Chapter 2 : Gentaur Products List

- WDSUB1 contains 1 SAM sterile alpha motif domain 1 U box domain and 7 WD repeats The function of WDSUB1 remains unknown
- RNF217 is an E3 ubiquitin protein ligase which accepts ubiquitin from E2 ubiquitin conjugating enzymes in the form of a thioester and then directly transfers the ubiquitin to targeted substrates
- TRIM60 contains a RING finger domain a motif present in a variety of functionally distinct proteins and known to be involved in protein protein and protein DNA interactions The protein encoded by thi
- RNF182 is a multi pass membrane protein It contains 1 RING type zinc finger The function of RNF182 remains unknown
- HECTD2 is a probable E3 ubiquitin protein ligase which accepts ubiquitin from an E2 ubiquitin conjugating enzyme in the form of a thioester and then directly transfers the ubiquitin to targeted substr
- TRIM54 contains a RING finger motif and is highly similar to the ring finger proteins RNF28 MURF1 and RNF29 MURF2 In vitro studies demonstrated that this protein RNF28 and RNF29 form heterodimers
- RNF212 contains 1 RING type zinc finger The function of the RNF212 protein remains unknown
- RNF148 is a single pass membrane protein It contains 1 PA protease associated domain and 1 RING type zinc finger The exact function of RNF148 remains unknown
- LONRF2 contains 1 Lon domain 1 RING type zinc finger and 6 TPR repeats The function of the LONRF2 protein remains unknown
- RNF207 contains 1 B box type zinc finger and 1 RING type zinc finger The function of the RNF207 protein remains unknown
- Glutamic oxaloacetic transaminase is a pyridoxal phosphate dependent enzyme which exists in cytoplasmic and inner membrane mitochondrial forms GOT1 and GOT2 respectively GOT plays a role in amino a
- The specific function of DPY19L1 is not yet known
- MAOB belongs to the flavin monoamine oxidase family It is a enzyme located in the mitochondrial outer membrane It catalyzes the oxidative deamination of biogenic and xenobiotic amines and plays an i
- Carboxypeptidases are enzymes that hydrolyze C terminal peptide bonds The carboxypeptidase family includes metallo serine and cysteine carboxypeptidases According to their substrate specificity
- ADH4 class II alcohol dehydrogenase 4 pi subunit which is a member of the alcohol dehydrogenase family Members of this enzyme family metabolize a wide variety of substrates including ethanol reti
- GTP cyclohydrolase I feedback regulatory protein binds to and mediates tetrahydrobiopterin inhibition of GTP cyclohydrolase I The regulatory protein GCHFR consists of a homodimer It is postulated
- CREBBP is involved in the transcriptional coactivation of many different transcription factors First isolated as a nuclear protein that binds to cAMP response element binding protein CREB this gen
- The membrane associated protein encoded by this gene is a member of the superfamily of ATP binding cassette ABC transporters ABC proteins transport various molecules across extra and intra cellula
- ABCC3 is a member of the superfamily of ATP binding cassette ABC transporters ABC proteins transport various molecules across extra and intra cellular membranes ABC genes are divided into seven d
- ABCC1 is a member of the superfamily of ATP binding cassette ABC transporters ABC proteins transport various molecules across extra and intra cellular membranes ABC genes are divided into seven di
- ABCD4 is a member of the superfamily of ATP binding cassette ABC transporters ABC proteins transport various molecules across extra and intra cellular membranes ABC genes are divided into seven d
- ABCC9 is a member of the superfamily of ATP binding cassette ABC transporters ABC proteins transport various molecules across extra and intra cellular membranes ABC genes are divided into seven d
- CYP46A1 is a member of the cytochrome P450 superfamily of enzymes The cytochrome P450 proteins are monooxygenases which catalyze many reactions involved in drug metabolism and synthesis of cholestero
- The membrane associated protein ABCB8 is a member of the superfamily of ATP binding cassette ABC transporters ABC proteins transport various molecules across extra and intra cellular membranes AB
- DLG3 is required for learning most likely through its role in synaptic plasticity following NMDA receptor signaling Defects in DLG3 are the cause of mental retardation X linked type 90 MRX90
- SLC25A20 is one of several closely related mitochondrial membrane carrier proteins that shuttle substrates between cytosol and the intramitochondrial matrix space It mediates the transport of acylcarn
- The sodium iodide symporter NIS or SLC5A5 is a key plasma membrane protein that mediates active I uptake in thyroid lactating breast and other tissues with an electrogenic stoichiometry of 2 Na
- SLC2A9 is a member of the SLC2A facilitative glucose transporter family Members of this family play a significant role in maintaining glucose homeostasis SLC2A9 may play a role in the development an
- SLC41A3 is a multi pass membrane protein It belongs to the SLC41A transporter family The exact function of SLC41A3 remains unknown
- SLC27A6 is a member of the fatty acid transport protein family FATP FATPs are involved in the uptake of long chain fatty acids and have unique expression patterns Alternatively spliced transcript
- SLC10A7 belongs to the sodium bile acid symporter family It is a multi pass membrane protein The function of SLC10A7 remains unknown
- Zinc is an essential cofactor for more than 50 classes of enzymes It is involved in protein nucleic acid carbohydrate and lipid metabolism as well as in the control of gene transcription growth
- SLC37A4 transports glucose 6 phosphate from the cytoplasm to the lumen of the endoplasmic reticulum It forms with glucose 6 phosphatase the complex responsible for glucose production through glycogen
- This gene is one of several tumor suppressing subtransferable fragments located in the imprinted gene domain of 11p15 5 an important tumor suppressor gene region Alterations in this region have been
- SLC25A11 catalyzes the transport of 2 oxoglutarate across the inner mitochondrial membrane in an electroneutral exchange for malate or other dicarboxylic acids and plays an important role in several
- SLC27A2 is an isozyme of long chain fatty acid coenzyme A ligase family Although differing in substrate specificity subcellular localization and tissue distribution all isozymes of this family con
- SLC13A2 belongs to the SLC13A transporter TC 2 A 47 family NADC subfamily It is a multi pass membrane protein SLC13A2 cotransports of sodium ions and dicarboxylates such as succinate and citrate
- SLC22A13 is a member of the organic cation transporter family SLC22A13 is a transmembrane protein involved in the transport of small molecules This protein can function to mediate urate uptake and i
- SLC16A6 is a proton linked monocarboxylate transporter It catalyzes the rapid transport across the plasma membrane of many monocarboxylates such as lactate pyruvate branched chain oxo acids derived
- SLC24A1 belongs to a family of potassium dependent sodium calcium exchangers Members of this family have 2 large hydrophilic loops and 2 sets of multiple transmembrane spanning segments SLC24A1 belon
- SLC33A1 is required for the formation of O acetylated Ac gangliosides It is predicted to contain 6 to 10 transmembrane domains and a leucine zipper motif in transmembrane domain III Studies indic
- SLC22A14 is a member of the organic cation transporter family SLC22A14 is a transmembrane protein which is thought to transport small molecules and since this protein is conserved among several speci
- SLC27A4 is involved in translocation of long chain fatty acids LFCA across the plasma membrane It appears to be the principal fatty acid transporter in small intestinal enterocytes SLC27A4 plays a
- The absorption of vitamin C into the body and its distribution to organs requires two sodium dependent vitamin C transporters This gene encodes one of the two required transporters and the encoded pr
- Retrovirus receptors allow infection of human and murine cells by various retroviruses The receptors that have been identified at the molecular level include CD4 MIM 186940 for human immunodeficien
- SLCO2B1 mediates the Na independent transport of organic anions such as taurocholate the prostaglandins PGD2 PGE1 PGE2 leukotriene C4 thromboxane B2 and iloprost
- SLCO3A1 mediates the Na independent transport of organic anions such as estrone 3 sulfate It mediates transport of prostaglandins PG E1 and E2 thyroxine T4 deltorphin II BQ 123 and vasopressi
- Sodium hydrogen exchangers NHEs such as SLC9A8 are integral transmembrane proteins that exchange extracellular Na for intracellular H NHEs have multiple functions including intracellular pH ho
- SLCO1C1 is a member of the organic anion transporter family SLCO1C1 is a transmembrane receptor that mediates the sodium independent uptake of thyroid hormones in brain tissues This protein has part
- SLC35A5 belongs to the nucleotide sugar transporter family SLC35A subfamily It is a multi pass membrane protein The function of the SLC35A5 protein remains unknown
- SLC6A15 shows structural characteristics of an Na and Cl dependent neurotransmitter transporter including 12 transmembrane TM domains intracellular N and C termini and large extracellular
- SLC25A36 belongs to the mitochondrial carrier family It contains 3 Solcar repeats SLC25A36 is a multi pass membrane protein The function of the SLC25A36 protein remains unknown
- SLC22A11 is involved in the sodium independent transport and excretion of organic anions some of which are potentially toxic SLC22A11 is an integral membrane protein and is found mainly in the kidne
- SLC37A1 a member of the sugar phosphate transport family transports glycerol 3 phosphate G3P between cellular compartments for its utilization in several compartment specific biochemical pathways
- SLC15A2 belongs to the PTR2 POT transporter TC 2 A 17 family It is a multi pass membrane protein The expression activity of PEPT2 SLC15A2 may be a critical factor in the modulation of opioidergi
- SLC24A6 belongs to a family of potassium dependent sodium calcium exchangers that maintain cellular calcium homeostasis through the electrogenic countertransport of 4 sodium ions for 1 calcium ion and
- SLC25A21 is a homolog of the S cerevisiae ODC proteins mitochondrial carriers that transport C5 C7 oxodicarboxylates across inner mitochondrial membranes One of the species transported by ODC is 2
- SLC25A28 is a mitochondrial iron transporter that mediates iron uptake It is probably required for heme synthesis of hemoproteins and Fe S cluster assembly in non erythroid cells The iron delivered
- Organelles of the secretory and endocytic pathways are distinguished by their luminal acidity which is generated by the activity of an electrogenic vacuolar type hydrogen ATPase Progressive acidific
- SLC8A3 is a member of the sodium calcium exchanger integral membrane protein family Three mammalian isoforms in family 8 have been identified Na Ca2 exchange proteins are involved in maintaining C
- SLC2A13 is an H myo inositol cotransporter It can also transport related stereoisomers
- SLC39A4 is a member of the zinc iron regulated transporter like protein ZIP family The transmembrane protein is required for zinc uptake in the intestine Mutations in the gene encoding SLC39A4 res
- SLC25A46 is a members of the solute carrier family 25 SLC25 which is known to transport molecules over the mitochondrial membrane SLC25A46 belongs to the SLC25 family of mitochondrial carrier protei
- SLC39A11 belongs to the ZIP transporter TC 2 A 5 family It is a multi pass membrane protein SLC39A11 may act as a zinc influx transporter
- SLC23A3 is a multi pass membrane protein It belongs to the xanthine uracil permease family SLC23A subfamily The exact function of SLC23A3 remains unknown
- SLC44A3 is a multi pass membrane protein It belongs to the CTL choline transporter like family The function of the RBM34 protein remains unknown
- SLC15A4 is the proton oligopeptide cotransporter It transports free histidine and certain di and tripeptides
- SLC25A16 is a protein that contains three tandemly repeated mitochondrial carrier protein domains The protein is localized in the inner membrane and facilitates the rapid transport and exchange of mo
- SLC35F3 is a multi pass membrane proteinPotential It belongs to the SLC35F solute transporter family SLC35F3 is a putative solute transporter
- Zinc is an essential cofactor for hundreds of enzymes It is involved in protein nucleic acid carbohydrate and lipid metabolism as well as in the control of gene transcription growth development
- SLC41A1 belongs to the SLC41A transporter family It acts as a magnesium transporter that is responsive to magnesium balance
- SLC25A42 belongs to the SLC25 family of mitochondrial

carrier proteins The exact function of SLC25A42 remains unknown SLC25A42 belongs to the SLC25 family of mitochondrial carrier proteins Haitina et

- SLC36A2 is involved in a pH dependent electrogenic neuronal transport and sequestration of small amino acids amino acids such as glycine alanine and proline SLC36A2 is inhibited by sarcosine
- SLC25A35 belongs to the mitochondrial carrier family It contains 3 Solcar repeats It is a multi pass membrane protein The functions of SLC25A35 remain unknown SLC25A35 belongs to the SLC25 family o
- SLC25A34 is a multi pass membrane protein It belongs to the mitochondrial carrier family and contains 3 Solcar repeats The function of the SLC25A34 protein remains unknown SLC25A34 belongs to the S
- The erythropoietin receptor is a member of the cytokine receptor family Upon erythropoietin binding the erythropoietin receptor activates Jak2 tyrosine kinase which activates different intracellular
- G6PC hydrolyzes glucose 6 phosphate to glucose in the endoplasmic reticulum It forms with the glucose 6 phosphate transporter SLC37A4 G6PT the complex responsible for glucose production through glyc
- SGCB is a member of the sarcoglycan family Sarcoglycans are transmembrane components in the dystrophin glycoprotein complex which help stabilize the muscle fiber membranes and link the muscle cytoske
- OCA2 is believed to be an integral membrane protein involved in small molecule transport specifically tyrosine a precursor of melanin Mutations in the gene encoding OCA2 result in type 2 oculocuta
- ROM1 is an integral membrane protein found in the photoreceptor disk rim of the eye It can form homodimers or can heterodimerize with another photoreceptor retinal degeneration slow RDS It is ess
- CYBB is a critical component of the membrane bound oxidase of phagocytes that generates superoxide It is the terminal component of a respiratory chain that transfers single electrons from cytoplasmic
- EXT2 is one of two glycosyltransferases involved in the chain elongation step of heparan sulfate biosynthesis This gene encodes one of two glycosyltransferases involved in the chain elongation step of
- UGT1A1 is a UDP glucuronosyltransferase an enzyme of the glucuronidation pathway that transforms small lipophilic molecules such as steroids bilirubin hormones and drugs into water soluble excr
- TYRP1 catalyses the oxidation of 5 6 dihydroxyindole 2 carboxylic acid DHICA into indole 5 6 quinone 2 carboxylic acid It may regulate or influence the type of melanin synthesized
- Hepatocyte growth factor regulates cell growth cell motility and morphogenesis by activating a tyrosine kinase signaling cascade after binding to the proto oncogenic c Met receptor Hepatocyte growt
- ATP4B belongs to a family of P type cation transporting ATPases The gastric H K ATPase is a heterodimer consisting of a high molecular weight catalytic alpha subunit and a smaller but heavily glyc
- GGCX is an enzyme which catalyzes the posttranslational modification of vitamin K dependent protein Many of these vitamin K dependent proteins are involved in coagulation so the function of the encod
- KITLG is the ligand of the tyrosine kinase receptor encoded by the KIT locus This ligand is a pleiotropic factor that acts in utero in germ cell and neural cell development and hematopoiesis all be
- The exact function of PRRG1 remains unknown
- TRPM2 is a calcium permeable cation channel that is regulated by free intracellular ADP ribose The encoded protein is activated by oxidative stress and confers susceptibility to cell death The protei
- ATP2B3 gene belongs to the family of P type primary ion transport ATPases characterized by the formation of an aspartyl phosphate intermediate during the reaction cycle These enzymes remove bivalent
- ATP2B4 belongs to the family of P type primary ion transport ATPases characterized by the formation of an aspartyl phosphate intermediate during the reaction cycle These enzymes remove bivalent calci
- The functions of C14orf37 remain unknown
- DGAT2L4 is acyltransferase that predominantly esterify long chain wax alcohols with acyl CoA derived fatty acids to produce wax esters Wax esters are enriched in sebum suggesting that it plays a c
- GPR177 has signal transducer activity It is positive regulation of I kappaB kinase NF kappaB cascade
- MCTP1 belongs to the MCTP family It contains 3 C2 domains MCTP1 is a multi pass membrane protein It binds calcium via the C2 domains in absence of phospholipids The function of MCTP1 remains unknow
- The exact function of C1orf95 remains unknown
- TTMB is a multi pass membrane protein It belongs to the TMEM200 family The function of the TTMB protein remains unknown
- UCRC is a subunit of mitochondrial complex III ubiquinol cytochrome c reductase EC 1 10 2 2 which forms the middle segment of the respiratory chain of the inner mitochondrial membrane UCRC is a su
- OSBPL8 is a member of the oxysterol binding protein OSBP family a group of intracellular lipid receptors Like most members OSBPL8 contains an N terminal pleckstrin homology domain and a highly co
- TMEM195 belongs to the TMEM195 family It is a multi pass membrane protein The function of the TMEM195 protein remains
- The exact function of LINGO4 remains unknown
- FAM19A3 is a member of the TAFA family which is composed of five highly homologous small secreted proteins These proteins contain conserved cysteine residues at fixed positions and are distantly rel
- TTYH1 is a member of the tweety family of proteins Members of this family function as chloride anion channels TTYH1 functions as a calcium 2 independent volume sensitive large conductance chlori
- EDA is a type II membrane protein that can be cleaved by furin to produce a secreted form It belongs to the tumor necrosis factor family acts as a homotrimer and may be involved in cell cell signali
- WDR33 is a member of the WD repeat protein family WD repeats are minimally conserved regions of approximately 40 amino acids typically bracketed by gly his and trp asp GH WD which may facilitate f
- PDPN is a type I integral membrane glycoprotein with diverse distribution in human tissues The physiological function of this protein may be related to its mucin type character The homologous protei
- CISD2 is a zinc finger protein that localizes to the endoplasmic reticulum It binds an iron sulfur cluster and may be involved in calcium homeostasis Defects in this gene are a cause of Wolfram synd
- TPST2 catalyzes the O sulfation of tyrosine residues within acidic regions of proteins TPST2 is a type II integral membrane protein found in the Golgi body The protein encoded by this gene catalyzes
- CST9 is part of the cystatin superfamily which encompasses proteins that contain multiple cystatin like sequences Some of the members are active cysteine protease inhibitors while others have lost o
- NIPA2 belongs to the NIPA family It is a multi pass membrane protein The function of the NIPA2 protein remains unknown
- The exact function of LST 3TM12 remains unknown
- Neuregulins are a family of growth and differentiation factors that are related to epidermal growth factor
- PAP2D is a type 2 member of the phosphatidic acid phosphatase PAP family All type 2 members of this protein family contain 6 transmembrane regions and a consensus N glycosylation site PAPs conver
- PTPLAD2 is a multi pass membrane protein It belongs to the PTPLA family The function of the PTPLAD2 protein remains unknown
- The exact function of C10orf38 remains unknown
- GLT8D1 is a member of the glycosyltransferase family The specific function of this protein has not been determined Three alternatively spliced variants encoding the same isoform have been described
- LECT1 is a glycosylated transmembrane protein that is cleaved to form a mature secreted protein The mature protein promotes chondrocyte growth and inhibits angiogenesis The mature protein likely pl
- Sulfatases such as ARSH hydrolyze sulfate esters from sulfated steroids carbohydrates proteoglycans and glycolipids They are involved in hormone biosynthesis modulation of cell signaling and d
- The exact function of GRAMD2 remains unknown
- RP11 50D16 3 contains 4 NHL repeats The function of the RP11 50D16 3 protein remains unknown
- TMEM82 is a multi pass membrane protein It belongs to the TMEM82 family The function of the TMEM82 protein remains unknown
- VSIG8 contains 2 Ig like V type immunoglobulin like domains VSIG8 is single pass type I membrane protein The function of the VSIG8 protein remains unknown
- TCTN3 may be involved in apoptosis regulation
- TMEM93 belongs to the TMEM93 family It is a multi pass membrane protein The function of the TMEM93 protein remains unknown
- FOLH1 is a type II transmembrane glycoprotein belonging to the M28 peptidase family The protein acts as a glutamate carboxypeptidase on different alternative substrates including the nutrient folate
- MPG functions in the hydrolysis of the deoxyribose N glycosidic bond to excise 3 methyladenine and 7 methylguanine from the damaged DNA polymer formed by alkylation lesions
- IGSF11 functions as a cell adhesion molecule through homophilic interaction IGSF11 stimulates cell growth IGSF11 is an immunoglobulin Ig superfamily member that is preferentially expressed in brain
- TMEM30B belongs to the CDC50 LEM3 family It is a multi pass membrane protein The function of the TMEM30B protein remains unknown
- LRP8 is an apolipoprotein E receptor a member of the low density lipoprotein receptor LDLR family Apolipoprotein E is a small lipophilic plasma protein and a component of lipoproteins such as chyl
- The exact function of LOC339977 remains unknown
- LRRC24 contains 1 Ig like C2 type immunoglobulin like domain and 7 LRR leucine rich repeats It is a single pass membrane protein The function of the LRRC24 protein remains unknown
- The function of the C3orf17 protein remains unknown
- PLD3 is a ingle pass type II membrane protein It belongs to the phospholipase D family PLD3 contains 2 PLD phosphodiesterase domains The exact function of PLD3 remains unknown
- The mitochondrial oxidation of long chain fatty acids is initiated by the sequential action of carnitine palmitoyltransferase I which is located in the outer membrane and is detergent labile and car
- TMPO may be involved in the structural organization of the nucleus and in the post mitotic nuclear assembly It plays an important role together with LMNA in the nuclear anchorage of RB1
- The exact function of C1orf151 remains unknown
- RHOT1 is mitochondrial GTPase involved in mitochondrial trafficking It is probably involved in control of anterograde transport of mitochondria and their subcellular distribution
- Mitochondrial GTPase involved in mitochondrial trafficking RHOT1 is probably involved in control of anterograde transport of mitochondria and their subcellular distribution
- SI belongs to the glycosyl hydrolase 31 family It plays an important role in the final stage of carbohydrate digestion
- GALC is a lysosomal protein which hydrolyzes the galactose ester bonds of galactosylceramide galactosylsphingosine lactosylceramide and monogalactosyldiglyceride Mutations in this gene have been a
- SIL1 is a resident endoplasmic reticulum ER N linked glycoprotein with an N terminal ER targeting sequence 2 putative N glycosylation sites and a C terminal ER retention signal This protein func
- CEACAM16 is a single pass type I membrane protein It belongs to the immunoglobulin superfamily CEA family It contains 2 Ig like C2 type immunoglobulin like domains The exact function of CEACAM16 r
- The function of the LOC253012 protein remains unknown
- KIAA0317 contains 1 filamin repeat and 1 HECT E6AP type E3 ubiquitin protein ligase domain The exact function of KIAA0317 remains unknown
- KREMEN1 is a high affinity dickkopf homolog 1 DKK1 transmembrane receptor that functionally cooperates with DKK1 to block wingless WNT beta catenin signaling It is a component of a membrane compl
- ZDHHC19 belongs to the DHHC palmitoyltransferase family It contains 1 DHHC type zinc finger The exact function of ZDHHC19 remains unknown
- YIF1B belongs to the YIF1 family It is a multi pass membrane protein The functions of YIF1B remain unknown
- Proteoglycans which consist of a core protein and covalently linked glycosaminoglycans are components of the extracellular matrix SPOCK3 is a member of a novel Ca 2 binding proteoglycan familyPr
- LFNG is a member of the glycosyltransferase superfamily It is a single pass type II Golgi membrane protein that functions as a fucose specific glycosyltransferase adding an N acetylglucosamine to th
- CLDND1 belongs to the PMP 22 EMP MP20 family It is a multi pass membrane proteinPotential The exact function of CLDND1 remains unknown
- ASAHL is an N acylethanolamine hydrolyzing enzyme which is highly similar to acid ceramidase This gene encodes an N acylethanolamine hydrolyzing enzyme which is highly similar to acid ceramidase Mul
- POMT1 is an O mannosyltransferase that requires interaction with the product of the POMT2 gene for enzymatic function The encoded protein is found in the membrane of the endoplasmic reticulum Defect
- Various cellular organelles and vesicles are transported along the microtubules in the cytoplasm Likewise membrane recycling of the endoplasmic reticulum ER Golgi assembly at the microtubule orga
- It belongs to the TMTC family Its exact function remains unknown
- Copper amine oxidases catalyze the oxidative conversion

of amines to aldehydes and ammonia in the presence of copper and quinone cofactor The protein contains several conserved motifs including the a

- Breakdown products of phosphoinositides are ubiquitous second messengers that function downstream of many G protein coupled receptors and tyrosine kinases regulating cell growth calcium metabolism a
- Cytochrome c oxidase COX the terminal component of the mitochondrial respiratory chain catalyzes the electron transfer from reduced cytochrome c to oxygen COX10 is heme A farnesyltransferase wh
- DSCAM is a cell adhesion molecule that can mediate cation independent homophilic binding activity DSCAM could be involved in nervous system development
- ACP2 is the beta subunit of lysosomal acid phosphatase LAP LAP is chemically and genetically distinct from red cell acid phosphatase The protein belongs to a family of distinct isoenzymes which hy
- CDH4 gene is a classical cadherin from the cadherin superfamily The protein is a calcium dependent cell cell adhesion glycoprotein comprised of five extracellular cadherin repeats a transmembrane re
- CEACAM4 belongs to the immunoglobulin superfamily
- DSC3 is a calcium dependent glycoprotein that is a member of the desmocollin subfamily of the cadherin superfamily These desmosomal family members along with the desmogleins are found primarily in
- Desmosomes are cell cell junctions between epithelial myocardial and certain other cell types DSG2 is a calcium binding transmembrane glycoprotein component of desmosomes in vertebrate epithelial c
- ITGB8 is a member of the integrin beta chain family and is a single pass type I membrane protein with a VWFA domain and four cysteine rich repeats This protein noncovalently binds to an alpha subunit
- The Notch signaling pathway is an intercellular signaling mechanism that is essential for proper embryonic development Members of the Notch protein family are transmembrane receptors that are critica
- LRCH4 is a protein that contains leucine rich repeats LRR at its amino terminus and that is known to be involved in ligand binding The carboxyl terminus may act as a membrane anchor Identified str
- This gene is a member of the protocadherin gamma gene cluster one of three related clusters tandemly linked on chromosome five These gene clusters have an immunoglobulin like organization suggestin
- This gene belongs to the protocadherin gene family a subfamily of the cadherin superfamily PCDH8 is an integral membrane protein that is thought to function in cell adhesion in a CNS specific manner
- PI3 is an elastase specific inhibitor that functions as an antimicrobial peptide against Gram positive and Gram negative bacteria PI3 contains a WAP type four disulfide core WFDC domain and is thu
- ROBO2 belongs to the ROBO family part of the immunoglobulin superfamily proteins that are highly conserved from fly to human ROBO2 is a receptor for SLIT2 molecules known to function in axon guidan
- TFR2 a member of the transferrin receptor like family is a single pass type II membrane protein with a protease associated PA domain an M28 peptidase domain and a transferrin receptor like dimeriza
- ICAM5 is a member of the intercellular adhesion molecule ICAM family All ICAM proteins are type I transmembrane glycoproteins contain 2 9 immunoglobulin like C2 type domains and bind to the leuko
- TSPAN6 is a member of the transmembrane 4 superfamily also known as the tetraspanin family Most of these members are cell surface proteins that are characterized by the presence of four hydrophobic
- Galactocerebrosides are abundant sphingolipids of the myelin membrane of the central nervous system and peripheral nervous system and are also present in small amounts in kidney The key enzymatic ste
- TMEM187 is a multi pass membrane protein The exact function of TMEM187 remains unknown
- CNTNAP1 was initially identified as a 190 kD protein associated with the contactin PTPRZ1 complex The 1 384 amino acid protein also designated p190 or CASPR for contactin associated protein inclu
- Diacylglycerol kinases are thought to be involved mainly in the regeneration of phosphatidylinositol PI from diacylglycerol in the PI cycle during cell signal transduction When expressed in mammali
- DEGS1 is a member of the membrane fatty acid desaturase family which is responsible for inserting double bonds into specific positions in fatty acids This protein contains three His containing consen
- TMEFF1 may inhibit NODAL and BMP signaling during neural patterning It may be a tumor suppressor in brain cancers
- GALNT4 catalyzes the initial reaction in O linked oligosaccharide biosynthesis the transfer of an N acetyl D galactosamine residue to a serine or threonine residue on the protein receptor It has a h
- Hairy enhancer of split related proteins such as HEY1 are basic helix loop helix bHLH transcription factors implicated in cell fate decision and boundary formation HEY genes are direct transcript
- RORC encodes a protein which is a DNA binding transcription factor and is a member of the NR1 subfamily of nuclear hormone receptors The specific functions of this protein are not known however stu
- NR1I3 mediates the induction of transcription of cytochrome P450 CYP genes by phenobarbital PB and PB type inducers NR1I3 activation induces hepatic expression of detoxification enzymes and trans
- Coup chicken ovalbumin upstream promoter transcription factor binds to the ovalbumin promoter and in conjunction with another protein S300 II stimulates initiation of transcription NR2F1 binds t
- IGFBP4 is a member of the insulin like growth factor binding protein IGFBP family IGFBP4 is a protein with an IGFBP domain and a thyroglobulin type I domain The protein binds both insulin like gro
- BAAT is a liver enzyme that catalyzes the transfer of C24 bile acids from the acyl CoA thioester to either glycine or taurine the second step in the formation of bile acid amino acid conjugates The
- HAL is a cytosolic enzyme catalyzing the first reaction in histidine catabolism the nonoxidative deamination of L histidine to trans urocanic acid HAL defects cause histidinemia which is characteriz
- ECHS1 functions in the second step of the mitochondrial fatty acid beta oxidation pathway It catalyzes the hydration of 2 trans enoyl coenzyme A CoA intermediates to L 3 hydroxyacyl CoAs The prote
- HSD11B1 is a microsomal enzyme that catalyzes the conversion of the stress hormone cortisol to the inactive metabolite cortisone In addition HSD11B1 can catalyze the reverse reaction the conversion
- Tryptophan 2 3 dioxygenase EC 1 13 11 11 plays a role in catalyzing the first and rat limiting step in the kynurenine pathway the major pathway of tryptophan metabolism
- MST1 belongs to the peptidase S1 family plasminogen subfamily It contains 4 kringle domains 1 PAN domain and 1 peptidase S1 domain MST1 probably has no proteolytic activity since crucial characte
- GYS2 transfers the glycosyl residue from UDP Glc to the non reducing end of alpha 1 4 glucan Defects in GYS2 are the cause of glycogen storage disease type 0 GSD0
- DGKH is a member of the diacylglycerol kinase DGK enzyme family of proteins specifically the type II DGK subfamily Members of this family are involved in regulating the intracellular concentration
- The specific function of NCRNA00114 is not yet known
- The exact function of C21orf87 remains unknown
- PSMG1 is a chaperone protein which promotes assembly of the 20S proteasome as part of a heterodimer with PSMG2 The PSMG1 PSMG2 heterodimer binds to the PSMA5 and PSMA7 proteasome subunits promotes a
- The function of the C21orf2 protein remains unknown
- PWP2 belongs to the WD repeat PWP2 family It contains 14 WD repeats The exact function of PWP2 is not known
- RRP1B belongs to the RRP1 family It may be a novel susceptibility gene for breast cancer progression and metastasis
- POFUT2 catalyzes the reaction that attaches fucose through an O glycosidic linkage to a conserved serine or threonine residue in thrombospondin type 1 repeats Fucose is typically found as a terminal
- The exact function of C21orf91 remains unknown
- The exact function of C21orf62 remains unknown
- RIPK4 is a serine threonine protein kinase that interacts with protein kinase C delta The protein can also activate NFkappaB and is required for keratinocyte differentiation This kinase undergoes au
- The function of the C21orf59 protein remains unknown
- SAMSN1 is a member of a novel protein family of putative adaptors and scaffold proteins containing SH3 and SAM sterile alpha motif domains SAMSN1 is a member of a novel gene family of putative adapt
- The exact function of C21orf56 remains unknown
- The function of the C21orf13 protein remains unknown
- KRTAP11 1 belongs to the PMG family In the hair cortex hair keratin intermediate filaments are embedded in an interfilamentous matrix consisting of hair keratin associated proteins KRTAP which a
- In the hair cortex hair keratin intermediate filaments are embedded in an interfilamentous matrix consisting of hair keratin associated proteins KRTAP which are essential for the formation of a r
- NCF4 is a cytosolic regulatory component of the superoxide producing phagocyte NADPH oxidase a multicomponent enzyme system important for host defense It interacts primarily with neutrophil cytosoli
- Soluble guanylate cyclase sGC a heterodimeric protein consisting of an alpha subunit and a beta subunit typically GUCY1B3 catalyzes conversion of GTP to the second messenger cGMP and functions as
- RRM2 provides the precursors necessary for DNA synthesis RRM2 catalyzes the biosynthesis of deoxyribonucleotides from the corresponding ribonucleotides RRM2 inhibits Wnt signaling Ribonucleotide red
- This protein is a nuclear encoded mitochondrial bifunctional enzyme with methylenetetrahydrofolate dehydrogenase and methenyltetrahydrofolate cyclohydrolase activities The enzyme functions as a homod
- MAP4K1 belongs to the protein kinase superfamily STE Ser Thr protein kinase family STE20 subfamily MAP4K1 may play a role in the response to environmental stress It appears to act upstream of the
- SKAP1 Is a T cell adaptor protein a class of intracellular molecules with modular domains capable of recruiting additional proteins but that exhibit no intrinsic enzymatic activity The encoded prote
- PAICS is a bifunctional enzyme containing phosphoribosylaminoimidazole carboxylase activity in its N terminal region and phosphoribosylaminoimidazole succinocarboxamide synthetase in its C terminal re
- Crystallins are separated into two classes taxon specific or enzyme and ubiquitous The latter class constitutes the major proteins of vertebrate eye lens and maintains the transparency and refract
- CTH is a cytoplasmic enzyme in the trans sulfuration pathway that converts cystathione derived from methionine into cysteine Glutathione synthesis in the liver is dependent upon the availability of c
- HSPA4 Hsp70 belongs to the heat shock protein 70 family It was isolated as a putative Rictor interacting protein and interaction with membranes acts as a platform for its release into the extracell
- The elongation of primed DNA templates by DNA polymerase delta and epsilon requires the action of the accessory proteins proliferating cell nuclear antigen PCNA and activator 1 This subunit may be
- Aminoacyl tRNA synthetases are a class of enzymes that charge tRNAs with their cognate amino acids EPRS is a multifunctional aminoacyl tRNA synthetase that catalyzes the aminoacylation of glutamic ac
- The promoters and first exons of the MAGEA genes show considerable variability suggesting that the existence of this gene family enables the same function to be expressed under different transcriptio
- PDK3 belongs to the PDK BCKDK protein kinase family It contains 1 histidine kinase domain PDK3 inhibits the mitochondrial pyruvate dehydrogenase complex by phosphorylation of the E1 alpha subunit t
- Aminoacyl tRNA synthetases catalyze the aminoacylation of tRNA by their cognate amino acid Because of their central role in linking amino acids with nucleotide triplets contained in tRNAs aminoacyl
- Purines are necessary for many cellular processes including DNA replication transcription and energy metabolism Ten enzymatic steps are required to synthesize inosine monophosphate IMP in the de
- PDSS1 is an enzyme that elongates the prenyl side chain of coenzyme Q or ubiquinone one of the key elements in the respiratory chain PDSS1 catalyzes the formation of all trans polyprenyl pyrophosph
- DLG7 is a potential cell cycle regulator that may play a role in carcinogenesis of cancer cells It is a mitotic phosphoprotein regulated by the ubiquitin proteasome pathway DLG7 is the key regulator
- BOP1 is the component of the PeBoW complex which is required for maturation of 28S and 5 8S ribosomal RNAs and formation of the 60S ribosome
- NCAPH is a member of the barr family and a regulatory subunit of the condensin complex This complex is required for the conversion of interphase chromatin into condensed chromosomes The protein is a
- PIP3 E enhances the promotion of guanine nucleotide exchange by PSCD2 on ARF6 in a concentration dependent manner
- The specific function of FAM82B is not yet known
- The yeast heterotetrameric GINS complex is made up of Sld5 Psf1 Psf2 and Psf3 The formation of this complex is essential for the initiation of DNA replication in yeast and Xenopus egg extracts The
- WBP11 is a nuclear protein which colocalizes with mRNA splicing factors and intermediate filament containing perinuclear networks WBP11has 95 amino acid sequence identity to the mouse Wbp11 protein
- NUSAP1 is a microtubule associated protein with the

capacity to bundle and stabilize microtubules It may associate with chromosomes and promote the organization of mitotic spindle microtubules around

