCA1, REGION:Interaction with CREBBP, REGION:MTAD, REGION:Necessary for interaction with H2AX, REGION:Necessary for interaction with RNA polymerase II holoenzyme, REGION:OB-fold, REGION:RGG, REGION:siRNA-binding,

FRMD5	FERM domain containing 5(FRMD5)	Related Genes	Homo sapiens
GOTERM_BP_DIRECT	regulation of cell migration, actomyosin structure organization, positive regulation of cell adhesion, negative regulation of cell motility,
GOTERM_CC_DIRECT	cytoskeleton, adherens junction, membrane,
GOTERM_MF_DIRECT	integrin binding, protein binding, cytoskeletal protein binding, protein kinase binding,
INTERPRO	FERM_domain, Ez/rad/moesin-like, PH-like_dom_sf, FERM/acyl-CoA-bd_prot_sf, FA, FERM_N, FERM_PH-like_C, FERM_CS, FERM_central, Band_41_domain, Ubiquitin-like_domsf, FERM_2,
OMIM_DISEASE	Neurodevelopmental disorder with eye movement abnormalities and ataxia,
SMART	B41, FA, FERM_C,
UP_KW_CELLULAR_COMPONENT	Membrane, Cell junction,
UP_KW_DISEASE	Disease variant, Intellectual disability,
UP_KW_DOMAIN	Transmembrane, Transmembrane helix,
UP_KW_PTM	Phosphoprotein,
UP_SEQ_FEATURE	COMPBIAS:Polar residues, DOMAIN:FERM, DOMAIN:FERM C-terminal PH-like, DOMAIN:FERM adjacent, REGION:Disordered, REGION:Interaction with ROCK1, TRANSMEM:Helical,

FRYL	FRY like transcription coactivator(FRYL)	Related Genes	Homo sapiens
GOTERM_BP_DIRECT	cell morphogenesis, neuron projection development,
GOTERM_CC_DIRECT	cell cortex, site of polarized growth,
INTERPRO	ARM-type_fold, Cell_Morphogen_C, Cell_morpho_N, MOR2-PAG1_mid, Furry/Tao3/Mor2, Fry_C,
UP_KW_BIOLOGICAL_PROCESS	Transcription, Transcription regulation,
UP_KW_DOMAIN	Coiled coil,
UP_KW_PTM	Acetylation, Phosphoprotein,
UP_SEQ_FEATURE	COMPBIAS:Acidic residues, COMPBIAS:Polar residues, DOMAIN:Cell morphogenesis central region, DOMAIN:Cell morphogenesis protein C-terminal, DOMAIN:Cell morphogenesis protein N-terminal, DOMAIN:Protein furry C-terminal, REGION:Disordered, SITE:Breakpoint for insertion to form KMT2A/MLL1-AFF4 fusion protein,

NAA10	N-alpha-acetyltransferase 10, NatA catalytic subunit(NAA10)	Related Genes	Homo sapiens
GOTERM_BP_DIRECT	protein acetylation, N-terminal protein amino acid acetylation, internal protein amino acid acetylation, chromosome organization, negative regulation of maintenance of mitotic sister chromatid cohesion, centromeric,
GOTERM_CC_DIRECT	nucleus, nucleolus, cytoplasm, cytosol, membrane, NatA complex,
GOTERM_MF_DIRECT	peptide alpha-N-acetyltransferase activity, protein binding, N-acetyltransferase activity, acetyltransferase activity, ribosome binding, peptide-serine-N-acetyltransferase activity, peptide-glutamate-N-acetyltransferase activity,
INTERPRO	GNAT_dom, Acyl_CoA_acyltransferase, Ard1-like,
OMIM_DISEASE	Ogden syndrome, Microphthalmia, syndromic 1,
UP_KW_CELLULAR_COMPONENT	Nucleus, Cytoplasm,
UP_KW_DISEASE	Disease variant, Microphthalmia,
UP_KW_MOLECULAR_FUNCTION	Acyltransferase, Transferase,
UP_KW_PTM	Acetylation, Phosphoprotein,
UP_SEQ_FEATURE	COMPBIAS:Basic and acidic residues, DOMAIN:N-acetyltransferase, MUTAGEN:K->R: Loss of its ability to acetylate HSPA1A and HSPA1B., MUTAGEN:S->A: Abolishes phosphorylation by IKKB and reduces cell growth., REGION:Disordered, REGION:Interaction with NAA15,

PPFIA3	PTPRF interacting protein alpha 3(PPFIA3)	Related Genes	Homo sapiens
GOTERM_BP_DIRECT	neurotransmitter secretion, synaptic vesicle docking, regulation of short-term neuronal synaptic plasticity, synapse organization,
GOTERM_CC_DIRECT	acrosomal vesicle, cytosol, presynaptic active zone, presynaptic active zone cytoplasmic component, epididymosome, glutamatergic synapse,
GOTERM_MF_DIRECT	protein binding,
INTERPRO	SAM, SAM/pointed_sf, Liprin, Liprin-alpha_SAM_rpt_1, Liprin-alpha_SAM_rpt_2, Liprin-alpha_SAM_rpt_3,
SMART	SAM,
UP_KW_CELLULAR_COMPONENT	Cytoplasm, Cytoplasmic vesicle,
UP_KW_DOMAIN	Coiled coil, Repeat,
UP_KW_PTM	Phosphoprotein,
UP_SEQ_FEATURE	COMPBIAS:Basic and acidic residues, COMPBIAS:Polar residues, DOMAIN:SAM, DOMAIN:SAM 1, DOMAIN:SAM 2, DOMAIN:SAM 3, REGION:Disordered,

POLR2A	RNA polymerase II subunit A(POLR2A)	Related Genes	Homo sapiens
BIOCARTA	CARM1 and Regulation of the Estrogen Receptor, Repression of Pain Sensation by the Transcriptional Regulator DREAM, Chromatin Remodeling by hSWI/SNF ATP-dependent Complexes, The information-processing pathway at the IFN-beta enhancer, Nuclear receptors coordinate the activities of chromatin remodeling complexes and coactivators to facilitate initiation of transcription in carcinoma cells, Telomeres, Telomerase, Cellular Aging, and Immortality,
GOTERM_BP_DIRECT	transcription, RNA-templated, DNA-templated transcription, termination, regulation of transcription, DNA-templated, transcription from RNA polymerase II promoter, response to organic cyclic compound, positive regulation of RNA splicing, cellular response to oxygen levels,
GOTERM_CC_DIRECT	DNA-directed RNA polymerase complex, euchromatin, Prp19 complex, nucleus, nucleoplasm, DNA-directed RNA polymerase II, core complex, chromosome, cytoplasm,
GOTERM_MF_DIRECT	core promoter sequence-specific DNA binding, RNA polymerase II activity, DNA binding, RNA binding, DNA-directed 5'-3' RNA polymerase activity, RNA-directed 5'-3' RNA polymerase activity, protein binding, kinase binding, ubiquitin protein ligase binding, metal ion binding, microfibril binding, promoter-specific chromatin binding,
INTERPRO	RNA_pol_II_repeat_euk, RNA_pol_asu, RNA_pol_N, RNA_pol_Rpb1_3, RNA_pol_Rpb1_7, RNA_pol_Rpb1_6, RNA_pol_Rpb1_1, RNA_pol_Rpb1_5, RNA_pol_Rpb1_4, Rpb1_funnel_sf, RNA_pol_Rpb1_7_sf, RNA_pol_Rpb1_3_sf, RNA_pol_Rpb1_clamp_domain, DNA-dir_RpoC_beta_prime,
KEGG_PATHWAY	RNA polymerase, Nucleotide excision repair, Huntington disease,
OMIM_DISEASE	Neurodevelopmental disorder with hypotonia and variable intellectual and behavioral abnormalities,
SMART	RPOLA_N,
UP_KW_BIOLOGICAL_PROCESS	Transcription, Host-virus interaction,
UP_KW_CELLULAR_COMPONENT	Chromosome, DNA-directed RNA polymerase, Nucleus, Cytoplasm, DNA-directed RNA polymerase,
UP_KW_DISEASE	Disease variant, Intellectual disability,
UP_KW_DOMAIN	Repeat,
UP_KW_LIGAND	Magnesium, Metal-binding, Zinc,
UP_KW_MOLECULAR_FUNCTION	DNA-binding, Nucleotidyltransferase, RNA-directed RNA polymerase, Transferase,
UP_KW_PTM	Acetylation, Methylation, Phosphoprotein, Ubl conjugation, Isopeptide bond,