- USP18 a member of the deubiquitinating protease family of enzymes removes ubiquitin adducts from a broad range of protein substrates USP18 a member of the deubiquitinating protease family of enzyme
- Mitochondrial ribosomes mitoribosomes consist of a small 28S subunit and a large 39S subunit MRPL39 is a 39S subunit protein Mammalian mitochondrial ribosomal proteins are encoded by nuclear genes
- OXSM is a mitochondrial beta ketoacyl synthase EC 2 3 1 41 involved in mitochondrial fatty acid synthesis It is required for catalysis of the chain elongating condensation reaction OXSM is a mitoch
- TMEM48 is a component of the nuclear pore complex NPC which plays a key role in de novo assembly and insertion of NPC in the nuclear envelope TMEM48 is required for NPC and nuclear envelope assemb
- TSR1 belongs to the BMS1 TSR1 family and TSR1 subfamily TSR1 is required during maturation of the 40S ribosomal subunit in the nucleolus
- CEP55 plays a role in mitotic exit and cytokinesis Not required for microtubule nucleation
- Myristate a rare 14 carbon saturated fatty acid is cotranslationally attached by an amide linkage to the N terminal glycine residue of cellular and viral proteins with diverse functions N myristoyl
- DTNB is dystrobrevin beta a component of the dystrophin associated protein complex DPC The DPC consists of dystrophin and several integral and peripheral membrane proteins including dystroglycans
- The centromere is a specialized chromatin domain present throughout the cell cycle that acts as a platform on which the transient assembly of the kinetochore occurs during mitosis All active centro
- The function of the C2orf47 protein remains unknown
- RMI1 is an essential component of the RMI complex a complex that plays an important role in the processing of homologous recombination intermediates to limit DNA crossover formation in cells RMI1 pr
- ANP32E inhibits activity of protein phosphatase 2A PP2A It does not inhibit protein phosphatase 1 It may play a role in cerebellar development and synaptogenesis process by modulating PP2A activit
- The nuclear lamina consists of a two dimensional matrix of proteins located next to the inner nuclear membrane The lamin family of proteins make up the matrix and are highly conserved in evolution D
- ADAM15 is a member of the ADAM a disintegrin and metalloproteinase protein family ADAM family members are type I transmembrane glycoproteins known to be involved in cell adhesion and proteolytic ec
- ADAM9 is a member of the ADAM a disintegrin and metalloprotease domain family Members of this family are membrane anchored proteins structurally related to snake venom disintegrins and have been i
- SGCE is a member of the sarcoglycan family Sarcoglycans are transmembrane components in the dystrophin glycoprotein complex which help stabilize the muscle fiber membranes and link the muscle cytoske
- Oncostatin M is a member of the IL6 family of cytokines Functional receptors for IL6 family cytokines are multisubunit complexes involving members of the hematopoietin receptor superfamily Many IL6
- NINJ1 is a homophilic cell adhesion molecule that promotes axonal growth NINJ1 may play a role in nerve regeneration and in the formation and function of other tissues
- PIGQ is involved in the first step in glycosylphosphatidylinositol GPI anchor biosynthesis The GPI anchor is a glycolipid found on many blood cells and serves to anchor proteins to the cell surface
- SEMA4F has growth cone collapse activity against retinal ganglion cell axons
- N acetylglucosamine 6 O sulfotransferases such as CHST2 catalyze the transfer of sulfate from 3 prime phosphoadenosine 5 prime phosphosulfate PAPS to position 6 of a nonreducing N acetylglucosamin
- ACSL3 is an isozyme of the long chain fatty acid coenzyme A ligase family Although differing in substrate specificity subcellular localization and tissue distribution all isozymes of this family c
- Interleukin 11 is a stromal cell derived cytokine that belongs to a family of pleiotropic and redundant cytokines that use the gp130 transducing subunit in their high affinity receptors IL11RA is the
- NDUFC2 is the accessory subunit of the mitochondrial membrane respiratory chain NADH dehydrogenase Complex I It is believed to be not involved in catalysis reaction Complex I functions in the tran
- TM4SF4 is a member of the transmembrane 4 superfamily also known as the tetraspanin family Most of these members are cell surface proteins that are characterized by the presence of four hydrophobic
- SYNGR2 is an integral membrane protein containing four transmembrane regions and a C terminal cytoplasmic tail that is tyrosine phosphorylated The exact function of this protein is unclear but studi
- Proteins of the matrix metalloproteinase MMP family are involved in the breakdown of extracellular matrix in normal physiological processes such as embryonic development reproduction and tissue r
- NDST3 is a member of the heparan sulfate heparin GlcNAc N deacetylase N sulfotransferase family NDST3 is a type II transmembrane protein that resides in the Golgi apparatus This monomeric bifunctio
- The Golgi apparatus which participates in glycosylation and transport of proteins and lipids in the secretory pathway consists of a series of stacked cisternae flattened membrane sacs Interaction
- Deletions of the 22q11 2 have been associated with a wide range of developmental defects classified under the acronym CATCH 22 The DGCR2 is a novel putative adhesion receptor protein which could pla
- ATP2A3 is one of the SERCA Ca 2 ATPases which are intracellular pumps located in the sarcoplasmic or endoplasmic reticula of muscle cells This enzyme catalyzes the hydrolysis of ATP coupled with
- IFNGR2 is the non ligand binding beta chain of the gamma interferon receptor Human interferon gamma receptor is a heterodimer of IFNGR1 and IFNGR2 Defects in IFNGR2 are a cause of mendelian suscepti
- DLL1 is a human homolog of the Notch Delta ligand and is a member of the delta serrate jagged family It plays a role in mediating cell fate decisions during hematopoiesis It may play a role in cell
- TSPAN3 is a member of the transmembrane 4 superfamily also known as the tetraspanin family Most of these members are cell surface proteins that are characterized by the presence of four hydrophobic
- TSPAN2 is a member of the transmembrane 4 superfamily also known as the tetraspanin family Most of these members are cell surface proteins that are characterized by the presence of four hydrophobic
- It may catalyze the formation of the NeuAc alpha 2 3 Gal beta 1 3 GalNAc or NeuAc alpha 2 3 Gal beta 1 3 GlcNAc sequences found in terminal carbohydrate groups of glycoproteins and glycolipids It ma
- GCS1 is the first enzyme in the N linked oligosaccharide processing pathway The enzyme cleaves the distal alpha 1 2 linked glucose residue from the Glc 3 Man 9 GlcNAc 2 oligosaccharide precurso
- Serine palmitoyltransferase which consists of two different subunits is the key enzyme in sphingolipid biosynthesis It converts L serine and palmitoyl CoA to 3 oxosphinganine with pyridoxal 5 phos
- Erlin 1 belongs to the band 7 mec 2 family Erlin 1 and erlin 2 are novel members of the prohibitin family of proteins that define lipid raft like domains of the ER
- PTPRE is a member of the protein tyrosine phosphatase PTP family PTPs are known to be signaling molecules that regulate a variety of cellular processes including cell growth differentiation mitot
- The WNT family consists of several secreted signaling proteins These proteins have been implicated in oncogenesis and in several developmental processes including regulation of cell fate and pattern
- CSPG5 may function as a growth and differentiation factor involved in neuritogenesis It may induce ERBB3 activation
- The function of the KLRA1 protein remains unknown
- LYVE1 is a type I integral membrane glycoprotein It acts as a receptor and binds to both soluble and immobilized hyaluronan This protein may function in lymphatic hyaluronan transport and have a rol
- Alpha mannosidases function at different stages of N glycan maturation in mammalian cells See MAN2A1 MIM 154582 for general information Alpha mannosidases function at different stages of N glycan m
- The specific function of BTNL3 is not yet known
- AFG3L2 is a protein localized in mitochondria and closely related to paraplegin The paraplegin gene is responsible for an autosomal recessive form of hereditary spastic paraplegia AFG3L2 gene is a c
- CKAP4 p63 is a substrate of DHHC2 a putative tumor suppressor CK MNF116 and p63 were useful in identifying squamous cell carcinomas with single cell infiltration Those results suggested a role of C
- TMED1 was identified by its interaction with interleukin 1 receptor like 1 IL1RL1 This protein lacks any similarity to other interleukin 1 ligands The functional significance of its interaction wi
- MMP23B is a protease This gene MMP23B encodes a member of the matrix metalloproteinase MMP family and it is part of a duplicated region of chromosome 1p36 3 Proteins of the matrix metalloprotein
- The specific function of TMEM115 is not yet known
- RER1 is involved in the retrieval of endoplasmic reticulum membrane proteins from the early Golgi compartment
- GALNT6 is a member of the UDP N acetyl alpha D galactosamine polypeptide N acetylgalactosaminyltransferase GalNAc T family of enzymes GalNAc Ts initiate mucin type O linked glycosylation in the Gol
- The exact function of C20orf103 remains unknown
- TRAM2 is a component of the translocon a gated macromolecular channel that controls the posttranslational processing of nascent secretory and membrane proteins at the endoplasmic reticulum ER membr
- ICMT is the third of three enzymes that posttranslationally modify isoprenylated C terminal cysteine residues in certain proteins and target those proteins to the cell membrane This enzyme localizes
- Neuroplastin is a type I transmembrane protein belonging to the Ig superfamily The protein is believed to be involved in cell cell interactions or cell substrate interactions The alpha and beta tran
- SYNGR4 is an integral membrane protein The gene belongs to the synaptogyrin gene family Like other members of the family the protein contains four transmembrane regions The exact function of this p
- ALG6 is a member of the ALG6 ALG8 glucosyltransferase family It catalyzes the addition of the first glucose residue to the growing lipid linked oligosaccharide precursor of N linked glycosylation Mu
- POMT2 is an integral membrane protein of the endoplasmic reticulum ER that shares significant sequence similarity with a family of protein O mannosyltransferases of S cerevisiae POMT2 encodes an in
- Paired receptors consist of highly related activating and inhibitory receptors and are widely involved in the regulation of the immune system PILRB is thought to act as a cellular signaling activatin
- ASTN2 may play an important role in neuronal functioning
- UNC50 belongs to the unc 50 family It binds RNA UNC50 may be involved in cell surface expression of neuronal nicotinic receptors
- GALNT5 can catalyze the initial reaction in O linked oligosaccharide biosynthesis the transfer of an N acetyl D galactosamine residue to a serine or threonine residue on the protein receptor GALNT5 h
- P type ATPases such as ATP11B are phosphorylated in their intermediate state and drive uphill transport of ions across membranes Several subfamilies of P type ATPases have been identified One subf
- KIAA0247 is a single pass type I membrane protein It contains 1 Sushi CCP SCR domain The function of the KIAA0247 protein remains unknown
- PTDSS1 is a multi pass membrane protein It belongs to the phosphatidyl serine synthase family PTDSS1 catalyzes a base exchange reaction in which the polar head group of phosphatidylcholine is replac
- KIAA1024 is a single pass membrane proteinPotential It belongs to the UPF0258 family The function of the KIAA1024 protein remains unknown
- ZDHHC17 is a palmitoyltransferase specific for a subset of neuronal proteins including SNAP25 DLG4 PSD95 GAD2 SYT1 and HD It may be involved in the sorting or targeting of critical proteins invol
- DULLARD is a serine threonine phosphatase which may be required for proper nuclear membrane morphology DULLARD was involved in LPIN1 dephosphorylation It may antagonize BMP signaling
- ABI3BP contains 2 fibronectin type III domains The loss of ABI3BP expression could play a functional role in thyroid tumorigenesis It also presumably represents a trigger gene for evoking cellular s
- DKFZP564J0863 ATL3 atlastin GTPase 3 belongs to the GBP family In the family of human GTPases atlastin 2 and 3 are closely related to atlastin 1
- GALNAC4S 6ST is a sulfotransferase that transfers sulfate from 3 phosphoadenosine 5 phosphosulfate PAPS to the C 6 hydroxyl group of the GalNAc 4 sulfate residue of chondroitin sulfate A and forms
- The specific function of TEX264 is not yet known
- PIGT is a protein that is involved in glycosylphosphatidylinositol GPI anchor biosynthesis The GPI anchor is a glycolipid found on many blood cells and serves to anchor proteins to the cell surface
- TMEM66 is a multi pass membrane protein It belongs to the TMEM66 family The exact function of TMEM66 remains unknown
- A4GNT is a protein from the glycosyltransferase 32 family The enzyme catalyzes the transfer of N acetylglucosamine GlcNAc to core 2 branched O glycans It forms a unique glycan GlcNAcalpha1 4Gal

- Interphotoreceptor matrix proteoglycan 2 IMPG2 is part of an extracellular complex occupying the interface between photoreceptors and the retinal pigment epithelium in th e fundus of the eye Interph
- Glycoprotein VI GP6 is a 58 kD platelet membrane glycoprotein that plays a crucial role in the collagen induced activation and aggregation of platelets Collagen receptor involved in collagen induce
- PTPLAD1 is a multi pass membrane protein It belongs to the PTPLA family and contains 1 CS domain PTPLAD1 hB ind1 plays a crucial role in HCV RNA replication and the propagation of JFH1 virus throu
- TMEM9 belongs to the TMEM9 family It may be involved in intracellular transport
- TMEM138 is a multi pass membrane protein It belongs to the TMEM138 family The function of the TMEM138 protein remains unknown
- This protein can induce apoptosis in a caspase dependent manner and plays a role in p53 TP53 dependent apoptosis
- CEND1 is a neuron specific protein The similar protein in pig enhances neuroblastoma cell differentiation in vitro and may be involved in neuronal differentiation in vivo The protein encoded by this
- PCDH12 belongs to the protocadherin protein family a subfamily of the cadherin superfamily It consists of an extracellular domain containing 6 cadherin repeats a transmembrane domain and a cytoplas
- FKBP11 belongs to the FKBP family of peptidyl prolyl cis trans isomerases which catalyze the folding of proline containing polypeptides The peptidyl prolyl isomerase activity of FKBP proteins is inh
- DLL3 is a member of the delta protein ligand family This family functions as Notch ligands that are characterized by a DSL domain EGF repeats and a transmembrane domain Mutations in this gene caus
- IL1RAPL2 is a member of the interleukin 1 receptor family This protein is similar to the interleukin 1 accessory proteins and is most closely related to interleukin 1 receptor accessory protein like
- CECR1 a member of a subfamily of the adenosine deaminase protein family It may act as a growth factor and have adenosine deaminase activity This gene may be responsible for some of the phenotypic fe
- QPCTL is a single pass membrane proteinPotential It belongs to the glutaminyl peptide cyclotransferase family The exact function of QPCTL remains unknown
- LAX1 is a single pass type III membrane protein It negatively regulates TCR T cell antigen receptor mediated signaling in T cells and BCR B cell antigen receptor mediated signaling in B cells
- TMEM127 is a multi pass membrane protein The exact function of TMEM127 remains unknown
- The exact function of C2orf18 remains unknown
- CLN6 is one of eight which have been associated with neuronal ceroid lipofuscinoses NCL Also referred to as Batten disease NCL comprises a class of autosomal recessive neurodegenerative disorders
- TMCO3 belongs to the monovalent cation proton antiporter 2 CPA2 transporter TC 2 A 37 family It is a multi pass membrane protein TMCO3 is a probable Na H antiporter
- The exact function of FAM70A remains unknown
- The exact function of C17orf80 remains unknown
- SUSD4 contains 4 Sushi CCP SCR domains It is a single pass type I membrane protein The function of the SUSD4 protein remains unknown
- TMEM51 is a multi pass membrane protein The function of the TMEM51 protein remains unknown
- TMEM16K is a multi pass membrane protein It belongs to the anoctamin family TMEM16K may act as a calcium activated chloride channel
- NETO2 is a predicted transmembrane protein containing two extracellular CUB domains followed by a low density lipoprotein class A LDLa domain It also has an intracellular FXNPXY like motif which h
- TMEM38B is a monovalent cation channel required for maintenance of rapid intracellular calcium release It may act as a potassium counter ion channel that functions in synchronization with calcium rel
- The exact function of this protein remains unknown
- The exact function of FLJ10769 remains unknown
- KIRREL NEPH1 is a member of the nephrin like protein family which includes NEPH2 and NEPH3 The cytoplasmic domains of these proteins interact with the C terminus of podocin NPHS2 and the genes
- The exact function of C6orf64 remains unknown
- LRRN3 is a single pass type I membrane protein It contains 1 fibronectin type III domain 1 Ig like C2 type immunoglobulin like domain and 12 LRR leucine rich repeats The function of the LRRN3 p
- TMEM144 belongs to the TMEM144 family It is a multi pass membrane protein The function of the TMEM144 protein remains unknown
- Mitochondrial creatine kinase MtCK is responsible for the transfer of high energy phosphate from mitochondria to the cytosolic carrier creatine It belongs to the creatine kinase isoenzyme family
- ChGn transfers 1 4 N acetylgalactosamine GalNAc from UDP GalNAc to the non reducing end of glucuronic acid GlcUA This protein is required for addition of the first GalNAc to the core tetrasacchar
- LAPTM4B is a multi pass membrane protein It belongs to the LAPTM4 LAPTM5 transporter family LAPTM4b has active role in disease progression of malignant cells and is involved in cell proliferation an
- Glycosylation of proteins affects cell cell interaction interactions with the matrix and the functions of intracellular molecules ST6GALNAC1 transfers a sialic acid N acetylneuraminic acid NeuAc
- SAC belongs to a distinct class of mammalian adenylyl cyclase that is soluble and insensitive to G protein or forskolin regulation It is localized in the cytoplasm and is thought to function as a gen
- KRT19 is a member of the keratin family The keratins are intermediate filament proteins responsible for the structural integrity of epithelial cells and are subdivided into cytokeratins and hair kera
- KRT23 is a member of the keratin family The keratins are intermediate filament proteins responsible for the structural integrity of epithelial cells and are subdivided into cytokeratins and hair kera
- ETV3L is a transcriptional regulator which belongs to the ETS family and contains 1 ETS DNA binding domain
- ARGFX belongs to the paired homeobox family Homeobox genes encode DNA binding proteins many of which are thought to be involved in early embryonic development Homeobox genes encode a DNA binding dom
- EMX1 belongs to the EMX homeobox family It is transcription factor which in cooperation with EMX2 acts to generate the boundary between the roof and archipallium in the developing brain The protein
- DRGX is a transcription factor required for the formation of correct projections from nociceptive sensory neurons to the dorsal horn of the spinal cord and normal perception of pain
- The POU6F1 gene encodes a protein that is part of a family of transcription factors which exhibit distinct temporal and spatial patterns of expression
- ZNF131 belongs to the krueppel C2H2 type zinc finger protein family It contains 1 BTB POZ domain and 6 C2H2 type zinc fingers It may be involved in transcriptional regulation ZNF131 plays a role
- NCKAP1L is a member of the HEM family of tissue specific transmembrane proteins which are highly conserved from invertebrates through mammals This gene is only expressed in hematopoietic cells while
- Cellular senescence the terminal nondividing state that normal cells enter following completion of their proliferative potential is the dominant phenotype in hybrids of normal and immortal cells Fu
- PSMC3IP plays an important role in meiotic recombination It stimulates DMC1 mediated strand exchange required for pairing homologous chromosomes during meiosis The complex PSMC3IP MND1 binds DNA st
- TCF25 acts as a transcriptional repressor It has been shown to repress transcription of SRF in vitro and so may play a role in heart development
- Similarity to a transcriptional repressor suggests that C21orf66 is involved in the regulation of transcription Alternative splicing of this gene results in three transcript variants encoding differe
- UBN1 may be required for replication independent chromatin assembly
- BARHL2 and BARHL1 are two homeobox genes in mouse and human which are highly related to the Bar Drosophila genes
- MEIS3 belongs to the TALE MEIS homeobox family It contains 1 homeobox DNA binding domain The function of the MEIS3 protein remains unknown
- MTA3 plays a role in maintenance of the normal epithelial architecture through the repression of SNAI1 transcription in a histone deacetylase dependent manner and thus the regulation of E cadherin le
- HOMEZ contains 2 homeobox DNA binding domains It may function as a transcriptional regulator
- Translocation t 2 17 p23 q25 with ALK a chromosomal aberration involving KIAA1618 ALO17 is associated with anaplastic large cell lymphoma ALCL
- METT10D belongs to the methyltransferase superfamily METT10D rlmF family The exact function of METT10D remains unknown
- ZNF452 SCAND3 contains 1 integrase catalytic domain and 1 SCAN box domain The function of ZNF452 remains unknown
- ZNF41 belongs to the krueppel C2H2 type zinc finger protein family It contains 18 C2H2 type zinc fingers and 1 KRAB domain ZNF41 may be involved in transcriptional regulation A chromosomal aberrati
- FOXD4 contains 1 fork head DNA binding domain The W148R mutation in the forkhead domain of FOXD4 possibly resultsin reduced DNA binding capacity and altered transcriptional activity
- ZNF154 may be involved in transcriptional regulation
- FBP2 is a gluconeogenesis regulatory enzyme which catalyzes the hydrolysis of fructose 1 6 bisphosphate to fructose 6 phosphate and inorganic phosphate This gene encodes a gluconeogenesis regulatory e
- CCNY belongs to the cyclin family Cyclin Y subfamily It contains 1 cyclin N terminal domain Single nucleotide polymorphism in CCNY gene is associated with Crohn s disease and ulcerative colitis
- NDE1 is required for centrosome duplication and formation and function of the mitotic spindle It is essential for the development of the cerebral cortex NDE1 may regulate the production of neurons b
- ZNF420 contains 19 C2H2 type zinc fingers and 1 KRAB domain ZNF420 may be involved in transcriptional regulation
- CKLF is a cytokine This gene is one of several chemokine like factor genes located in a cluster on chromosome 16 CKLF is a potent chemoattractant for neutrophils monocytes and lymphocytes It also
- The exact function of PLAC9 remains unknown
- Members of the F box protein family such as FBXO42 are characterized by an approximately 40 amino acid F box motif SCF complexes formed by SKP1 cullin and F box proteins act as protein ubiquiti
- PPP1R13B is a member of the ASPP apoptosis stimulating protein of p53 family of p53 interacting proteins The protein contains four ankyrin repeats and an SH3 domain involved in protein protein inte
- Complex II of the respiratory chain which is specifically involved in the oxidation of succinate carries electrons from FADH to CoQ The complex is composed of four nuclear encoded subunits and is l
- The function of the C1orf111 protein remains unknown
- SRRD belongs to the SRR1 family It may be involved in a circadian clock input pathway
- NEXN is involved in regulating cell migration through association with the actin cytoskeleton
- PPP2R5A belongs to the phosphatase 2A regulatory subunit B family Protein phosphatase 2A is one of the four major Ser Thr phosphatases and it is implicated in the negative control of cell growth and
- REC8 is required during meiosis for separation of sister chromatids and homologous chromosomes Proteolytic cleavage of REC8 on chromosome arms by separin during anaphase I allows for homologous chrom
- TMEM173 acts as a facilitator of innate immune signaling It is able to activate both NF kappa B and IRF3 transcription pathways to induce expression of type I interferon IFN alpha and IFN beta and
- TNNI3K may play a role in cardiac physiology
- AKT1S1 may play an important role in phosphatidylinositol 3 kinase PI3K AKT1 survival signaling It is the substrate for AKT1 phosphorylation but can also be activated by AKT1 independent mechanism
- IL28RA belongs to the class II cytokine receptor family This protein forms a receptor complex with interleukine 10 receptor beta IL10RB The receptor complex has been shown to interact with three
- MYH9 is a myosin IIA heavy chain that contains an IQ domain and a myosin head like domain The protein is involved in several important functions including cytokinesis cell motility and maintenance
- SELS is a selenoprotein which contains a selenocysteine Sec residue at its active site The selenocysteine is encoded by the UGA codon that normally signals translation termination The 3 UTR of s
- RNASE9 belongs to the pancreatic ribonuclease family It may be involved in host defense
- OAT is a key enzyme in the pathway that converts arginine and ornithine into the major excitatory and inhibitory neurotransmitters glutamate and GABA Mutations of this enzyme cause the autosomal rece
- TPI1 belongs to the triosephosphate isomerase family Defects in TPI1 are the cause of triosephosphate isomerase deficiency TPI deficiency TPI deficiency is an autosomal recessive disorder It is
- OPRT UMPS is involved in early events of pancreatic and gallbladder carcinogenesis and invasion of hepatocellular carcinomas Orotate phosphoribosyltransferase is involved in the invasion and metast
- Adenylate kinase is an enzyme involved in regulating the adenine nucleotide composition within a cell by catalyzing the reversible transfer of phosphate group among adinine nucleotides Three isozymes
- The pyruvate dehydrogenase complex catalyzes the

overall conversion of pyruvate to acetyl CoA and CO2 It contains multiple copies of three enzymatic components pyruvate dehydrogenase E1 dihydroli

- Ribosomes the complexes that catalyze protein synthesis consist of a small 40S subunit and a large 60S subunit Together these subunits are composed of 4 RNA species and approximately 80 structurall
- Chromosomal region 7p12 which contains GBAS is amplified in approximately 40 of glioblastomas the most common and malignant form of central nervous system tumor The predicted 286 amino acid protei
- EIF3E belongs to the eIF 3 subunit E family It is a component of the eukaryotic translation initiation factor 3 eIF 3 complex which is required for several steps in the initiation of protein synthe
- ACAA1 is an enzyme operative in the beta oxidation system of the peroxisomes Deficiency of this enzyme leads to pseudo Zellweger syndrome Acetyl Coenzyme A acyltransferase ACAA1 is an enzyme operat
- APEH is the enzyme acylpeptide hydrolase which catalyzes the hydrolysis of the terminal acetylated amino acid preferentially from small acetylated peptides The acetyl amino acid formed by this hydro
- ATP5F1 is a subunit of mitochondrial ATP synthase Mitochondrial ATP synthase catalyzes ATP synthesis utilizing an electrochemical gradient of protons across the inner membrane during oxidative phosp
- The immunosuppressant drug cyclosporin A blocks a calcium dependent signal from the T cell receptor TCR that normally leads to T cell activation When bound to cyclophilin B cyclosporin A binds and
- EEF1A2 is an isoform of the alpha subunit of the elongation factor 1 complex which is responsible for the enzymatic delivery of aminoacyl tRNAs to the ribosome This isoform alpha 2 is expressed in
- Isocitrate dehydrogenases catalyze the oxidative decarboxylation of isocitrate to 2 oxoglutarate These enzymes belong to two distinct subclasses one of which utilizes NAD as the electron accepto
- The 26S proteasome is a multicatalytic proteinase complex with a highly ordered structure composed of 2 complexes a 20S core and a 19S regulator PSMD8 is a non ATPase subunit of the 19S regulator T
- SH3BGRL belongs to the SH3BGR family Mutations in predicted EVH1 binding domain of SH3BGRL had a modest effect on suppression of v Rel transformation
- STK16 is a protein kinase that acts on both serine and threonine residues
- SELENBP1 belongs to the selenium binding protein family Selenium is an essential nutrient that exhibits potent anticarcinogenic properties and deficiency of selenium may cause certain neurologic dis
- DRG1 belongs to the GTP1 OBG family It may play a role in cell proliferation differentiation and death
- SEP15 is a selenoprotein which contains a selenocysteine Sec residue at its active site Studies in mouse suggest that this selenoprotein may have redox function and may be involved in the quality
- The exact function of C1orf63 remains unknown
- THOC6 belongs to the WD repeat THOC6 family It contains 7 WD repeats The function of the THOC6 protein remains unknown
- FKSG24 is a multi pass membrane proteinPotential It belongs to the peroxisomal membrane protein PXMP2 4 family The exact function of FKSG24 remains unknown
- NUDCD1 CML66 contains 1 CS domain It may play an oncogenic role in ways of favoring tumor cells proliferation invasion and metastasis associated with multiple pathways
- EPSTI1 was up regulated in breast carcinomas The exact function of EPSTI1 is not known
- WDR34 is a member of the WD repeat protein family WD repeats are minimally conserved regions of approximately 40 amino acids typically bracketed by gly his and trp asp GH WD which may facilitate f
- Microsomal long and very long chain fatty acid elongation uses malonyl CoA as the 2 carbon donor and consists of 4 sequential reactions GPSN2 catalyzes the final step reducing trans 2 3 enoyl CoA to
- ADSSL1 is a muscle isozyme of adenylosuccinate synthase EC 6 3 4 4 which catalyzes the initial reaction in the conversion of inosine monophosphate IMP to adenosine monophosphate AMP
- KLHDC8B contains 8 Kelch repeats The exact function of KLHDC8B remains unknown
- ATPIF1 is a mitochondrial ATPase inhibitor It is thought to be a regulatory component of the ATP synthesizing complex in the mitochondria This gene encodes a mitochondrial ATPase inhibitor Alternati
- The function of the C19orf47 protein remains unknown
- HPRT1 has a central role in the generation of purine nucleotides through the purine salvage pathway HPRT1 catalyzes conversion of hypoxanthine to inosine monophosphate and guanine to guanosine monoph
- Cytosolic and membrane bound forms of glutathione S transferase are encoded by two distinct supergene families At present eight distinct classes of the soluble cytoplasmic mammalian glutathione S tr
- Glutathione S transferase GST theta 1 GSTT1 is a member of a superfamily of proteins that catalyze the conjugation of reduced glutathione to a variety of electrophilic and hydrophobic compounds H
- HS3ST6 is a single pass type II membrane protein It belongs to the sulfotransferase 1 family It transfers a sulfuryl group to heparan sulfate The substrate specific O sulfation generates an enzyme
- NAT12 belongs to the acetyltransferase family MAK3 subfamily It contains 1 N acetyltransferase domain It is a probable N acetyltransferase
- TRMT11 belongs to the methyltransferase superfamily It is a catalytic subunit of an S adenosyl L methionine dependent tRNA methyltransferase complex that mediates the methylation of the guanosine nuc
- SULT6B1 belongs to the sulfotransferase 1 family SULT6B1 may catalyze the sulfate conjugation of many drugs xenobiotic compounds hormones and neurotransmitters
- GGPS1 is a member of the prenyltransferase family and has geranylgeranyl diphosphate GGPP synthase activity The enzyme catalyzes the synthesis of GGPP from farnesyl diphosphate and isopentenyl diph
- MBOAT1 shares structural similarity with a superfamily of membrane bound O acetyltransferases that transfer organic compounds usually fatty acids e g cholesterol diacylglycerol palmitoyl onto
- GATM is a mitochondrial enzyme that belongs to the amidinotransferase family This enzyme is involved in creatine biosynthesis whereby it catalyzes the transfer of a guanido group from L arginine to
- This enzyme condenses acetyl CoA with acetoacetyl CoA to form HMG CoA which is the substrate for HMG CoA reductase
- N alpha acetylation is one of the most common protein modifications that occurs during protein synthesis and involves the transfer of an acetyl group from acetyl coenzyme A to the protein alpha amino
- In the de novo synthesis of purine nucleotides IMP is the branch point metabolite at which point the pathway diverges to the synthesis of either guanine or adenine nucleotides In the guanine nucleot
- CpG methylation is an epigenetic modification that is important for embryonic development imprinting and X chromosome inactivation Studies in mice have demonstrated that DNA methylation is required
- MAP4K2 is a member of the serine threonine protein kinase family Although this kinase is found in many tissues its expression in lymphoid follicles is restricted to the cells of germinal centre whe
- RABGGTB catalyzes the transfer of a geranyl geranyl moiety from geranyl geranyl pyrophosphate to both cysteines in Rab proteins with an XXCC XCXC and CCXX C terminal such as RAB1A RAB3A and RAB5
- Sulfotransferase enzymes catalyze the sulfate conjugation of many hormones neurotransmitters drugs and xenobiotic compounds These cytosolic enzymes are different in their tissue distributions and
- SPTLC2 is a long chain base subunit of serine palmitoyltransferase Serine palmitoyltransferase which consists of two different subunits is the key enzyme in sphingolipid biosynthesis It catalyzes
- POLR2K is one of the smallest subunits of RNA polymerase II the polymerase responsible for synthesizing messenger RNA in eukaryotes This subunit is shared by the other two DNA directed RNA polymeras
- ST8SIA4 catalyzes the polycondensation of alpha 2 8 linked sialic acid required for the synthesis of polysialic acid a modulator of the adhesive properties of neural cell adhesion molecule NCAM1 S
- The glycine N acyltransferase protein conjugates glycine with acyl CoA substrates in the mitochondria The protein is thought to be important in the detoxification of endogenous and xenobiotic acyl Co
- PECI is an auxiliary enzyme that catalyzes an isomerization step required for the beta oxidation of unsaturated fatty acids PECI is an auxiliary enzyme that catalyzes an isomerization step required fo
- POLR3F is one of more than a dozen subunits forming eukaryotic RNA polymerase III RNA Pol III which transcribes 5S ribosomal RNA and tRNA genes This protein has been shown to bind both TFIIIB90 an
- SULT1C4 catalyzes the sulfate conjugation of many drugs xenobiotic compounds hormones and neurotransmitters It may be involved in the activation of carcinogenic hyroxylamines SULT1C4 shows activi
- N methylation of endogenous and xenobiotic compounds is a major method by which they are degraded This gene encodes an enzyme that N methylates indoles such as tryptamine N methylation of endogenous
- SDF2 is believed to be a secretory protein It has regions of similarity to hydrophilic segments of yeast mannosyltransferases Its expression is ubiquitous and the gene appears to be relatively conse
- ATE1 is an arginyltransferase an enzyme that is involved in posttranslational conjugation of arginine to N terminal aspartate or glutamate residues Conjugation of arginine to the N terminal aspartat
- QPCT is responsible for the biosynthesis of pyroglutamyl peptides QPCT has a bias against acidic and tryptophan residues adjacent to the N terminal glutaminyl residue and a lack of importance of chai
- The Aspergillus nidulans never in mitosis A NIMA gene encodes a serine threonine kinase that controls initiation of mitosis NIMA related kinases NEKs are a group of protein kinases that are hom
- LCMT2 belongs to the highly variable methyltransferase superfamily This gene is the inferred homolog of the Saccharomyces cerevisiae carboxymethyltransferase gene PPM2 that is essential for the synth
- POLR1D belongs to the archaeal rpoL eukaryotic RPB11 RPC19 RNA polymerase subunit family DNA dependent RNA polymerase catalyzes the transcription of DNA into RNA using the four ribonucleoside triphos
- POLK belongs to the DNA polymerase type Y family It contains 2 Rad18 type zinc fingers and 1 umuC domain POLK is a DNA polymerase specifically involved in DNA repair It plays an important role in t
- RSF1 HBXAP is involved in transcription repression transcription coactivation when associated with hepatitis B virus X protein HBX and chromatin remodeling and spacing when associated with SNF2H
- GALNT10 belongs to the polypeptide N acetylgalactosaminyltransferase pp GalNAc T family Polypeptide GalNAc transferases initiate the synthesis of mucin type oligosaccharides by transferring GalNAc
- Maturation of cytoplasmic tRNAs includes splicing of introns which are located 1 nucleotide 3 prime from the anticodon in all intron containing tRNA genes In tRNA leu CAA the first position of th
- ECHDC2 belongs to the enoyl CoA hydratase isomerase family The exact function of ECHDC2 remains unknown
- PHF10 is a protein with two zinc finger domains The function of the PHF10 protein is not known This gene contains a predicted ORF that encodes a protein with two zinc finger domains The function of
- ECHDC1 belongs to the enoyl CoA hydratase isomerase family The exact function of ECHDC1 remains unknown
- PBK is a serine threonine kinase related to the dual specific mitogen activated protein kinase kinase MAPKK family Evidence suggests that mitotic phosphorylation is required for its catalytic activ
- CMAS is an enzyme that catalyzes the activation of Neu5Ac to Cytidine 5 prime monophosphate N acetylneuraminic acid CMP Neu5Ac which provides the substrate required for the addition of sialic acid
- UGCGL2 recognizes glycoproteins with minor folding defects UGCGL2 reglucosylates single N glycans near the misfolded part of the protein thus providing quality control for protein folding in the end
- tRNAs contain as many as 13 or 14 nucleotides that are modified posttranscriptionally by enzymes that are highly specific for particular nucleotides in the tRNA structure TRMT5 methylates the N1 posi
- CHST6 catalyzes the transfer of sulfate to position 6 of non reducing N acetylglucosamine GlcNAc residues of keratan It mediates sulfation of keratan in cornea Keratan sulfate plays a central role
- QTRTD1 belongs to the queuine tRNA ribosyltransferase family The function of the QTRTD1 protein remains unknown
- NUDT18 belongs to the Nudix hydrolase family It contains 1 nudix hydrolase domain NUDT18 probably mediates the hydrolysis of some nucleoside diphosphate derivatives
- Dehydrodolichyl diphosphate dedol PP synthase catalyzes cis prenyl chain elongation to produce the polyprenyl backbone of dolichol a glycosyl carrier lipid required for the biosynthesis of several
- TRMT2B CXorf34 is probable S adenosyl L methionine dependent methlytransferase that catalyzes the formation of 5 methyl uridine at position 54 M 5 U54 in all tRNA And it may also have a role in t
- THUMPD2 belongs to the methyltransferase superfamily It contains 1 THUMP domain The function of the THUMPD2 protein remains unknown
- B3GNT4 is a member of the beta 1 3 N acetylglucosaminyltransferase protein family The protein is involved in the biosynthesis of poly N acetyllactosamine chains and prefers lacto N neotetraose as a s