ATP2B1	ATPase plasma membrane Ca2+ transporting 1(ATP2B1)	Related Genes	Homo sapiens
UP_SEQ_FEATURE	COMPBIAS:Polar residues, COMPBIAS:Pro residues, CROSSLNK:Glycyl lysine isopeptide (Lys-Gly) (interchain with G-Cter in ubiquitin); by NEDD4, DOMAIN:RNA polymerase N-terminal, MUTAGEN:K->R: Impairs ubiquitination, interaction with the TFIIH complex, and its degradation during transcription stress., MUTAGEN:K->R: Loss of acetylation and loss of regulation of growth-factor-induced gene expression; when associated with R-1838; R-1859; R-1866; R-1873; R-1887; R-1908 and R-1922., MUTAGEN:K->R: Loss of acetylation and loss of regulation of growth-factor-induced gene expression; when associated with R-1838; R-1859; R-1866; R-1873; R-1887; R-1908 and R-1936., MUTAGEN:K->R: Loss of acetylation and loss of regulation of growth-factor-induced gene expression; when associated with R-1838; R-1859; R-1866; R-1873; R-1908; R-1922 and R-1936., MUTAGEN:K->R: Loss of acetylation and loss of regulation of growth-factor-induced gene expression; when associated with R-1838; R-1859; R-1866; R-1887; R-1908; R-1922 and R-1936., MUTAGEN:K->R: Loss of acetylation and loss of regulation of growth-factor-induced gene expression; when associated with R-1838; R-1866; R-1873; R-1887; R-1908; R-1922 and R-1936., MUTAGEN:K->R: Loss of acetylation and loss of regulation of growth-factor-induced gene expression; when associated with R-1859; R-1859; R-1873; R-1887; R-1908; R-1922 and R-1936., MUTAGEN:K->R: Loss of acetylation and loss of regulation of growth-factor-induced gene expression; when associated with R-1859; R-1866; R-1873; R-1887; R-1908; R-1922 and R-1936., MUTAGEN:K->R: Loss of acetylation and loss of regulation of growth-factor-induced gene expression; when associated with R.1838; R-1859; R-1866; R-1873; R-1887; R-1922 and R-1936., MUTAGEN:Missing: Decreases cell viability., MUTAGEN:R->A: Misexpression of a variety of small nuclear RNAs and small nucleolar RNAs. Loss of interaction with TDRD3 and SMN1/SMN2., REGION:Bridging helix, REGION:C-terminal domain (CTD); 52 X 7 AA approximate tandem repeats of Y-[ST]-P-[STQ]-[ST]-P-[SRTEVKGN], REGION:Disordered, REPEAT:1, REPEAT:10, REPEAT:11, REPEAT:12, REPEAT:13, REPEAT:14, REPEAT:15, REPEAT:16, REPEAT:17, REPEAT:18, REPEAT:19, REPEAT:20, REPEAT:21, REPEAT:22, REPEAT:23, REPEAT:24, REPEAT:25, REPEAT:26, REPEAT:27, REPEAT:28, REPEAT:29, REPEAT:2; approximate, REPEAT:3, REPEAT:30, REPEAT:31, REPEAT:32, REPEAT:33, REPEAT:34, REPEAT:35, REPEAT:36, REPEAT:37, REPEAT:38, REPEAT:39, REPEAT:4, REPEAT:40, REPEAT:41, REPEAT:42, REPEAT:43, REPEAT:44, REPEAT:45, REPEAT:46, REPEAT:47, REPEAT:48, REPEAT:49, REPEAT:5, REPEAT:50, REPEAT:51; approximate, REPEAT:52; approximate, REPEAT:6, REPEAT:7, REPEAT:8, REPEAT:9,		

POLR3A	RNA polymerase III subunit A(POLR3A)	Related Genes	Homo sapiens
GOTERM_BP_DIRECT	transcription, DNA-templated, transcription from RNA polymerase III promoter, positive regulation of interferon-beta production, tRNA transcription from RNA polymerase III promoter, innate immune response, defense response to virus,		
GOTERM_CC_DIRECT	DNA-directed RNA polymerase complex, nucleus, nucleoplasm, DNA-directed RNA polymerase III complex, cytoplasm, cytosol, membrane, nuclear lumen,		
GOTERM_MF_DIRECT	magnesium ion binding, RNA polymerase III activity, DNA binding, chromatin binding, DNA-directed 5'-3' RNA polymerase activity, protein binding, zinc ion binding, metal ion binding, DNA/RNA hybrid binding,		
INTERPRO	RNA_pol_asu, RNA_pol_N, RNA_pol_Rpb1_3, RNA_pol_Rpb1_1, RNA_pol_Rpb1_5, RNA_pol_Rpb1_4, RNAP_III_RPC1_N, RNAP_III_Rpc1_C, Rpb1_funnel_sf, RNA_pol_Rpb1_3_sf, RNA_pol_Rpb1_clamp_domain, DNA-dir_RpoC_beta_prime,		
KEGG_PATHWAY	RNA polymerase, Cytosolic DNA-sensing pathway,		
OMIM_DISEASE	Wiedemann-Rautenstrauch syndrome, Leukodystrophy, hypomyelinating, 7, with or without oligodontia and/or hypogonadotropic hypogonadism,		
SMART	RPOLA_N,		
UP_KW_BIOLOGICAL_PROCESS	Antiviral defense, Immunity, Innate immunity, Transcription,		
UP_KW_CELLULAR_COMPONENT	DNA-directed RNA polymerase, Nucleus, Cytoplasm, DNA-directed RNA polymerase,		
UP_KW_DISEASE	Disease variant, Leukodystrophy,		
UP_KW_LIGAND	Magnesium, Metal-binding, Zinc,		
UP_KW_MOLECULAR_FUNCTION	Nucleotidyltransferase, Transferase,		
UP_KW_PTM	Acetylation,		
UP_SEQ_FEATURE	DOMAIN:RNA polymerase N-terminal, DOMAIN:RNA polymerase Rpb1, REGION:Bridging helix,		

ADGRL1	adhesion G protein-coupled receptor L1(ADGRL1)	Related Genes	Homo sapiens
GOTERM_BP_DIRECT	heterophilic cell-cell adhesion via plasma membrane cell adhesion molecules, cell surface receptor signaling pathway, G-protein coupled receptor signaling pathway, adenylate cyclase-activating G-protein coupled receptor signaling pathway, calcium-mediated signaling using intracellular calcium source, positive regulation of synapse maturation,		
GOTERM_CC_DIRECT	plasma membrane, membrane, axon, growth cone, presynaptic membrane, neuron projection, synapse,		
GOTERM_MF_DIRECT	G-protein coupled receptor activity, protein binding, latrotoxin receptor activity, carbohydrate binding, cell adhesion molecule binding,		
INTERPRO	GPS, GPCR_2_secretin-like, Lectin_gal-bd_dom, GPCR_2_extracellular_dom, Olfac-like_dom, GPCR_2_latrophilin_rcpt_C, GPCR_2_latrophilin, GPCR_2-like_7TM, GPCR_2_secretin-like_CS, Latrophilin-1_TM, GAIN_dom_N, GPCR_2_extracell_dom_sf, Lectin_gal-bd_sf, GAIN_dom_sf,		
OMIM_DISEASE	Developmental delay, behavioral abnormalities, and neuropsychiatric disorders,		
SMART	HormR, OLF, GPS,		
UP_KW_CELLULAR_COMPONENT	Membrane, Synapse, Synaptosome, Cell projection, Cell membrane,		
UP_KW_DISEASE	Disease variant, Intellectual disability, Autism spectrum disorder,		
UP_KW_DOMAIN	Signal, Transmembrane, Transmembrane helix,		
UP_KW_LIGAND	Lectin,		
UP_KW_MOLECULAR_FUNCTION	G-protein coupled receptor, Receptor, Transducer,		
UP_KW_PTM	Autocatalytic cleavage, Glycoprotein, Methylation, Phosphoprotein, Disulfide bond,		
UP_SEQ_FEATURE	CARBOHYD:N-linked (GlcNAc...) asparagine, COMPBIAS:Polar residues, COMPBIAS:Pro residues, DOMAIN:GAIN, DOMAIN:GPCR family 2 latrophilin C-terminal, DOMAIN:GPS, DOMAIN:Olfactomedin-like, DOMAIN:SUEL-type lectin, REGION:Disordered, SITE:Cleavage; by autolysis, TOPO_DOM:Cytoplasmic, TOPO_DOM:Extracellular, TRANSMEM:Helical; Name=1, TRANSMEM:Helical; Name=2, TRANSMEM:Helical; Name=3, TRANSMEM:Helical; Name=4, TRANSMEM:Helical; Name=5, TRANSMEM:Helical; Name=6, TRANSMEM:Helical; Name=7,		

CDH2	cadherin 2(CDH2)	Related Genes	Homo sapiens
GOTERM_BP_DIRECT	cell morphogenesis, type B pancreatic cell development, cell-cell junction assembly, cell adhesion, homophilic cell adhesion via plasma membrane adhesion molecules, heterophilic cell-cell adhesion via plasma membrane cell adhesion molecules, multicellular organism development, synapse assembly, brain development, glial cell differentiation, neural crest cell development, calcium-dependent cell-cell adhesion via plasma membrane cell adhesion molecules, cerebral cortex development, adherens junction organization, detection of muscle stretch, positive regulation of MAPK cascade, cell-cell adhesion mediated by cadherin, blood vessel morphogenesis, brain morphogenesis, homeostasis of number of cells, regulation of axonogenesis, striated muscle cell differentiation, regulation of synaptic transmission, glutamatergic, radial glial cell differentiation, neuroepithelial cell differentiation, regulation of oligodendrocyte progenitor proliferation, protein localization to plasma membrane, negative regulation of canonical Wnt signaling pathway, mesenchymal cell migration, synaptic vesicle clustering, neuroligin clustering involved in postsynaptic membrane assembly, neuronal stem cell population maintenance, cell-cell adhesion, regulation of postsynaptic density protein 95 clustering, positive regulation of synaptic vesicle clustering,		
GOTERM_CC_DIRECT	cytoplasm, endoplasmic reticulum lumen, plasma membrane, cell-cell junction, adherens junction, fascia adherens, focal adhesion, cell surface, postsynaptic density, intercalated disc, membrane, basolateral plasma membrane, apical plasma membrane, apicolateral plasma membrane, catenin complex, lamellipodium, cell junction, desmosome, cortical actin cytoskeleton, sarcolemma, neuron projection, plasma membrane raft, apical part of cell, presynapse,		
GOTERM_MF_DIRECT	RNA binding, calcium ion binding, protein binding, beta-catenin binding, protein kinase binding, protein phosphatase binding, identical protein binding, alpha-catenin binding, gamma-catenin binding, cadherin binding,		
INTERPRO	Cadherin_Y-type_LIR, PH_domain, Cadherin-like_dom, Cadherin_pro_dom, Cadherin-like_sf, Cadherin_CS, Catenin-bd_sf, Cadherin,		
KEGG_PATHWAY	Cell adhesion molecules, Arrhythmogenic right ventricular cardiomyopathy,		
OMIM_DISEASE	Arrhythmogenic right ventricular dysplasia 14, Agenesis of corpus callosum, cardiac, ocular, and genital syndrome, Attention deficit-hyperactivity disorder 8,		
SMART	CA, Cadherin_pro,		
UP_KW_BIOLOGICAL_PROCESS	Cell adhesion,		
UP_KW_CELLULAR_COMPONENT	Membrane, Cell junction, Cell membrane,		
UP_KW_DISEASE	Cardiomyopathy, Disease variant, Intellectual disability,		
UP_KW_DOMAIN	Repeat, Signal, Transmembrane, Transmembrane helix,		
UP_KW_LIGAND	Calcium, Metal-binding,		
UP_KW_PTM	Cleavage on pair of basic residues, Glycoprotein, Phosphoprotein,		
UP_SEQ_FEATURE	CARBOHYD:N-linked (GlcNAc...) asparagine, COMPBIAS:Polar residues, DOMAIN:Cadherin, DOMAIN:Cadherin 1, DOMAIN:Cadherin 2, DOMAIN:Cadherin 3, DOMAIN:Cadherin 4, DOMAIN:Cadherin 5, DOMAIN:PH, REGION:Disordered, TOPO_DOM:Cytoplasmic, TOPO_DOM:Extracellular, TRANSMEM:Helical,		

CAMK2D	calcium/calmodulin dependent protein kinase II delta(CAMK2D)	Related Genes	Homo sapiens
BIOCARTA	Bioactive Peptide Induced Signaling Pathway, Ca++/ Calmodulin-dependent Protein Kinase Activation, Transcription factor CREB and its extracellular signals, Regulation of PGC-1a, Stathmin and breast cancer resistance to antimicrotubule agents,		
GOTERM_BP_DIRECT	regulation of cell growth, regulation of the force of heart contraction, regulation of membrane depolarization, regulation of transcription from RNA polymerase II promoter, protein phosphorylation, regulation of heart contraction, positive regulation of cardiac muscle hypertrophy, regulation of cell communication by electrical coupling, positive regulation of cardiac muscle cell apoptotic process, regulation of release of sequestered calcium ion into cytosol by sarcoplasmic reticulum, regulation of cardiac muscle contraction by regulation of the release of sequestered calcium ion, phosphorylation, peptidyl-serine phosphorylation, peptidyl-threonine phosphorylation, endoplasmic reticulum calcium ion homeostasis, protein autophosphorylation, relaxation of cardiac muscle, regulation of ryanodine-sensitive calcium-release channel activity, regulation of cellular localization, cellular response to calcium ion, cardiac muscle cell contraction, regulation of heart rate by cardiac conduction, regulation of cardiac muscle cell action potential, regulation of cardiac muscle cell action potential involved in regulation of contraction, regulation of cell communication by electrical coupling involved in cardiac conduction, regulation of relaxation of cardiac muscle, negative regulation of sodium ion transmembrane transport, regulation of calcium ion transmembrane transport via high voltage-gated calcium channel, negative regulation of sodium ion transmembrane transporter activity,		
GOTERM_CC_DIRECT	nucleus, nucleoplasm, cytoplasm, cytosol, calcium- and calmodulin-dependent protein kinase complex, membrane, endocytic vesicle membrane, sarcoplasmic reticulum membrane, sarcolemma, neuron projection, organelle,		