- tRNA guanine transglycosylase TGT EC 2 4 2 29 synthesizes queuosine Q which is found in tRNAs that recognize NAU and NAC codons encoding tyr asn asp and his Prokaryotic TGT is a single prot
- PWWP2A contains 1 PWWP domain The exact function of PWWP2A remains unknown
- GPT and GPT2 EC 2 6 1 2 also known as alanine transaminases are pyridoxal enzymes that catalyze the reversible transamination between alanine and 2 oxoglutarate to form pyruvate and glutamate By
- NIMA related kinases share high amino acid sequence identity with the gene product of the Aspergillus nidulans never in mitosis A gene which controls initiation of mitosis NIMA related kinases shar
- Human patatin like phospholipases such as PNPLA5 have been implicated in regulation of adipocyte differentiation and have been induced by metabolic stimuli Human patatin like phospholipases such as
- TTC16 contains 8 TPR repeats The exact function of TTC16 remains unknown
- GLYATL2 belongs to the glycine N acyltransferase family GLYATL2 is a mitochondrial acyltransferase which transfers the acyl group to the N terminus of glycine It can conjugate a multitude of substra
- B3GNT7 belongs to the glycosyltransferase 31 family It may be involved in keratane sulfate biosynthesis B3GNT7 transfers N acetylgalactosamine on to keratan sulfate related glycans It may play a ro
- B3GALNT2 is the beta 1 3 N acetylgalactosaminyltransferase active in synthesizing a unique carbohydrate structure GalNAc beta 1 3GlcNAc on N and O glycans B3GALNT2 has no galactose nor galactosami
- METT5D1 belongs to the methyltransferase superfamily mraW family METT5D1 is a probable S adenosyl L methionine dependent methyltransferase
- NEK3 is a member of the NimA never in mitosis A family of serine threonine protein kinases It differs from other NimA family members in that it is not cell cycle regulated and is found primarily in
- CHST13 catalyzes the transfer of sulfate to position 4 of the N acetylgalactosamine GalNAc residue of chondroitin Chondroitin sulfate constitutes the predominant proteoglycan present in cartilage a
- Heparan sulfate HS sulfotransferases such as HS6ST3 modify HS to generate structures required for interactions between HS and a variety of proteins These interactions are implicated in proliferat
- B4GALNT3 transfers N acetylgalactosamine GalNAc onto glucosyl residues to form N N prime diacetyllactosediamine LacdiNAc or LDN a unique terminal structure of cell surface N glycans It mediates
- UDP glucuronosyltransferases catalyze phase II biotransformation reactions in which lipophilic substrates are conjugated with glucuronic acid to increase water solubility and enhance excretion They a
- TMTC1 is a multi pass membrane protein It belongs to the TMTC family and contains 10 TPR repeats The exact function of TMTC1 remains unknown
- GGTL3 is an enzymes involved in both the metabolism of glutathione and in the transpeptidation of amino acids Changes in the activity of gamma glutamyltransferase may signal preneoplastic or toxic co
- GLT6D1 is a single pass type II membrane protein It belongs to the glycosyltransferase 6 family The exact function of GLT6D1 remains unknown
- The omega class glutathione transferases GST EC 2 5 1 18 have poor activity with common GST substrates but exhibit novel glutathione dependent thioltransferase dehydroascorbate reductase and mon
- GALNTL4 may catalyze the initial reaction in O linked oligosaccharide biosynthesis the transfer of an N acetyl D galactosamine residue to a serine or threonine residue on the protein receptor
- TGM5 belongs to the transglutaminase superfamily transglutaminase family It catalyzes the cross linking of proteins and the conjugation of polyamines to proteins It contributes to the formation of
- GMPPA is a GDP mannose pyrophosphorylase This enzyme catalyzes the reaction which converts mannose 1 phosphate and GTP to GDP mannose which is involved in the production of N linked oligosaccharides
- LOC399818 belongs to the methyltransferase superfamily
- The exact function of LOC641515 remains unknown
- The exact function of C6orf140 remains unknown
- The exact function of C9orf46 remains unknown
- Heparan sulfate proteoglycans HSPGs act as coreceptors for numerous heparin binding growth factors and cytokines and are involved in cell signaling Heparan sulfate 6 O endosulfatases such as SULF2
- PCDHAC2 is a potential calcium dependent cell adhesion protein It may be involved in the establishment and maintenance of specific neuronal connections in the brain This gene is a member of the proto
- PCDHA12 is a potential calcium dependent cell adhesion protein PCDHA12 may be involved in the establishment and maintenance of specific neuronal connections in the brain This gene is a member of the
- The gene encoding PCDHA5 is a member of the protocadherin alpha gene cluster one of three related gene clusters tandemly linked on chromosome five that demonstrate an unusual genomic organization sim
- PCDHGA4 is a single pass type I membrane protein It contains 6 cadherin domains PCDHGA4 is a potential calcium dependent cell adhesion protein It may be involved in the establishment and maintenanc
- PCDHGB1 is a single pass type I membrane protein It contains 6 cadherin domains PCDHGB1 is a potential calcium dependent cell adhesion protein It may be involved in the establishment and maintenanc
- PCDHGC4 is a single pass type I membrane protein It contains 6 cadherin domains PCDHGC4 is a potential calcium dependent cell adhesion protein It may be involved in the establishment and maintenance
- CLN8 is a transmembrane protein belonging to a family of proteins containing TLC domains which are postulated to function in lipid synthesis transport or sensing The protein localizes to the endop
- HLA F belongs to the HLA class I heavy chain paralogues It is a non classical heavy chain that forms a heterodimer with a beta 2 microglobulin light chain with the heavy chain anchored in the membra
- YIPF1 is a multi pass membrane protein It belongs to the YIP1 family The exact function of YIPF1 remains unknown
- FAM105A belongs to the FAM105 family The exact function of FAM105A remains unknown
- ALG1 catalyzes the first mannosylation step in the biosynthesis of lipid linked oligosaccharides Defects in ALG1 are the cause of congenital disorder of glycosylation type 1K CDG1K The biosynthesis
- LRRC8A is a protein belonging to the leucine rich repeat family of proteins which are involved in diverse biological processes including cell adhesion cellular trafficking and hormone receptor int
- MDM1 is a nuclear protein similar to the mouse double minute 1 protein The mouse gene is located in double minute DM chromatin particles and is amplified in the mouse transformed 3T3 cell line and
- The exact function of C15orf24 remains unknown
- CNNM4 belongs to the ACDP family It is a metal transporter The interaction with the metal ion chaperone COX11 suggests that CNNM4 may play a role in sensory neuron functions
- The exact function of C2orf33 remains unknown
- SEMA4B is a single pass type I membrane protein It belongs to the semaphorin family SEMA4B contains 1 Ig like C2 type immunoglobulin like domain 1 PSI domain and 1 Sema domain It inhibits axonal
- FAM20C belongs to the FAM20 family FAM20C is a calcium binding protein which may play a role in dentin mineralization Mutations in FAM20C are associated with lethal osteosclerotic bone dysplasia Ra
- ENTPD7 is a multi pass membrane protein It belongs to the GDA1 CD39 NTPase family It preferentially hydrolyzes nucleoside 5 triphosphates The order of activity with respect to possible substrates i
- DOLPP1 is a multi pass membrane proteinBy similarity It belongs to the dolichyldiphosphatase family It is required for efficient N glycosylation and is necessary for maintaining optimal levels of do
- ATP10D is a multi pass membrane protein It belongs to the cation transport ATPase P type family type IV subfamily The exact function of ATP10D remains unknown
- IL22 belongs to the IL 10 family It is a cytokine that contributes to the inflammatory response in vivo
- The exact function of C20orf3 remains unknown
- Junctional complexes between the plasma membrane and endoplasmic sarcoplasmic reticulum are a common feature of all excitable cell types and mediate cross talk between cell surface and intracellular i
- GALNTL1 belongs to the glycosyltransferase 2 family GalNAc T subfamily It contains 1 ricin B type lectin domain GALNTL1 may catalyze the initial reaction in O linked oligosaccharide biosynthesis t
- NLGN4X is a member of a family of neuronal cell surface proteins Members of this family may act as splice site specific ligands for beta neurexins and may be involved in the formation and remodeling
- KIAA1324 belongs to the UPF0577 family It may play a role as a marker of hyperestrogenic state and estrogen related type I endometrial carcinoma
- TXNDC16 contains 1 thioredoxin domain The exact function of TXNDC16 remains unknown
- IGSF9 belongs to the immunoglobulin superfamily turtle family It contains 2 fibronectin type III domains and 5 Ig like immunoglobulin like domains It functions in dendrite outgrowth and synapse m
- ISLR2 is a single pass membrane protein It contains 1 Ig like immunoglobulin like domain and 5 LRR leucine rich repeats The exact function of ISLR2 remains unknown
- Semaphorins are a large family including both secreted and membrane associated proteins many of which have been implicated as inhibitors or chemorepellents in axon pathfinding fasciculation and bra
- CACHD1 belongs to the calcium channel subunit alpha 2 delta family It contains 2 cache domains and 1 VWFA domain CACHD1 may regulate voltage dependent calcium channels
- NGL1 LRRC4C is a specific binding partner for netrin G1 NTNG1 which is a member of the netrin family of axon guidance molecules It may promote neurite outgrowth of developing thalamic neurons NG
- SCUBE2 contains 1 CUB domain and 9 EGF like domains The function of the SCUBE2 protein remains unknown
- B3GALT1 is a member of the beta 1 3 galactosyltransferase beta3GalT family This family are type II membrane bound glycoproteins with diverse enzymatic functions using different donor substrates UD
- HAI 2 SPINT2 is a candidate tumour suppressor gene that is frequently hypermethylated and underexpressed in human HCCs and the KD 1 domain of HAI 2 is the key region responsible for its anti invasi
- Reticulons are associated with the endoplasmic reticulum and are involved in neuroendocrine secretion or in membrane trafficking in neuroendocrine cells This gene belongs to the family of reticulon e
- TXNDC13 is a single pass type I membrane protein It contains 1 thioredoxin domain The exact function of TXNDC13 remains unknown
- A cluster of genes BAT1 BAT5 has been localized in the vicinity of the genes for TNF alpha and TNF beta These genes are all within the human major histocompatibility complex class III region BAT5
- SRPRB has similarity to mouse protein which is a subunit of the signal recognition particle receptor SR This subunit is a transmembrane GTPase belonging to the GTPase superfamily It anchors alpha
- TMEM35 is a multi pass membrane protein The exact function of TMEM35 remains unknown
- SIGIRR acts as a negative regulator of the Toll like and IL 1R receptor signaling pathways It attenuates the recruitment of receptor proximal signaling components to the TLR4 receptor probably throu
- ELOVL5 plays a role in elongation of long chain polyunsaturated fatty acids ELOVL5 plays a role in elongation of long chain polyunsaturated fatty acids Leonard et al 2000 PubMed 10970790
- FAM38B is a multi pass membrane proteinPotential It belongs to the FAM38 family The exact function of FAM38B remains unknown
- TNMD is a single pass type II membrane proteinPotential It belongs to the chondromodulin 1 family and contains 1 BRICHOS domain TNMD may be an angiogenesis inhibitor
- XYLT2 is an isoform of xylosyltransferase which belongs to a family of glycosyltransferases This enzyme transfers xylose from UDP xylose to specific serine residues of the core protein and initiates
- EDAR is a member of the tumor necrosis factor receptor family It is a receptor for the soluble ligand ectodysplasin A and can activate the nuclear factor kappaB JNK and caspase independent cell de
- POPDC3 is a member of the POP family of proteins containing three putative transmembrane domains The protein is expressed in cardiac and skeletal muscle and may play an important role in these tissue
- DNAJC1 contains 1 J domain and 2 SANT domains The exact function of DNAJC1 remains unknown
- STRA6 may act as a high affinity cell surface receptor for the complex retinol retinol binding protein RBP RBP4 STRA6 acts by removing retinol from RBP RBP4 and transports it across the plasma memb
- ARL6IP2 is a multi pass membrane proteinPotential It belongs to the GBP family Atlastin GTPases are required for Golgi apparatus and ER morphogenesis
- RHBDF1 is a seven transmembrane protein with a long N terminal cytoplasmic extension that comprises half of the polypeptide sequence and is found in the endoplasmic reticulum and Golgi but not on th
- Cadherins are calcium dependent cell adhesion proteins They preferentially interact with themselves in a homophilic manner in connecting cells cadherins may thus contribute to the sorting of heterog
- TMEM168 is a multi pass membrane protein It belongs to the TMEM168 family The exact function of TMEM168 remains unknown
- SFXN1 might be involved in the transport of a component

required for iron utilization into or out of the mitochondria

- The specific function of MPPE1 is not yet known
- GALNT14 EC 2 4 1 41 belongs to a large subfamily of glycosyltransferases residing in the Golgi apparatus GALNT enzymes catalyze the first step in the O glycosylation of mammalian proteins by transf
- TMEM149 is a single pass type I membrane protein The exact function of TMEM149 remains unknown
- The specific function of ACBD4 is not yet known
- ACBD4 is a member of the acyl coenzyme A binding domain containing protein family All family members contain the conserved acyl Coenzyme A binding domain which binds acyl CoA thiol esters They are
- The exact function of C12orf49 remains unknown
- UGT2A3 is a single pass type I membrane proteinPotential It belongs to the UDP glycosyltransferase family UDP glucuronosyltransferases catalyze phase II biotransformation reactions in which lipophil
- NPAL2 is a multi pass membrane protein and it belongs to the NIPA family The exact function of NPAL2 remains unknown
- This protein mediates receptor activity
- Dietary fat absorption from the small intestine is facilitated by acyl CoA monoacylglycerol transferase MOGAT and acyl CoA diacylglycerol acyltransferase DGAT activities MOGAT catalyzes the joini
- The exact function of C10orf57 is not known
- ITFG1 belongs to the TIP family It contains 1 FG GAP repeat ITFG1 is a modulator of T cell function It has a protective effect in graft versus host disease model
- SFXN3 is a potential iron transporter
- TMEM16C is a multi pass membrane proteinPotential It belongs to the anoctamin family TMEM16C may act as a calcium activated chloride channel
- PCDHA3 is a single pass type I membrane protein It contains 6 cadherin domains PCDHA3 is a potential calcium dependent cell adhesion protein It may be involved in the establishment and maintenance
- FAM62C belongs to the extended synaptotagmin family It is a single pass membrane protein and contains 3 C2 domains FAM62C may play a role as calcium regulated intrinsic membrane protein
- TSPAN10 belongs to the tetraspanin TM4SF family It is a multi pass membrane protein The exact function of TSPAN10 remains unknown
- The exact function of FAM14A remains unknown
- KIRREL2 is a single pass type I membrane protein KIRREL2 protein is a beta cell expressed Ig domain protein and may be involved in pancreas development or beta cell function
- The exact function of FLJ23356 remains unknown
- TMEM117 is a multi pass membrane protein It belongs to the TMEM117 family The exact function of TMEM117 remains unknown
- SYT3 may be involved in Ca 2 dependent exocytosis of secretory vesicles through Ca 2 and phospholipid binding to the C2 domain or may serve as Ca 2 sensors in the process of vesicular traffic
- TMEM79 is a multi pass membrane protein The exact function of TMEM79 remains unknown
- PIGO is a protein that is involved in glycosylphosphatidylinositol GPI anchor biosynthesis The GPI anchor is a glycolipid which contains three mannose molecules in its core backbone The GPI anchor
- Receptors for the Fc fragment of IgG or FCGRs are cell surface glycoproteins of the Ig superfamily IgSF These receptors mediate phagocytosis of IgG coated pathogens and promote activation of effe
- Tight junctions represent one mode of cell to cell adhesion in epithelial or endothelial cell sheets forming continuous seals around cells and serving as a physical barrier to prevent solutes and wat
- ORAI2 is a multi pass membrane protein and it belongs to the Orai family It is a Ca 2 release activated Ca 2 like CRAC like channel subunit which mediates Ca 2 influx and increase in Ca
- DIRC2 is a membrane bound protein from the major facilitator superfamily of transporters Disruption of DIRC2 by translocation has been associated with haplo insufficiency and renal cell carcinomas A
- FIBCD1 is a single pass membrane protein It contains 1 fibrinogen C terminal domain The exact function of FIBCD1 remains unknown
- ABHD13 is a single pass type II membrane protein It belongs to the serine esterase family The exact function of ABHD13 remains unknown Western blots using two different antibodies against two unique
- GAL3ST3 is a member of the galactose 3 O sulfotransferase protein family It catalyzes sulfonation by transferring a sulfate group to the 3 position of galactose in N acetyllactosamine in both type 2
- SURF4 is a conserved integral membrane protein containing multiple putative transmembrane regions In eukaryotic cells protein transport between the endoplasmic reticulum and Golgi compartments is me
- LMF2 belongs to the lipase maturation factor family LMF2 is involved in the maturation of specific proteins in the endoplasmic reticulum It may be required for maturation and transport of active lip
- Potassium channels play a role in many cellular processes including maintenance of the action potential muscle contraction hormone secretion osmotic regulation and ion flow KCNK4 is one of the me
- PERLD1 is involved in the lipid remodeling steps of GPI anchor maturation Lipid remodeling steps consist in the generation of 2 saturated fatty chains at the sn 2 position of GPI anchors proteins It
- MMEL1 is a member of the neutral endopeptidase NEP or membrane metallo endopeptidase MME family Family members play important roles in pain perception arterial pressure regulation phosphate met
- The exact function of C6orf192 remains unknown This gene encodes a protein which has high sequence similarity to rat xenopus and zebrafish proteins The protein function is unknown
- N glycosylation of proteins follows a highly conserved pathway that begins with the synthesis of a
- The exact function of PIK3IP1 remains unknown
- ELFN2 is a single pass membrane protein It contains 1 fibronectin type III domain and 5 LRR leucine rich repeats The exact function of ELFN2 remains unknown
- TMEM132B single pass type I membrane protein It belongs to the TMEM132 family The exact function of TMEM132B is not known
- Members of the SLITRK family such as SLITRK1 are integral membrane proteins with 2 N terminal leucine rich repeat LRR domains similar to those of SLIT proteins Most SLITRKs but not SLITRK1 also
- The GALNT13 protein is a member of the UDP N acetyl alpha D galactosamine polypeptide N acetylgalactosaminyltransferase GalNAcT EC 2 4 1 41 family which initiate O linked glycosylation of mucins b
- SLAMF6 is a type I transmembrane protein belonging to the CD2 subfamily of the immunoglobulin superfamily SLAMF6 is expressed on Natural killer NK T and B lymphocytes It undergoes tyrosine phos
- TMEM123 is a highly glycosylated transmembrane protein with a high content of threonine and serine residues in its extracellular domain similar to a broadly defined category of proteins termed mucins
- Acyl CoA monoacylglycerol acyltransferase MOGAT EC 2 3 1 22 catalyzes the synthesis of diacylglycerols the precursor of physiologically important lipids such as triacylglycerol and phospholipids A
- AQP10 is a member of the aquaglyceroporin family of integral membrane proteins Members of this family function as water permeable channels in the epithelia of organs that absorb and excrete water AQ
- COX3 is a multi pass membrane protein It belongs to the cytochrome c oxidase subunit 3 family Defects in COX3 are a cause of Leber hereditary optic neuropathy LHON and cytochrome c oxidase deficie
- ND5 is the core subunit of the mitochondrial membrane respiratory chain NADH dehydrogenase Complex I that is believed to belong to the minimal assembly required for catalysis Complex I functions in
- The exact function of ND6 remains unknown
- CYTB belongs to the cytochrome b family It is a component of the ubiquinol cytochrome c reductase complex complex III or cytochrome b c1 complex which is a respiratory chain that generates an elec
- B3GALT6 Beta 1 3 galactosyltransferase transfers galactose from UDP galactose to substrates with a terminal beta linked galactose residue It has a preference for galactose beta 1 4 xylose that is f
- BRI3BP is involved in the structural dynamics of the ER and affects mitochondrial viability It is widely expressed in animal cell types that seems to possess a pro apoptotic property and can potentia
- The exact function of DPCR1 remains unknown
- ASB5 is a member of the
- COLEC12 is a member of the C lectin family
- LRRC15 may contribute to regulation of cell matrix adhesion interactions with respect to astrocyte recruitment around senile plaques in Alzheimer s disease brain LRRC15 is induced by EWS WT1 KTS i
- UNC5A belongs to a family of netrin 1 receptors thought to mediate the chemorepulsive effect of netrin 1 on specific axons For more information on UNC5 proteins see UNC5C UNC5A belongs to a family o
- EMID1 contains 1 collagen like domain and 1 EMI domain The exact function of EMID1 remains unknown
- SPOPL belongs to the Tdpoz family It contains 1 BTB POZ domain and 1 MATH domain In complex with a cullin SPOPL may act in ubiquitination and proteasomal degradation processes
- BC37295 3 ZNF835 belongs to the krueppel C2H2 type zinc finger protein family It contains 14 C2H2 type zinc fingers BC37295 3 may be involved in transcriptional regulation
- ZNF780B belongs to the krueppel C2H2 type zinc finger protein family It contains 23 C2H2 type zinc fingers and 1 KRAB domain ZNF780B may be involved in transcriptional regulation
- TCEAL8 is a member of the transcription elongation factor A SII like TCEAL gene family Members of this family contain TFA domains and may function as nuclear phosphoproteins that modulate transcr
- TCEAL4 is a member of the transcription elongation factor A SII like TCEAL gene family Members of this family contain TFA domains and may function as nuclear phosphoproteins that modulate transcr
- SPOP may modulate the transcriptional repression activities of death associated protein 6 DAXX which interacts with histone deacetylase core histones and other histone associated proteins In mou
- PHF19 contains 2 PHD type zinc fingers It acts as a transcritpional repressor Isoform 1 and isoform 2 inhibit transcription from an HSV tk promoter
- ZNF766 belongs to the krueppel C2H2 type zinc finger protein family It contains 10 C2H2 type zinc fingers and 1 KRAB domain ZNF766 may be involved in transcriptional regulation
- ZNF780A belongs to the krueppel C2H2 type zinc finger protein family It contains 17 C2H2 type zinc fingers and 1 KRAB domain ZNF780A may be involved in transcriptional regulation
- The exact function of PURG is not known however it is highly similar to purine rich element binding protein A The latter is a DNA binding protein which binds preferentially to the single strand of
- ARID3C is a member of the ARID AT rich interaction domain family of proteins The ARID domain is a helix turn helix motif based DNA binding domain ARID family members have roles in embryonic patter
- ZMYND17 contains 1 MYND type zinc finger The exact function of ZMYND17 remains unknown
- FEZF1 is a transcription repressor It is involved in the axonal projection and proper termination of olfactory sensory neurons OSN It plays a role in rostro caudal patterning of the diencephalon a
- DBX1 could have a role in patterning the central nervous system during embryogenesis DBX1 has a key role in regulating the distinct phenotypic features that distinguish two major classes of ventral i
- PHF12 acts as a transcriptional repressor It is involved in recruitment of functional SIN3A complexes to DNA PHF12 represses transcription at least in part through the activity of an associated hist
- ZNF284 belongs to the krueppel C2H2 type zinc finger protein family It contains 15 C2H2 type zinc fingers and 1 KRAB domain ZNF284 may be involved in transcriptional regulation
- The specific function of LOC728957 is not yet known
- The exact function of FLJ44894 remains unknown
- ZXDC belongs to the ZXD family It contains 10 C2H2 type zinc fingers ZXDC cooperates with CIITA to promote transcription of MHC class I and MHC class II genes
- ZFYVE19 contains 1 FYVE type zinc finger A chromosomal aberration translocation t 11 15 q23 q14 with MLL HRX involving ZFYVE19 is associated with acute myeloblastic leukemia AML
- ZNF433 belongs to the krueppel C2H2 type zinc finger protein family It contains 19 C2H2 type zinc fingers and 1 KRAB domain ZNF433 may be involved in transcriptional regulation
- The exact function of LOC643641 remains unknown
- The specific function of ZNF578 is not yet known
- FHL3 contains 4 LIM zinc binding domains It is expressed only in skeletal muscle FHL3 association with MyoD may contribute to the regulation of MyoD dependent transcription of muscle genes and there
- ZNHIT3 contains 1 HIT type zinc finger The exact function of ZNHIT3 remains unknown
- AIM2 is a member of the IFI20X IFI16 family It plays a putative role in tumorigenic reversion and may control cell proliferation Interferon gamma induces expression of AIM2 AIM2 is a member of the
- SPRY1 belongs to the sprouty family It contains 1 SPR sprouty domain SPRY1 may function as an antagonist of fibroblast growth factor FGF pathways and may negatively modulate respiratory organoge
- SMYD5 contains 1 MYND type zinc finger and 1 SET domain The exact function of SMYD5 remains unknown
- YAP1 is the human ortholog of chicken YAP protein which binds to the SH3 domain of the Yes proto oncogene product

YAP1 contains a WW domain that is found in various structural regulatory and signali