ATP2B1	ATPase plasma membrane Ca2+ transporting 1(ATP2B1)	Related Genes	Homo sapiens
GOTERM_MF_DIRECT	protein kinase activity, protein serine/threonine kinase activity, calmodulin-dependent protein kinase activity, protein binding, calmodulin binding, ATP binding, sodium channel inhibitor activity, titin binding, identical protein binding, protein homodimerization activity, ion channel binding,		
INTERPRO	Prot_kinase_dom, Ser/Thr_kinase_AS, Kinase-like_dom_sf, Ca/CaM-dep_prot_kinase-assoc, Protein_kinase_ATP_BS, NTF2-like_dom_sf,		
KEGG_PATHWAY	ErbB signaling pathway, Calcium signaling pathway, cAMP signaling pathway, HIF-1 signaling pathway, Oocyte meiosis, Efferocytosis, Necroptosis, Adrenergic signaling in cardiomyocytes, Wnt signaling pathway, Axon guidance, Circadian entrainment, Long-term potentiation, Neurotrophin signaling pathway, Cholinergic synapse, Dopaminergic synapse, Olfactory transduction, Inflammatory mediator regulation of TRP channels, Insulin secretion, GnRH signaling pathway, Melanogenesis, Oxytocin signaling pathway, Glucagon signaling pathway, Aldosterone synthesis and secretion, Cushing syndrome, Gastric acid secretion, Parkinson disease, Pathways of neurodegeneration - multiple diseases, Amphetamine addiction, Tuberculosis, Pathways in cancer, Proteoglycans in cancer, Glioma, Diabetic cardiomyopathy, Lipid and atherosclerosis,		
SMART	S_TKc,		
UP_KW_CELLULAR_COMPONENT	Membrane, Sarcoplasmic reticulum, Cell membrane,		
UP_KW_DOMAIN	Transmembrane, Transmembrane helix,		
UP_KW_LIGAND	ATP-binding, Nucleotide-binding,		
UP_KW_MOLECULAR_FUNCTION	Calmodulin-binding, Kinase, Serine/threonine-protein kinase, Transferase,		
UP_KW_PTM	Acetylation, Phosphoprotein,		
UP_SEQ_FEATURE	ACT_SITE:Proton acceptor, COMPBIAS:Polar residues, DOMAIN:Calcium/calmodulin-dependent protein kinase II association-domain, DOMAIN:Protein kinase, REGION:Autoinhibitory domain, REGION:Calmodulin-binding, REGION:Disordered, TRANSMEM:Helical,		
CSNK1G1	casein kinase 1 gamma 1(CSNK1G1)	Related Genes	Homo sapiens
GOTERM_BP_DIRECT	endocytosis, signal transduction, Wnt signaling pathway, phosphorylation, peptidyl-serine phosphorylation, positive regulation of canonical Wnt signaling pathway,		
GOTERM_CC_DIRECT	nucleus, cytoplasm, cytosol, plasma membrane, membrane,		
GOTERM_MF_DIRECT	protein kinase activity, protein serine/threonine kinase activity, protein binding, ATP binding,		
INTERPRO	Prot_kinase_dom, Ser/Thr_kinase_AS, Kinase-like_dom_sf, Protein_kinase_ATP_BS, Casein_kinase-1_gamma_C,		
KEGG_PATHWAY	Hedgehog signaling pathway,		
SMART	S_TKc,		
UP_KW_BIOLOGICAL_PROCESS	Wnt signaling pathway,		
UP_KW_CELLULAR_COMPONENT	Membrane, Cytoplasm,		
UP_KW_DISEASE	Disease variant,		
UP_KW_DOMAIN	Transmembrane, Transmembrane helix,		
UP_KW_LIGAND	ATP-binding, Nucleotide-binding,		
UP_KW_MOLECULAR_FUNCTION	Kinase, Serine/threonine-protein kinase, Transferase,		
UP_KW_PTM	Phosphoprotein,		
UP_SEQ_FEATURE	ACT_SITE:Proton acceptor, COMPBIAS:Basic and acidic residues, COMPBIAS:Polar residues, DOMAIN:Casein kinase 1 gamma C-terminal, DOMAIN:Protein kinase, MUTAGEN:N->A: Loss of kinase activity., REGION:Disordered, TRANSMEM:Helical,		
CERT1	ceramide transporter 1(CERT1)	Related Genes	Homo sapiens
GOTERM_BP_DIRECT	cell morphogenesis, in utero embryonic development, receptor recycling, heart morphogenesis, ceramide metabolic process, muscle contraction, immune response, mitochondrion organization, endoplasmic reticulum organization, endosome organization, signal transduction, cell proliferation, response to endoplasmic reticulum stress, ER to Golgi ceramide transport, ceramide transport, retrograde transport, endosome to Golgi, lipid homeostasis, mitochondrion morphogenesis, ceramide 1-phosphate transport,		
GOTERM_CC_DIRECT	nucleoplasm, mitochondrion, early endosome, endoplasmic reticulum, endoplasmic reticulum membrane, Golgi apparatus, trans-Golgi network, cytosol, clathrin-coated vesicle, perinuclear region of cytoplasm, recycling endosome,		
GOTERM_MF_DIRECT	protein binding, lipid binding, kinase activity, identical protein binding, phosphatidylinositol-4-phosphate binding, ceramide binding, ceramide 1-phosphate binding, ceramide 1-phosphate transporter activity,		
INTERPRO	PH_domain, START_lipid-bd_dom, PH-like_dom_sf, START-like_dom_sf, STARD11_START, Boi1/Boi2-like,		
OMIM_DISEASE	Intellectual developmental disorder, autosomal dominant 34,		
SMART	PH, START,		
UP_KW_BIOLOGICAL_PROCESS	Lipid transport, Transport,		
UP_KW_CELLULAR_COMPONENT	Endoplasmic reticulum, Golgi apparatus, Cytoplasm, Endosome, Cytoplasmic vesicle,		
UP_KW_DISEASE	Disease variant, Intellectual disability,		
UP_KW_DOMAIN	Coiled coil,		
UP_KW_LIGAND	Lipid-binding,		
UP_KW_PTM	Phosphoprotein,		
UP_SEQ_FEATURE	COMPBIAS:Polar residues, DOMAIN:PH, DOMAIN:START, MOTIF:FFAT, MUTAGEN:D->A: Impairs the endoplasmic reticulum-to-Golgi ceramide trafficking and abolishes the interaction with VAPA and MOSPD2., MUTAGEN:E->A: Reduces ceramide transfer., MUTAGEN:N->A: Reduces ceramide transfer., MUTAGEN:Q->A: No effect on ceramide transfer activity., MUTAGEN:S->A: Abolishes the phosphorylation. Strongly reduces the interaction with phosphatidylinositol 4-phosphate. Increases the ceramide transfer activity., MUTAGEN:W->A: Abolishes ceramide transfer; when associated with A-499., MUTAGEN:W->A: Reduces affinity for membranes. Abolishes ceramide transfer; when associated with A-588., REGION:Disordered,		
CBX1	chromobox 1(CBX1)	Related Genes	Homo sapiens
GOTERM_BP_DIRECT	negative regulation of transcription from RNA polymerase II promoter, chromatin organization, cellular response to DNA damage stimulus, negative regulation of transcription, DNA-templated,		
GOTERM_CC_DIRECT	chromosome, centromeric region, chromosome, telomeric region, chromatin, heterochromatin, female pronucleus, male pronucleus, nucleus, nucleoplasm, pericentric heterochromatin, spindle, chromocenter, nuclear body, intracellular membrane-bounded organelle, site of DNA damage,		
GOTERM_MF_DIRECT	DNA binding, chromatin binding, protein binding, enzyme binding, methylated histone binding, identical protein binding, binding, bridging, histone methyltransferase binding,		
INTERPRO	Chromo/chromo_shadow_dom, Chromo_shadow_dom, Chromo-like_dom_sf, Chromo_dom_subgr, Chromodomain_CS, Chromo_domain,		
SMART	CHROMO, ChSh,		
UP_KW_CELLULAR_COMPONENT	Nucleus,		
UP_KW_DOMAIN	Repeat,		
UP_KW_PTM	Phosphoprotein, Ubl conjugation, Isopeptide bond,		
UP_SEQ_FEATURE	COMPBIAS:Basic and acidic residues, CROSSLNK:Glycyl lysine isopeptide (Lys-Gly) (interchain with G-Cter in SUMO2), DOMAIN:Chromo, DOMAIN:Chromo 1, DOMAIN:Chromo 2; shadow subtype, MUTAGEN:I->E: Abolishes homodimer formation and binding to EMSY., REGION:Disordered, SITE:Histone H3A7 binding, SITE:Histone H3K9me2 binding, SITE:Interacts with the PxVxL motif of TRIM28/TIF1B,		
CDK19	cyclin dependent kinase 19(CDK19)	Related Genes	Homo sapiens
GOTERM_BP_DIRECT	protein phosphorylation, phosphorylation, positive regulation of apoptotic process, cell division, regulation of cell cycle, cellular response to lipopolysaccharide,		
GOTERM_CC_DIRECT	nucleus, nucleoplasm, cytosol, perinuclear region of cytoplasm, CKM complex,		
GOTERM_MF_DIRECT	protein kinase activity, protein serine/threonine kinase activity, cyclin-dependent protein serine/threonine kinase activity, ATP binding,		
INTERPRO	Prot_kinase_dom, Ser/Thr_kinase_AS, Kinase-like_dom_sf, Protein_kinase_ATP_BS,		
OMIM_DISEASE	Developmental and epileptic encephalopathy 87,		
SMART	S_TKc,		
UP_KW_BIOLOGICAL_PROCESS	Cell cycle, Cell division,		
UP_KW_CELLULAR_COMPONENT	Nucleus, Cytoplasm,		
UP_KW_DISEASE	Disease variant, Epilepsy,		
UP_KW_LIGAND	ATP-binding, Nucleotide-binding,		
UP_KW_MOLECULAR_FUNCTION	Kinase, Serine/threonine-protein kinase, Transferase,		
UP_KW_PTM	Acetylation, Phosphoprotein,		
UP_SEQ_FEATURE	ACT_SITE:Proton acceptor, COMPBIAS:Polar residues, DOMAIN:Protein kinase, REGION:Disordered,		
FGF13	fibroblast growth factor 13(FGF13)	Related Genes	Homo sapiens
GOTERM_BP_DIRECT	MAPK cascade, neuron migration, sodium ion transport, negative regulation of microtubule depolymerization, signal transduction, cell-cell signaling, nervous system development, learning, memory, hippocampus development, cerebral cortex cell migration, establishment of neuroblast polarity, microtubule polymerization, negative regulation of collateral sprouting, branching morphogenesis of a nerve, protein localization to plasma membrane, regulation of cardiac muscle cell action potential involved in regulation of contraction, inhibitory synapse assembly, regulation of voltage-gated sodium channel activity, positive regulation of voltage-gated sodium channel activity,		
GOTERM_CC_DIRECT	nucleus, cytoplasm, cytosol, microtubule, plasma membrane, intercalated disc, lateral plasma membrane, filopodium, axon, dendrite, growth cone, sarcolemma, neuron projection,		
GOTERM_MF_DIRECT	protein binding, microtubule binding, growth factor activity, sodium channel regulator activity, ion channel binding, beta-tubulin binding,		
INTERPRO	Fibroblast_GF_fam, IL1/FGF,		
OMIM_DISEASE	Developmental and epileptic encephalopathy 90, Intellectual developmental disorder, X-linked 110,		

ATP2B1	ATPase plasma membrane Ca2+ transporting 1(ATP2B1)	Related Genes	Homo sapiens
SMART	FGF,		
UP_KW_BIOLOGICAL_PROCESS	Neurogenesis,		
UP_KW_CELLULAR_COMPONENT	Membrane, Microtubule, Nucleus, Cytoplasm, Cell projection, Cell membrane,		
UP_KW_DISEASE	Disease variant, Epilepsy, Intellectual disability,		
UP_KW_PTM	Phosphoprotein,		
UP_SEQ_FEATURE	COMPBIAS:Basic and acidic residues, MUTAGEN:P->Q: Loss of interaction with SCN1A., REGION:Disordered, REGION:Mediates interaction with sodium channels, REGION:Mediates targeting to the nucleus,		

MACF1	microtubule actin crosslinking factor 1(MACF1)	Related Genes	Homo sapiens
GOTERM_BP_DIRECT	regulation of epithelial cell migration, Wnt signaling pathway, positive regulation of Wnt signaling pathway, regulation of cell migration, regulation of microtubule-based process, wound healing, Golgi to plasma membrane protein transport, intermediate filament cytoskeleton organization, positive regulation of axon extension, regulation of focal adhesion assembly,		
GOTERM_CC_DIRECT	cytoplasm, Golgi apparatus, cytoskeleton, microtubule, intermediate filament, plasma membrane, actin cytoskeleton, membrane, cell junction, ruffle membrane, cell projection,		
GOTERM_MF_DIRECT	RNA binding, actin binding, structural molecule activity, calcium ion binding, protein binding, microtubule binding, cadherin binding, microtubule minus-end binding, actin filament binding,		
INTERPRO	Plectin_repeat, SH3_domain, Actinin_actin-bd_CS, CH_dom, Spectrin_repeat, EF_hand_dom, GAR_dom, EF-hand-dom_pair, Spectrin/alpha-actinin, EF_Hand_1_Ca_BS, Plakin_repeat_sf, GAR_dom_sf, CH_dom_sf, MCAF1-like, Desmoplakin_Spectrin-like, Desmoplakin_SH3, Plakin,		
OMIM_DISEASE	Lissencephaly 9 with complex brainstem malformation,		
SMART	CH, EFh, SPEC, GAS2, PLEC, DELLA,		
UP_KW_BIOLOGICAL_PROCESS	Wnt signaling pathway,		
UP_KW_CELLULAR_COMPONENT	Cytoskeleton, Golgi apparatus, Membrane, Microtubule, Cytoplasm, Cell projection, Cell membrane,		
UP_KW_DISEASE	Disease variant, Lissencephaly,		
UP_KW_DOMAIN	Coiled coil, Leucine-rich repeat, Repeat, SH3 domain, Transmembrane, Transmembrane helix,		
UP_KW_LIGAND	Calcium, Metal-binding,		
UP_KW_MOLECULAR_FUNCTION	Actin-binding,		
UP_KW_PTM	Acetylation, Phosphoprotein,		
UP_SEQ_FEATURE	COMPBIAS:Basic and acidic residues, COMPBIAS:Polar residues, COMPBIAS:Pro residues, DOMAIN:Calponin-homology (CH), DOMAIN:Calponin-homology (CH) 1, DOMAIN:Calponin-homology (CH) 2, DOMAIN:EF-hand, DOMAIN:EF-hand 1, DOMAIN:EF-hand 2, DOMAIN:GAR, DOMAIN:SH3, REGION:13 X 13 AA approximate tandem repeat of P-T-S-P-A-A-A-V-P-T-P-E-E, REGION:4 X 4 AA tandem repeats of [GS]-S-R-[AR], REGION:Actin-binding, REGION:C-terminal tail, REGION:Disordered, REPEAT:1, REPEAT:10, REPEAT:11, REPEAT:12, REPEAT:13, REPEAT:2, REPEAT:3, REPEAT:4, REPEAT:5, REPEAT:6, REPEAT:7, REPEAT:8, REPEAT:9, REPEAT:LRR 1, REPEAT:LRR 10, REPEAT:LRR 11, REPEAT:LRR 12, REPEAT:LRR 13, REPEAT:LRR 14, REPEAT:LRR 15, REPEAT:LRR 16, REPEAT:LRR 17, REPEAT:LRR 18, REPEAT:LRR 19, REPEAT:LRR 2, REPEAT:LRR 20, REPEAT:LRR 21, REPEAT:LRR 22, REPEAT:LRR 23, REPEAT:LRR 24, REPEAT:LRR 3, REPEAT:LRR 4, REPEAT:LRR 5, REPEAT:LRR 6, REPEAT:LRR 7, REPEAT:LRR 8, REPEAT:LRR 9, REPEAT:Plectin 1, REPEAT:Plectin 10, REPEAT:Plectin 11, REPEAT:Plectin 2, REPEAT:Plectin 3, REPEAT:Plectin 4, REPEAT:Plectin 5, REPEAT:Plectin 6, REPEAT:Plectin 7, REPEAT:Plectin 8, REPEAT:Plectin 9, REPEAT:Spectrin 1, REPEAT:Spectrin 10, REPEAT:Spectrin 11, REPEAT:Spectrin 12, REPEAT:Spectrin 13, REPEAT:Spectrin 14, REPEAT:Spectrin 15, REPEAT:Spectrin 16, REPEAT:Spectrin 17, REPEAT:Spectrin 2, REPEAT:Spectrin 3, REPEAT:Spectrin 4, REPEAT:Spectrin 5, REPEAT:Spectrin 6, REPEAT:Spectrin 7, REPEAT:Spectrin 8, REPEAT:Spectrin 9, TRANSMEM:Helical,		

MSX2	msh homeobox 2(MSX2)	Related Genes	Homo sapiens
GOTERM_BP_DIRECT	negative regulation of transcription from RNA polymerase II promoter, osteoblast differentiation, chondrocyte development, osteoblast development, outflow tract septum morphogenesis, cardiac conduction system development, epithelial to mesenchymal transition involved in endocardial cushion formation, endochondral bone growth, regulation of transcription from RNA polymerase II promoter, negative regulation of cell proliferation, anterior/posterior pattern specification, signal transduction involved in regulation of gene expression, BMP signaling pathway, positive regulation of BMP signaling pathway, embryonic forelimb morphogenesis, embryonic hindlimb morphogenesis, wound healing, spreading of epidermal cells, embryonic nail plate morphogenesis, negative regulation of apoptotic process, negative regulation of fat cell differentiation, negative regulation of keratinocyte differentiation, positive regulation of osteoblast differentiation, negative regulation of transcription, DNA-templated, embryonic morphogenesis, stem cell differentiation, positive regulation of timing of catagen, bone trabecula formation, cranial suture morphogenesis, frontal suture morphogenesis, branching involved in mammary gland duct morphogenesis, cell surface receptor signaling pathway involved in heart development, enamel mineralization, cellular response to estradiol stimulus, activation of meiosis, mesenchymal cell apoptotic process, positive regulation of mesenchymal cell apoptotic process,		
GOTERM_CC_DIRECT	chromatin, nucleus, transcription factor complex, cytosol, nuclear speck,		
GOTERM_MF_DIRECT	transcription regulatory region sequence-specific DNA binding, RNA polymerase II regulatory region sequence-specific DNA binding, RNA polymerase II core promoter proximal region sequence-specific DNA binding, RNA polymerase II transcription factor activity, sequence-specific DNA binding, transcriptional repressor activity, RNA polymerase II transcription regulatory region sequence-specific binding, protein binding, sequence-specific DNA binding, sequence-specific double-stranded DNA binding,		
INTERPRO	Homeobox_dom, Homeobox-like_sf, Homeobox_CS, Homeobox_metazoa,		
KEGG_PATHWAY	Human T-cell leukemia virus 1 infection,		
OMIM_DISEASE	Parietal foramina 1, Parietal foramina with cleidocranial dysplasia, Craniosynostosis 2,		
SMART	HOX,		
UP_KW_BIOLOGICAL_PROCESS	Transcription, Transcription regulation, Osteogenesis,		
UP_KW_CELLULAR_COMPONENT	Nucleus,		
UP_KW_DISEASE	Disease variant, Craniosynostosis,		
UP_KW_DOMAIN	Homeobox,		
UP_KW_MOLECULAR_FUNCTION	Developmental protein, DNA-binding, Repressor, Developmental protein,		
UP_SEQ_FEATURE	DNA_BIND:Homeobox, MUTAGEN:T->A: Does not bind DNA but still suppresses OCFRE activation., REGION:Disordered,		

PABPC1	poly(A) binding protein cytoplasmic 1(PABPC1)	Related Genes	Homo sapiens
BIOCARTA	Regulation of eIF4e and p70 S6 Kinase,		
GOTERM_BP_DIRECT	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay, mRNA splicing, via spliceosome, mRNA polyadenylation, gene silencing by RNA, positive regulation of viral genome replication, mRNA stabilization, positive regulation of nuclear-transcribed mRNA poly(A) tail shortening, CRD-mediated mRNA stabilization, negative regulation of nuclear-transcribed mRNA catabolic process, deadenylation-dependent decay, positive regulation of nuclear-transcribed mRNA catabolic process, deadenylation-dependent decay, negative regulation of nuclear-transcribed mRNA catabolic process, nonsense-mediated decay, positive regulation of cytoplasmic translation,		
GOTERM_CC_DIRECT	nucleus, cytoplasm, cytosol, focal adhesion, cytoplasmic stress granule, membrane, lamellipodium, cell leading edge, cytoplasmic ribonucleoprotein granule, extracellular exosome, catalytic step 2 spliceosome, ribonucleoprotein complex,		
GOTERM_MF_DIRECT	RNA binding, mRNA binding, mRNA 3'-UTR binding, protein binding, poly(A) binding, poly(U) RNA binding, translation activator activity,		
INTERPRO	RRM_dom, PABP_HYD, RRM_dom_euk, PABP_1234, Nucleotide-bd_a/b_plait_sf, PABP_RRM1, RBD_domain_sf, PABP-dom, RRM2_I_PABPs,		
KEGG_PATHWAY	mRNA surveillance pathway, RNA degradation,		
SMART	RRM, RRM_1, PolyA,		
UP_KW_BIOLOGICAL_PROCESS	mRNA processing, mRNA splicing, Nonsense-mediated mRNA decay, Host-virus interaction,		
UP_KW_CELLULAR_COMPONENT	Nucleus, Spliceosome, Cytoplasm, Cell projection,		
UP_KW_DOMAIN	Repeat,		
UP_KW_MOLECULAR_FUNCTION	RNA-binding,		
UP_KW_PTM	Acetylation, Methylation, Phosphoprotein,		
UP_SEQ_FEATURE	COMPBIAS:Polar residues, DOMAIN:PABC, DOMAIN:RRM, DOMAIN:RRM 1, DOMAIN:RRM 2, DOMAIN:RRM 3, DOMAIN:RRM 4, MUTAGEN:R->A: Greatly reduces methylation by CARM1 (in vitro); when associated with A-455., MUTAGEN:R->A: Greatly reduces methylation by CARM1 (in vitro); when associated with A-460., REGION:(Microbial infection) Binding to HRSV M2-1 protein, REGION:CSDE1-binding, REGION:Disordered,		

PJA1	praja ring finger ubiquitin ligase 1(PJA1)	Related Genes	Homo sapiens
GOTERM_BP_DIRECT	protein catabolic process,		
GOTERM_CC_DIRECT	cytoplasm,		
GOTERM_MF_DIRECT	protein binding, ligase activity, metal ion binding, ubiquitin protein ligase activity,		
INTERPRO	Znf_RING, Znf_RING/FYVE/PHD,		
SMART	RING,		
UP_KW_BIOLOGICAL_PROCESS	Ubl conjugation pathway,		
UP_KW_DOMAIN	Zinc-finger,		
UP_KW_LIGAND	Metal-binding, Zinc,		
UP_KW_MOLECULAR_FUNCTION	Ligase, Transferase,		
UP_KW_PTM	Phosphoprotein, Ubl conjugation,		
UP_SEQ_FEATURE	COMPBIAS:Basic and acidic residues, COMPBIAS:Polar residues, DOMAIN:RING-type, REGION:Disordered, ZN_FING:RING-type,		

PRPF8	pre-mRNA processing factor 8(PRPF8)	Related Genes	Homo sapiens
GOTERM_BP_DIRECT	spliceosomal tri-snRNP complex assembly, RNA splicing, via transesterification reactions, mRNA splicing, via spliceosome, mRNA processing, RNA splicing, cellular response to lipopolysaccharide, cellular response to tumor necrosis factor,		
GOTERM_CC_DIRECT	nucleus, nucleoplasm, spliceosomal complex, U5 snRNP, membrane, nuclear speck, U4/U6 x U5 tri-snRNP complex, U2-type precatalytic spliceosome, U2-type catalytic step 1 spliceosome, U2-type catalytic step 2 spliceosome, catalytic step 2 spliceosome,		