- PTTG2 belongs to the securin family The N terminal destruction box D box acts as a recognition signal for degradation via the ubiquitin proteasome pathway
- ZNF460 belongs to the krueppel C2H2 type zinc finger protein family It contains 11 C2H2 type zinc fingers and 1 KRAB domain ZNF460 may be involved in transcriptional regulation Zinc finger proteins
- CAND2 may play a role in the assembly of ubiquitin ligase complexes and modulate the ubiquitination of target proteins And it may be also a transcription regulator
- TMED4 contains 1 GOLD domain and belongs to the EMP24 GP25L family The function remains unknown
- LIMD1 may be involved in cell anchoring via focal adhesions and in the cell cycle particularly during mitosis LIMD1 functionally interacts with pRB and the loss of which promotes lung carcinogenesis
- SIN3B acts as a transcriptional repressor It interacts with MXI1 to repress MYC responsive genes and antagonize MYC oncogenic activities It also interacts with MAD MAX heterodimers by binding to MAD
- SIN3B acts as a transcriptional repressor It interacts with MXI1 to repress MYC responsive genes and antagonize MYC oncogenic activities Also it interacts with MAD MAX heterodimers by binding to MA
- ZZZ3 contains 1 HTH myb type DNA binding domain and 1 ZZ type zinc finger The exact function of ZZZ3 remains unknown
- BRPF3 contains 1 bromo domain 1 PHD type zinc finger and 1 PWWP domain The exact function of BRPF3 remains unknown
- PTOV1 belongs to the Mediator complex subunit 25 family PTOV1 subfamily It may activate transcription and is required for nuclear translocation of FLOT1 PTOV1 promotes cell proliferation
- ZNF708 belongs to the krueppel C2H2 type zinc finger protein family It contains 15 C2H2 type zinc fingers and 1 KRAB domain ZNF708 may be involved in transcriptional regulation
- SMYD3 is a member of an RNA polymerase complex Within the RNA polymerase complex it acts as a histone methyltransferase that plays a role in transcriptional regulation SMYD3 is a histone methyltrans
- ANKRA2 contains 3 ANK repeats It may facilitate endocytosis by linking megalin to components of the cytoskeleton or endocytic machinery
- SCRT2 belongs to the snail C2H2 type zinc finger protein family It contains 5 C2H2 type zinc fingers SCRT2 may be involved in transcriptional regulation
- ZNF418 belongs to the krueppel C2H2 type zinc finger protein family It contains 16 C2H2 type zinc fingers and 1 KRAB domain ZNF418 is a transcriptional repressor
- ZMYND19 is a MYND zinc finger domain containing protein that binds to the C terminus of melanin concentrating hormone receptor 1 MCHR1 MIM 601751 and to the N termini of alpha tubulin TUBA1 MIM
- ZNF700 belongs to the krueppel C2H2 type zinc finger protein family It contains 18 C2H2 type zinc fingers and 1 KRAB domain ZNF700 may be involved in transcriptional regulation
- MGC29891 GABPB2 contains 5 ANK repeats It may function as transcription factor capable of interacting with purine rich repeats GA repeats
- SRFBP1 may be involved in regulating transcriptional activation of cardiac genes during the aging process It may play a role in biosynthesis and or processing of SLC2A4 in adipose cells
- ZNF781 belongs to the krueppel C2H2 type zinc finger protein family It contains 4 C2H2 type zinc fingers ZNF781 may be involved in transcriptional regulation The protein encoded by this gene is a m
- DCP1B may play a role in the degradation of mRNAs both in normal mRNA turnover and in nonsense mediated mRNA decay It may remove the 7 methyl guanine cap structure from mRNA molecules yielding a 5
- HYAL1 is a lysosomal hyaluronidase Hyaluronidases intracellularly degrade hyaluronan one of the major glycosaminoglycans of the extracellular matrix Hyaluronan is thought to be involved in cell pro
- ZNF680 belongs to the krueppel C2H2 type zinc finger protein family It contains 12 C2H2 type zinc fingers and 1 KRAB domain ZNF680 may be involved in transcriptional regulation
- ASCL4 a basic helix loop helix transcription factor is essential for the determination of cell fate and the development and differentiation of numerous tissues It could be a transcriptional regulat
- Members of the ARID protein family including ARID5A have diverse functions but all appear to play important roles in development tissue specific gene expression and regulation of cell growth Membe
- The amino acid sequence of hCG 1646157 is derived from an annotated genomic sequence NT 024477 using gene prediction method GNOMON supported by mRNA and EST evidence The exact function of hCG 164
- The exact function of LOC391524 remains unknown
- The exact function of ZNF724P remains unknown
- The exact function of LOC732272 remains unknown
- The exact function of LOC344167 remains unknown
- The function of LOC391764 remains unknown
- The exact function of LOC388553 remains unknown
- The exact function of LOC116412 remains unknown
- MSL3L2 contains 1 chromo domain It may be involved in chromatin remodeling and transcriptional regulation
- The exact function of C6orf94 remains unknown
- CES7 belongs to the type B carboxylesterase lipase family It is involved in the detoxification of xenobiotics and in the activation of ester and amide prodrugs
- DCLRE1C is a nuclear protein that is involved in V D J recombination and DNA repair The protein has single strand specific 5 3 exonuclease activity it also exhibits endonuclease activity on 5 an
- Cytokine that binds to and signals through IL1RL1 ST2 and its stimulation recruits MYD88 IRAK1 IRAK4 and TRAF6 followed by phosphorylation of MAPK3 ERK1 and or MAPK1 ERK2 MAPK14 and MAPK8 IL33
- The function of the PRR11 protein remains unknown
- LCN6 may play a role in male fertility
- There are 2 forms of glucose 6 phosphate dehydrogenase G form is X linked and H form is autosomally linked This H form shows activity with other hexose 6 phosphates especially galactose 6 phosphate
- The function of the C2orf60 protein remains unknown
- PHF13 contains 1 PHD type zinc finger The function of the PHF13 protein remains unknown
- PHF23 contains 1 PHD type zinc finger It belongs to the PHF23 family A chromosomal aberration involving PHF23 translocation t 11 17 p15 p13 with NUP98 is found in a patient with acute myeloid
- PHF6 is a member of the plant homeodomain PHD like finger PHF family PHF6 is a protein with two PHD type zinc finger domains indicating a potential role in transcriptional regulation that local
- PYGO2 is involved in signal transduction through the Wnt pathway
- SETD3 contains 1 SET domain The function of the SETD3 protein remains unknown
- Transcription factor TFIID is one of the general factors required for accurate and regulated initiation by RNA polymerase II TFIID is a multimeric protein complex that plays a central role in mediati
- Cytoplasmic dyneins are large enzyme complexes with a molecular mass of about 1 200 kD They contain two force producing heads formed primarily from dynein heavy chains and stalks linking the heads t
- The exact function of C10orf33 remains unknown
- Troponin T is the tropomyosin binding subunit of troponin the thin filament regulatory complex which confers calcium sensitivity to striated muscle actomyosin ATPase activity
- P2RY12 belongs to the family of G protein coupled receptors This family has several receptor subtypes with different pharmacological selectivity which overlaps in some cases for various adenosine a
- Heterotrimeric G proteins transduce extracellular signals received by cell surface receptors into integrated cellular responses GPSM2 belongs to a group of proteins that modulate activation of G prot
- MGP is associates with the organic matrix of bone and cartilage MGP is thought to act as an inhibitor of bone formation
- CDC45L was identified by its strong similarity with Saccharomyces cerevisiae Cdc45 an essential protein required to the initiation of DNA replication Cdc45 is a member of the highly conserved multip
- The sperm specific protein Izumo named for a Japanese shrine dedicated to marriage is essential for sperm egg plasma membrane binding and fusion The sperm specific protein Izumo named for a Japanes
- This protein is a member of the 2 5A synthetase family essential proteins involved in the innate immune response to viral infection The encoded protein is induced by interferons and uses adenosine t
- The GTPBP1 gene is upregulated by interferon gamma and the protein is a member of the AGP11 GTPBP1 family of GTP binding proteins A structurally similar protein has been found in mouse where disrupt
- SERTAD2 acts at E2F responsive promoters to integrate signals provided by PHD and or bromodomain containing transcription factors
- KLHDC5 contains 1 BTB POZ domain and 6 Kelch repeats It is phosphorylated upon DNA damage probably by ATM or ATR The exact functions of KLHDC5 remain unknown
- INTS4 is a subunit of the Integrator complex which associates with the C terminal domain of RNA polymerase II large subunit POLR2A and mediates 3 prime end processing of small nuclear RNAs U1 RNU1
- TP53I13 may act as a tumor suppressor TP53I13 inhibits tumor cell growth when overexpressed
- FUBP3 may interact with single stranded DNA from the far upstream element FUSE FUBP3 may activate gene expression
- ADA is an enzyme that catalyzes the hydrolysis of adenosine to inosine Various mutations have been described for this gene and have been linked to human diseases Deficiency in this enzyme causes a f
- 4 aminobutyrate aminotransferase ABAT is responsible for catabolism of gamma aminobutyric acid GABA an important mostly inhibitory neurotransmitter in the central nervous system into succinic s
- CYP27A1 is a member of the cytochrome P450 superfamily of enzymes The cytochrome P450 proteins are monooxygenases which catalyze many reactions involved in drug metabolism and synthesis of cholestero
- Deoxycytidine kinase DCK is required for the phosphorylation of several deoxyribonucleosides and their nucleoside analogs Deficiency of DCK is associated with resistance to antiviral and anticancer
- The Escherichia coli AlkB protein protects against the cytotoxicity of methylating agents by repair of the specific DNA lesions generated in single stranded DNA ALKBH2 and ALKBH3 MIM 610603 are E
- MTX2 is highly similar to the metaxin 2 protein from mouse which has been shown to interact with the mitochondrial membrane protein metaxin 1 Because of this similarity it is thought that the encod
- The exact function of C18orf25 remains unknown
- The specific function of LOC201725 is not yet known
- PM20D2 belongs to the peptidase M20A family The function of PM20D2 remains unknown
- The exact function of FAM78B remains unknown
- GPHN is a neuronal assembly protein that anchors inhibitory neurotransmitter receptors to the postsynaptic cytoskeleton via high affinity binding to a receptor subunit domain and tubulin dimers In no
- CHCHD4 a component of human mitochondria belongs to a protein family whose members share 6 highly conserved cysteine residues constituting a CXC CX 9 C CX 9 C motif in the C terminus CHCHD4 a c
- CYP11A1 is a member of the cytochrome P450 superfamily of enzymes The cytochrome P450 proteins are monooxygenases which catalyze many reactions involved in drug metabolism and synthesis of cholestero
- Carboxypeptidase N is a plasma metallo protease that cleaves basic amino acids from the C terminal of peptides and proteins The enzyme is important in the regulation of peptides like kinins and anaph
- DPH2 gene is one of two human genes similar to the yeast gene dph2 The yeast gene was identified by its ability to complement a diphthamide mutant strain and thus probably functions in diphthamide b
- Casein kinase II is a serine threonine protein kinase that phosphorylates acidic proteins such as casein The kinase exists as a tetramer and is composed of an alpha an alpha prime and two beta subu
- Elastases form a subfamily of serine proteases that hydrolyze many proteins in addition to elastin Humans have six structurally similar proteins elastase 1 2 2A 2B 3A and 3B Unlike other elasta
- The aldehyde dehydrogenases are a family of isozymes that may play a major role in the detoxification of aldehydes generated by alcohol metabolism and lipid peroxidation ALDH3B1 is highly expressed i
- CTTN is overexpressed in breast cancer and squamous cell carcinomas of the head and neck CTTN is localized in the cytoplasm and in areas of the cell substratum contacts It has two roles 1 regulat
- Protein disulfide isomerases such as PDIA6 are endoplasmic reticulum ER resident proteins that catalyze formation reduction and isomerization of disulfide bonds in proteins and are thought to pl
- NET1 acts as guanine nucleotide exchange factor GEF for RhoA GTPase It may be involved in activation of the SAPK JNK pathway
- HAX1 is known to associate with hematopoietic cell specific Lyn substrate 1 a substrate of Src family tyrosine kinases It also interacts with the product of the polycystic kidney disease 2 gene mut
- ANP32B is a multifunctional protein working as a cell cycle progression factor as well as a cell survival factor ANP32B is required for the progression from the G1 to the S phase ANP32B is an anti a
- The exact function of MTHFS remains unknown
- The specific function of RASL10A is not yet known
- AP3M2 is part of the AP 3 complex an adaptor related complex which is not clathrin associated The complex is

associated with the Golgi region as well as more peripheral structures It facilitates th
- RAB40B has similarity to a yeast protein which suggests a role of the gene product in regulating secretory vesicles The protein encoded by this gene has similarity to a yeast protein which suggests a
- EXOC3 is a component of the exocyst complex a multiple protein complex essential for targeting exocytic vesicles to specific docking sites on the plasma membrane Though best characterized in yeast
- GABARAPL2 belongs to the MAP1 LC3 family It modulates intra Golgi transport through coupling between NSF activity and SNAREs activation The protein first stimulates the ATPase activity of NSF which
- SPON2 is a cell adhesion protein that promote adhesion and outgrowth of hippocampal embryonic neurons Binds directly to bacteria and their components and functions as an opsonin for macrophage phagoc
- PFDN6 binds specifically to cytosolic chaperonin c CPN and transfers target proteins to it PFDN6 binds to nascent polypeptide chain and promotes folding in an environment in which there are many co
- Adducins are heteromeric proteins composed of different subunits referred to as adducin alpha beta and gamma The three subunits are encoded by distinct genes and belong to a family of membrane skele
- KRT24 is a member of the type I acidic keratin family which belongs to the superfamily of intermediate filament IF proteins Keratins are heteropolymeric structural proteins which form the interm
- CAPN10 is the calcium regulated non lysosomal thiol protease which catalyzes limited proteolysis of substrates involved in cytoskeletal remodeling and signal transduction Calpains are ubiquitous well
- ASB8 may be a substrate recognition component of a SCF like ECS Elongin Cullin SOCS box protein E3 ubiquitin protein ligase complex which mediates the ubiquitination and subsequent proteasomal degra
- MED8 is a protein that is one of more than 20 subunits of the mediator complex first identified in S cerevisiae that is required for activation of transcription MED8 also interacts with elongins B
- The specific function of KLHL32 is not yet known
- GLMN is a phosphorylated protein that is a member of a Skp1 Cullin F box like complex The protein is essential for normal development of the vasculature and mutations in this gene have been associate
- DNAJB6 is a member of the DNAJ protein family DNAJ family members are characterized by a highly conserved amino acid stretch called the J domain and function as one of the two major classes of mole
- The specific function of C20orf160 is not yet known
- NEU4 belongs to a family of glycohydrolytic enzymes which remove sialic acid residues from glycoproteins and glycolipids This gene belongs to a family of glycohydrolytic enzymes which remove sialic ac
- ASB12 is a member of the ankyrin repeat and SOCS box containing ASB family of proteins They contain ankyrin repeat sequence and a SOCS box domain The SOCS box serves to couple suppressor of cytoki
- ACOT12 contains 2 acyl coenzyme A hydrolase domains and 1 START domain It hydrolyzes acetyl CoA to acetate and CoA
- DYX1C1contains 1 CS domain and 3 TPR repeats A chromosomal aberration translocation t 2 15 q11 q21 involving DYX1C1 may be a cause of dyslexia
- The exact function of KIAA1958 remains unknown
- NUP35 is a member of the nucleoporin family The protein is localized to the nuclear rim and is part of the nuclear pore complex NPC All molecules entering or leaving the nucleus either diffuse thr
- The specific function of ACTRT1 is not yet known
- The specific function of JOSD2 is not yet known
- The exact function of FAM83F remains unknown
- The exact function of C6orf150 remains unknown
- The function of LOC116349 remains unknown
- ICA1L contains 1 AH domain The function of the ICA1L protein remains
- The exact function of C11orf74 remains unknown
- CANT1 belongs to the apyrase family It is a calcium dependent nucleotidase with a preference for UDP The order of activity with different substrates is UDP GDP UTP GTP The enzyme has very low
- ARL8A belongs to the small GTPase superfamily Arf family ARL8A m ay play a role in lysosomes motility Alternatively may play a role in chromosomes segregation
- GALM is an enzyme that catalyzes the epimerization of hexose sugars such as glucose and galactose It is expressed in the cytoplasm and has a preference for galactose The protein may be required for
- DPPA2 may play a role in maintaining cell pluripotentiality ECSA DPPA2 is a promising target for antigen specific immunotherapy in non small cell lung cancers
- The specific function of RDHE2 is not yet known RDHE2 belongs to a family of short chain alcohol dehydrogenases reductases that catalyze the first and rate limiting step that generates retinaldehyde f
- The exact function of ALS2CR12 remains unknown
- The exact function of C16orf71 remains unknown
- LRRC28 contains 11 LRR leucine rich repeats The function of the LRRC28 protein is not known
- The exact function of C16orf78 remains unknown
- Septins such as SEPT12 are conserved GTP binding proteins that function as dynamic regulatable scaffolds for the recruitment of other proteins They are involved in membrane dynamics vesicle traff
- The exact function of CYB5D2 remains unknown
- PPM1M belongs to the PP2C family It contains 1 PP2C like domain The exact function of PPM1M is not known
- ADHFE1 is hydroxyacid oxoacid transhydrogenase which is responsible for the oxidation of 4 hydroxybutyrate in mammalian tissues The ADHFE1 gene encodes hydroxyacid oxoacid transhydrogenase EC 1 1 99
- LETM2 contains 1 LETM1 domain The function of the LETM1 protein remains unknown
- FAM76B belongs to the FAM76 family The function of the FAM76B protein remains unknown
- WDR66 contains 9 WD repeats The functions of WDR66 remain unknown
- AIFM3 induces apoptosis through a caspase dependent pathway AIFM3 reduces mitochondrial membrane potential
- TEKT4 belongs to the tektin family TEKT4 is a structural component of ciliary and flagellar microtubules It forms filamentous polymers in the walls of ciliary and flagellar microtubules
- FAM82A belongs to the FAM82 RMD family It is a single pass membrane protein The function of the FAM82A protein remains unknown
- The specific function of CCDC52 is not yet known
- RP13 102H20 1 is the GTPase activator for the Rho type GTPases by converting them to an inactive GDP bound state
- DENND1B contains 1 dDENN domain 1 DENN domain and 1 uDENN domain The function of the DENND1B protein remains unknown
- The function of the CCDC138 protein remains unknown
- SLFNL1 belongs to the Schlafen family The function of the SLFNL1 protein remains unknown
- ARL13B has an evolutionarily conserved role mediating cilia function in multiple organs N and C domains of ARL13B cooperatively regulate its ciliary localization and that N domain dependent self asso
- STK32A belongs to the protein kinase superfamily Ser Thr protein kinase family It contains 1 protein kinase domain The function of the STK32A protein remains unknown
- CDC42 a small Rho GTPase regulates the formation of F actin containing structures through its interaction with the downstream effector proteins The protein encoded by this gene is a member of the B
- DIRAS1 belongs to a distinct branch of the functionally diverse Ras superfamily of monomeric GTPases DIRAS1 belongs to a distinct branch of the functionally diverse Ras see HRAS MIM 190020 superfam
- FAM84A belongs to the FAM84 family Up regulation of FAM84A may play a critical role in progression of colon cancer
- VTI1A is a V SNARE that mediates vesicle transport pathways through interactions with t SNAREs on the target membrane These interactions are proposed to mediate aspects of the specificity of vesicle
- SPATA5 may be involved in morphological and functional mitochondrial transformations during spermatogenesis
- DDIT4L inhibits cell growth by regulating the FRAP1 pathway upstream of the TSC1 TSC2 complex and downstream of AKT1
- RNASE11 belongs to the pancreatic ribonuclease family The function of RNASE11 remains unknown
- Mammalian mitochondrial ribosomal proteins are encoded by nuclear genes and help in protein synthesis within the mitochondrion Mitochondrial ribosomes mitoribosomes consist of a small 28S subunit a
- LRRC25 is a single pass type I membrane protein It contains 2 LRR leucine rich repeats LRRC25 may be involved in the activation of cells of innate and acquired immunity
- FAM119A is a multi pass membrane protein It belongs to the FAM119 family The function of the FAM119A protein remains unknown
- The exact function of ANKRD9 remains unknown
- The specific function of TC2N is not yet known
- The exact function of C15orf27 remains unknown
- The exact function of C16orf46 remains unknown
- SPATA2L belongs to the SPATA2 family The exact function of SPATA2L is not known
- LSM12 belongs to the LSM12 family The exact function of LSM12 is not known
- The exact function of ANKRD13B remains unknown
- The exact function of C17orf57 remains unknown
- KRT222P belongs to the intermediate filament family The exact function of KRT222P is not known
- TNFAIP8L1 belongs to the TNFAIP8 family The exact function of TNFAIP8L is not known
- BBS5 is a protein that has been directly linked to Bardet Biedl syndrome The primary features of this syndrome include retinal dystrophy obesity polydactyly renal abnormalities and learning disabi
- The exact function of IQCF1 is not known
- The exact function of OCIAD2 is not known
- TRAM1L1 is stimulatory or required for the translocation of secretory proteins across the ER membrane
- GRPEL2 is an essential component of the PAM complex a complex required for the translocation of transit peptide containing proteins from the inner membrane into the mitochondrial matrix in an ATP dep
- VPS37A is a component of the ESCRT I complex a regulator of vesicular trafficking process Required for the sorting of endocytic ubiquitinated cargos into multivesicular bodies VPS37A may be involve
- RDH12 is an NADPH dependent retinal reductase whose highest activity is toward 9 cis and all trans retinol RDH12 also plays a role in the metabolism of short chain aldehydes but does not exhibit ster
- ZADH1 is an enzyme involved in the metabolism of prostaglandins ZADH1 catalyzes the NADPH dependent conversion of 15 keto prostaglandin E2 to 15 keto 13 14 dihydro prostaglandin E2 ZADH1 may also be
- The specific function of LRFN5 is not yet known
- The specific function of LYSMD4 is not yet known
- EME1 and MUS81 MIM 606591 form an endonuclease complex that cleaves branched DNA structures especially those arising during stalled DNA replication EME1 and MUS81 MIM 606591 form an endonuclease
- The specific function of C1orf74 is not yet known
- The specific function of ENTHD1 is not yet known
- The specific function of CCNYL1 is not yet known
- The specific function of BTNL9 is not yet known
- The specific function of FAM81B is not yet known
- The specific function of C11orf65 is not yet known
- The exact functions of FSIP1 remain unknown
- The specific function of C1orf177 is not yet known
- The specific function of C1orf65 is not yet known
- SGMS2 is a bidirectional lipid cholinephosphotransferase capable of converting phosphatidylcholine PC and ceramide to sphingomyelin SM and diacylglycerol DAG and vice versa Direction is depende
- The specific function of FAM46D is not yet known
- The specific function of FAM76A is not yet known
- 3 hydroxyisobutyrate dehydrogenase 3 hydroxy 2 methylpropanoate NAD oxidoreductase EC 1 1 1 31 is a dimeric mitochondrial enzyme that catalyzes the NAD dependent reversible oxidation of 3
- The specific function of SASP is not yet known
- The specific function of PDIK1L is not yet known
- The specific function of NKAIN4 is not yet known
- The specific function of C5orf33 is not yet known
- TMEM74 plays an essential role in autophagy TMEM74 induced autophagy may involve PI3K signal transduction
- RPESP belongs to the thrombospondin family It contains 1 SMB somatomedin B domain and 1 TSP type 1 domain The exact function of RPESP remains unknown
- FBXO39 is a substrate recognition component of the SCF SKP1 CUL1 F box protein type E3 ubiquitin ligase complex Members of the F box protein family such as FBXO39 are characterized by an approxima
- The exact functions of ATXN7L2 remain unknown
- ENPP6 is a choline specific glycerophosphodiester phosphodiesterase ENPP6 hydrolyzes the classical substrate for phospholipase C p nitrophenyl phosphorylcholine while it does not hydrolyze the clas
- The exact functions of TMEM161B remain unknown
- The exact functions of MGC42105 remain unknown
- The exact functions of C5orf35 remain unknown
- The exact functions of CREG2 remain unknown
- DCAL1 is a type II transmembrane C type lectin like protein expressed on dendritic cells DCs and B cells It interacts with subsets of T cells as a costimulatory molecule that enhances interleukin
- RDH10 is a retinol dehydrogenase with a clear preference for NADP RDH10 converts all trans retinol to all trans retinal RDH10 has no detectable activity towards 11 cis retinol 9 cis retinol and 13
- PLEKHH2 contains 1 FERM domain 1 MyTH4 domain and 2 PH domains It is a Single pass membrane protein The exact function of PLEKHH2 remains unknown
- The exact function of C19orf21 remains unknown
- PIP5KL1 may act as a scaffold to localize and regulate

type I PI 4 P 5 kinases to specific compartments within the cell where they generate PI 4 5 P2 for actin nucleation signaling and scaffold pr

- MPP7 acts as an important adapter that promotes epithelial cell polarity and tight junction formation via its interaction with DLG1 MPP7 is involved in the assembly of protein complexes at sites of c
- The exact function of FLJ90709 remains unknown
- RLBP1L1 contains 1 CRAL TRIO domain It may be used as a marker for human hepatocellular carcinomas
- The exact function of C15orf26 remains unknown
- The exact function of C18orf54 remains unknown
- The specific function of C17orf49 is not yet known
- Members of the F box protein family such as FBXO36 are characterized by an approximately 40 amino acid F box motif SCF complexes formed by SKP1 MIM 601434 cullin see CUL1 MIM 603134 and F b
- Fatty acid amide hydrolases such as FAAH1 and FAAH2 hydrolyze primary fatty acid amide substrates and may play a role in fatty acid catabolism Fatty acid amide hydrolases such as FAAH1 FAAH MIM 6
- The exact function of SAMD14 remains unknown
- The exact function of ZPLD1 remains unknown
- C17orf74 is a single pass membrane protein The exact function of C17orf74 remains unknown
- KLB is a single pass type III membrane protein It contributes to the transcriptional repression of cholesterol 7 alpha hydroxylase CYP7A1 the rate limiting enzyme in bile acid synthesis KLB is pr
- The exact function of ODF3L1 remains unknown
- TRA16 may act as a repressor of NR2C2 mediated transactivation by suppressing the binding between NR2C2 TR4 and the TR4 response element in target genes
- KLC3 is a member of the kinesin light chain gene family Kinesins are molecular motors involved in the transport of cargo along microtubules and are composed of two kinesin heavy chain KHC and two
- TRAPPC6B is a component of TRAPP complexes which are tethering complexes involved in vesicle transport TRAPPC6B is a component of TRAPP complexes which are tethering complexes involved in vesicle tr
- ASB6 belongs to a family of ankyrin repeat proteins that along with four other protein families contain a C terminal SOCS box motif Growing evidence suggests that the SOCS box similar to the F box
- FAM134C belongs to the FAM134 family
- WDR49 contains 8 WD repeats The exact function of WDR49 remains unknown
- Cmtm8 gene belongs to the chemokine like factor gene superfamily a novel family that is similar to the chemokine and the transmembrane 4 superfamilies This gene is one of several chemokine like fact
- MFSD4 is a multi pass membrane protein It belongs to the major facilitator superfamily
- The exact function of CCDC67 remains unknown
- FAM101A belongs to the FAM101 family The exact function of FAM101A remains unknown
- The exact function of OLFML2A is not known
- The specific function of CCDC38 is not yet known
- THAP5 contains 1 THAP type zinc finger The exact function of THAP5 remains unknown
- TCTE1 contains 7 LRR leucine rich repeats The exact function of TCTE1 remains unknown
- The Rho family of small GTPases act as molecular switches to control a wide range of cellular processes Guanine nucleotide exchange factors GEFs like GEFT activate Rho GTPases by accelerating GDP
- PRELID2 contains 1 PRELI MSF1 domain The exact function of PRELID2 remains unknown
- EIF5 catalyzes the hydrolysis of GTP bound to the 40S ribosomal initiation complex 40S mRNA Met tRNA F eIF 2 GTP with the subsequent joining of a 60S ribosomal subunit resulting in the release of e
- PHACTR3 is associated with the nuclear scaffold in proliferating cells It was found to bind to the catalytic subunit of protein phosphatase 1 PP1 and inhibit PP1 activity suggesting that this prot
- LYPD6 contains 1 UPAR Ly6 domain The exact function of LYPD6 is not known
- FAM36A is a multi pass membrane protein It belongs to the FAM36 family The exact function of FAM36A remains unknown
- The specific function of DENND2C is not yet known
- The exact function of LOC134145 remains unknown
- ADAMTS18 is a member of the ADAMTS a disintegrin and metalloproteinase with thrombospondin motifs protein family ADAMTS family members share several distinct protein modules including a propeptide
- LRRC23 contains 5 LRR leucine rich repeats The exact function of LRRC23 remains unknown
- FAM47A belongs to the FAM47 family The exact function of FAM47A remains unknown
- Cytokine mediated signal transduction in the JAK STAT cascade requires the involvement of adaptor molecules One such signal transducing adaptor molecule contains an SH3 domain that is required for in
- FAM116A belongs to the FAM116 family The exact function of FAM116A remains unknown
- ARHGAP28 contains 1 Rho GAP domain ARHGAP28 is a GTPase activator for the Rho type GTPases by converting them to an inactive GDP bound state
- The metallocarboxypeptidase family of enzymes is divided into 2 subfamilies based on sequence similarities The pancreatic carboxypeptidase like and the regulatory B type carboxypeptidase subfamilies
- Cylicin II CYCL2 is specifically expressed in testis and is part of the cytoskeletal calyx of mammalian sperm heads Cylicin II may play a role in the morphogenesis of the sperm head Cylicin II CYC
- ACRV1 is a testis specific differentiation antigen acrosomal vesicle protein 1 that arises within the acrosomal vesicle during spermatogenesis and is associated with the acrosomal membranes and ma
- CSNK2A2 belongs to the protein kinase superfamily Ser Thr protein kinase family CK2 subfamily It contains 1 protein kinase domain Casein kinases are operationally defined by their preferential uti
- INHA joins either the beta A or beta B subunit to form a pituitary FSH secretion inhibitor Inhibin has been shown to regulate gonadal stromal cell proliferation negatively and to have tumour suppress
- DNALI1 is the human homolog of the Chlamydomonas inner dynein arm gene p28 The precise function of this gene is not known however it is a potential candidate for immotile cilia syndrome ICS Ult
- LPP may play a structural role at sites of cell adhesion in maintaining cell shape and motility In addition to these structural functions it may also be implicated in signaling events and activation
- ST6GALNAC2 belongs to a family of sialyltransferases that add sialic acids to the nonreducing ends of glycoconjugates At the cell surface these modifications have roles in cell cell and cell substra
- FGFR1OP is a largely hydrophilic protein postulated to be a leucine rich protein family member A t 6 8 q27 p11 chromosomal translocation fusing this gene and the fibroblast growth factor recepto
- Strong TKTL1 protein expression has been correlated with a certain type of glucose metabolism aerobic glycolysis Warburg effect and to cells which are affected by chronic complications of diabetic
- TBL2 is a member of the beta transducin protein family Most proteins of the beta transducin family are involved in regulatory functions This protein is possibly involved in some intracellular signal
- LRRC6 may be involved in spermatocytogenesis or prophase of meiosis
- SSX2IP belongs to an adhesion system which plays a role in the organization of homotypic interneuronal and heterotypic cell cell adherens junctions AJs It may connect the nectin afadin and E cadh
- HSPA4L possesses chaperone activity in vitro where it inhibits aggregation of citrate synthase
- HSPA4L belongs to the heat shock protein 70 family HSPA4L possesses chaperone activity in vitro where it inhibits aggregation of citrate synthase
- The exact function of C20orf10 remains unknown
- The specific function of C17orf81 is not yet known
- SCCPDH belongs to the saccharopine dehydrogenase family The exact function of SCCPDH remains unknown
- The exact function of C2orf42 remains unknown
- ANKRD7 contains 5 ANK repeats The exact function of ANKRD7 remains unknown
- MLF1 is involved in lineage commitment of primary hemopoietic progenitors by restricting erythroid formation and enhancing myeloid formation It interferes with erythopoietin induced erythroid termina
- The exact function of C17orf39 remains unknown The multiprotein Mediator complex is a coactivator required for activation of RNA polymerase II transcription by DNA bound transcription factors The pro
- The exact function of C20orf195 remains unknown
- C14orf140 belongs to the UPF0418 family The exact function of C14orf140 remains unknown
- CLPB belongs to the clpA clpB family It contains 4 ANK repeats CLPB may function as a regulatory ATPase and be related to secretion protein trafficking process
- CLPB may function as a regulatory ATPase and be related to secretion protein trafficking process
- ACSBG2 belongs to the ATP dependent AMP binding enzyme family bubblegum subfamily ACSBG2 mediates activation of long chain fatty acids for both synthesis of cellular lipids and degradation via beta
- The specific function of CCDC70 is not yet known
- CCDC46 is a protein with filament myosin tail and ATPase domains Orthologs of the gene exist in mouse rat and chimp
- This gene represents a candidate gene for human lipodystrophy characterized by loss of body fat fatty liver hypertriglyceridemia and insulin resistance Mouse studies suggest that LPIN1 functions
- PAOX belongs to the flavin monoamine oxidase family PAOX is a flavoenzyme which catalyzes the oxidation of N 1 acetylspermine to spermidine and is thus involved in the polyamine back conversion It
- ACADS is a a tetrameric mitochondrial flavoprotein which is a member of the acyl CoA dehydrogenase family This enzyme catalyzes the initial step of the mitochondrial fatty acid beta oxidation pathwa
- Epoxide hydrolase is a critical biotransformation enzyme that converts epoxides from the degradation of aromatic compounds to trans dihydrodiols which can be conjugated and excreted from the body Epo
- Excision repair cross complementing rodent repair deficiency complementation group 5 xeroderma pigmentosum complementation group G is involved in excision repair of UV induced DNA damage Mutation
- ETFA participates in catalyzing the initial step of the mitochondrial fatty acid beta oxidation It shuttles electrons between primary flavoprotein dehydrogenases and the membrane bound electron trans
- FTL is the light subunit of the ferritin protein Ferritin is the major intracellular iron storage protein in prokaryotes and eukaryotes It is composed of 24 subunits of the heavy and light ferritin
- Alpha L fucosidase EC 3 2 1 51 is a lysosomal enzyme involved in the degradation of fucose containing glycoproteins and glycolipids At least 2 separate polymorphic alpha L fucosidases are recognize
- GSN binds to the plus ends of actin monomers and filaments to prevent monomer exchange It is a calcium regulated protein which functions in both assembly and disassembly of actin filaments Defect
- Hexokinases phosphorylate glucose to produce glucose 6 phosphate thus committing glucose to the glycolytic pathway HK2 hexokinase 2 is the predominant form found in skeletal muscle It localizes t
- LIG1is DNA ligase I with functions in DNA replication and the base excision repair process Mutations in LIG1 that lead to DNA ligase I deficiency result in immunodeficiency and increased sensitivity
- Anti Mullerian hormone is a member of the transforming growth factor beta gene family which mediates male sexual differentiation Anti Mullerian hormone causes the regression of Mullerian ducts which
- The enzyme system for cleavage of glycine glycine cleavage system EC 2 1 2 10 which is confined to the mitochondria is composed of 4 protein components P protein a pyridoxal phosphate dependent
- IL9 is a cytokine that acts as a regulator of a variety of hematopoietic cells This cytokine stimulates cell proliferation and prevents apoptosis It functions through the interleukin 9 receptor IL9
- IGF binding proteins prolong the half life of the IGFs and have been shown to either inhibit or stimulate the growth promoting effects of the IGFs on cell culture They alter the interaction of IGFs w
- GSR belongs to the class I pyridine nucleotide disulfide oxidoreductase family It maintains high levels of reduced glutathione in the cytosol Both glutathione and glutathione reductase are inducible
- Delta aminolevulinate synthase ALAS EC 2 3 1 37 catalyzes the condensation of glycine with succinyl CoA to form delta aminolevulinic acid This nuclear encoded mitochondrial enzyme is the first and
- IMPDH1 acts as a homotetramer to regulate cell growth It is an enzyme that catalyzes the synthesis of xanthine monophosphate XMP from inosine 5 monophosphate IMP This is the rate limiting step
- IMPDH2 is the rate limiting enzyme in the de novo guanine nucleotide biosynthesis It is thus involved in maintaining cellular guanine deoxy and ribonucleotide pools needed for DNA and RNA synthesis
- LTA4H hydrolyzes an epoxide moiety of leukotriene A4 LTA 4 to form leukotriene B4 LTB 4 The enzyme also has some peptidase activity
- NPAL2 is a multi pass membrane protein and it belongs to the NIPA family The exact function of NPAL2 remains unknown Western blots using two different antibodies against two unique regions of this pr
- FAM13C1 belongs to the FAM13 family The exact function of FAM13C1 remains unknown
- Tusc1 gene is located within the region of chromosome 9p that harbors tumor suppressor genes critical in carcinogenesis It is an intronless gene which is downregulated in non small cell lung cancer a