ATP2B1	ATPase plasma membrane Ca2+ transporting 1(ATP2B1)	Related Genes	Homo sapiens
GOTERM_MF_DIRECT	RNA binding, protein binding, metallopeptidase activity, U6 snRNA binding, U1 snRNA binding, U2 snRNA binding, U5 snRNA binding, K63-linked polyubiquitin binding, pre-mRNA intronic binding,		
INTERPRO	JAMM/MPN+_dom, RNaseH-like_sf, PRO8NT, PROCN, PROCT, Prp8_U6-snRNA-bd, Prp8_U5-snRNA-bd, RRM_spliceosomal_PrP8, PRP8_domainIV, PRP8, MPN, Prp8_U5-snRNA-bd_sf, Prp8_domainIV_palm, Prp8_domainIV_fingers,		
KEGG_PATHWAY	Spliceosome,		
OMIM_DISEASE	Retinitis pigmentosa 13,		
SMART	JAB_MPN,		
UP_KW_BIOLOGICAL_PROCESS	mRNA processing, mRNA splicing,		
UP_KW_CELLULAR_COMPONENT	Nucleus, Spliceosome,		
UP_KW_DISEASE	Disease variant, Retinitis pigmentosa,		
UP_KW_MOLECULAR_FUNCTION	Ribonucleoprotein, RNA-binding,		
UP_KW_PTM	Acetylation, Methylation, Phosphoprotein,		
UP_SEQ_FEATURE	COMPBIAS:Polar residues, DOMAIN:MPN, DOMAIN:PRO8NT, DOMAIN:PROCN, DOMAIN:PROCT, DOMAIN:RNA recognition motif spliceosomal PrP8, MUTAGEN:T->P: Strongly reduced interaction with RNA., MUTAGEN:V->D: Strongly reduced interaction with RNA., REGION:Disordered, REGION:Important for branch point selection, REGION:Involved in interaction with pre-mRNA 5' splice site, REGION:Linker, REGION:RNase H homology domain, REGION:Required for interaction with EFTUD2 and SNRNP200, REGION:Restriction endonuclease homology domain, REGION:Reverse transcriptase homology domain,		
PPP3CA	**protein phosphatase 3 catalytic subunit alpha(PPP3CA)**	**Related Genes**	**Homo sapiens**
BIOCARTA	BCR Signaling Pathway, Effects of calcineurin in Keratinocyte Differentiation, Regulation of ck1/cdk5 by type 1 glutamate receptors, Fc Epsilon Receptor I Signaling in Mast Cells, fMLP induced chemokine gene expression in HMC-1 cells, Signaling Pathway from G-Protein Families, Control of skeletal myogenesis by HDAC & calcium/calmodulin-dependent kinase (CaMK), Role of MEF2D in T-cell Apoptosis, Endocytotic role of NDK, Phosphins and Dynamin, NFAT and Hypertrophy of the heart (Transcription in the broken heart), Nitric Oxide Signaling Pathway, Regulation of PGC-1a, T Cell Receptor Signaling Pathway, Neuropeptides VIP and PACAP inhibit the apoptosis of activated T cells,		
GOTERM_BP_DIRECT	G1/S transition of mitotic cell cycle, response to amphetamine, protein dephosphorylation, protein import into nucleus, calcium ion transport, epidermis development, positive regulation of gene expression, negative regulation of gene expression, transition between fast and slow fiber, cardiac muscle hypertrophy in response to stress, dephosphorylation, negative regulation of signaling, keratinocyte differentiation, positive regulation of cell migration, calcineurin-NFAT signaling cascade, multicellular organismal response to stress, wound healing, positive regulation of activated T cell proliferation, T cell activation, skeletal muscle tissue regeneration, positive regulation of osteoblast differentiation, positive regulation of osteoclast differentiation, positive regulation of cell adhesion, positive regulation of endocytosis, positive regulation of transcription from RNA polymerase II promoter, negative regulation of insulin secretion, positive regulation of saliva secretion, skeletal muscle fiber development, dendrite morphogenesis, negative regulation of dendrite morphogenesis, modulation of synaptic transmission, response to calcium ion, excitatory postsynaptic potential, regulation of cell proliferation involved in kidney morphogenesis, peptidyl-serine dephosphorylation, positive regulation of calcineurin-NFAT signaling cascade, cellular response to glucose stimulus, positive regulation of glomerulus development, renal filtration, calcineurin-mediated signaling, positive regulation of cardiac muscle hypertrophy in response to stress, positive regulation of connective tissue replacement, positive regulation of calcium ion import across plasma membrane,		
GOTERM_CC_DIRECT	nucleus, nucleoplasm, cytoplasm, mitochondrion, cytosol, plasma membrane, calcineurin complex, protein serine/threonine phosphatase complex, cytoplasmic side of plasma membrane, extrinsic component of plasma membrane, Z disc, slit diaphragm, sarcolemma, dendritic spine, Schaffer collateral - CA1 synapse, postsynapse, glutamatergic synapse,		
GOTERM_MF_DIRECT	protein serine/threonine phosphatase activity, calcium ion binding, protein binding, calmodulin binding, cyclosporin A binding, myosin phosphatase activity, enzyme binding, calmodulin-dependent protein phosphatase activity, macromolecular complex binding, protein dimerization activity, ATPase binding,		
INTERPRO	Calcineurin-like_PHP_ApaH, Ser/Thr-sp_prot-phosphatase, Metallo-depent_PP-like, MPP_PP2B, PP2B,		
KEGG_PATHWAY	MAPK signaling pathway, Calcium signaling pathway, cGMP-PKG signaling pathway, Oocyte meiosis, Cellular senescence, Wnt signaling pathway, Axon guidance, VEGF signaling pathway, Osteoclast differentiation, C-type lectin receptor signaling pathway, Natural killer cell mediated cytotoxicity, Th1 and Th2 cell differentiation, Th17 cell differentiation, T cell receptor signaling pathway, B cell receptor signaling pathway, Long-term potentiation, Glutamatergic synapse, Dopaminergic synapse, Oxytocin signaling pathway, Glucagon signaling pathway, Renin secretion, Alzheimer disease, Amyotrophic lateral sclerosis, Prion disease, Pathways of neurodegeneration - multiple diseases, Amphetamine addiction, Tuberculosis, Human cytomegalovirus infection, Human T-cell leukemia virus 1 infection, Kaposi sarcoma-associated herpesvirus infection, Human immunodeficiency virus 1 infection, PD-L1 expression and PD-1 checkpoint pathway in cancer, Lipid and atherosclerosis,		
OMIM_DISEASE	Developmental and epileptic encephalopathy 91, Arthrogryposis, cleft palate, craniosynostosis, and impaired intellectual development,		
SMART	PP2Ac,		
UP_KW_CELLULAR_COMPONENT	Membrane, Synapse, Cytoplasm, Cell projection, Cell membrane,		
UP_KW_DISEASE	Disease variant, Dwarfism, Epilepsy, Craniosynostosis, Intellectual disability,		
UP_KW_LIGAND	Iron, Metal-binding, Zinc,		
UP_KW_MOLECULAR_FUNCTION	Calmodulin-binding, Hydrolase, Protein phosphatase,		
UP_KW_PTM	Acetylation, Phosphoprotein, Nitration,		
UP_SEQ_FEATURE	ACT_SITE:Proton donor, COMPBIAS:Polar residues, DOMAIN:Serine/threonine specific protein phosphatases, MOTIF:SAPNY motif, MUTAGEN:Missing: Loss of Ca(2+)-mediated transcription factor NFAT activation; when associated with F-341., MUTAGEN:Y->F: Partial loss of Ca(2+)-mediated transcription factor NFAT activation; when associated with F-341., MUTAGEN:Y->F: Resistant to cyclosporin A-mediated inhibition. Loss of Ca(2+)-mediated transcription factor NFAT activation; when associated with N-288, A-228 or 328-V--R-332 DEL. Partial loss in Ca(2+)-mediated transcription factor NFAT activation; when associated with F-288., MUTAGEN:Y->N,A: Loss of Ca(2+)-mediated transcription factor NFAT activation; when associated with F-341., REGION:Autoinhibitory domain, REGION:Autoinhibitory segment, REGION:Calcineurin B binding, REGION:Calmodulin-binding, REGION:Catalytic, REGION:Disordered, REGION:Interaction with PxIxIF motif in substrate, SITE:Interaction with PxVP motif in substrate,		
RIMS2	**regulating synaptic membrane exocytosis 2(RIMS2)**	**Related Genes**	**Homo sapiens**
GOTERM_BP_DIRECT	intracellular protein transport, exocytosis, adenylate cyclase-modulating G-protein coupled receptor signaling pathway, calcium ion regulated exocytosis, regulation of exocytosis, insulin secretion, cell differentiation, regulation of membrane potential, regulation of synaptic plasticity, calcium ion-regulated exocytosis of neurotransmitter, positive regulation of synaptic transmission, spontaneous neurotransmitter secretion, positive regulation of inhibitory postsynaptic potential, positive regulation of dendrite extension, regulation of synaptic vesicle exocytosis, positive regulation of excitatory postsynaptic potential,		
GOTERM_CC_DIRECT	membrane, presynaptic membrane, cell projection, synapse, presynaptic active zone, cytoskeleton of presynaptic active zone, extracellular exosome,		
GOTERM_MF_DIRECT	protein binding, small GTPase binding, ion channel binding, metal ion binding,		
INTERPRO	C2_dom, PDZ, Rab_BD, Znf_FYVE_PHD, Znf_RING/FYVE/PHD, Znf_FYVE-rel, C2_domain_sf, PDZ_sf, Rim-like, FYVE_2, PDZ_6,		
KEGG_PATHWAY	Insulin secretion,		
OMIM_DISEASE	Cone-rod synaptic disorder syndrome, congenital nonprogressive,		
SMART	PDZ, C2,		
UP_KW_BIOLOGICAL_PROCESS	Differentiation,		
UP_KW_CELLULAR_COMPONENT	Membrane, Synapse, Cell projection, Cell membrane,		
UP_KW_DISEASE	Disease variant,		
UP_KW_DOMAIN	Coiled coil, Repeat, Zinc-finger,		
UP_KW_LIGAND	Metal-binding, Zinc,		
UP_KW_PTM	Phosphoprotein,		
UP_SEQ_FEATURE	COMPBIAS:Basic and acidic residues, COMPBIAS:Polar residues, DOMAIN:C2, DOMAIN:C2 1, DOMAIN:C2 2, DOMAIN:FYVE-type, DOMAIN:PDZ, DOMAIN:RabBD, REGION:Disordered, ZN_FING:FYVE-type,		
RFX4	**regulatory factor X4(RFX4)**	**Related Genes**	**Homo sapiens**
GOTERM_BP_DIRECT	regulation of transcription from RNA polymerase II promoter, telencephalon development, negative regulation of smoothened signaling pathway involved in ventral spinal cord patterning, positive regulation of transcription from RNA polymerase II promoter, cilium assembly, regulation of protein processing,		
GOTERM_CC_DIRECT	chromatin, nucleus,		
GOTERM_MF_DIRECT	RNA polymerase II core promoter proximal region sequence-specific DNA binding, RNA polymerase II transcription factor activity, sequence-specific DNA binding, transcriptional activator activity, RNA polymerase II transcription regulatory region sequence-specific binding, DNA binding, transcription factor activity, sequence-specific DNA binding, protein binding, sequence-specific double-stranded DNA binding,		
INTERPRO	DNA-bd_RFX, WH-like_DNA-bd_sf, WH_DNA-bd_sf, RFX-like,		
UP_KW_BIOLOGICAL_PROCESS	Transcription, Transcription regulation,		
UP_KW_CELLULAR_COMPONENT	Nucleus,		
UP_KW_MOLECULAR_FUNCTION	Activator, DNA-binding,		
UP_SEQ_FEATURE	COMPBIAS:Basic and acidic residues, DNA_BIND:RFX-type winged-helix, DOMAIN:RFX-type winged-helix, REGION:Disordered, REGION:Necessary for dimerization,		
RFX7	**regulatory factor X7(RFX7)**	**Related Genes**	**Homo sapiens**
GOTERM_BP_DIRECT	regulation of transcription from RNA polymerase II promoter, positive regulation of transcription from RNA polymerase II promoter,		
GOTERM_CC_DIRECT	chromatin, nucleus,		
GOTERM_MF_DIRECT	RNA polymerase II core promoter proximal region sequence-specific DNA binding, RNA polymerase II core promoter sequence-specific DNA binding, RNA polymerase II transcription factor activity, sequence-specific DNA binding, DNA binding, transcription factor activity, sequence-specific DNA binding, protein binding, sequence-specific double-stranded DNA binding,		

ATP2B1	ATPase plasma membrane Ca2+ transporting 1(ATP2B1)	Related Genes	Homo sapiens
INTERPRO	DNA-bd_RFX, WH-like_DNA-bd_sf, WH_DNA-bd_sf, RFX-like, RFX5_N, RFX5_N_sf,		
OMIM_DISEASE	Intellectual developmental disorder, autosomal dominant 71, with behavioral abnormalities,		
UP_KW_BIOLOGICAL_PROCESS	Transcription, Transcription regulation,		
UP_KW_CELLULAR_COMPONENT	Nucleus,		
UP_KW_DISEASE	Disease variant, Intellectual disability, Autism spectrum disorder,		
UP_KW_MOLECULAR_FUNCTION	DNA-binding,		
UP_KW_PTM	Acetylation, Phosphoprotein,		
UP_SEQ_FEATURE	COMPBIAS:Basic and acidic residues, COMPBIAS:Polar residues, COMPBIAS:Pro residues, DNA_BIND:RFX-type winged-helix, DOMAIN:RFX-type winged-helix, MOTIF:PxLPxI/L motif; mediates interaction with ANKRA2 and RFXANK, REGION:Disordered,		
SRSF1	serine and arginine rich splicing factor 1(SRSF1)	Related Genes	Homo sapiens
GOTERM_BP_DIRECT	alternative mRNA splicing, via spliceosome, mRNA 5'-splice site recognition, mRNA splicing, via spliceosome, mRNA splice site selection, mRNA processing, positive regulation of RNA splicing, regulation of RNA splicing, oligodendrocyte differentiation, mRNA transport, liver regeneration,		
GOTERM_CC_DIRECT	nucleus, nucleoplasm, cytoplasm, nuclear speck, exon-exon junction complex, catalytic step 2 spliceosome,		
GOTERM_MF_DIRECT	RNA binding, mRNA binding, protein binding, protein kinase B binding, DNA topoisomerase binding,		
INTERPRO	RRM_dom, Nucleotide-bd_a/b_plait_sf, SRSF1_RRM2, SRSF1_RRM1, RBD_domain_sf,		
KEGG_PATHWAY	Spliceosome, IL-17 signaling pathway, Herpes simplex virus 1 infection,		
OMIM_DISEASE	Neurodevelopmental disorder with dysmorphic facies and behavioral abnormalities,		
SMART	RRM,		
UP_KW_BIOLOGICAL_PROCESS	mRNA processing, mRNA splicing, mRNA transport, Transport,		
UP_KW_CELLULAR_COMPONENT	Nucleus, Spliceosome, Cytoplasm,		
UP_KW_DOMAIN	Repeat,		
UP_KW_MOLECULAR_FUNCTION	RNA-binding,		
UP_KW_PTM	Acetylation, Methylation, Phosphoprotein, Ubl conjugation, Isopeptide bond,		
UP_SEQ_FEATURE	COMPBIAS:Basic residues, CROSSLNK:Glycyl lysine isopeptide (Lys-Gly) (interchain with G-Cter in SUMO2), CROSSLNK:Glycyl lysine isopeptide (Lys-Gly) (interchain with G-Cter in SUMO2); alternate, DOMAIN:RRM, DOMAIN:RRM 1, DOMAIN:RRM 2, MUTAGEN:F->A: In AV; loss of ability to activate splicing. Great reduction in splice site switching activity and no effect on RNA-binding., MUTAGEN:F->D: Reduced nucleocytoplasmic shuttling; when associated with D-162., MUTAGEN:F->D: Reduced nucleocytoplasmic shuttling; when associated with D-190., MUTAGEN:FV->SR: In FV1; loss of ability to activate splicing. Slight reduction in splice site switching activity and no effect on RNA-binding., MUTAGEN:FV->SR: In FV2; loss of ability to activate splicing. Great reduction in splice site switching activity and RNA-binding., MUTAGEN:Missing: In MR-A; loss of ability to activate splicing., MUTAGEN:Missing: In MR-B; strongly inhibits splicing., MUTAGEN:Missing: In MR-D; loss of ability to activate splicing., MUTAGEN:Missing: In MR-E; loss of ability to activate splicing., MUTAGEN:Missing: In RS-A; loss of ability to activate splicing but retains splice site switching., MUTAGEN:Missing: In RS-B; retains both splice activation and splice site switching., MUTAGEN:Missing: In RS-C; loss of ability to activate splicing but retains splice site switching., MUTAGEN:R->A: Predominantly localizes to cytoplasm and fails to modulate splicing of endogenous pre-mRNAs; when associated with Ala-93 and Ala-109., MUTAGEN:R->A: Predominantly localizes to cytoplasm and fails to modulate splicing of endogenous pre-mRNAs; when associated with Ala-93 and Ala-97., MUTAGEN:R->A: Predominantly localizes to cytoplasm and fails to modulate splicing of endogenous pre-mRNAs; when associated with Ala-97 and Ala-109., REGION:Disordered, REGION:Interaction with SAFB1,		
TCEAL1	transcription elongation factor A like 1(TCEAL1)	Related Genes	Homo sapiens
GOTERM_CC_DIRECT	nucleus, nucleoplasm,		
GOTERM_MF_DIRECT	protein binding,		
INTERPRO	TF_A-like/BEX,		
OMIM_DISEASE	Hijazi-Reis syndrome,		
UP_KW_BIOLOGICAL_PROCESS	Transcription, Transcription regulation,		
UP_KW_CELLULAR_COMPONENT	Nucleus,		
UP_KW_DISEASE	Disease variant, Intellectual disability,		
UP_KW_PTM	Phosphoprotein,		
UP_SEQ_FEATURE	COMPBIAS:Acidic residues, COMPBIAS:Basic and acidic residues, MUTAGEN:SS->AA: Loss of transcriptional repression., MUTAGEN:SS->AA: No effect on transcriptional repression., REGION:Disordered,		
TRIM8	tripartite motif containing 8(TRIM8)	Related Genes	Homo sapiens
GOTERM_BP_DIRECT	I-kappaB kinase/NF-kappaB signaling, positive regulation of autophagy, stem cell population maintenance, negative regulation of viral transcription, positive regulation of I-kappaB kinase/NF-kappaB signaling, negative regulation by host of viral release from host cell, innate immune response, positive regulation of transcription, DNA-templated, negative regulation of viral entry into host cell, positive regulation of sequence-specific DNA binding transcription factor activity, positive regulation of NF-kappaB transcription factor activity, protein K63-linked ubiquitination, positive regulation of protein localization to nucleus,		
GOTERM_CC_DIRECT	nucleus, cytoplasm, cytosol, PML body,		
GOTERM_MF_DIRECT	transcription coactivator activity, protein binding, zinc ion binding, mitogen-activated protein kinase kinase kinase binding, identical protein binding, protein homodimerization activity, metal ion binding, ubiquitin protein ligase activity,		
INTERPRO	Znf_RING, Znf_RING/FYVE/PHD, Znf_RING_CS, Znf-RING_euk,		
OMIM_DISEASE	Focal segmental glomerulosclerosis and neurodevelopmental syndrome,		
SMART	RING,		
UP_KW_BIOLOGICAL_PROCESS	Immunity, Innate immunity, Ubl conjugation pathway,		
UP_KW_CELLULAR_COMPONENT	Nucleus, Cytoplasm,		
UP_KW_DISEASE	Disease variant,		
UP_KW_DOMAIN	Coiled coil, Repeat, Zinc-finger,		
UP_KW_LIGAND	Metal-binding, Zinc,		
UP_KW_MOLECULAR_FUNCTION	Transferase,		
UP_SEQ_FEATURE	DOMAIN:RING-type, MUTAGEN:C->A: Complete loss of ubiquitination activity on MAP3K7/TAK1., MUTAGEN:C->S: Complete loss of ubiquitination activity on TICAM1., REGION:Disordered, ZN_FING:B box-type 1, ZN_FING:B box-type 2, ZN_FING:RING-type,		
YWHAG	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein gamma(YWHAG)	Related Genes	Homo sapiens
GOTERM_BP_DIRECT	negative regulation of protein kinase activity, protein targeting, signal transduction, regulation of signal transduction, cellular response to insulin stimulus, cellular response to glucose starvation, regulation of neuron differentiation, regulation of synaptic plasticity, negative regulation of TORC1 signaling,		
GOTERM_CC_DIRECT	cytoplasm, cytosol, focal adhesion, membrane, extracellular exosome, presynapse,		
GOTERM_MF_DIRECT	RNA binding, protein kinase C binding, insulin-like growth factor receptor binding, protein binding, protein kinase C inhibitor activity, protein domain specific binding, receptor tyrosine kinase binding, identical protein binding, phosphoserine binding,		
INTERPRO	14-3-3, 14-3-3_CS, 14-3-3_domain, 14-3-3_dom_sf,		
KEGG_PATHWAY	Cell cycle, Oocyte meiosis, PI3K-Akt signaling pathway, Hippo signaling pathway, Hepatitis C, Viral carcinogenesis,		
OMIM_DISEASE	Developmental and epileptic encephalopathy 56,		
PIR_SUPERFAMILY	14-3-3,		
SMART	14_3_3,		
UP_KW_CELLULAR_COMPONENT	Cytoplasm,		
UP_KW_DISEASE	Disease variant, Epilepsy,		
UP_KW_PTM	Acetylation, Phosphoprotein,		
UP_SEQ_FEATURE	DOMAIN:14-3-3, SITE:Interaction with phosphoserine on interacting protein,		
ZFHX3	zinc finger homeobox 3(ZFHX3)	Related Genes	Homo sapiens
GOTERM_BP_DIRECT	negative regulation of transcription from RNA polymerase II promoter, regulation of transcription, DNA-templated, regulation of transcription from RNA polymerase II promoter, muscle organ development, circadian regulation of gene expression, negative regulation of myoblast differentiation, positive regulation of myoblast differentiation, regulation of neuron differentiation, positive regulation of cell adhesion, positive regulation of transcription, DNA-templated, positive regulation of transcription from RNA polymerase II promoter, response to transforming growth factor beta, regulation of locomotor rhythm,		
GOTERM_CC_DIRECT	chromatin, nucleus, nucleoplasm, transcription factor complex, cytoplasm, nuclear body,		
GOTERM_MF_DIRECT	transcription regulatory region sequence-specific DNA binding, RNA polymerase II core promoter proximal region sequence-specific DNA binding, RNA polymerase II transcription factor activity, sequence-specific DNA binding, transcriptional repressor activity, RNA polymerase II transcription regulatory region sequence-specific binding, nucleic acid binding, transcription factor activity, sequence-specific DNA binding, protein binding, zinc ion binding, enzyme binding,		
INTERPRO	Homeobox_dom, Matrin/U1-like-C_Znf_C2H2, Homeobox-like_sf, Znf_C2H2_type, Homeobox_CS, Znf_C2H2_sf,		
KEGG_PATHWAY	Signaling pathways regulating pluripotency of stem cells,		
OMIM_DISEASE	Prostate cancer, somatic, Spinocerebellar ataxia 4, Atrial fibrillation 8, susceptibility to,		
SMART	ZnF_C2H2, HOX, ZnF_U1,		
UP_KW_BIOLOGICAL_PROCESS	Myogenesis, Transcription, Transcription regulation,		