- The exact function of LOC402573 remains unknown
- GALE is an UDP galactose 4 epimerase which catalyzes two distinct but analogous reactions the epimerization of UDP glucose to UDP galactose and the epimerization of UDP N acetylglucosamine to UDP N
- The exact function of C9orf153 remains unknown
- MAGEA4 is a member of the MAGEA family The members of this family are proteins with 50 to 80 sequence identity to each other The promoters and first exons of the MAGEA genes show considerable varia
- CENPP is the component of the CENPA CAD nucleosome distal complex a complex recruited to centromeres which is involved in assembly of kinetochore proteins mitotic progression and chromosome segreg
- The exact function of C9orf117 remains unknown
- C6orf173 is up regulated in many cancer tissues It suggests that C6orf173 may act as an oncogene
- RP11 269F19 9 also known as TCTEX1D4 belongs to the dynein light chain Tctex type family The exact function of RP11 269F19 9 remains unknown
- The exact function of LOC387856 remains unknown
- The exact function of LOC388969 remains unknown
- The exact function of LOC400566 remains unknown
- C5orf39 may act as a receptor for annexin II on marrow stromal cells to induce osteoclast formation
- HMBS is a member of the hydroxymethylbilane synthase superfamily It is the third enzyme of the heme biosynthetic pathway and catalyzes the head to tail condensation of four porphobilinogen molecules
- The exact function of LOC284009 remains unknown
- The exact function of CCDC7 remains unknown
- KCTD21 contains 1 BTB POZ domain The exact function of KCTD21 remains unknown
- The specific function of WDR21B is not yet known
- SUNC1 is a single pass membrane protein It contains 1 Unc84 SUN domain
- The exact function of C12orf40 remains unknown
- ACADVL is targeted to the inner mitochondrial membrane where it catalyzes the first step of the mitochondrial fatty acid beta oxidation pathway This acyl Coenzyme A dehydrogenase is specific to long
- The exact function of LOC285033 remains unknown
- Several proteins have been found to be prenylated and methylated at their carboxyl terminal ends Prenylation was initially believed to be important only for membrane attachment However another role
- PRAMEF10 belongs to the PRAME family It contains 3 LRR leucine rich repeats The function of the PRAMEF10 protein remains unknown
- DCUN1D4 contains 1 DCUN1 domain The exact function of DCUN1D4 remains unknown
- HAGH is classified as a thiolesterase and is responsible for the hydrolysis of S lactoyl glutathione to reduced glutathione and D lactate The enzyme encoded by this gene is classified as a thiolester
- Klkbl4 is a secreted protein Klkbl4 belongs to the peptidase S1 family plasma kallikrein subfamily It contains 1 peptidase S1 domain
- TMEM184A is a multi pass membrane proteinPotential It belongs to the UPF0206 family The exact function of TMEM184A remains unknown
- Toll like receptors TLRs and IL1R IL1R1 are part of the innate immune response aimed at mobilizing defense mechanisms in response in infection or injury Pellino proteins such as PELI3 are inter
- The exact function of C12orf42 remains unknown
- SOHLH1 contains 1 basic helix loop helix bHLH domain It is a probable transcription factor required during spermatogenesis and oogenesis
- AMN1 belongs to the AMN1 family The exact function of AMN1 remains unknown
- Arginase catalyzes the hydrolysis of arginine to ornithine and urea At least two isoforms of mammalian arginase exists types I and II which differ in their tissue distribution subcellular localiza
- GLE1 is a predicted 75 kDa polypeptide with high sequence and structure homology to yeast Gle1p which is nuclear protein with a leucine rich nuclear export sequence essential for poly A RNA export
- IFRD1 belongs to the IFRD family It could play a role in regulating gene activity in the proliferative and or differentiative pathways induced by NGF IFRD1 may be an autocrine factor that attenuates
- Short branched chain acyl CoA dehydrogenase ACADSB is a member of the acyl CoA dehydrogenase family of enzymes that catalyze the dehydrogenation of acyl CoA derivatives in the metabolism of fatty ac
- The gene that encodes ARCN1 maps in a region which includes the mixed lineage leukemia and Friend leukemia virus integration 1 genes where multiple disease associated chromosome translocations occur
- ARF6 is a member of the human ARF family which is part of the RAS superfamily They are small guanine nucleotide binding proteins that stimulate the ADP ribosyltransferase activity of cholera toxin a
- FAU is a fusion protein consisting of the ubiquitin like protein fubi at the N terminus and ribosomal protein S30 at the C terminus It has been proposed that the fusion protein is post translationall
- FES is the human cellular counterpart of a feline sarcoma retrovirus protein with transforming capabilities FES has tyrosine specific protein kinase activity and that activity is required for mainten
- Fibromodulin is a member of a family of small interstitial proteoglycans containing a central region composed of leucine rich repeats with 4 keratan sulfate chains flanked by disulfide bonded termina
- The specific function of FRK is not yet known The protein encoded by this gene belongs to the TYR family of protein kinases This tyrosine kinase is a nuclear protein and may function during G1 and S
- FTH1 is the heavy subunit of ferritin the major intracellular iron storage protein in prokaryotes and eukaryotes It is composed of 24 subunits of the heavy and light ferritin chains Variation in fe
- Glutamate cysteine ligase also known as gamma glutamylcysteine synthetase is the first rate limiting enzyme of glutathione synthesis The enzyme consists of two subunits a heavy catalytic subunit a
- Guanine nucleotide binding proteins G proteins form a large family of signal transducing molecules They are found as heterotrimers made up of alpha beta and gamma subunits Members of the G prote
- Guanine nucleotide binding proteins G proteins are involved as modulators or transducers in various transmembrane signaling systems The G i proteins are involved in hormonal regulation of adenyla
- HSPE1 is a major heat shock protein which functions as a chaperonin Its structure consists of a heptameric ring which binds to another heat shock protein in order to form a symmetric functional hete
- Recombination activating proteins RAG1 and RAG2 regulate and mediate V D J recombination the process by which genes for immunoglobulins and T cell receptors are generated Several other ubiquitously
- Imported proteins require a nuclear localization sequence NLS which generally consists of a short region of basic amino acids or 2 such regions spaced about 10 amino acids apart Proteins involved i
- The transport of molecules between the nucleus and the cytoplasm in eukaryotic cells is mediated by the nuclear pore complex NPC which consists of 60 100 proteins and is probably 120 million daltons
- The nuclear import of karyophilic proteins is directed by short amino acid sequences termed nuclear localization signals NLSs Karyopherins or importins are cytoplasmic proteins that recognize NLS
- Plastins are a family of actin binding proteins that are conserved throughout eukaryote evolution and expressed in most tissues of higher eukaryotes In humans two ubiquitous plastin isoforms L and
- FDXR is a mitochondrial flavoprotein that initiates electron transport for cytochromes P450 receiving electrons from NADPH This gene encodes a mitochondrial flavoprotein that initiates electron transp
- GBPs are characterized by their ability to specifically bind guanine nucleotides GMP GDP and GTP GBP2 is a GTPase that converts GTP to GDP and GMP Interferons are cytokines that have antiviral e
- HABP2 is an extracellular serine protease that binds hyaluronic acid and is involved in cell adhesion It is synthesized as a single chain but then undergoes an autoproteolytic event to form the func
- IDI1 is a peroxisomally localized enzyme that catalyzes the interconversion of isopentenyl diphosphate IPP to its highly electrophilic isomer dimethylallyl diphosphate DMAPP which are the substr
- ICA1 is a protein with an arfaptin homology domain that is found both in the cytosol and as membrane bound form on the Golgi complex and immature secretory granules This protein is believed to be an
- Histones are basic nuclear proteins that are responsible for the nucleosome structure of the chromosomal fiber in eukaryotes Nucleosomes consist of approximately 146 bp of DNA wrapped around a histon
- Histones are basic nuclear proteins responsible for nucleosome structure of the chromosomal fiber in eukaryotes Two molecules of each of the four core histones H2A H2B H3 and H4 form an octamer
- HADH functions in the mitochondrial matrix to catalyze the oxidation of straight chain 3 hydroxyacyl CoAs as part of the beta oxidation pathway Its enzymatic activity is highest with medium chain len
- LDHA catalyzes the conversion of L lactate and NAD to pyruvate and NADH in the final step of anaerobic glycolysis The protein is found predominantly in muscle tissue and belongs to the lactate dehydr
- The galectins are a family of beta galactoside binding proteins implicated in modulating cell cell and cell matrix interactions LGALS3BP has been found elevated in the serum of patients with cancer a
- LOXL1 is a member of the lysyl oxidase family The prototypic member of the family is essential to the biogenesis of connective tissue encoding an extracellular copper dependent amine oxidase that ca
- IPP is a member of the kelch family of proteins which is characterized by a 50 amino acid repeat which interacts with actin The protein encoded by this gene is a member of the kelch family of protein
- SFN is an adapter protein implicated in the regulation of a large spectrum of both general and specialized signaling pathway SFN binds to a large number of partners usually by recognition of a phosp
- Multiprotein complexes are key determinants of Golgi apparatus structure and its capacity for intracellular transport and glycoprotein modification Several complexes have been identified including t
- CCT5 is a molecular chaperone that is member of the chaperonin containing TCP1 complex CCT also known as the TCP1 ring complex TRiC This complex consists of two identical stacked rings each con
- Glutamate dehydrogenase EC 1 4 1 3 catalyzes the reversible oxidative deamination of glutamate to alpha ketoglutarate using NAD and or NADP as cofactors Glutamate dehydrogenase EC 1 4 1 3 catalyze
- PRDX5 is a member of the peroxiredoxin family of antioxidant enzymes which reduce hydrogen peroxide and alkyl hydroperoxides The encoded protein may play an antioxidant protective role in different
- CDC42EP4 is a member of the CDC42 binding protein family Members of this family interact with Rho family GTPases and regulate the organization of the actin cytoskeleton The protein has been shown to
- CHORDC1 may be play a role in the regulation of NOD1 via its interaction with HSP90AA1
- DDAH1 belongs to the dimethylarginine dimethylaminohydrolase DDAH family This enzyme plays a role in nitric oxide generation by regulating cellular concentrations of methylarginines which in turn
- FBXO22 is a member of the F box protein family which is characterized by an approximately 40 amino acid motif the F box The F box proteins constitute one of the four subunits of the ubiquitin protei
- FBXO8 is a member of the F box protein family which is characterized by an approximately 40 amino acid motif the F box The F box proteins constitute one of the four subunits of the ubiquitin protein
- GTP binding proteins are GTPases and function as molecular switches that can flip between two states active when GTP is bound and inactive when GDP is bound Active in this context usually means
- TTC33 contains 3 TPR repeats The function of the TTC33 protein remains unknown
- PLDN may play a role in intracellular vesicle trafficking It interacts with Syntaxin 13 which mediates intracellular membrane fusion The protein encoded by this gene may play a role in intracellular
- PITPNB is found in the cytoplasm where it catalyzes the transfer of phosphatidylinositol and phosphatidylcholine between membranes The protein encoded by this gene is found in the cytoplasm where it
- IFIT5 belongs to the IFIT family It contains 8 TPR repeats The exact function of IFIT5 remains unknown
- Meiotic recombination and chromosome segregation require the formation of double strand breaks DSBs in paired chromosome homologs During meiosis in yeast a meiotic recombination protein is covalen
- VPS4A is a member of the AAA protein family ATPases associated with diverse cellular activities and is the homolog of the yeast Vps4 protein In humans two paralogs of the yeast protein have been
- POLL is a repair polymerase It is involved in base excision repair BER responsible for repair of lesions that give rise to abasic AP sites in DNA Has both DNA polymerase and terminal transferase
- POLM seems to act as an Ig mutase which is responsible for immunoglobulin Ig gene hypermutation
- The exact function of C12orf24 remains unknown
- EPN1 is an endocytic accessory protein that interacts with EPS15 MIM 600051 the alpha subunit of the clathrin adaptor AP2 AP2A1 MIM 601026 and clathrin see MIM 118960 as well as with other a
- Replication protein A RPA is an essential factor for DNA double strand break repair and cell cycle checkpoint activation RPA4 is the 32 kDa subunit of the RPA which associates with the 70 and 13

- Transportin 2 TNPO2 mediates nuclear import of HuR protein in vitro It also participates in mRNA export from the nucleus
- NOB1 may play a role in mRNA degradation
- THYN1 is a protein that is highly conserved among vertebrates and plant species and may be involved in the induction of apoptosis This gene encodes a protein that is highly conserved among vertebrates
- ITPK1 is the kinase that can phosphorylate various inositol polyphosphate such as Ins 3 4 5 6 P4 or Ins 1 3 4 P3 It may also act as an isomerase that interconverts the inositol tetraphosphate isome
- ITGB3BP is a transcription coregulator that can have both coactivator and corepressor functions Isoform 1 but not other isoforms is involved in the coactivation of nuclear receptors for retinoid X
- TBC1D22A contains 1 Rab GAP TBC domain It may act as a GTPase activating protein for Rab family protein s
- SNX5 is a member of the sorting nexin family Members of this family contain a phox PX domain which is a phosphoinositide binding domain and are involved in intracellular trafficking This protein
- DHDH is an enzyme that belongs to the family of dihydrodiol dehydrogenases which exist in multiple forms in mammalian tissues and are involved in the metabolism of xenobiotics and sugars These enzym
- PDLIM3 contains a PDZ domain and a LIM domain indicating that it may be involved in cytoskeletal assembly In support of this PDLIM3 has been shown to bind the spectrin like repeats of alpha actinin
- TMOD3 belongs to the tropomodulin family It blocks the elongation and depolymerization of the actin filaments at the pointed end The Tmod TM complex contributes to the formation of the short actin p
- TMOD2 is a neuronal specific member of the tropomodulin family of actin regulatory proteins It caps the pointed end of actin filaments preventing both elongation and depolymerization The capping act
- The covalent modification of proteins by the small ubiquitin like protein SUMO is implicated in the regulation of nucleocytoplasmic transport genomic stability gene transcription and other processe
- FAM120A may participate in mRNA transport in the cytoplasm FAM120A is the critical component of the oxidative stress induced survival signaling It activates src family kinases and acts as a scaffold
- The function of KIAA0182 remains unknown
- R3HDM2 contains 1 R3H domain The function of R3HDM2 remains unknown
- Functions of the cell cortex including motility adhesion and cytokinesis are mediated by the reorganization of the actin cytoskeleton and recent evidence suggests a role for the Formin homology F
- WDTC1 contains 2 TPR repeats and 7 WD repeats WDTC1 the ortholog of Drosophila Adipose Gene associates with human obesity modulated by MUFA intake
- PDXDC1 belongs to the group II decarboxylase family The function of PDXDC1 remains unknown
- KIAA0692 is a single pass membrane protein It contains 1 ANK repeat and 1 LEM domain It contains 1 RING type zinc finger The function of KIAA0692 remains unknown
- FCHO1 is involved in clathrin coated vesicle formation
- TBC1D1 is the founding member of a family of proteins sharing a 180 to 200 amino acid TBC domain presumed to have a role in regulating cell growth and differentiation These proteins share significan
- Members of the F box protein family such as FBXO28 are characterized by an approximately 40 amino acid F box motif SCF complexes formed by SKP1 cullin and F box proteins act as protein ubiquiti
- KIAA0460 contains 1 CID domain The function of KIAA0460 remains unknown
- Inositol phosphates IPs and diphosphoinositol phosphates PP IPs also known as inositol pyrophosphates act as cell signaling molecules HISPPD1 has both IP6 kinase EC 2 7 4 21 and PP IP5 also
- The function of C22orf9 remains unknown
- KIAA0892 belongs to the mau 2 family It contains 4 TPR repeats The function of KIAA0892 remains unknown
- PPWD1 is a putative peptidylprolyl isomerase PPIase PPIases accelerate the folding of proteins It catalyzes the cis trans isomerization of proline imidic peptide bonds in oligopeptides PPWD1 may
- WDSOF1 belongs to the WD repeat WDSOF1 family It contains 7 WD repeats WDSOF1 is a possible role in ribosomal RNA processing
- RP11 529I10 4 DPCD belongs to the DPCD family It may play a role in the formation or function of ciliated cells Deletion of the DPCD gene may be a cause of primary ciliary dyskinesia PCD
- SAMHD1 contains 1 HD domain and 1 SAM sterile alpha motif domain SAMHD1 may play a role in mediating proinflammatory responses to TNF alpha signaling
- FAM98A belongs to the FAM98 family The function of FAM98A remains unknown
- The function of C18orf10 remains unknown
- RAI14 contains 7 ANK repeats The function of RAI14 remains unknown
- Sm like proteins were identified in a variety of organisms based on sequence homology with the Sm protein family Sm like proteins contain the Sm sequence motif which consists of 2 regions separated
- WDR21A is a WD repeat containing protein The function of WDR21A remains unknown This gene encodes a WD repeat containing protein Multiple alternatively spliced transcript variants have been found fo
- The function of CCDC69 remains unknown
- IRF2BP1 acts as a transcriptional repressor IRF2BP1 also acts as a transcriptional corepressor in a IRF2 dependent manner This repression is not mediated at least in part by histone deacetylase acti
- SDCBP2 contains 2 PDZ DHR domains The function of SDCBP2 remains unknown
- The function of C2orf25 remains unknown Vitamin B12 cobalamin is an essential cofactor in several metabolic pathways Intracellular conversion of cobalamin to adenosylcobalamin in mitochondria and t
- VGLL3 belongs to the vestigial family It may act as a specific coactivator for the mammalian TEFs
- MKNK2 may play a role in the response to environmental stress and cytokines It appears to regulate transcription by phosphorylating EIF4E thus increasing the affinity of this protein for the 7 methy
- SSBP3 may be involved in transcription regulation of the alpha 2 I collagen gene where it binds to the single stranded polypyrimidine sequences in the promoter region
- GSPT2 is closely related to GSPT1 a GTP binding protein that plays an essential role at the G1 to S phase transition of the cell cycle in yeast and human cells GSPT1 is a positive regulator of tran
- NKIRAS1 is an atypical Ras like protein that acts as a potent regulator of NF kappa B activity by preventing the degradation of NF kappa B inhibitor beta NFKBIB by most signals explaining why NFKBI
- IFNA7 belongs to the alpha beta interferon family IFNA7 is produced by macrophages IFN alpha have antiviral activities Interferon stimulates the production of two enzymes a protein kinase and an o
- TRIB2 is one of three members of the Tribbles family The Tribbles members share a Trb domain which is homologous to protein serine threonine kinases but lacks the active site lysine and probably la
- TSPYL4 belongs to the nucleosome assembly protein NAP family The functions of TSPYL4 remain unknown
- The Fanconi anemia complementation group FANC currently includes FANCA FANCB FANCC FANCD1 also called BRCA2 FANCD2 FANCE FANCF FANCG FANCI FANCJ also called BRIP1 FANCL FANCM and FANC
- HSPA2 belongs to the heat shock protein 70 family In cooperation with other chaperones HSPA2 stabilize preexistent proteins against aggregation and mediate the folding of newly translated polypeptide
- The exact function of C11orf67 remains unknown
- PHACTR1 belongs to the phosphatase and actin regulator family It contains 4 RPEL repeats The function of the PHACTR1 protein remains unknown
- GABARAPL1 increases cell surface expression of kappa type opioid receptor through facilitating anterograde intracellular trafficking of the receptor
- Phototransduction in rod and cone photoreceptors is regulated by groups of signaling proteins GNGT2 is thought to play a crucial role in cone phototransduction It belongs to the G protein gamma fami
- The function of the KIAA0157 protein remains unknown
- KRAS is a member of the small GTPase superfamily A single amino acid substitution is responsible for an activating mutation The transforming protein that results is implicated in various malignancie
- The exact functions of FAM78A remain unknown
- FGF13 is probably involved in nervous system development and function The protein encoded by this gene is a member of the fibroblast growth factor FGF family FGF family members possess broad mitoge
- Activated Goalpha interacted directly with PLZF and enhanced its function as a transcriptional and cell growth suppressor Goalpha might play a role in mediating extracellular signal regulated kinase
- In vitro MAPK15 phosphorylates MBP
- The Escherichia coli AlkB protein protects against the cytotoxicity of methylating agents by repair of the specific DNA lesions generated in single stranded DNA ALKBH2 MIM 610602 and ALKBH3 are E
- DAGLB belongs to the AB hydrolase superfamily It catalyzes the hydrolysis of diacylglycerol DAG to 2 arachidonoyl glycerol 2 AG the most abundant endocannabinoid in tissues This protein is requi
- EHD4 is involved in the control of trafficking at the early endosome and regulates exit of cargo toward both the recycling compartment and the late endocytic pathway
- Defects in RPIA are the cause of ribose 5 phosphate isomerase deficiency The exact function of RPIA remains unknown
- The exact function of SUSD3 remains unknown
- The function of the CCDC11 protein remains unknown
- The function of the C6orf199 protein remains unknown
- The exact function of this protein remains unknown The protein is weakly similar to transposase like proteins in human and mouse This gene encodes a protein of unknown function The protein is weakly
- The exact function of LRRC51 remains unknown
- RASGEF1A is the guanine nucleotide exchange factor GEF for KRAS HRAS and NRAS in vitro It plays a role in cell migration
- SGMS1 is predicted to be a five pass transmembrane protein This gene may be predominately expressed in brain The protein encoded by this gene is predicted to be a five pass transmembrane protein Thi
- The function of this protein has not been determined The protein encoded by this gene has homologs that have been identified in mouse and macaque The mouse and human proteins have a putative prenyl g
- Condensin complexes I and II play essential roles in mitotic chromosome assembly and segregation Both condensins contain 2 invariant structural maintenance of chromosome SMC subunits SMC2 and SMC4
- IQCE contains 2 IQ domains The functions of IQCE remain unknown
- ATP6V0D2 is the subunit of the integral membrane V0 complex of vacuolar ATPase Vacuolar ATPase is responsible for acidifying a variety of intracellular compartments in eukaryotic cells thus providin
- The exact function of MGC26647 remains unknown
- The exact function of ATXN7L1 remains unknown
- YTHDF3 contains 1 YTH domain The functions of YTHDF3 remain unknown
- The specific function of C4orf22 is not yet known
- The specific function of TCP11L2 is not yet known
- TMEM146 is a single pass type I membrane protein The functions of TMEM146 remain unknown
- GCET2 is a protein which may function in signal transduction pathways and whose expression is elevated in germinal cell lymphomas It contains a putative PDZ interacting domain an immunoreceptor tyro
- The function of the C9orf43 protein remains unknown
- IF 3 binds to the 28S ribosomal subunit and shifts the equilibrum between 55S ribosomes and their 39S and 28S subunits in favor of the free subunits thus enhancing the availability of 28S subunits on
- The exact function of PXT1 remains unknown
- The exact function of MGC45491 remains unknown
- The exact function of LRRC57 remains unknown
- EML3 may modify the assembly dynamics of microtubules such that microtubules are slightly longer but more dynamic
- FBXW8 is a member of the F box protein family members of which are characterized by an approximately 40 amino acid motif the F box The F box proteins constitute one of the four subunits of ubiquiti
- The exact function of C10orf56 remains unknown
- The exact functions of CCDC96 remain unknown
- HTRA4 is a member of the HtrA family of proteases The protein contains a putative signal peptide an insulin growth factor binding domain a Kazal protease inhibitor domain a conserved trypsin domai
- IL15 is a cytokine that regulates T and natural killer cell activation and proliferation This cytokine and interleukine 2 share many biological activities They are found to bind common hematopoietin
- WDR51B contains 7 WD repeats The function of the WDR51B protein remains unknown
- The correlation of anti sperm antibodies with cases of unexplained infertility implicates a role for these antibodies in blocking fertilization Improved diagnosis and treatment of immunologic inferti
- APBB2 may modulate the internalization of beta amyloid precursor protein The protein encoded by this gene interacts with the cytoplasmic domains of amyloid beta A4 precursor protein and amyloid beta
- The specific function of ARMC3 is not yet known Armadillo beta catenin CTNNB1 MIM 116806 like ARM domains are imperfect 45 amino acid repeats involved in protein protein interactions ARM domain
- The specific function of TRIML2 is not yet known
- The specific function of C14orf80 is not yet known
- The specific function of FAM98B is not yet known
- The exact functions of FLJ37543 remain unknown
- Members of the RGS regulator of G protein signaling family

have been shown to modulate the functioning of G proteins by activating the intrinsic GTPase activity of the alpha guanine nucleotide bind

- COX18 is required for the insertion of integral membrane proteins into the mitochondrial inner membrane COX18 is essential for the activity and assembly of cytochrome c oxidase COX18 plays a central
- RASGEF1C is a guanine nucleotide exchange factor GEF
- RHOC Is a member of the Rho family of small GTPases which cycle between inactive GDP bound and active GTP bound states and function as molecular switches in signal transduction cascades Rho proteins
- The exact functions of PRR18 remain unknown
- ARL5A lacks ADP ribosylation enhancing activity The protein encoded by this gene belongs to the ARF family of GTP binding proteins With its distinctive nuclear nucleolar localization and interaction
- The exact functions of ANGPTL5 remain unknown
- The exact functions of C1orf110 remain unknown
- The exact functions of C2orf53 remain unknown
- TSPAN33 plays an important role in normal erythropoiesis It has a role in the differentiation of erythroid progenitors
- SPDYA regulates the G1 S phase transition of the cell cycle by binding and activating CDC2 CDK2 and CDKN1B KIP1 SPDYA can activate CDK2 without promoting CDK2 phosphorylation SPDYA mediates cell su
- MAT2B belongs to the methionine adenosyltransferase MAT family MAT catalyzes the biosynthesis of S adenosylmethionine from methionine and ATP This protein is the regulatory beta subunit of MAT The
- The function of the HEATR4 protein remains unknown
- Xaa Pro dipeptidase is a cytosolic dipeptidase that hydrolyzes dipeptides with proline or hydroxyproline at the carboxy terminus but not Pro Pro It is important in collagen metabolism because of th
- The function of the PBLD protein remains unknown
- ACO2 belongs to the aconitase IPM isomerase family It is an enzyme that catalyzes the interconversion of citrate to isocitrate via cis aconitate in the second step of the TCA cycle This protein is e
- PPP1R7 is the regulatory subunit of protein phosphatase 1
- PRELP is a leucine rich repeat protein present in connective tissue extracellular matrix This protein functions as a molecule anchoring basement membranes to the underlying connective tissue This pr
- The proteasome is a multicatalytic proteinase complex with a highly ordered ring shaped 20S core structure The core structure is composed of 4 rings of 28 non identical subunits 2 rings are composed
- SCP2 protein is thought to be an intracellular lipid transfer protein SCP2 is highly expressed in organs involved in lipid metabolism and may play a role in Zellweger syndrome in which cells are de
- SFRP2 is a member of the SFRP family that contains a cysteine rich domain homologous to the putative Wnt binding site of Frizzled proteins SFRPs act as soluble modulators of Wnt signaling Methylatio
- SH3BP2 has an N terminal pleckstrin homology PH domain an SH3 binding proline rich region and a C terminal SH2 domain The protein binds to the SH3 domains of several proteins including the ABL1 a
- PRKRIR is upstream regulator of interferon induced serine threonine protein kinase R PKR PRKRIR may block the PKR inhibitory function of P58IPK resulting in restoration of kinase activity and supp
- SEPT2 is required for normal progress through mitosis SEPT2 is involved in cytokinesis
- Phosphoinositide specific phospholipase C PLC acts as a signal transducer that generates 2 second messengers diacylglycerol and inositol 1 4 5 trisphosphate by hydrolyzing inositol phospholipids
- PPP2R1A is a constant regulatory subunit of protein phosphatase 2 Protein phosphatase 2 is one of the four major Ser Thr phosphatases and it is implicated in the negative control of cell growth and
- FAM108B1 belongs to the AB hydrolase superfamily fAM108 family The exact function of FAM108B1 remains unknown
- The specific function of LACTB2 is not yet known
- COPS4 is one of eight subunits composing COP9 signalosome a highly conserved protein complex that functions as an important regulator in multiple signaling pathways The structure and function of COP
- Protein phosphatase methylesterase 1 catalyzes the demethylation of the protein phosphatase 2A catalytic subunit Protein phosphatase methylesterase 1 catalyzes the demethylation of the protein phospha
- 17 beta hydroxysteroid dehydrogenases such as HSD17B14 are primarily involved in metabolism of steroids at the C17 position and also of other substrates such as fatty acids prostaglandins and xen
- Defects in GLRX5 are the cause of anemia sideroblastic pyridoxine refractory autosomal recessive PRARSA The specific function of GLRX5 is not yet known
- SEPT11 belongs to the conserved septin family of filament forming cytoskeletal GTPases that are involved in a variety of cellular functions including cytokinesis and vesicle trafficking
- The function of the SPATA7 protein remains unknown
- RCC2 is required for completion of mitosis and cytokinesis RCC2 may function as a guanine nucleotide exchange factor for the small GTPase RAC1
- Pyridoxal 5 prime phosphate PLP is the active form of vitamin B6 that acts as a coenzyme in maintaining biochemical homeostasis The preferred degradation route from PLP to 4 pyridoxic acid involves
- MATN2 is a member of the von Willebrand factor A domain containing protein family This family of proteins is thought to be involved in the formation of filamentous networks in the extracellular matri
- MYL6 contains 3 EF hand domains It is the regulatory light chain of myosin MYL6 does not bind calcium Myosin is a hexameric ATPase cellular motor protein It is composed of two heavy chains two no
- RNH1 is the inhibitor of pancreatic RNase and angiogenin RNH1 may also function in the modulation of cellular activities
- GABPB2 is the GA binding protein transcription factor beta subunit This protein forms a tetrameric complex with the alpha subunit and stimulates transcription of target genes The protein may be in
- TFAP2B belongs to the AP 2 family which is developmentally regulated and have distinct overlapping functions in the regulation of many genes governing growth and differentiation TFAP2B binds DNA as a
- TUB functions in signal transduction from heterotrimeric G protein coupled receptors It could be involved in the hypothalamic regulation of body weight This gene encodes a member of the Tubby family
- The human gene C19orf6 localizes to chromosome 19p13 3 Splice variant membralin 1 is encoded by 11 exons translating into 620 amino acids Membralin is a novel tumor associated marker in ovarian ser
- TRIM31 encodes for a member of the tripartite motif TRIM family The TRIM motif includes three zinc binding domains a RING a B box type 1 and a B box type 2 and a coiled coil region The protein
- ERCC8 is a WD repeat protein which interacts with Cockayne syndrome type B CSB protein and with p44 protein a subunit of the RNA polymerase II transcription factor IIH Mutations in this gene have
- v ets erythroblastosis virus E26 oncogene like isoform 2 ERG is a transcriptional regulator It may participate in transcriptional regulation through the recruitment of SETDB1 histone methyltransfer
- L glutamate is the major excitatory neurotransmitter in the central nervous system and activates both ionotropic and metabotropic glutamate receptors Glutamatergic neurotransmission is involved in mo
- GTF2B is the general transcription factor IIB one of the ubiquitous factors required for transcription initiation by RNA polymerase II The protein localizes to the nucleus where it forms a complex
- GTF2I is a multifunctional phosphoprotein with roles in transcription and signal transduction It is deleted in Williams Beuren syndrome a multisystem developmental disorder caused by the deletion of
- UBE2K belongs to the ubiquitin conjugating enzyme family This protein interacts with RING finger proteins and it can ubiquitinate huntingtin the gene product for Huntington s disease Known functio
- ZBTB48 contains 1 BTB POZ domain and 11 C2H2 type zinc fingers It belongs to the krueppel C2H2 type zinc finger protein family and binds to and regulates the J and or S elements in MHC II promoter
- HOXB5 belongs to ANTP homeobox family It is a nuclear protein with a homeobox DNA binding domain HOXB5 gene is included in a cluster of homeobox B genes located on chromosome 17 The protein function
- TBX10 a member of the Tbx1 subfamily of conserved developmental genes is located at human chromosome 11q13 and proximal mouse chromosome 19
- NFE2 is required for activity at the locus control region LCR upstream of the globin gene complexes It requires p18 NF E2 for binding to the NF E2 motif NFE2 may play a role in all aspects of hemog
- The PAX genes including PAX1 are a highly conserved family of developmental control genes that encode transcription factors and have been shown to play a role in pattern formation during embryogenes
- POLE3 is a histone fold protein that interacts with other histone fold proteins to bind DNA in a sequence independent manner These histone fold protein dimers combine within larger enzymatic complexe
- ZNF334 belongs to the krueppel C2H2 type zinc finger protein family It contains 14 C2H2 type zinc fingers and 1 KRAB domain ZNF334 may be involved in transcriptional regulation
- The 26S proteasome is a multicatalytic proteinase complex with a highly ordered structure composed of 2 complexes a 20S core and a 19S regulator The 20S core is composed of 4 rings of 28 non identic
- NKX3 2 is a member of the NK family of homeobox containing proteins It may play a role in skeletal development This gene encodes a member of the NK family of homeobox containing proteins The encoded
- The first mRNA transcript isolated for C2orf3 gene was part of an artificial chimera derived from two distinct gene transcripts and a primer used in the cloning process see Genbank accession M29204
- ZFPL1 is expressed strongly in the exocrine pancreas as a 1 4 kb polyadenylated RNA encoding a putative protein of 310 amino acids
- JMJD5 is a histone lysine demethylase Studies of a similar protein in mouse indicate a potential role for this protein as a tumor suppressor JMJD5 is a putative histone lysine demethylase that contai
- TRIM15 is a member of the tripartite motif TRIM family The TRIM motif includes three zinc binding domains a RING a B box type 1 and a B box type 2 and a coiled coil region The protein localizes
- SOX13 is a member of the SOX SRY related HMG box family of transcription factors involved in the regulation of embryonic development and in the determination of cell fate The encoded protein may ac
- GTF2A1 belongs to the TFIIA subunit 1 family It is a component of the transcription machinery of RNA polymerase II and plays an important role in transcriptional activation This protein induces a co
- PSMC3 is a subunit of the 26S proteasome 26S proteasome is a multicatalytic proteinase complex with a highly ordered structure composed of 2 complexes a 20S core and a 19S regulator The 20S core is
- RNF5 contains a RING finger which is a motif known to be involved in protein protein interactions This protein is a membrane bound ubiquitin ligase It can regulate cell motility by targeting paxill
- ZNF442 Belongs to the krueppel C2H2 type zinc finger protein family It contains 16 C2H2 type zinc fingers and 1 KRAB domain ZNF442 may be involved in transcriptional regulation
- Ataxin 2 binding protein 1 A2BP1 has an RNP motif that is highly conserved among RNA binding proteins This protein binds to the C terminus of ataxin 2 and may contribute to the restricted pathology
- TFPI2 may play a role in the regulation of plasmin mediated matrix remodeling It inhibits trypsin plasmin factor VIIa tissue factor and weakly factor Xa TFPI2 has no effect on thrombin
- SUMO proteins such as SUMO3 and ubiquitin see MIM 191339 posttranslationally modify numerous cellular proteins and affect their metabolism and function However unlike ubiquitination which targe
- Histones are basic nuclear proteins that are responsible for the nucleosome structure of the chromosomal fiber in eukaryotes Two molecules of each of the four core histones H2A H2B H3 and H4 for
- NPM2 belongs to the nucleoplasmin family It probably involved in sperm DNA decondensation during fertilization
- SMARCD1 is a member of the SWI SNF family of proteins whose members display helicase and ATPase activities and which are thought to regulate transcription of certain genes by altering the chromatin s
- SYCP3 is a component of the transverse filaments of synaptonemal complexes SCS formed between homologous chromosomes during meiotic prophase It has an essential meiotic function in spermatogenesis
- TINF2 is a component of the shelterin complex telosome that is involved in the regulation of telomere length and protection Shelterin associates with arrays of double stranded TTAGGG repeats added
- USP22 is a subunit of the SAGA transcriptional cofactor complex It deubiquitylates histone H2B and is recruited to specific genes by activators like Myc USP22 is needed for cell cycle progression I
- IGF2BP1 is a member of the IGF II mRNA binding protein IMP family The protein contains four K homology domains and two RNA recognition motifs It functions by binding to the 5 UTR of the insulin l
- MUC3B is major glycoprotein component of a variety of mucus gels It is thought to provide a protective lubricating barrier against particles and infectious agents at mucosal surfaces
- Alpha actinin is an actin binding protein with multiple roles in different cell types In nonmuscle cells the cytoskeletal isoform is found along microfilament bundles and adherens