ATP2B1	ATPase plasma membrane Ca2+ transporting 1(ATP2B1)	Related Genes	Homo sapiens
UP_KW_CELLULAR_COMPONENT	Nucleus, Cytoplasm,		
UP_KW_DOMAIN	Coiled coil, Homeobox, Repeat, Zinc-finger,		
UP_KW_LIGAND	Metal-binding, Zinc,		
UP_KW_MOLECULAR_FUNCTION	Activator, DNA-binding, Repressor,		
UP_KW_PTM	Phosphoprotein, Ubl conjugation, Isopeptide bond,		
UP_SEQ_FEATURE	COMPBIAS:Acidic residues, COMPBIAS:Basic and acidic residues, COMPBIAS:Polar residues, COMPBIAS:Pro residues, CROSSLNK:Glycyl lysine isopeptide (Lys-Gly) (interchain with G-Cter in SUMO1), CROSSLNK:Glycyl lysine isopeptide (Lys-Gly) (interchain with G-Cter in SUMO1); alternate, CROSSLNK:Glycyl lysine isopeptide (Lys-Gly) (interchain with G-Cter in SUMO2); alternate, DNA_BIND:Homeobox 1, DNA_BIND:Homeobox 2, DNA_BIND:Homeobox 3, DNA_BIND:Homeobox 4, DOMAIN:C2H2-type, MOTIF:Nuclear localization signal, MUTAGEN:K->A: Loss of sumoylation., MUTAGEN:KRK->AAA: Loss of nuclear localization., REGION:Disordered, ZN_FING:C2H2-type 10; atypical, ZN_FING:C2H2-type 11; atypical, ZN_FING:C2H2-type 12, ZN_FING:C2H2-type 13, ZN_FING:C2H2-type 14, ZN_FING:C2H2-type 15, ZN_FING:C2H2-type 16, ZN_FING:C2H2-type 17, ZN_FING:C2H2-type 18, ZN_FING:C2H2-type 19; atypical, ZN_FING:C2H2-type 1; degenerate, ZN_FING:C2H2-type 2, ZN_FING:C2H2-type 20, ZN_FING:C2H2-type 21, ZN_FING:C2H2-type 22, ZN_FING:C2H2-type 23, ZN_FING:C2H2-type 3, ZN_FING:C2H2-type 4, ZN_FING:C2H2-type 5, ZN_FING:C2H2-type 6; atypical, ZN_FING:C2H2-type 7; degenerate, ZN_FING:C2H2-type 8; atypical, ZN_FING:C2H2-type 9; atypical,		

ZFX	zinc finger protein X-linked(ZFX)	Related Genes	Homo sapiens
GOTERM_BP_DIRECT	ovarian follicle development, regulation of transcription, DNA-templated, regulation of transcription from RNA polymerase II promoter, spermatogenesis, fertilization, post-embryonic development, multicellular organism growth, positive regulation of transcription from RNA polymerase II promoter, oocyte development, homeostasis of number of cells, parental behavior,		
GOTERM_CC_DIRECT	chromatin, nucleus, nucleoplasm, chromosome, nucleolus,		
GOTERM_MF_DIRECT	RNA polymerase II core promoter proximal region sequence-specific DNA binding, transcriptional activator activity, RNA polymerase II transcription regulatory region sequence-specific binding, DNA binding, chromatin insulator sequence binding, metal ion binding,		
INTERPRO	Transcrp_activ_Zfx/Zfy-dom, Znf_C2H2_type, Znf_C2H2_sf,		
SMART	ZnF_C2H2,		
UP_KW_BIOLOGICAL_PROCESS	Transcription, Transcription regulation,		
UP_KW_CELLULAR_COMPONENT	Nucleus,		
UP_KW_DOMAIN	Repeat, Zinc-finger,		
UP_KW_LIGAND	Metal-binding, Zinc,		
UP_KW_MOLECULAR_FUNCTION	Activator, DNA-binding,		
UP_KW_PTM	Phosphoprotein,		
UP_SEQ_FEATURE	DOMAIN:C2H2-type, DOMAIN:Transcriptional activator Zfx / Zfy, REGION:Disordered, ZN_FING:C2H2-type 1, ZN_FING:C2H2-type 10, ZN_FING:C2H2-type 11, ZN_FING:C2H2-type 12, ZN_FING:C2H2-type 13, ZN_FING:C2H2-type 2, ZN_FING:C2H2-type 3, ZN_FING:C2H2-type 4, ZN_FING:C2H2-type 5, ZN_FING:C2H2-type 6, ZN_FING:C2H2-type 7, ZN_FING:C2H2-type 8, ZN_FING:C2H2-type 9,		