type junctions wh

- ACTR1A is a 42 6 kD subunit of dynactin a macromolecular complex consisting of 10 11 subunits ranging in size from 22 to 150 kD Dynactin binds to both microtubules and cytoplasmic dynein It is invo
- ALDH1B1 belongs to the aldehyde dehydrogenases family of proteins Aldehyde dehydrogenase is the second enzyme of the major oxidative pathway of alcohol metabolism This gene does not contain introns
- Adenine phosphoribosyltransferase APRT belongs to the purine pyrimidine phosphoribosyltransferase family A conserved feature of this gene is the distribution of CpG dinucleotides This enzyme catal
- ARHGAPs such as ARHGAP25 are negative regulators of Rho GTPases which are implicated in actin remodeling cell polarity and cell migration ARHGAPs such as ARHGAP25 encode negative regulators of
- Carbonic anhydrases CAs are a large family of zinc metalloenzymes that catalyze the reversible hydration of carbon dioxide They participate in a variety of biological processes including respirati
- CAPS is a calcium binding protein which may play a role in the regulation of ion transport A similar protein was first described as a potentially important regulatory protein in the dog thyroid and
- COL1A2 is the pro alpha2 chain of type I collagen whose triple helix comprises two alpha1 chains and one alpha2 chain Type I is a fibril forming collagen found in most connective tissues and is abund
- CPE is a carboxypeptidase that cleaves C terminal amino acid residues and is involved in the biosynthesis of peptide hormones and neurotransmitters including insulin It is a peripheral membrane prot
- DLD is the L protein of the mitochondrial glycine cleavage system The L protein also named dihydrolipoamide dehydrogenase is also a component of the pyruvate dehydrogenase complex the alpha ketogl
- EPHA5 belongs to the ephrin receptor subfamily of the protein tyrosine kinase family EPH and EPH related receptors have been implicated in mediating developmental events particularly in the nervous
- ERLIN2 plays an important role in the early steps of the endoplasmic reticulum associated degradation ERAD pathway It is involved in ITPR1 degradation by the ERAD pathway
- The GLP2 receptor GLP2R is a G protein coupled receptor superfamily member closely related to the glucagon receptor ans GLP1 receptor Glucagon like peptide 2 GLP2 is a 33 amino acid proglucagon d
- HNRPH1 belongs to the subfamily of ubiquitously expressed heterogeneous nuclear ribonucleoproteins hnRNPs The hnRNPs are RNA binding proteins and they complex with heterogeneous nuclear RNA hnRNA
- KLHL15 is a member of the kelch like family of proteins that share a common domain structure consisting of an N terminal broad complex tramtrack bric a brac poxvirus and zinc finger domain and C ter
- KPTN may be involved in actin dynamics KPTN may play a role in producing the sensory apparatus in hair cells KPTN may also play a role in actin rearrangements that accompany platelet activation and
- LCN12 may play a role in male fertility LCN12 may act as a retinoid carrier protein within the epididymis
- Neuromedin B receptor binds neuromedin B a potent mitogen and growth factor for normal and neoplastic lung and for gastrointestinal epithelial tissue Neuromedin B receptor binds neuromedin B a poten
- The function of this protein is binding oxidoreductase activity and transcription repressor activity
- OR10X1 is an odorant receptor Olfactory receptors interact with odorant molecules in the nose to initiate a neuronal response that triggers the perception of a smell The olfactory receptor proteins
- PGLS belongs to the glucosamine galactosamine 6 phosphate isomerase family 6 phosphogluconolactonase subfamily It is implicated in the hydrolysis of 6 phosphogluconolactone to 6 phosphogluconate
- PNPO catalyzes the terminal rate limiting step in the synthesis of pyridoxal 5 phosphate also known as vitamin B6 Vitamin B6 is a required co factor for enzymes involved in both homocysteine metab
- SAMD8 is a multi pass membrane protein It belongs to the sphingomyelin synthase family and contains 1 SAM sterile alpha motif domain The function of the SAMD8 protein remains unknown
- The exact function of SCRN2 remains unknown
- SLC25A6 catalyzes the exchange of ADP and ATP across the mitochondrial inner membrane SLC25A6 may participate in the formation of the permeability transition pore complex PTPC responsible for the r
- TUFM is a protein which participates in protein translation in mitochondria Mutations in this gene have been associated with combined oxidative phosphorylation deficiency resulting in lactic acidosis
- TXNDC5 is a protein disulfide isomerase Its expression is induced by hypoxia and its role may be to protect hypoxic cells from apoptosis This gene encodes a protein disulfide isomerase Its expressio
- Low density lipoprotein receptor related protein 1 2 macroglobulin receptor LRP1 is a multifunctional endocytic receptor with an important role in regulating the activity of proteinases in the ex
- EVI1 promotes cell proliferation by interacting with BRG1 and blocking the repression of BRG1 on E2F1 activity
- ARPC2 is one of seven subunits of the human Arp2 3 protein complex The Arp2 3 protein complex has been implicated in the control of actin polymerization in cells and has been conserved through evolut
- ATP6V1C1 is a component of vacuolar ATPase V ATPase a multisubunit enzyme that mediates acidification of intracellular compartments of eukaryotic cells V ATPase dependent acidification is necessar
- BPNT1 also called bisphosphate 3 prime nucleotidase or BPntase is a member of a magnesium dependent phosphomonoesterase family Lithium a major drug used to treat manic depression acts as an unco
- Calreticulins such as CALR3 are Ca 2 binding chaperones localized mainly in the endoplasmic sarcoplasmic reticulum Calreticulins such as CALR3 are Ca 2 binding chaperones localized mainly in
- The specific function of CCDC54 is not yet known
- DDAH2 hydrolyzes N G N G dimethyl L arginine ADMA and N G monomethyl L arginine MMA which act as inhibitors of NOS DDAH2 has therefore a role in nitric oxide generation This gene belongs to
- EFHD2 may regulate B cell receptor BCR induced immature and primary B cell apoptosis It plays a role as negative regulator of the canonical NF kappa B activating branch EFHD2 controls spontaneous
- The specific function of ESSPL is not yet known
- FN3KRP phosphorylates psicosamines and ribulosamines but not fructosamines on the third carbon of the sugar moiety Protein bound psicosamine 3 phosphates and ribulosamine 3 phosphates are unstable
- GLRX3 may play a role in regulating the function of the thioredoxin system
- The specific function of LYPD4 is not yet known
- Lysophospholipases are enzymes that act on biological membranes to regulate the multifunctional lysophospholipids Lysophospholipases are enzymes that act on biological membranes to regulate the multif
- Cytosolic 5 prime nucleotidases such as NT5C1B catalyze production of adenosine which regulates diverse physiologic processes Cytosolic 5 prime nucleotidases such as NT5C1B catalyze production of
- The 2 oxoglutarate dehydrogenase complex catalyzes the overall conversion of 2 oxoglutarate to succinyl CoA and CO2 It contains multiple copies of three enzymatic components 2 oxoglutarate dehydroge
- PPP1CA is one of the three catalytic subunits of protein phosphatase 1 PP1 PP1 is a serine threonine specific protein phosphatase known to be involved in the regulation of a variety of cellular pro
- SPATA16 is involved in the formation of sperm acrosome which implicated its potential role in spermatogenesis and sperm egg fusion Defects in SPATA16 are a cause of globozoospermia also called Roun
- SPATA22 is highly expressed in adult testis The specific function of SPATA22 is not yet known
- Tissue specific transplantation antigen P35B is a NADP H binding protein It catalyze the two step epimerase and the reductase reactions in GDP D mannose metabolism converting GDP 4 keto 6 D deoxym
- UCHL3 is an ubiquitin protein hydrolase involved both in the processing of ubiquitin precursors and of ubiquitinated proteins This enzyme is a thiol protease that recognizes and hydrolyzes a peptide
- The specific function of FLJ14803 is not yet known
- This protein is an intracellular F actin binding protein The protein is expressed in lymphocytes neutrophils macrophages and endothelium and may regulate neutrophil motility adhesion to fibrinoge
- WDR3 is a nuclear protein containing 10 WD repeats WD repeats are approximately 30 to 40 amino acid domains containing several conserved residues which usually include a trp asp at the C terminal e
- CCNT1 belongs to the highly conserved cyclin family whose members are characterized by a dramatic periodicity in protein abundance through the cell cycle Cyclins function as regulators of CDK kinase
- CDK5 is probably involved in the control of the cell cycle It interacts with D1 and D3 type G1 cyclins The protein can phosphorylate histone H1 tau MAP2 and NF H and NF M And it is also thought t
- CDC25C gene is highly conserved during evolution and it plays a key role in the regulation of cell division The protein is a tyrosine phosphatase and belongs to the Cdc25 phosphatase family It direc
- FOXM1 is a transcriptional activatory factor It may play a role in the control of cell proliferation
- CCR4 belongs to the G protein coupled receptor family It is a receptor for the CC chemokine MIP 1 RANTES TARC and MCP 1 Chemokines are a group of small polypeptide structurally related molecul
- The function of CXCL9 has not been specifically defined however it is thought to be involved in T cell trafficking This gene has been localized to 4q21 with INP10 which is also a member of the che
- CCL8 gene is one of several cytokine genes clustered on the q arm of chromosome 17 Cytokines are a family of secreted proteins involved in immunoregulatory and inflammatory processes The protein is
- CMKLR1 mediates the Resolvin E1 signal to attenuate nuclear factor kappaB
- TRAF4 is a member of the TNF receptor associated factor TRAF family TRAF proteins are associated with and mediate signal transduction from members of the TNF receptor superfamily It has been show
- The regulator of G protein signaling RGS proteins are signal transduction molecules that have structural homology to SST2 of Saccharomyces cerevisiae and EGL 10 of Caenorhabditis elegans Multiple g
- CAV2 is a major component of the inner surface of caveolae small invaginations of the plasma membrane and is involved in essential cellular functions including signal transduction lipid metabolism
- In response to double strand DNA breaks TP53INP1 promotes p53 TP53 phosphorylation on Ser 46 and subsequent apoptosis TP53INP1s and HIPK2 could be partners in regulating p53 activity TP531NP1 pla
- KIF20A interacts with guanosine triphosphate GTP bound forms of RAB6A and RAB6B It may act as a motor required for the retrograde RAB6 regulated transport of Golgi membranes and associated vesicles
- APBA3 is a member of the X11 protein family It is an adapter protein that interacts with the Alzheimer s disease amyloid precursor protein This protein is believed to be involved in signal transduct
- For background information on the acetylcholine receptor AChR see CHRNA1 Two forms of AChR are found in mammalian skeletal muscle cells The mature form is predominant in innervated adult muscle a
- GABRG2 is a gamma aminobutyric acid GABA receptor GABA is the major inhibitory neurotransmitter in the mammlian brain where it acts at GABA A receptors which are ligand gated chloride channels G
- Galanin is small neuropeptide that functions as a cellular messenger within the central and peripheral nervous systems modulating diverse physiologic functions
- HTR2A belongs to the G protein coupled receptor 1 family It is one of the several different receptors for 5 hydroxytryptamine serotonin a biogenic hormone that functions as a neurotransmitter a h
- The neurotransmitter serotonin 5 hydroxytryptamine 5 HT has been implicated in a wide range of psychiatric conditions and also has vasoconstrictive and vasodilatory effects HTR5A is a member of 5
- OPRK1 is a multi pass membrane protein It belongs to the G protein coupled receptor 1 family OPRK1 inhibits neurotransmitter release by reducing calcium ion currents and increasing potassium ion con
- RAB8A is a member of the RAS superfamily which are small GTP GDP binding proteins with an average size of 200 amino acids The RAS related proteins of the RAB YPT family may play a role in the transpo
- STXBP1 belongs to the STXBP unc 18 SEC1 family It may participate in the regulation of synaptic vesicle docking and fusion possibly through interaction with GTP binding proteins The protein is esse
- OAS1 is a member of the 2 5A synthetase family essential proteins involved in the innate immune response to viral infection It is induced by interferons and uses adenosine triphosphate in 2 specifi
- DEK is a protein with one SAP domain This protein binds to cruciform and induces positive supercoils into closed circular DNA and is also involved in splice site selection durin
- TLX1 contains 1 homeobox DNA binding domain TLX1 controls the genesis of the spleen A chromosomal aberration involving TLX1 translocation t 10 14 q24 q11 with TCRD may be a cause of a form of
- MHC class II gene expression is controlled primarily at the transcriptional level by transcription factors that bind to the X and Y boxes two highly conserved elements in the proximal promoter of MHC
- The gene encodes the DMRT1 protein is found in a cluster

with two other members of the gene family having in common a zinc finger like DNA binding motif DM domain The DM domain is an ancient cons

- SOX8 is a member of the SOX SRY related HMG box family of transcription factors involved in the regulation of embryonic development and in the determination of the cell fate It may act as a transcr
- REL is a member of the Rel NFKB family which also includes RELA RELB NFKB1 and NFKB2 These proteins are related through a highly conserved N terminal region termed the Rel domain which is resp
- Brg or hBrm associated factor BAF complexes a chromatin remodeling complex family of mammalian cells facilitate transcriptional activity by remodeling nucleosome structure Brg1 is the core subun
- The protein encoded by E2F1 is a member of the E2F family of transcription factors The E2F family plays a crucial role in the control of cell cycle and action of tumor suppressor proteins and is also
- GATA1 is a protein which belongs to the GATA family of transcription factors The protein plays an important role in erythroid development by regulating the switch of fetal hemoglobin to adult hemoglo
- ELK3 is a member of the ETS domain transcription factor family and the ternary complex factor TCF subfamily Proteins in this subfamily regulate transcription when recruited by serum response factor
- PAX2 encodes paired box gene 2 one of many human homologues of the Drosophila melanogaster gene prd The central feature of this transcription factor gene family is the conserved DNA binding paired b
- GTF2E1 belongs to the TFIIE alpha subunit family It recruits TFIIH to the initiation complex and stimulates the RNA polymerase II C terminal domain kinase and DNA dependent ATPase activities of TFIIH
- NFKBIL2 is thought to be a negative regulator of NF kappa B mediated transcription It may bind NF kappa B complexes and trap them in the cytoplasm preventing them from entering the nucleus and inter
- Lymphoid enhancer binding factor 1 LEF1 is a 48 kD nuclear protein that is expressed in pre B and T cells It binds to a functionally important site in the T cell receptor alpha TCRA enhancer and
- GTF2H2 gene is part of a 500 kb inverted duplication on chromosome 5q13 This duplicated region contains at least four genes and repetitive elements which make it prone to rearrangements and deletions
- Homeobox containing genes are thought to have a role in controlling development In Drosophila the engrailed en gene plays an important role during development in segmentation where it is requir
- The helix loop helix HLH proteins are a family of putative transcription factors some of which have been shown to play an important role in growth and development of a wide variety of tissues and s
- ID2 belongs to the inhibitor of DNA binding ID family members of which are transcriptional regulators that contain a helix loop helix HLH domain but not a basic domain Members of the ID family i
- HSF2 binds specifically to the heat shock element and has homology to HSFs of other species Heat shock transcription factors activate heat shock response genes under conditions of heat or other stres
- CCNH belongs to the highly conserved cyclin family whose members are characterized by a dramatic periodicity in protein abundance through the cell cycle Cyclins function as regulators of CDK kinases
- The polycomb group PcG protein HPC2 which functions as a transcriptional suppressor is a candidate of KyoT2 binding proteins Pc2 dramatically enhances CtBP sumoylation Pc2 is a SUMO E3 and Poly
- The growth arrest specific 7 GAS7 gene is expressed primarily in terminally differentiated brain cells and predominantly in mature cerebellar Purkinje neurons GAS7 plays a putative role in neuronal
- Familial incontinentia pigmenti IP is a genodermatosis that segregates as an X linked dominant disorder and is usually lethal prenatally in males In affected females it causes highly variable abno
- This gene which is located on chromosome 20 is predicted to encode for a signal protein with unknown function
- FLJ14768 is homologous to mouse and bovine Fiz1 flt 3 interacting zinc finger It interacts with NRL neural retina leucine zipper Possible role for Fiz1 as a transcriptional repressor
- Zinc Finger Protein 341 is a new candidate transcription factor
- The ZNF341 gene is located on chromosome 20
- ZNF499 is located on chromosome 19
- The ZNF499 gene is located on chromosome 19 and encodes a protein with unknown function
- SMARCA5 is a member of the SWI SNF family of proteins Members of this family have helicase and ATPase activities and are thought to regulate transcription of certain genes by altering the chromatin s
- In mouse Hes7 expression is associated with somitogenesis and is controlled by Notch signaling
- Members of the Kruppel like zinc finger protein family such as GLIS2 function as activators and or repressors of gene transcription
- SUPT3H is a component of the multiprotein SPT ADA GCN5 acetyltransferase SAGA complex that integrates proteins with transcription coactivator adaptor functions ADAs and GCN5 histone acetyltransfe
- Mutations in the winged helix transcription factor gene at the nude locus in mice and rats produce the pleiotropic phenotype of hairlessness and athymia resulting in a severely compromised immune sys
- The function of ZMAT1 has not been determined
- ZNF512 is a new candidate transcription factor
- ZNF541 is a new candidate transcription factor
- ZNF394 belongs to the krueppel C2H2 type zinc finger protein family and may be involved in transcriptional regulation
- EEA1 is involved in neuronal synaptic vesicle function and axonal transport and growth EEA1 may undergo calcium dependent conformational changes that are required for binding to SNAP 25
- MIXL1 is a novel human Mix like homeobox gene In normal hematopoiesis its expression appears to be restricted to immature B and T lymphoid cells
- TFAP2D has significantly high homology to transcription factor AP 2 gene of human It is highly expressed in adult thymus prostate small intestine skeletal muscle placenta brain and testis tissu
- MXD3 contains 1 basic helix loop helix bHLH domain It is a transcriptional repressor and binds with MAX to form a sequence specific DNA binding protein complex which recognizes the core sequence 5
- GFI1B acts in the late stage of erythroid differentiation as a transcriptional repressor GATA 1 and NF Y both contribute to erythroid specific transcriptional activation of the Gfi 1B promoter This
- EOMES is a member of a conserved protein family that shares a common DNA binding domain the T box T box genes encode transcription factors involved in the regulation of developmental processes A si
- RBM10 contains RNA recognition motif found in a variety of RNA binding proteins including various hnRNP proteins proteins implicated in regulation of alternative splicing and protein components of
- ELL was shown to encode a previously uncharacterized elongation factor that can increase the catalytic rate of RNA polymerase II transcription by suppressing transient pausing by polymerase at multipl
- TSC22D4 is a leucine zipper containing protein that is highly conserved during evolution It is transcriptionally up regulated by many different stimuli including anti cancer drugs and growth inhibit
- Although C1orf25 is similar to N2 N2 dimethylguanosine tRNA methyltransferase from other organisms the true function of C1orf25 protein is not known
- Calreticulin is a multifunctional protein that acts as a major Ca 2 binding storage protein in the lumen of the endoplasmic reticulum It is also found in the nucleus suggesting that it may have
- YEATS4 is found in the nucleoli It has high sequence homology to human MLLT1 and yeast and human MLLT3 proteins Both MLLT1 and MLLT3 proteins belong to a class of transcription factors indicating
- CCNB1 is a regulatory protein involved in mitosis CCNB1 complexes with p34 cdc2 to form the maturation promoting factor MPF The protein encoded by this gene is a regulatory protein involved in mi
- HSPB1 like the other heat shock proteins is part of a complex system of molecular chaperones in epidermal keratinocytes
- RAD17 is highly similar to the gene product of Schizosaccharomyces pombe rad17 a cell cycle checkpoint gene required for cell cycle arrest and DNA damage repair in response to DNA damage This protei
- Regulator of G protein signaling RGS family members are regulatory molecules that act as GTPase activating proteins GAPs for G alpha subunits of heterotrimeric G proteins RGS proteins are able to
- TERF2 is a telomere specific protein TERF2 which is a component of the telomere nucleoprotein complex This protein is present at telomeres in metaphase of the cell cycle is a second negative regul
- In response to DNA damage and replication blocks cell cycle progression is halted through the control of critical cell cycle regulators CHEK2 is a cell cycle checkpoint regulator and putative tumor
- Fadd is apoptotic adaptor molecule that recruits caspase 8 or caspase 10 to the activated Fas CD95 or TNFR 1 receptors The resulting aggregate called the death inducing signaling complex DISC per
- PDPK1 phosphorylates and activates not only PKB AKT but also PKA PKC zeta RPS6KA1 and RPS6KB1 It may play a general role in signaling processes and in development
- Apoptosis is a cell death process that removes toxic and or useless cells during mammalian development The apoptotic process is accompanied by shrinkage and fragmentation of the cells and nuclei and
- BCL2L1 encodes a protein which belongs to the BCL 2 protein family The proteins encoded by BCL2L1 are located at the outer mitochondrial membrane and have been shown to regulate outer mitochondrial
- MAP3K8 is a member of the serine threonine protein kinase family This kinase can activate both the MAP kinase and JNK kinase pathways This kinase was shown to activate IkappaB kinases and thus indu
- CCBP2 is a beta chemokine receptor which is predicted to be a seven transmembrane protein similar to G protein coupled receptors Chemokines and their receptor mediated signal transduction are critic
- PBX1 binds the sequence 5 ATCAATCAA 3 It acts as a transcriptional activator of PF4 in complex with MEIS1 It may be converted into a potent transcriptional activator by the 1 19 translocation I
- RBPSUH is a DNA binding protein that activates a full transcriptional response but only demonstrates partial anti apoptotic activity RTA mediated redirection of RBPSUH activity from repression to act
- The protein encoded by this gene is a member of the E2F family of transcription factors The E2F family plays a crucial role in the control of cell cycle and action of tumor suppressor proteins It is
- ELK1 is a member of the Ets family of transcription factors and of the ternary complex factor TCF subfamily Proteins of the TCF subfamily form a ternary complex by binding to the the serum response
- ISGF3G functions to recruit RNA polymerase II to the promoter of interferon stimulated genes and requires histone deacetylases Defects in ISGF3 can cause resistance to IFN 2a treatment
- N Oct 3 POU3F2 is a protein belonging to a large family of transcription factors that bind to the octameric DNA sequence ATGCAAAT Most of these proteins share a highly homologous region referred t
- The protein encoded by this intronless gene CEBPB is a bZIP transcription factor which can bind as a homodimer to certain DNA regulatory regions It can also form heterodimers with the related prote
- NFYA is one subunit of a trimeric complex forming a highly conserved transcription factor that binds to CCAAT motifs in the promoter regions in a variety of genes Subunit A associates with a tight d
- CREB1 is a transcription factor that is a member of the leucine zipper family of DNA binding proteins This protein binds as a homodimer to the cAMP responsive element an octameric palindrome The pr
- The Fos gene family consists of 4 members FOS FOSB FOSL1 and FOSL2 which encode leucine zipper proteins that can dimerize with proteins of the JUN family thereby forming the transcription factor
- TCEB2 is the protein elongin B which is a subunit of the transcription factor B SIII complex The SIII complex is composed of elongins A A2 B and C It activates elongation by RNA polymerase II by
- ATF1 binds the cAMP response element CRE consensus 5 GTGACGT AC AG 3 a sequence present in many viral and cellular promoters ATF1 binds to the Tax responsive element TRE of HTLV I ATF1
- POU4F2 is a member of the POU domain family of transcription factors POU domain proteins have been observed to play important roles in control of cell identity in several systems A class IV POU doma
- KLF9 is a transcription factor that binds to GC box elements located in the promoter Binding of the encoded protein to a single GC box inhibits mRNA expression while binding to tandemly repeated GC b
- Homeobox containing genes are thought to have a role in controlling development The human engrailed homologs 1 and 2 encode homeodomain containing proteins and have been implicated in the control of
- The Fos gene family consists of 4 members FOS FOSB FOSL1 and FOSL2 These genes encode leucine zipper proteins that can dimerize with proteins of the JUN family thereby forming the transcription
- HOXB6 belongs to the homeobox family The homeobox genes encode a highly conserved family of transcription factors that play an important role in morphogenesis in all multicellular organisms Mammals
- HOXD4 belongs to the homeobox family of genes The homeobox genes encode a highly conserved family of

transcription factors that play an important role in morphogenesis in all multicellular organisms

- LYL1 contains 1 basic helix loop helix bHLH domain A chromosomal aberration translocation t 7 19 q35 p13 with TCRB involving LYL1 may be a cause of a form of T cell acute lymphoblastic leukem
- Slightly proximal to the Huntington disease locus the human MSX1 gene is deleted in patients with Wolf Hirschhorn syndrome This gene is also called HOX7 The Msx family of vertebrate HOX genes was o
- The function remains unknown This gene encodes a mitochondrial transcription factor that is a key activator of mitochondrial transcription as well as a participant in mitochondrial genome replication
- Expression of the c myc gene which produces an oncogenic transcription factor is tightly regulated in normal cells but is frequently deregulated in human cancers The MXI1 gene encodes a transcripti
- SPI1 MIM 165170 and SPIB are members of a subfamily of ETS see ETS1 MIM 164720 transcription factors ETS proteins share a conserved ETS domain that mediates specific DNA binding SPIB and SPI1 b
- TAFs may participate in basal transcription serve as coactivators function in promoter recognition or modify general transcription factors GTFs to facilitate complex assembly and transcription ini
- GTF2E2 alpha s interaction with RNA polymerase II is subsequent to the entry of RNA polymerase II into the transcription cycle
- GTF2F2 synergizes with HIV 1 Tat and the cellular coactivator Tat SF1 during Tat mediated transactivation of the HIV 1 LTR promoter This gene is required for both basal and HIV 1 Tat activated transc
- GTranscription Factor Antibodies2F2 is required for both basal and HIV 1 Tat activated transcription GTranscription Factor Antibodies2F2 synergizes with HIV 1 Tat and the cellular co activator Tat SF
- GTF2F2 synergizes with HIV 1 Tat and the cellular coactivator Tat SF1 during Tat mediated transactivation of the HIV 1 LTR promoter
- GTranscription Factor Antibodies2H3 interacts with HIV 1 Tat as a component of the HIV 1 transcription pre initiation complex but is released from the elongation complex which includes P TEFb It syn
- HHEX encodes a member of the homeobox family of transcription factors many of which are involved in developmental processes Expression in specific hematopoietic lineages suggests that this protein m
- HOXB5 belongs to the homeobox family The homeobox genes encode a highly conserved family of transcription factors that play an important role in morphogenesis in all multicellular organisms Mammals
- Histones play a critical role in transcriptional regulation cell cycle progression and developmental events Histone acetylation deacetylation alters chromosome structure and affects transcription f
- THRAP5 is part of the human thyroid hormone receptor associated protein TRAP Mediator family which acts as a coactivator for a broad range of nuclear hormone receptors as well as other classes of tr
- PQBP1 is a nuclear polyglutamine binding protein that contains a WW domain Mutations in this gene are associated with X linked mental retardation
- YAF2 interacts with YY1 a zinc finger protein involved in negative regulation of muscle restricted genes YAF2 contains a single N terminal C2 X10 C2 zinc finger and in contrast to YY1 is up regula
- OLIG2 is a basic helix loop helix transcription factor which is expressed in oligodendroglial tumors of the brain OLIG2 is an essential regulator of ventral neuroectodermal progenitor cell fate It i
- CDX2 encodes a protein that plays an important role in gallbladder carcinogenesis with intestinal differentiation Cdx2 is a highly sensitive marker for Barrett s esophagus
- The gene corresponding to embryonic lung protein also known as Solute carrier family 30 Zinc transporter member 9 SLC30A9 is likely to be an evolutionarily conserved housekeeping gene that pla
- CDX are homeodomain transcription factors related to the Drosophila caudal gene The vertebrate CDX have been implicated in the development of the posterior embryo Several signaling molecules notabl
- KLF1 is a transcription factor originally identified in this laboratory which plays a crucial role as a transcriptional activator at the adult beta globin locus
- TCFL5 is a new bHLH transcription factor that negatively regulates upstream transcription factor dependent transcription
- ZNF274 is a zinc finger protein containing five C2H2 type zinc finger domains one or two Kruppel associated box A KRAB A domains and a leucine rich domain The protein has been suggested to be a t
- RIPK3 is a member of the receptor interacting protein RIP family of serine threonine protein kinases and contains a C terminal domain unique from other RIP family members The protein is predominan
- The SALF mRNA is an infrequent but naturally occurring co transcribed product of the neighboring SBLF and ALF genes This rare transcript encodes a fusion protein composed of greater than 95 each of
- PMF1 is part of the MIS12 complex which is required for normal chromosome alignment and segregation and kinetochore formation during mitosis It may act as a cotranscription partner of NFE2L2 involved
- ELL encodes an RNA polymerase II transcription factor that undergoes frequent translocation in acute myeloid leukemia AML In addition to its elongation activity ELL contains a novel type of RNA po
- KLF8 is abnormally expressed in female patients with X autosome translocation t X 21 p11 2 q22 3 and non syndromic mental retardation
- Osr2 is a zinc finger containing protein related to Drosophila Odd skipped Its mRNA expression is specifically activated in the nascent palatal mesenchyme at the onset of palatal outgrowth Osr2 muta
- Zinc finger proteins Zfp are encoded by a large family of genes present in many organisms including yeast and human Some of them are transcriptional activators and bind specifically to DNA by zinc
- ZFP1 is part of a large family of genes present in many organisms including yeast and human Some of them are transcriptional activators and bind specifically to DNA by zinc mediated folded structures
- DBP is a member of the PAR bZIP proline and acidic amino acid rich basic leucine zipper transcription factor family Khatib et al 1994
- ZNF342 contains 6 C2H2 type zinc fingers and belongs to the krueppel C2H2 type zinc finger protein family It may be involved in transcriptional regulation
- The adipocyte enhancer binding protein 1 AEBP1 is a transcriptional repressor with carboxypeptidase CP activity This protein binds to a regulatory sequence adipocyte enhancer 1 AE 1 located i
- Many vertebrate homeo box containing genes have been identified on the basis of their sequence similarity with Drosophila developmental genes Members of the Dlx gene family contain a homeobox that is
- E2F2 is a member of the E2F family of transcription factors The E2F family plays a crucial role in the control of cell cycle and action of tumor suppressor proteins and is also a target of the transf
- EBF1 belongs to the COE family It contains 1 IPT TIG domain EBF1 is a transcriptional activator which recognizes variations of the palindromic sequence 5 ATTCCCNNGGGAATT 3
- SP7 is a C2H2 type zinc finger transcription factor of the SP gene family and a putative master regulator of bone cell differentiation
- SP7 is a C2H2 type zinc finger transcription factor of the SP gene family and a putative master regulator of bone cell differentiation SP7 is a C2H2 type zinc finger transcription factor of the SP gen
- Aryl hydrocarbon receptor AHR is a ligand activated transcription factor involved in the regulation of biological responses to planar aromatic hydrocarbons AHR has been shown to regulate xenobiotic
- The ELF2 gene encodes a protein that physically interacts with AML1 and mediates opposing effects on AML1 mediated transcription of the B cell specific blk gene
- The homeodomain transcription factor EMX2 is critical for central nervous system and urogenital development EMX1 along with EMX2 is related to the empty spiracles gene expressed in the developing D
- ZNF449 belongs to the krueppel C2H2 type zinc finger protein family It contains 7 C2H2 type zinc fingers and 1 SCAN box domain ZNF449 may be involved in transcriptional regulation
- The gene encoding the hypothetical protein LASS3 is located on chromosome 15
- ESR2 is a member of the family of estrogen receptors and superfamily of nuclear receptor transcription factors The gene product contains an N terminal DNA binding domain and C terminal ligand binding
- ESRRB encodes a protein with similarity to the estrogen receptor Its function is unknown however a similar protein in mouse plays an essential role in placental development Sequence Note The sequ
- ERRs which are coexpressed with ERs in prostatic cells could regulate cell growth and modulate ER mediated pathways via interference on ERalpha transcription in prostatic cells Not only PNRC2 but a
- ETV5 Contains 1 ETS DNA binding domain and belongs to the ETS family The ETV5 gene expression is regulated by the conventional PKC cPKC pathway ETV5 is subject to SUMO modification and this post tr
- FGD1 contains Dbl DH and pleckstrin PH homology domains It can bind specifically to the Rho family GTPase Cdc42Hs and stimulate the GDP GTP exchange of the isoprenylated form of Cdc42Hs It also
- Novel short isoforms of this gene ZNFN1A2 are overexpressed in a patient with T cell acute lymphoblastic leukemia and may contribute to the development of T cell malignancies
- ZNF652 is a new candidate transcription factor
- Zinc Finger Protein 365 is a new candidate transcription factor
- Kin is a nuclear protein that forms intranuclear foci during proliferation and is redistributed in the nucleoplasm during the cell cycle Short wave ultraviolet light provokes the relocalization of th
- FOXF1 belongs to the forkhead family of transcription factors which is characterized by a distinct forkhead domain The specific function of this gene has not yet been determined however it may play
- TRIM32 is a member of the tripartite motif TRIM family The TRIM motif includes three zinc binding domains a RING a B box type 1 and a B box type 2 and a coiled coil region TRIM32 localizes to c
- FOXF2 encodes forkhead box F2 one of many human homologues of the Drosophila melanogaster transcription factor forkhead FOXF2 is expressed in lung and placenta and has been shown to transcriptional
- FBXL11 is a member of the F box protein family which is characterized by an approximately 40 amino acid motif the F box The F box proteins constitute one of the four subunits of ubiquitin protein li
- FOXC2 belongs to the forkhead family of transcription factors which is characterized by a distinct DNA binding forkhead domain The specific function of this gene has not yet been determined however
- The function of ZNF609 remains unknown
- FOXD2 belongs to the forkhead family of transcription factors which is characterized by a distinct forkhead domain The specific function of this gene has not yet been determined
- TLR6 is a member of the Toll like receptor TLR family which plays a fundamental role in pathogen recognition and activation of innate immunity TLRs are highly conserved from Drosophila to humans an
- ZNF297B is a candidate transcription factor
- PTDSR is required during embryogenesis and differentiation of multiple organs during embryogenesis PTDSR probably acts as a key regulator of hematopoietic differentiation PTDSR may not be required f
- SEC14L2 encodes a cytosolic protein which belongs to a family of lipid binding proteins including Sec14p alpha tocopherol transfer protein and cellular retinol binding protein The encoded protein s
- SSBP2 is a member of a closely related evolutionarily conserved and ubiquitously expressed gene family It is also a potential tumor suppressor
- ZFP95 is a zinc finger protein of the Kruppel family It contains a SCAN box and a KRAB A domain A similar protein in mouse is differentially expressed in spermatogenesis
- NR5A2 binds to the sequence element 5 AACGACCGACCTTGAG 3 of the enhancer II of hepatitis B virus genes a critical cis element of their expression and regulation It may be responsable for the liver
- NR5A1 is an important regulator of steroidogeneisis which is present in human skin and its appendages It plays a role in regulating p450scc expression with TReP 132 and CBP p300 The protein encoded
- ZNF620 is a new candidate transcription factor
- EB1 family proteins are evolutionarily conserved proteins that bind microtubule plus ends and centrosomes and regulate the dynamics and organization of microtubules Human EB1 family proteins which i
- PTF1A is a pancreas specific transcription factor Mammalian studies have implicated important roles for the basic helix loop helix transcription factor PTF1A p48 in the development of both exocrine a
- PDEF is an ETS transcription factor expressed in prostate epithelial cells It acts as an androgen independent transactivator of PSA expression PDEF is an ETS transcription factor expressed in prostat
- The function of the C20orf194 gene has not yet been determined
- Results suggest that RZF is a shuttling regulatory protein expressed in photoreceptors of the human retina that may be involved in mRNA or protein regulation of photoreceptor specific genes and theref
- ZNF500 is a new candidate transcription factor
- ZBTB20 is a 733 residue protein with a BTB POZ domain at the N terminal and 4 C2H2 zinc fingers at C terminal It is localized on chromosome 3 It is widely expressed in

hematopoietic tissues

- The GATA family of transcription factors which contain zinc fingers in their DNA binding domain have emerged as candidate regulators of gene expression in hematopoietic cells is essential for normal
- A murine NKX2 8 was isolated from the Hepal 6 cell line and showed oligonucleotide binding competitive with fetoprotein transcription factor Nkx2 8 bound to the active AFP promoter and antisense inh
- The MYCBP gene encodes a protein that binds to the N terminal region of MYC and stimulates the activation of E box dependent transcription by MYC
- EHF belongs to an ETS transcription factor subfamily characterized by epithelial specific expression ESEs The encoded protein acts as a transcriptional repressor and may be associated with asthma s
- Altered expression of GBX2 part of the homeobox containing human family of DNA binding transcription factors is associated with therapy failure and death in patients with multiple types of cancer
- HEYL belongs to hairy related bHLH transcription factor family HEY genes are candidates for several human or mouse disease loci
- The AATF gene encodes a protein that was identified on the basis of its interaction with MAP3K12 DLK a protein kinase known to be involved in the induction of cell apoptosis This gene product contai
- GFI1 may be a transcription factor involved in regulating the expression of genes active in the S phase during cell cycle progression in T cells GFI1 may be involved in tumor progression Defects in
- ZBTB32 may play an essential role during the proliferative stages of primitive hematopoietic progenitors possibly acting in concert with a subset of the Fanconi anemia proteins This gene can also
- Whereas most DNA sequence specific transcription factors increase the rate of initiation and interact with enhancer or promoter DNA human immunodeficiency virus 1 HIV 1 Tat predominantly stimulates
- GLI2 encodes a protein which belongs to the C2H2 type zinc finger protein subclass of the Gli family Members of this subclass are characterized as transcription factors which bind DNA through zinc fi
- MKX is a member of the TALE superclass of atypical homeobox genes that is most closely related to the Iroquois class
- The function of the C13orf8 gene has not yet been determined
- ZNF545 belongs to the krueppel C2H2 type zinc finger protein family and may be involved in transcriptional regulation
- ZNF326 is a candidate transcription factor
- Rho GTPases control a variety of cellular processes There are 3 subtypes of Rho GTPases in the Ras superfamily of small G proteins RHO RAC and CDC42 GTPase activating proteins GAPs bind activat
- GTF2I encodes a multifunctional phosphoprotein with roles in transcription and signal transduction It is deleted in Williams Beuren syndrome a multisystem developmental disorder caused by the deleti
- TFCP2L1 is a candidate CP2 family member It is expressed in a developmentally regulated fashion in vivo and acts as a direct repressor of transcription CP2 related proteins comprise a family of DNA
- TBX21 is a member of a phylogenetically conserved family of genes that share a common DNA binding domain the T box T box genes encode transcription factors involved in the regulation of developmenta
- Retinal Homeobox Protein Rx RAX is a member of homeobox family of transcription factors Mutations mouse and fish RAX lead to defects in retinal development and result in animal models of anophthalm
- HCLS1 is a substrate for caspase cleavage during apoptosis
- HCLS1 Tyr phosphorylation catalyzed by Syk and Lyn plays a crucial role in the translocation of the protein to the membrane and is involved in the cytoskeleton rearrangement triggered by thrombin in h
- CSEN is a member of the family of voltage gated potassium Kv channel interacting proteins KCNIPs which belong to the recoverin branch of the EF hand superfamily Members of the KCNIP family are s
- This protein is a member of the non histone chromosomal high mobility group family The proteins of this family are chromatin associated and ubiquitously distributed in the nucleus of higher eukaryoti
- NR4A1 is a member of the steroid thyroid hormone retinoid receptor superfamily Expression is induced by phytohemagglutinin in human lymphocytes and by serum stimulation of arrested fibroblasts The e
- NR4A1 encodes a member of the steroid thyroid hormone retinoid receptor superfamily Expression is induced by phytohemagglutinin in human lymphocytes and by serum stimulation of arrested fibroblasts
- FOXA3 encodes a member of the forkhead class of DNA binding proteins These hepatocyte nuclear factors are transcriptional activators for liver specific transcripts such as albumin and transthyretin
- The protein encoded by HNF4A is a nuclear transcription factor which binds DNA as a homodimer The encoded protein controls the expression of several genes including hepatocyte nuclear factor 1 alpha
- HNF4 was first identified as a DNA binding activity in rat liver nuclear extracts and then was found to be an orphan member of the nuclear receptor superfamily Binding sites for this factor were iden
- HOXC4 belongs to the homeobox family of genes The homeobox genes encode a highly conserved family of transcription factors that play an important role in morphogenesis in all multicellular organisms
- HOXD3 homeobox D3 belongs to the homeobox family of genes The homeobox genes encode a highly conserved family of transcription factors that play an important role in morphogenesis in all multicellu
- HOXD11 belongs to the homeobox family This family play an important role in morphogenesis in all multicellular organisms The mouse Hoxd11 plays a role in forelimb morphogenesis This gene belongs to
- Human CHX10 is expressed in progenitor cells of the developing neuroretina and in the inner nuclear layer of the mature retina The strong conservation in vertebrates of the CHX10 sequence pattern of
- LOC339123 is a candidate transcription factor located on chromosome 16
- LOC344191 is a new candidate transcription factor
- LOC346157 is a new candidate transcription factor
- ZFP57 is a protein similar to zinc finger protein 57 It is derived from an annotated genomic sequence NT 007592 using gene prediction method
- Zinc Finger Protein 81 is a new candidate transcription factor
- Insulinoma associated 1 INSM1 gene is intronless and encodes a protein containing both a zinc finger DNA binding domain and a putative prohormone domain This gene is a sensitive marker for neuroend
- IRF3 is interferon regulatory factor 3 a member of the interferon regulatory transcription factor IRF family IRF3 is found in an inactive cytoplasmic form that upon serine threonine phosphorylatio
- LMX1A is necessary for the expression of bone morphogenetic protein BMP and for the normal generation and differentiation of the dorsal most spinal cord neurons the dI1 interneurons
- ARNTL is a general dimerization partner for a subset of the basic helix loop helix bHLH PER ARNT SIM PAS superfamily of transcriptional regulators
- SMAD1 belongs to the SMAD family SMAD proteins are signal transducers and transcriptional modulators that mediate multiple signaling pathways SMAD1 mediates the signals of the bone morphogenetic pro
- SMAD4 is one of the Smad family members which are essential intracellular signalling components of the transforming growth factor beta TGF beta superfamily Smad2 and Smad3 are structurally highly
- SMAD5 undergoes copy number gain and increased expression rather than loss of expression and therefore does not act as a tumor suppressor gene in hepatocellular carcinoma Up regulated Smad5 mediate
- Smad7 acts to functionally inactivate RB and de repress E2F without blocking the activation of TbetaRI and the nuclear translocation of Smad2 3 allowing TGF beta1 to exert effects in a cancer cell th
- MBD1 belongs to a family of nuclear proteins related by the presence in each of a methyl CpG binding domain MBD Each of these proteins with the exception of MBD3 is capable of binding specificall
- MEFV was identified as the gene that when mutated causes Mediterranean fever a hereditary periodic fever syndrome MEFV is expressed in granulocytes and myeloid bone marrow precursors
- The zinc finger transcription factor MTF 1 metal responsive transcription factor 1 is conserved from insects to vertebrates The major role of MTF 1 in both organisms is to control the transcription
- MYCN is a member of the MYC family and encodes a protein with a basic helix loop helix bHLH domain It is located in the nucleus and must dimerize with another bHLH protein in order to bind DNA Amp
- NAB1 belongs to the NAB family and acts as a transcriptional repressor for zinc finger transcription factors EGR1 and EGR2
- NeuroD1is a members of bHLH family that involves in neuroendocrine differentiation
- NEUROD2 is a member of the neuroD family of neurogenic basic helix loop helix bHLH proteins Expression of NEUROD2 can induce transcription from neuron specific promoters such as the GAP 43 promote
- NFATC4 is a member of the nuclear factors of activated T cells DNA binding transcription complex This complex consists of at least two components a preexisting cytosolic component that translocates
- NFKB has been detected in numerous cell types that express cytokines chemokines growth factors cell adhesion molecules and some acute phase proteins in health and in various disease states NFKB i
- CNOT2 is one of the subunits of the CCR4 NOT complex which functions as general transcription regulation complex
- NOTCH3 encodes the third discovered human homologue of the Drosophilia melanogaster type I membrane protein notch In Drosophilia notch interaction with its cell bound ligands delta serrate establ
- PCSK6 is a calcium dependent serine endoprotease that can cleave precursor protein at their paired basic amino acid processing sites This gene is thought to play a role in tumor progression
- The tumor suppressor WT1 represses and activates transcription Anti Prostate Apoptosis Response Protein Par 4 PAWR is a WT1 interacting protein that itself functions as a transcriptional repressor
- PAX4 is a member of the paired box PAX family of transcription factors Members of this gene family typically contain a paired box domain an octapeptide and a paired type homeodomain These genes
- IRX4 is likely to be an important mediator of ventricular differentiation during cardiac development
- PBX2 is a ubiquitously expressed member of the TALE PBX homeobox family PBX2 gene was identified by its similarity to a homeobox gene which is involved in t 1 19 translocation in acute pre B cell l
- PBX3 is a transcriptional activator that binds the sequence 5 ATCAATCAA 3
- CGI 143 encodes proteins that seem to be involved in cell proliferation or cell cycle regulation but the molecular function is still unknown
- ZNF691 may be involved in transcriptional regulation
- DVL1 is a cytoplasmic phosphoprotein that regulates cell proliferation acting as a transducer molecule for developmental processes including segmentation and neuroblast specification DVL1 gene is a
- This gene belongs to the forkhead family of transcription factors which are characterized by a distinct forkhead domain The specific function of this gene has not yet been determined however it may
- Phosphoinositide 3 kinases PI3Ks phosphorylate the 3 prime OH position of the inositol ring of inositol lipids They have been implicated as participants in signaling pathways regulating cell growth
- MYF5 is a member of the myogenic basic helix loop helix family of transcription factors which can activate the muscle differentiation program
- MYF6 is a part of the myogenic basic helix loop helix family of transcription factors and can activate the muscle differentiation program
- TFIID is composed of the TATA binding protein TBP and a group of evolutionarily conserved proteins known as TBP associated factors or TAFs TAFs may participate in basal transcription serve as coac
- PRMT3 is a ribosomal protein methyltransferase that affects the cellular level of ribosomal subunits
- RNF12 is a RING H2 zinc finger protein It has been shown to be a ubiquitin protein ligase that targets LIM domain binding 1 LDB1 CLIM and causes proteasome dependent degradation of LDB1 This prot
- ZNF543 a gene located on chromosome 19 encodes a zinc finger protein
- CREBL1 bears sequence similarity with the Creb ATF subfamily of the bZip superfamily of transcription factors It localizes to both the cytoplasm and the nucleus The gene localizes to the major histo
- Pyrimidine 5 prime nucleotidase P5N also called uridine 5 prime monophosphate hydrolase UMPH catalyzes the dephosphorylation of the pyrimidine 5 prime monophosphates UMP and CMP to the correspon
- KLF3 is a zinc finger transcription factor that is known to function as a potent transcriptional repressor
- IRX2 is a member of the Iroquois homeobox gene family Members of this family appear to play multiple roles during pattern formation of vertebrate embryos
- ZFP1 is a candidate transcription factor
- D site binding protein DBP is a member of the PAR bZIP proline and acidic amino acid rich basic leucine zipper transcription factor family
- homeobox protein GSH 2
- DLX3 is a member of the Dlx gene family which contains a homeobox that is related to that of Distal less Dll a gene expressed in the head and limbs of the developing fruit fly

The Distal less home

- E2F6 encodes a member of the E2F transcription factor protein family E2F family members play a crucial role in control of the cell cycle and of the action of tumor suppressor proteins They are also
- E2F6 is a member of the E2F transcription factor protein family E2F family members play a crucial role in control of the cell cycle and of the action of tumor suppressor proteins They are also a tar
- The SOX30 gene encodes a member of the SOX SRY related HMG box family of transcription factors involved in the regulation of embryonic development and in the determination of the cell fate The enco
- The LOC442206 gene is similar to the putative G protein coupled receptor
- The LOC153222 gene is similar to hypothetical protein
- Early Growth Response Protein 1 EGR1 Krox 24 protein nerve growth factor induced protein A Transcription factor ETR103 Zinc finger protein 225 belongs to the EGR family of C2H2 type zinc finger
- AHR is a ligand activated transcription factor involved in the regulation of biological responses to planar aromatic hydrocarbons This receptor has been shown to regulate xenobiotic metabolizing enzy
- ELF3 is a novel highly tissue restricted member of the ets transcription factor oncogene family ELF3 contains two putative DNA binding domains an ETS domain which is unique in that the 5 half sho
- ELF4 contains 1 ETS DNA binding domain and belongs to the ETS family It is transcriptional activator that binds to DNA sequences containing the consensus 5 WGGA 3 It transactivates promoters of th
- Orphan nuclear receptor EAR 2 NR2F6 V erbA related protein EAR 2 is predicted to be a protein similar in primary structure to receptors for steroid hormones or thyroid hormone T3
- NR2F6 is a nuclear orphan receptor that belongs to the COUP TF subfamily
- The protein encoded by the ETV4 gene is known to play a role in ovarian and breast malignancies as well as in the early stage of colorectal carcinogenesis
- TFEC is an activator of transcription with two separate activation domains
- ZNF209 is a candidate transcription factor
- Zinc Finger Protein 365 Isoform B ZNF365 is a new candidate transcription factor
- ZNF365 is located on chromosome 10
- SKIIP Nuclear Protein SkiP nuclear receptor coactivator NCoA 62 ski interacting protein is a member of the SNW gene family encodes a coactivator that enhances transcription from some Pol II promo
- This gene belongs to the forkhead family of transcription factors which is characterized by a distinct forkhead domain The specific function of this gene has not yet been determined however it may
- FOXC1 belongs to the forkhead family of transcription factors which is characterized by a distinct DNA binding forkhead domain The specific function of this gene has not yet been determined however
- FOXL1 is a member of the forkhead family The forkhead domain is a monomeric DNA binding motif that defines a rapidly growing family of eukaryotic transcriptional regulators Genetic and biochemical d
- Forkhead Box Protein E3 FOXE3 forkhead related protein FKHL12 forkhead related transcription factor 8 is a forkhead winged helix transcription factor which is expressed in the developing lens fro
- Hepatocyte Nuclear Factor 1 HNF 1 Homeoprotein LFB3 Transcription factor 2 TCF2 Variant hepatic nuclear factor is a liver specific factor of the homeobox containing basic helix turn helix fa
- TCF2 encodes transcription factor 2 a liver specific factor of the homeobox containing basic helix turn helix family The TCF2 protein is believed to form heterodimers with another liver specific mem
- The bone morphogenetic proteins BMPs are a family of secreted signaling molecules that can induce ectopic bone growth Many BMPs are part of the transforming growth factor beta TGFB superfamily B
- Eyes absent homolog 3 EYA3 is a member of the eyes absent EYA family of proteins This protein may act as a transcriptional activator and have a role during development A similar protein in mice
- ID3 is a member of the ID family The members of the family of helix loop helix HLH proteins lack a basic DNA binding domain and inhibit transcription through formation of nonfunctional dimers that
- PSMD4 encodes one of the non ATPase subunits of the 19S regulator lid which is part of a multicatalytic proteinase complex of the 26S proteasome
- ASCL1 encodes a member of the basic helix loop helix BHLH family of transcription factors The protein activates transcription by binding to the E box 5 CANNTG 3 Dimerization with other BHLH pr
- ALX4 is a member of the ALX homeobox gene family in humans The paired type homeodomain has been shown to mediate high affinity sequence specific DNA binding to palindromic elements as either homodime
- The TLE genes are differentially expressed and encode nuclear proteins consistent with the presence of sequence motifs associated with nuclear functions These genes are the human homologues of Droso
- TBX19 is a member of a phylogenetically conserved family of genes that share a common DNA binding domain the T box T box genes encode transcription factors involved in the regulation of developmenta
- GLI1 is a protein which is a member of the Kruppel family of zinc finger proteins The function of this gene has not been determined however it may play a role in normal development gene transcripti
- SKIL belongs to the SKI family and may have regulatory role in cell division or differentiation in response to extracellular signals
- HES1 belongs to the basic helix loop helix family of transcription factors It is a transcriptional repressor of genes that require a bHLH protein for their transcription The protein has a particular
- LHX1 is a member of a large protein family which contains the LIM domain a unique cysteine rich zinc binding domain It may function as a transcriptional regulator and be involved in control of diffe
- RuvB Like 2 48 kDa TATA box binding protein interacting protein Reptin 52 RUVBL2 is the second human homologue of the bacterial RuvB gene Bacterial RuvB protein is a DNA helicase essential for ho
- RUVBL2 encodes the second human homologue of the bacterial RuvB gene Bacterial RuvB protein is a DNA helicase essential for homologous recombination and DNA double strand break repair Functional ana
- SIX6 is a member of SIX family It is the homologue of the chick Six6 Optx2 gene SIX6 is closely related to SIX3 and is expressed in the developing and adult human retina
- SIRT2 encodes a member of the sirtuin family of proteins homologs to the yeast Sir2 protein Members of the sirtuin family are characterized by a sirtuin core domain and grouped into four classes Th
- SIRT2 is included in class I of the sirtuin family which is characterized by a sirtuin core domain Human sirtuins may function as intracellular regulatory proteins with mono ADP ribosyltransferase ac
- SIRT2 is a member of the sirtuin family of proteins homologs to the yeast Sir2 protein Members of the sirtuin family are characterized by a sirtuin core domain and grouped into four classes The fun
- SIRT1 is a member of the sirtuin family of proteins homologs to the yeast Sir2 protein Members of the sirtuin family are characterized by a sirtuin core domain and grouped into four classes The fun
- SIRT3 is a member of the sirtuin family of proteins homologs to the yeast Sir2 protein Members of the sirtuin family are characterized by a sirtuin core domain and grouped into four classes The fun
- The SIRT3 gene encodes a member of the sirtuin family of proteins homologs to the yeast Sir2 protein The functions of human sirtuins have not yet been determined however yeast sirtuin proteins are
- SIRT3 is included in class I of the sirtuin family which is characterized by a sirtuin core domain Human sirtuins may function as intracellular regulatory proteins with mono ADP ribosyltransferase ac
- SIRT5 is a member of the sirtuin family of proteins homologs to the yeast Sir2 protein Members of the sirtuin family are characterized by a sirtuin core domain and grouped into four classes The fun
- PSMD6 acts as a regulatory subunit of the 26S proteasome which is involved in the ATP dependent degradation of ubiquitinated proteins
- MAP3K7IP2 is an activator of MAP3K7 TAK1 which is required for the IL 1 induced activation of NF B and MAPK8 JNK This protein forms a kinase complex with TRAF6 MAP3K7 and TAB1 thus serving as
- Lymphoid enhancer binding factor 1 LEF1 is a 48 kD nuclear protein that is expressed in pre B and T cells It binds to a functionally important site in the T cell receptor alpha enhancer and confers
- SIRT7 is a member of the sirtuin family of proteins homologs to the yeast Sir2 protein Members of the sirtuin family are characterized by a sirtuin core domain and grouped into four classes The fun
- SIRT6 encodes a member of the sirtuin family of proteins homologs to the yeast Sir2 protein Studies suggest that the human sirtuins may function as intracellular regulatory proteins with mono ADP ri
- Most X autosome translocations associated with premature ovarian failure do not interrupt X linked genes Only one of the six breakpoints disrupts the DACH2 gene
- BHLHB5 is a member of family of basic helix loop helix bHLH transcription factors Members of this family have been implicated in many aspects of neural development including cell growth different
- Homeobox protein OTX2 is a member of the bicoid sub family of homeodomain containing transcription factors This protein acts as a transcription factor and may play a role in brain and sensory organ d
- LHX3 is a member a large protein family which carry the LIM domain a unique cysteine rich zinc binding domain The encoded protein is a transcription factor that is required for pituitary development
- PAX3 is a member of the paired box PAX family of transcription factors Members of the PAX family typically contain a paired box domain and a paired type homeodomain These genes play critical roles
- POH1 pad one homolog 1 is a component of the 26S proteasome a multiprotein complex that degrades proteins targeted for destruction by the ubiquitin pathway
- POH1 pad one homolog 1 is a component of the 26S proteasome a multiprotein complex that degrades proteins targeted for destruction by the ubiquitin pathway Spataro et al 1997 PubMed 9374539
- POLR2B encodes the second largest subunit of RNA polymerase II the polymerase responsible for synthesizing messenger RNA in eukaryotes This subunit in combination with at least two other polymerase
- POLR2B is the second largest subunit of RNA polymerase II the polymerase responsible for synthesizing messenger RNA in eukaryotes This subunit in combination with at least two other polymerase subu
- The LOC391804 gene is similar to hypothetical protein
- NCOR2 forms a large corepressor complex that contains SIN3A B and histone deacetylases HDAC1 and HDAC2 This complex associates with the thyroid TR and the retinoid acid receptors RAR in the absen
- CBP and p300 are large nuclear proteins that bind to many sequence specific factors involved in cell growth and or differentiation including c jun and the adenoviral oncoprotein E1A PCAF associates
- The phosphoprotein C terminal binding protein 1 CTBP 1 binds the C terminus of adenovirus E1A protein CTBP 1 is a transcriptional repressor and may play a role during cellular proliferation A seco
- CTBP1 binds to the C terminus of adenovirus E1A proteins This phosphoprotein is a transcriptional repressor and may play a role during cellular proliferation This protein and the product of a second
- SUV39H1 a human homolog of the Drosophila position effect variegation modifier Su var 3 9 and of the S pombe silencing factor clr4 encodes a heterochromatic protein that transiently accumulates at
- NCOR1 mediates ligand independent transcription repression of thyroid hormone and retinoic acid receptors by promoting chromatin condensation and preventing access of the transcription machinery It i
- CBX5 is a methyl lysine binding protein localized at heterochromatin sites where it mediates gene silencing
- COLEC12 encodes a member of the C lectin family proteins that possess collagen like sequences and carbohydrate recognition domains This protein is a scavenger receptor a cell surface glycoprotein t
- GRIP1 is a steroid receptor coactivator family SRC member SRC proteins comprise a well characterized family of nuclear receptor NR coactivators that increase transcriptional activation by NRs via
- CIon Channel represents a new subfamily of the HMG box superfamily Expression of the Cic gene is predominantly restricted to immature granule cells in the cerebellum hippocampus and olfactory bulb i
- ZC3H7B is a protein that contains a tetratricopeptide repeat domain The encoded protein also interacts with the rotavirus non structural protein NSP3
- A chromosomal aberration involving SUZ12 may be a cause of endometrial stromal tumors Translocation t 7 17 p15 q21 with JAZF1 generates the JAZF1 SUZ12 oncogene consisting of the N terminus part
- The Fos gene family consists of 4 members FOS FOSB FOSL1 and FOSL2 They are leucine zipper proteins that can dimerize with proteins of the JUN family thereby forming the transcription factor com
- ZNF318 encodes a nuclear protein with a zinc finger motif of the Cys2 His2 type that is a novel corepressor of androgen receptor AR
- NR5A1 is a members of the orphan nuclear receptor superfamily that is critical regulatory components of the hypothalamic pituitary adrenal gonadal axis In adrenal and gonadal tissues they regulate th
- CCRN4L is highly similar to Nocturnin a gene identified as a circadian clock regulated gene in Xenopus laevis This

protein and Nocturnin protein share similarity with the C terminal domain of a yeas

- POU domain genes encode a family of highly conserved transacting factors that influence the transcriptional activity of several cell type specific and ubiquitous genes
- POU domain genes encode a family of highly conserved transacting factors that influence the transcriptional activity of several cell type specific and ubiquitous genes Studies have cloned and sequenc
- ZNF385 is a new candidate transcription factor
- Trans acting T cell specific transcription factor GATA 3 is a member of GATA family of transcription factors that regulates development of multiple tissues It is an important transcription factor in
- LHX6 is a member of a large protein family that contains the LIM domain a unique cysteine rich zinc binding domain The encoded protein may function as a transcriptional regulator and may be involved
- FOXD3 belongs to the forkhead family of transcription factors which is characterized by a distinct forkhead domain The specific function of this gene has not yet been determined
- SND1 was originally characterized as a transcriptional coactivator for Epstein Barr virus nuclear antigen 2 It is a STAT6 TAD interacting protein containing staphylococcal nuclease SN like domain a
- FOXP1 belongs to subfamily P of the forkhead box FOX transcription factor family Forkhead box transcription factors play important roles in the regulation of tissue and cell type specific gene tra
- MKX contains 1 homeobox DNA binding domain and belongs to the TALE IRO homeobox family It may act as a morphogenetic regulator of cell adhesion
- ZNF621 is a candidate transcription factor
- HIPK2 is a conserved serine threonine nuclear kinase that interacts with homeodomain transcription factors HIPK2 is a conserved serine threonine nuclear kinase that interacts with homeodomain transcri
- KLF15 is a Cys2 His2 zinc finger gene It is found abundantly expressed in the liver kidneys heart and skeletal muscle
- CHEK1 is required during normal S phase to avoid aberrantly increased initiation of DNA replication thereby protecting against DNA breakage Its expression is dispensable for somatic cell death and c
- L glutamate is the major excitatory neurotransmitter in the central nervous system and activates both ionotropic and metabotropic glutamate receptors The metabotropic glutamate receptors are a family
- Basal transcription of genes by RNA polymerase II requires the interaction of TATA binding protein TBP with the core region of class II promoters Studies in mouse suggest that the protein encoded b
- TFCP2L1 is a transcriptional suppressor TFCP2L1 may suppress UBP1 mediated transcriptional activation It modulates the placental expression of CYP11A1
- HS1 which is hematopoietic lineage cell specific protein 1 is a substrate of protein tyrosine kinases in lymphocytes it binds to F actin and promotes Arp2 3 complex mediated actin polymerization H
- Histone deacetylase 2 HDAC2 or transcriptional regulator homolog RPD3 L1 is highly homologous to the yeast transcription factor RPD3 reduced potassium dependency 3 gene As in yeast human HDA2
- HIon Channel1 is a transcriptional repressor HIon Channel1 may act as a tumor suppressor HIon Channel1 may be involved in development of head face limbs and ventral body wall Defects in HIon Chan
- HMX1 acts as a transcriptional antagonist and is part of the Hmx family of homeodomain proteins which are predominately expressed in discrete regions of developing sensory tissues
- FOXA1 is a member of the forkhead class of DNA binding proteins These hepatocyte nuclear factors are transcriptional activators for liver specific transcripts such as albumin and transthyretin and t
- HOXB9 belongs to the homeobox family of genes The homeobox genes encode a highly conserved family of transcription factors that play an important role in morphogenesis in all multicellular organisms
- HOXC10 belongs to the homeobox family The homeobox family is a highly conserved family of transcription factors that play an important role in morphogenesis in all multicellular organisms The protei
- HOXC11 belongs to the homeobox family The homeobox family is a highly conserved family of transcription factors that play an important role in morphogenesis in all multicellular organisms HOXC11 is
- HOXD12 belongs to the homeobox family of genes The homeobox genes encode a highly conserved family of transcription factors that play an important role in morphogenesis in all multicellular organisms
- The function of the protein encoded by the AIRE gene is not well defined However it contains zinc finger motifs suggestive of a transcription factor The protein isoform 1 is localized to both the
- AIRE is a transcriptional regulator that forms nuclear bodies and interacts with the transcriptional coactivator CBP At least three splice variant mRNAs products have been described including one whi
- Apurinic apyrimidinic AP sites occur frequently in DNA molecules by spontaneous hydrolysis by DNA damaging agents or by DNA glycosylases that remove specific abnormal bases AP sites are pre mutage
- Heat shock transcription factors HSFs activate heat shock response genes under conditions of heat or other stresses HSF4 lacks the carboxyl terminal hydrophobic repeat which is shared among all ver
- The insulinoma associated 1 INSM1 gene is intronless and encodes a protein containing both a zinc finger DNA binding domain and a putative prohormone domain This gene is a sensitive marker for neur
- IFN regulatory factor IRF 4 is a lymphoid myeloid restricted member of the IRF transcription factor family that plays an essential role in the homeostasis and function of mature lymphocytes IRF 4 e
- The TSFM gene encodes a protein that is expressed in all tissues with the highest levels of expression in skeletal muscle liver and kidney
- PTK2B encodes a cytoplasmic protein tyrosine kinase which is involved in calcium induced regulation of ion channels and activation of the map kinase signaling pathway The encoded protein may represen
- SMAD6 mothers against decapentaplegic homolog 6 is an antagonist of signaling by TGF beta transforming growth factor type 1 receptor superfamily members has been shown to inhibit selectively BMP
- MEOX1 belongs to a family of nonclustered diverged homeobox genes It may play a role in regulating growth and differentiation
- MEOX2 is a member of a subfamily of non clustered diverged antennapedia like homeobox containing genes MEOX2 may play a role in the regulation of vertebrate limb myogenesis Mutations in the relate
- MLLT1 is a homolog of the yeast SWI SNF subunit ANC1 TFG3 Moreover MLLT0 is a fusion partner for the gene product of MLL that is a common target for chromosomal translocations in human acute leukem
- CBP p300 interacting transactivator 1 CITED1 melanocyte specific protein 1 is a nuclear protein that shares two highly conserved domains CR1 and CR2 The CR2 domain is significantly acidic and ac
- MYBL1 is strong transcriptional activator DNA binding protein that specifically recognize the sequence 5 YAAC GT G 3 It could have a role in the proliferation and or differentiation of neurogenic
- MYC is a multifunctional nuclear phosphoprotein that plays a role in cell cycle progression apoptosis and cellular transformation It functions as a transcription factor that regulates transcription
- Nuclear factor I NFI proteins constitute a family of dimeric DNA binding proteins with similar and possibly identical DNA binding specificity They function as cellular transcription factors and a
- NFIB is a member of the nuclear factor I family of nuclear proteins which are known to be involved in viral and cellular transcription NFIB includes the proposed DNA binding and dimerization domain
- Nuclear factor I NFI proteins constitute a family of sequence specific transcription factors whose functional diversity is generated through transcription from four different genes NFI A NFI B NF
- NOTCH4 is a member of the Notch family Members of this Type 1 transmembrane protein family share structural characteristics including an extracellular domain consisting of multiple epidermal growth f
- NR4A2 is a member of the steroid thyroid hormone retinoid receptor superfamily The protein may act as a transcription factor Mutations in NR4A2 gene have been associated with disorders related to do
- MEF 2 is expressed early in the differentiation program and is suppressed by specific polypeptide growth factors The ability of MEF 2 to recognize conserved activating elements associated with multip
- PAX6 is one of many human homologues of the Drosophila melanogaster gene prd In addition to the hallmark feature of this gene family a conserved paired box domain the encoded protein also contains
- Forkhead box protein P3 FOXP3 Scurfin Zinc finger protein JM2 encodes a novel member of the forkhead family of transcription factors It presumably represses transcription playing a paramount rol
- ZFP67 is an early growth response gene that encodes a zinc finger containing transcription factor that binds to the promoter regions of type I collagen genes and has a role in development
- The CGI 62 gene encodes a hypothetical protein located on chromosome 8
- ZNFN1A1 has a role in progesterone activation of fatty acid amide hydrolase in human T lymphocytes
- HMG20A plays a role in neuronal differentiation as chromatin associated protein HMG20A acts as inhibitor of HMG20B HMG20A overcomes the repressive effects of the neuronal silencer REST and induces t
- PIAS3 is a member of the protein inhibitor of activated STAT PIAS family It also activates TGF beta SMAD transcriptional responses
- HUEL includes the putative nuclear receptor interaction motif nuclear localization and export signals zinc finger leucine zipper and acidic domains HUEL is likely to be an evolutionarily conserved
- CREB3 is a transcription factor that is a member of the leucine zipper family of DNA binding proteins This protein binds to the cAMP responsive element an octameric palindrome The protein interacts
- CC3 HTATIP2 is a member of the short chain dehydrogenases reductases SDR family It is a novel serine threonine kinase that phosphorylates the C terminal domain CTD of the largest RNA polymerase
- The function of Anti HTATIP2 has not yet been determined
- MXD4 is a member of the MAD gene family The MAD genes encode basic helix loop helix leucine zipper proteins that heterodimerize with MAX protein forming a transcriptional repression complex The MA
- ACSL1 encodes an isozyme of the long chain fatty acid coenzyme A ligase family Although differing in substrate specificity subcellular localization and tissue distribution all isozymes of this fam
- PDK4 is a member of the PDK BCKDK protein kinase family and is a mitochondrial protein with a histidine kinase domain This protein is located in the matrix of the mitochondria and inhibits the pyruv
- Acetyl Coenzyme A acetyltransferase 2 is an enzyme involved in lipid metabolism Reported patients with ACAT2 deficiency have shown severe mental retardation and hypotonus The ACAT2 gene shows comple
- Stearoyl CoA desaturase fatty acid desaturase SCD is expressed at high levels in several human tissues and is required for the biosynthesis of oleate 18 1 and palmitoleate 16 1 These monounsa
- Adiponectin ACDC is expressed in adipose tissue exclusively It is similar to collagens X and VIII and complement factor C1q Adiponectin circulates in the plasma and is involved with metabolic and
- PCK1 is a main control point for the regulation of gluconeogenesis The cytosolic enzyme encoded by this gene along with GTP catalyzes the formation of phosphoenolpyruvate from oxaloacetate with th
- Aquaporins major intrinsic protein MIP are a family of water selective membrane channels Aquaporin 7 has greater sequence similarity with AQP3 and AQP9 and they may be a subfamily Aquaporin 7 and
- Prohibitin is from an evolutionarily conserved gene that is ubiquitously expressed It is thought to be a negative regulator of cell proliferation and may be a tumor suppressor Mutations in PHB have
- IASPP is one of the most evolutionarily conserved inhibitors of p53 TP53 whereas ASPP1 and ASPP2 are activators of p53 IASPP is one of the most evolutionarily conserved inhibitors of p53 TP53 MIM
- TRAFD1 is a new candidate transcription factor
- The protein encoded by COPS5 is one of the eight subunits of COP9 signalosome a highly conserved protein complex that functions as an important regulator in multiple signaling pathways The structure
- The assembly and stability of the RNA polymerase II transcription pre initiation complex on a eukaryotic core promoter involves the effects of TFIIA on the interaction between TATA binding protein TB
- The assembly and stability of the RNA polymerase II transcription pre initiation complex on a eukaryotic core promoter involve the effects of TFIIA on the interaction between TATA binding protein TBP
- Checkpoint suppressor 1 is a member of the forkhead winged helix transcription factor family Checkpoints are eukaryotic DNA damage inducible cell cycle arrests at G1 and G2 Checkpoint suppressor 1 s
- SP140 is the nuclear body protein found specifically in all NP cells HIV 1 infection induced its partial dispersal from nuclear bodies into cytosolic colocalization with Vif
- DLX5 is a member of a homeobox transcription factor family DLX5 may play a role in bone development and fracture healing Mutation in this gene which is located in a tail to tail configuration with
- The function of Anti ZBTB7C has not yet been determined
- Vasculin is a novel vascular protein differentially expressed

in human atherogenesis

- PPARD is a member of the peroxisome proliferator activated receptor PPAR family PPARs are nuclear hormone receptors that bind peroxisome proliferators and control the size and number of peroxisomes
- PPARG is a regulator of adipocyte differentiation Additionally PPAR gamma has been implicated in the pathology of numerous diseases including obesity diabetes atherosclerosis and cancer
- APTX is a member of the histidine triad HIT superfamily some of which have nucleotide binding and diadenosine polyphosphate hydrolase activities APTX may play a role in single stranded DNA repair
- ZSCAN2 contains several copies of zinc finger motif which is commonly found in transcriptional regulatory proteins Studies in mice show that ZSCAN2 is expressed during embryonic development and spe
- HES6 belongs to a subfamily of basic helix loop helix transcription factors that includes Drosophila Hairy and Enhancer of split genes Like other members of the family HES6 features the WRPW motif w
- cDNA sequence of HSZFP36 is generated by Mammalian Gene Collection MGC Program Team
- C14orf131 is a protein predicted based on an ORF found in chromosome 14
- HR is a protein whose function has been linked to hair growth A similar protein in rat functions as a transcriptional corepressor for thyroid hormone and interacts with histone deacetylases Mutation
- FOXJ2 is a fork head factor that is expressed in many adult tissues In the embryo FOXJ2 expression showed a very early onset during the cleavage stages of preimplantation development It is capable
- JMJD1A is a zinc finger protein that contains a jumonji domain
- RNF130 contains a RING finger motif and is similar to g1 a Drosophila zinc finger protein that is expressed in mesoderm and involved in embryonic development The expression of the mouse counterpart
- DMAP1 is a subunit of several distinct complexes involved in the repression or activation of transcription The encoded protein can independently repress transcription and is targeted to replication
- BARX1 belongs to the Bar subclass of the homeobox gene family The function of this gene has not yet been determined however studies in the mouse and chick homolog suggest a role in developing teeth
- The regulation of the quinone reductase QR gene as well as other genes involved in detoxification is known to be mediated by an electrophile response element EpRE QR gene regulation by the anties
- GATAD2B contains 1GATA type zinc finger GATAD2B was identified as potent transcriptional repressors interacting with MBD2 and MBD3 GATAD2B one of the Mi 2 NuRD complex subunits mediate MBD2 and hi
- This gene located on chromosome 17 encodes a protein that is part of the zinc finger family
- The ZNF537 gene is located on chromosome 19
- RBAK encodes a nuclear protein which interacts with the tumor suppressor retinoblastoma 1 The two interacting proteins are thought to act as a transcriptional repressor for promoters which are activa
- RBAK is a nuclear protein which interacts with the tumor suppressor retinoblastoma 1 The two interacting proteins are thought to act as a transcriptional repressor for promoters which are activated b
- ZNF297B is a new candidate transcription factor
- NKX2C is a member of the NKX family of homeodomain containing transcription factors which are implicated in many aspects of cell type specification and maintenance of differentiated tissue functions
- LDB2 belongs to the LDB family LDB2 binds to the LIM domain of a wide variety of LIM domain containing transcription factors LIM domains are required for both inhibitory effects on LIM homeodomain t
- RNF138 contains a RING finger a motif present in a variety of functionally distinct proteins and known to be involved in protein DNA and protein protein interactions The protein encoded by this gene
- Prenylated proteins contain one of two isoprenoid lipids either the 15 carbon farnesyl or the 20 carbon geranylgeranyl covalently attached to cysteine residues at or near their C terminus PCYOX1 is
- The TTRAP gene encodes a member of a superfamily of divalent cation dependent phosphodiesterases The encoded protein associates with CD40 tumor necrosis factor TNF receptor 75 and TNF receptor ass
- PIAS4 is an inhibitor of TRIF induced ISRE and NF kappaB activation Its mRNA is selectively expressed in endothelial cells and its expression can be regulated by angiogenic growth factors
- LSR has a probable role in the clearance of triglyceride rich lipoprotein from blood It binds chylomicrons LDL and VLDL in presence of free fatty acids and allows their subsequent uptake in the cell
- Prefoldin 1 is a heterohexameric chaperone protein which assists in the correct folding of other proteins It binds specifically to cytosolic chaperonin and transfers target proteins Prefoldin may fu
- PHF1 has significant sequence similarity with Drosophila Polycomblike It contains a zinc finger like PHD plant homeodomain finger which is distinct from other classes of zinc finger motifs and whic
- PLRG1 is necessary for spliceosome assembly and for pre mRNA splicing
- SOX18 is a member of the SOX SRY related HMG box family of transcription factors involved in the regulation of embryonic development and in the determination of the cell fate The encoded protein ma
- SOX18 a member of the SOX SRY related HMG box family of transcription factors involved in the regulation of embryonic development and in the determination of the cell fate The encoded protein may a
- Under hypertonic conditions the induction of SLC38A2 SNAT2 leads to the stimulation of transport system A and to the increase in the cell content of amino acids Its amino acid response element along
- POU3F1 is a member of the POU domain family of proteins and regulates events during neurogenesis and myelination
- POU4F3 is capable of activating both BDNF and NT 3 promoters in inner ear sensory epithelial cell lines Mutant POU4F3 loses most of its transcriptional activity and most of its ability to bind to DNA
- Endoglin is a homodimeric transmembrane glycoprotein highly expressed by endothelial cells It is a component of the transforming growth factor beta receptor complex since it binds TGFB1 and TGFB3 wit
- Endoglin is a homodimeric transmembrane glycoprotein highly expressed by endothelial cells It is a component of the transforming growth factor beta receptor complex as it binds TGFB1 and TGFB3 with h
- Mutations in PHKG2 along with PHKA2 and PHKB all three different genes of phosphorylase kinase Phk subunits can give rise to glycogen storage disease of the liver The autosomal recessive liver s
- ARID4A encodes a ubiquitously expressed nuclear protein It binds directly with several other proteins to retinoblastoma protein pRB which regulates cell proliferation pRB represses transcription
- HSPA1A is a member of the heat shock protein 70 family In conjuction with other heat shock proteins this protein stabilizes existing proteins against aggregation and mediates the folding of newly tr
- PNMA1 encodes a protein that is highly restricted to the brain and testis Anti PNMA1 reacts mainly with subnuclear elements including the nucleoli and to a lesser degree the cytoplasm
- This gene encodes a protein which interacts with the nonstructural NS1 protein of the influenza A virus In noninfected cells affinity purified antibodies localized this protein in nuclear regions en
- IVNS1ABP is a novel human protein that interacts with the influenza A virus Nonstructural NS1 protein is relocalized in the nuclei of infected cells
- In infectious mononucleosis anti EBNA 1 antibodies are produced which cross react with multiple normal human proteins The cross reactivity is due to anti gly ala antibodies that cross react with hos
- Iron sulfur clusters are required for the function of many cellular enzymes The protein encoded by this gene supplies inorganic sulfur to these clusters by removing the sulfur from cysteine creating
- UBE2N encodes a member of the E2 ubiquitin conjugating enzyme family The modification of proteins with ubiquitin is an important cellular mechanism for targeting abnormal or short lived proteins for
- ZNF312 is a candidate transcription factor
- The ZNF654 gene located on chromosome 17 encodes a protein that is part of the zinc finger family
- Myoneurin belongs to the BTB POZ and zinc finger protein family The BTB POZ and zinc finger proteins BTB POZ ZF constitute a growing family of proteins with gene expression regulatory functions sin
- Myoneurin belongs to the BTB POZ and zinc finger protein family whose members have been implicated in regulatory functions of gene expression Myoneurin has been identified in various tissues but mus
- ZNF395 is a novel transcription factor shuttling between nucleus and cytoplasm and bind to the specific GCCGGCG which is an essential cis element for HD gene expression in neuronal cells ZNF395 migh
- ZNF313 may play a role in spermatogenesis
- The protein encoded by SLC2A4RG is a nuclear transcription factor involved in the activation of the solute carrier family 2 member 4 gene The encoded protein interacts with another transcription fact
- CCNL1 plays a critical role in the loco regional progression of HNSCC and may serve as an indicator for occult advanced tumour stages CCNL1 also plays a role in pre mRNA splicing has been shown to a
- TBX20 is a member of the T box transcription factor family expressed in the developing heart eye ventral neural tube and limbs indicating a possible role in regulating development of these tissues
- ODAG Ocular development associated gene a novel transcription factor located on chromosome 7 encodes a protein that may play a role in eye development mRNA profiling in multiple human tissue indi
- GRHL3 is a member of the grainyhead family of transcription factors GRHL3 interacts with leader binding protein 32 LBP 32 and brother of mammalian grainyhead BOM and may function as a transcript
- Retinoblastoma RB is an embryonic malignant neoplasm of retinal origin It almost always presents in early childhood and is often bilateral Spontaneous regression cure occurs in some cases
- DMRTA2 is involved in gonadal differentiation The gene is part of five novel human DM genes that map to three well defined regions of chromosomes 1 9 and 19 one gene on chromosome 19 having an add
- RFX4 is a transcription factors that contain a highly conserved winged helix DNA binding domain RFX4 is structurally related to regulatory factors X1 X2 X3 and X5 It has been shown to interact wi
- Alx4 is a member of the family of transcription factors that contain the paired type homeodomain In contrast to other types of homeodomains the paired type homeodomain has been shown to mediate high
- PRDM14 is part of a family of PR domain genes that are involved in tumorigenesis
- SEMA4A is a member of the semaphorin family of soluble and transmembrane proteins Semaphorins are involved in guidance of axonal migration during neuronal development and in immune responses
- Members of the Ikaros ZNFN1A1 MIM 603023 family of transcription factors which includes Eos are expressed in lymphocytes and are implicated in the control of lymphoid development
- Members of the Ikaros ZNFN1A1 MIM 603023 family of transcription factors which includes Pegasus are expressed in lymphocytes and are implicated in the control of lymphoid development
- ZFP106 is a new candidate transcription factor
- ZNF212 belongs to the C2H2 type zinc finger gene family The zinc finger proteins are involved in gene regulation and development and are quite conserved throughout evolution
- SNAI2 is a member of the Snail family of C2H2 type zinc finger transcription factors The protein acts as a transcriptional repressor that binds to E box motifs and is also likely to repress E cadheri
- ZNF447 contains 1 SCAN box domain and 2 C2H2 type zinc fingers It belongs to the kruppel C2H2 type zinc finger protein family and may be involved in transcriptional regulation
- SMARCC1 is a member of the SWI SNF family of proteins whose members display helicase and ATPase activities and which are thought to regulate transcription of certain genes by altering the chromatin s
- The Drosophila embryonic protein snail is a zinc finger transcriptional repressor which downregulates the expression of ectodermal genes within the mesoderm The nuclear protein encoded by this gene i
- SOX3 is a member of the SOX SRY related HMG box family of transcription factors involved in the regulation of embryonic development and in the determination of the cell fate The encoded protein may
- SOX5 encodes a member of the SOX SRY related HMG box family of transcription factors involved in the regulation of embryonic development and in the determination of the cell fate The encoded protei
- SOX10 is a member of the SOX SRY related HMG box family of transcription factors involved in the regulation of embryonic development and in the determination of the cell fate This protein may act a
- This intronless gene encodes a member of the SOX SRY related HMG box family of transcription factors involved in the regulation of embryonic development and in the determination of the cell fate Th
- Members of the SOX family of transcription factors are characterized by the presence of a DNA binding high mobility group HMG domain homologous to the HMG box of sex determining region Y SRY For
- C20orf20 is a component of the NuA4 histone acetyltransferase HAT complex which is involved in transcriptional activation of select genes principally by acetylation of nucleosomal histone H4 and H2A

- C20orf20 belongs to the EAF7 family It is a component of the NuA4 histone acetyltransferase HAT complex which is involved in transcriptional activation of select genes principally by acetylation of
- The screening of cDNA expression libraries from human tumors with serum antibody SEREX has proven to be a powerful method for identifying the repertoire of tumor antigens recognized by the immune sy
- FOXL2 is a member of the forkhead family The forkhead domain is a monomeric DNA binding motif that defines a rapidly growing family of eukaryotic transcriptional regulators Genetic and biochemical d
- Somatostatin acts at many sites to inhibit the release of many hormones and other secretory proteins The biologic effects of somatostatin are probably mediated by a family of G protein coupled recept
- SATB1 binds to DNA at special AT rich sequences at nuclear matrix or scaffold associated regions SATB1 was thought to recognize the sugar phosphate structure of double stranded DNA
- PKNOX2 is a TALE homeodomain protein that shows distinct homology with PKNOX1 It may interact with PBX proteins and play a tissue specific regulation of transcription
- STAT1 is a member of the STAT protein family In response to cytokines and growth factors STAT family members are phosphorylated by the receptor associated kinases and then form homo or heterodimer
- STAT4 is a member of the STAT family of transcription factors In response to cytokines and growth factors STAT family members are phosphorylated by the receptor associated kinases and then form hom
- TBX5 is a member of a phylogenetically conserved family of genes that share a common DNA binding domain the T box T box genes encode transcription factors involved in the regulation of developmental
- TBX6 is a member of a phylogenetically conserved family of genes that share a common DNA binding domain the T box T box genes encode transcription factors involved in the regulation of developmental
- The TBX6 gene is a member of a phylogenetically conserved family of genes that share a common DNA binding domain the T box T box genes encode transcription factors involved in the regulation of deve
- TCEA1 is necessary for efficient RNA polymerase II transcription elongation past template encoded arresting sites TCEA1 has a role in suppression of transient pausing which is the most important con
- The protein encoded by TCEA2 is found in the nucleus where it functions as an SII class transcription elongation factor Elongation factors in this class are responsible for releasing RNA polymerase
- Located on chromosome 1 the TCEA3 gene encodes a transcription elongation factor A protein with conserved N and C terminal domains separated by a linker region that is more variable in sequence and
- Polyclonal antibody produced in rabbits immunized with a synthetic peptide corresponding to a region of Human TCEA3 with an internal ID of P04456
- TBX3 is a member of a phylogenetically conserved family of genes that share a common DNA binding domain the T box T box genes encode transcription factors involved in the regulation of developmental
- The TCF21 gene encodes a transcription factor of the basic helix loop helix family The TCF21 product is mesoderm specific and expressed in embryonic epicardium mesenchyme derived tissues of lung g
- MLX belongs to the family of basic helix loop helix leucine zipper bHLH Zip transcription factors These factors form heterodimers with Mad proteins and play a role in proliferation determination a
- TEAD3 is a member of the transcriptional enhancer factor TEF family The family members contain the TEA ATTS DNA binding domain This member is preferentially expressed in placenta and transactivate
- TFAP4 acts in concert with AP 1 to activate SV40 late transcription in vitro
- Enhancer binding protein TFAP4 is a transcription factor that activates both viral and cellular genes by binding to the symmetrical DNA sequence CAGCTG
- The TFDP genes encode a family of transcription factors that can form heterodimers with E2F family proteins in vivo The E2F TFDP transcription factors are major regulators of genes that are required
- UBP1 is an important SF1 independent transcriptional activator stimulating P450scc expression in human placental JEG 3 cells whereas LBP 9 modulates the action of UBP1 exerting both positive and neg
- WHSC1 encodes a protein that contains four domains present in other developmental proteins a PWWP domain an HMG box a SET domain and a PHD type zinc finger It is expressed ubiquitously in early d
- The WNT family consists of sereval secreted signaling proteins These proteins have been implicated in oncogenesis and in several developmental processes including regulation of cell fate and pattern
- ZNF7 is a candidate transcription factor
- ZNF18 is a candidate transcription factor
- Located on chromosome X ZNF21 encodes a zinc finger protein 21
- ZNF23 GZF1 has a BTB POZ broad complex tramtrack and bric a brac poxvirus and zinc finger domain and 10 tandemly repeated zinc finger motifs with strong transcriptional repressive activity
- ZNF24 is a new candidate transcription factor
- ZNF37A is a new candidate transcription factor
- ZBTB25 contains 1 BTB POZ domain and 2 C2H2 type zinc fingers and belongs to the krueppel C2H2 type zinc finger protein family ZBTB25 may be involved in transcriptional regulation
- Ribosomes the organelles that catalyze protein synthesis consist of a small 40S subunit and a large 60S subunit Together these subunits are composed of 4 RNA species and approximately 80 structural
- PIK3R3 binds to activated phosphorylated protein tyrosine kinases through its SH2 domain and regulates their kinase activity During insulin stimulation it also binds to IRS 1
- APOBEC3G is a member of the cytidine deaminase gene family It is one of seven related genes or pseudogenes found in a cluster thought to result from gene duplication on chromosome 22 Members of th
- Anti APOBEC3G is a member of the cytidine deaminase gene family It is one of seven related genes or pseudogenes found in a cluster thought to result from gene duplication on chromosome 22 Members
- ANKRD11 is a member of a novel family of ankyrin repeats containing cofactors ANCOs that interact with p160 coactivators to inhibit ligand dependent transactivation ANKRD11 encodes a large nuclear
- Ankyrin repeats containing cofactors may recruit histone deacetylases to the p160 coactivators nuclear receptor complex to inhibit ligand dependent transactivation
- The protein encoded by BTG2 is a member of the BTG Tob family This family has structurally related proteins that appear to have antiproliferative properties This encoded protein is involved in the r
- Located on chromosome 19 this gene encodes for zinc finger protein 426
- ZNF426 gene located on chromosome 19
- IRX1 is a member of the Iroquois homeobox gene family Members of this family appear to play multiple roles during pattern formation of vertebrate embryos
- FLJ23436 is a hypothetical protein
- FLJ23436 is a hypothetical protein found in Chromosome 16
- Smad binding peptide aptamers can be developed to selectively inhibit TGF beta induced gene expression
- Zinc finger protein 750 is a new candidate transcription factor
- ZNF668 is a new candidate transcription factor
- The FLJ13798 gene located on chromosome 16 encodes a hypothetical protein with unknown function
- ZNF212 belongs to the C2H2 type zinc finger gene family The zinc finger proteins are involved in gene regulation and development and are quite conserved throughout evolution Like this gene product
- ZNF606 is a new candidate transcription factor
- ZNF306 is a new candidate transcription factor
- CLDN10 encodes a member of the claudin family Claudins are integral membrane proteins and components of tight junction strands Tight junction strands serve as a physical barrier to prevent solutes a
- CLDN17 clustered with CLDN8 at human chromosome 21q22 11 is a four transmembrane protein with WWCC motif defined by W X 17 22 W X 2 C X 8 10 C
- CLDN13 is a member of claudin family It is a four transmembrane protein with WWCC motif defined by W X 17 22 W X 2 C X 8 10 C
- CLDN9 is a member of claudin family It is a four transmembrane protein with WWCC motif defined by W X 17 22 W X 2 C X 8 10 C
- CLDN8 clustered with CLDN17 at human chromosome 21q22 11 is a four transmembrane protein with WWCC motif defined by W X 17 22 W X 2 C X 8 10 C
- CLDN11 belongs to the claudin family of tight junction associated proteins and is a major component of central nervous system myelin that is necessary for normal CNS function There is growing evidenc
- CLDN23 is a four transmembrane protein with WWCC motif defined by W X 17 22 W X 2 C X 8 10 C It is a candidate tumor suppressor gene implicated in intestinal type gastric cancer
- LHX3 encodes a member a large protein family which carry the LIM domain a unique cysteine rich zinc binding domain The encoded protein is a transcription factor that is required for pituitary develo
- ZNF436 is a candidate transcription factor
- PIR is a member of the cupin superfamily The protein is an Fe II containing nuclear protein expressed in all tissues of the body and concentrated within dot like subnuclear structures Interactions
- ZIon Channel5 is a member of the ZIon Channel family of C2H2 type zinc finger proteins Members of this family are important during development and have been associated X linked visceral heterotaxy a
- The NR1H4 gene encodes a protein that has a central role in lipid homeostasis and also regulates carbohydrate metabolism
- NR1I3 is a member of the nuclear receptor superfamily and is a key regulator of xenobiotic and endobiotic metabolism The protein binds to DNA as a monomer or a heterodimer with the retinoid X recept
- MAFB is a basic leucine zipper bZIP transcription factor that plays an important role in the regulation of lineage specific hematopoiesis The nuclear protein represses ETS1 mediated transcription o
- The ZFHX1B gene is a member of the delta EF1 Zfh1 family of 2 handed zinc finger homeodomain proteins ZFHX1B is strongly transcribed at an early stage in the developing peripheral and central nervous
- TSC22D2 belongs to the TSC 22 Dip Bun family and the function remains unknown
- Some high mobility group HMG box proteins e g LEF1 contain a single HMG box motif and bind DNA in a sequence specific manner while other members of this family e g HMG1 have multiple HMG bo
- MLL4 a protein which contains multiple domains including a CXXC zinc finger three PHD zinc fingers two FY rich domains and a SET suppressor of variegation enhancer of zeste and trithorax domain
- MORF4L2 is a member of the mortality factor MORF family of putative transcriptional regulators
- NFE2L3 activates erythroid specific globin gene expression
- GTF2IRD1 contains five GTF2I like repeats and each repeat possesses a potential helix loop helix HLH motif It may have the ability to interact with other HLH proteins and function as a transcriptio
- The TBX4 gene is a member of a phylogenetically conserved family of genes that share a common DNA binding domain the T box T box genes encode transcription factors involved in the regulation of deve
- CRSP9 is a subunit of the CRSP cofactor required for SP1 activation complex which along with TFIID is required for efficient activation by SP1 CRSP9 is also a component of other multisubunit com
- FOXQ1 contains 1 fork head DNA binding domain FOXQ1 mediates the interaction of Akt protein kinase B with TGFb2 Foxq1 regulates differentiation of hair in satin mice
- FOXP2 is an evolutionarily conserved transcription factor expressed in fetal and adult brain This transcription factor is a member of the forkhead winged helix FOX family of transcription factors
- PARP2 contains a catalytic domain and is capable of catalyzing a poly ADP ribosyl ation reaction This protein has a catalytic domain which is homologous to that of poly ADP ribosyl transferase bu
- PARP3 belongs to the PARP family These enzymes modify nuclear proteins by poly ADP ribosylation which is required for DNA repair regulation of apoptosis and maintenance of genomic stability PARP3
- Poly ADP ribose polymerases PARPs constitute a large family of 18 proteins encoded by different genes and displaying a conserved catalytic domain They are involved in DNA damage dependent post t
- The PARP11 gene is part of the poly ADP ribose polymerase family
- The ATP7A gene encodes the Menkes copper translocating P type ATPase a ubiquitous protein that regulates the absorption of copper in the gastrointestinal tract Inside cells this protein has a dual
- Erythrocyte membrane protein band 4 2 is an ATP binding protein which may regulate the association of protein 3 with ankyrin It probably has a role in erythrocyte shape and mechanical property regula
- The CD233 gene is located on chromosome 17q21 q22 and is part of the anion exchanger AE family CD233 is expressed in the erythrocyte plasma membrane where it functions as a chloride bicarbonate exc
- AFM is a member of the albumin gene family which is comprised of four genes that localize to chromosome 4 in a tandem arrangement These four genes encode structurally related serum transport protein
- ASGR1 is a cell surface receptor binds to galactose terminated glycoproteins It transports these glycoproteins via a series of membrane vesicles and tubules to an acidic sorting organelle where the r

- ASGR1 encodes for a cell surface receptor binds to galactose terminated glycoproteins It transports these glycoproteins via a series of membrane vesicles and tubules to an acidic sorting organelle wh
- SLC17A2 is a member of the solute carrier family
- A1BG is a plasma glycoprotein of unknown function It shows sequence similarity to the variable regions of some immunoglobulin supergene family member proteins
- A1BG is a plasma glycoprotein of unknown function It shows sequence similarity to the variable regions of some immunoglobulin supergene family member proteins The protein encoded by this gene is a p
- C4BPB is a member of a superfamily of proteins composed predominantly of tandemly arrayed short consensus repeats of approximately 60 amino acids A single unique beta chain encoded by this gene asse
- Alpha2 HS glycoprotein AHSG a glycoprotein present in the serum is synthesized by hepatocytes The AHSG molecule consists of two polypeptide chains which are both cleaved from a proprotein encode
- ASGR2 binds to galactose terminated glycoproteins It transports these glycoproteins via a series of membrane vesicles and tubules to an acidic sorting organelle where the receptor and ligand dissocia
- ASGR2 is a cell surface receptor that binds to galactose terminated glycoproteins It transports these glycoproteins via a series of membrane vesicles and tubules to an acidic sorting organelle where
- Fatty acid binding protein 3 FABP3 gene contains four exons and its function is to arrest growth of mammary epithelial cells This gene is a candidate tumor suppressor gene for human breast cancer
- The protein encoded by FABP7 is a brain fatty acid binding protein Fatty acid binding proteins FABPs are a family of small highly conserved cytoplasmic proteins that bind long chain fatty acids a
- PNLIP is a member of the lipase gene family It encodes a carboxyl esterase that hydrolyzes insoluble emulsified triglycerides and is essential for the efficient digestion of dietary fats This gene
- PNLIP is a member of the lipase gene family PNLIP is a carboxyl esterase that hydrolyzes insoluble emulsified triglycerides and is essential for the efficient digestion of dietary fats It is expre
- ARHGDIG is highly expressed in the entire brain with regional variations The mRNA is also present at high levels in kidney and pancreas and at moderate levels in spinal cord stomach and pituitary
- Three different forms of human pancreatic procarboxypeptidase A have been isolated The A1 and A2 forms are monomeric proteins with different biochemical properties Carboxypeptidase A1 is a monomeric
- KIF5A is a member of the kinesin family of proteins Members of this family are part of a multisubunit complex that functions as a microtubule motor in intracellular organelle transport Mutations in
- Located on chromosome 1 this gene encodes for acid sphingomyelinase like phosphodiesterase 3b precursor protein
- PHYHIP interacts with PHYH suggests a role in the development of the central system
- 2 3 Cyclic nucleotide 3 phosphodiesterase CNP1 and CNP2 is the major enzyme of central nervous system myelin It is associated with oligodendroglial plasma membrane and uncompacted myelin myelin
- PTHLH is a member of the parathyroid hormone family This hormone regulates endochondral bone development and epithelial mesenchymal interactions during the formation of the mammary glands and teeth
- KIF3C is a member of KIF3 family It is highly enriched in neural tissues such as brain spinal cord and retina It is an anterograde motor
- Kinesin is the founding member of a superfamily of microtubule based motor proteins that perform force generating tasks such as organelle transport and chromosome segregation Kinesin consists of heav
- The protein encoded by the KIF3B gene acts as a heterodimer with kinesin family member 3A to aid in chromosome movement during mitosis and meiosis The encoded protein is a plus end directed microtubu
- KIF1C represents a member of the Unc104 subfamily of kinesin like proteins that are involved in the transport of mitochondria or synaptic vesicles in axons KIF1C consists of an amino terminal motor d
- KIF3A B is a kinesin involved in intraflagellar transport and Golgi trafficking
- KIF22 a member of kinesin like protein family This family of proteins are microtubule dependent molecular motors that transport organelles within cells and move chromosomes during cell division The
- KIF21A belongs to a family of plus end directed kinesin motor proteins Neurons use kinesin and dynein microtubule dependent motor proteins to transport essential cellular components along axonal and
- KIF23 is a member of kinesin like protein family This family includes microtubule dependent molecular motors that transport organelles within cells and move chromosomes during cell division This pro
- The t 16 21 q24 q22 translocation is a rare but recurrent chromosomal abnormality associated with therapy related myeloid malignancies The translocation produces a chimeric gene made up of the 5
- RUNX1T1 is a putative zinc finger transcription factor and oncoprotein In acute myeloid leukemia especially in the M2 subtype the t 8 21 q22 q22 translocation is one of the most frequent karyot
- BHLHB2 is a basic helix loop helix protein expressed in various tissues Expression in the chondrocytes is responsive to the addition of Bt2cAMP Differentiated embryo chondrocyte expressed gene 1 is
- RGS16 belongs to the regulator of G protein signaling family It inhibits signal transduction by increasing the GTPase activity of G protein alpha subunits It also may play a role in regulating the
- The protein encoded by RGS13 is a member of the regulator of G protein signaling RGS family RGS family members share similarity with S cerevisiae SST2 and C elegans egl 10 proteins which contain
- RGS13 encodes a protein which is a member of the regulator of G protein signaling RGS family RGS proteins accelerate GTPase activity of G protein alpha subunits thereby driving G protein into thei
- Regulator of G protein signaling RGS proteins are regulatory and structural components of G protein coupled receptor complexes RGS proteins are GTPase activating proteins for Gi class G alpha prote
- Regulator of G protein signaling RGS proteins are regulatory and structural components of G protein coupled receptor complexes RGS proteins are GTPase activating proteins for Gi and Gq class G alph
- TCFL1 encodes the YL 1 protein which is a subunit of the TRRAP TIP60 HAT complex and also is a component of a novel mammalian multiprotein complex that includes the SNF2 related helicase SRCAP
- FLJ37300 is a hypothetical protein found on chromosome 17
- NPM1 is a member of Nucleophosmin NPM family NPM is a ubiquitously expressed nucleolar phosphoprotein that continuously shuttles between the nucleus and cytoplasm
- NPM2 is a member of Nucleophosmin NPM family NPM is a ubiquitously expressed nucleolar phosphoprotein that continuously shuttles between the nucleus and cytoplasm
- PTGER3 is a member of the G protein coupled receptor family This protein is one of four receptors identified for prostaglandin E2 PGE2 This receptor may have many biological functions which invol
- Peroxisome proliferators include hypolipidemic drugs herbicides leukotriene antagonists and plasticizers this term arises because they induce an increase in the size and number of peroxisomes Per
- NPM3 is a member of Nucleophosmin NPM family NPM is a ubiquitously expressed nucleolar phosphoprotein that continuously shuttles between the nucleus and cytoplasm
- The p70 p80 autoantigen is a nuclear complex consisting of two subunits with molecular masses of approximately 70 and 80 kDa The complex functions as a single stranded DNA dependent ATP dependent hel
- XRCC5 encodes the 80 kilodalton subunit of the Ku heterodimer protein which is also known as ATP dependant DNA helicase II or DNA repair protein XRCC5 Ku is the DNA binding component of the DNA depen
- LIG4 encodes a DNA ligase that joins single strand breaks in a double stranded polydeoxynucleotide in an ATP dependent reaction This protein is essential for V D J recombination and DNA double stran
- ZNF179 encodes a member of the RING finger protein family of transcription factors The protein is primarily expressed in brain The gene is located within the Smith Magenis syndrome region on chromos
- PREB encodes a protein that specifically binds to a Pit1 binding element of the prolactin PRL promoter This protein may act as a transcriptional regulator and is thought to be involved in some of t
- RCOR3 is a REST corepressor 3 protein located on chromosome 1
- Human membralin is unique and does not share significant sequence homology with other human genes only membralins of other species The membralin gene contains 11 exons which encode at least two spli
- Tryptophan hydroxylase TPH EC 1 14 16 4 is the rate limiting enzyme in the synthesis of serotonin 5 hydroxytryptamine or 5HT 5HT is causally involved in numerous central nervous activities and
- The protein encoded by the RFP2 gene is a member of the tripartite motif TRIM family The TRIM motif includes three zinc binding domains a RING a B box type 1 and a B box type 2 and a coiled coil
- The protein encoded by RFP2 is a member of the tripartite motif TRIM family The TRIM motif includes three zinc binding domains a RING a B box type 1 and a B box type 2 and a coiled coil region
- ATF2 encodes a transcription factor that is a member of the leucine zipper family of DNA binding proteins This protein binds to the cAMP responsive element CRE an octameric palindrome The protein
- SIAH1 is a protein that is a member of the seven in absentia homolog SIAH family The protein is an E3 ligase and is involved in ubiquitination and proteasome mediated degradation of specific protei
- The protein encoded by SMARCB1 is part of a complex that relieves repressive chromatin structures allowing the transcriptional machinery to access its targets more effectively The encoded nuclear pr
- SNAPC3 is part of the SNAPc complex required for the transcription of both RNA polymerase II and III small nuclear RNA genes SNAPC3 binds to the proximal sequence element PSE a non TATA box basal
- TRIM26 is a member of the tripartite motif TRIM family The TRIM motif includes three zinc binding domains a RING a B box type 1 and a B box type 2 and a coiled coil region The protein localizes
- The CSRP3 gene encodes a member of the CSRP family of LIM domain proteins which may be involved in regulatory processes important for development and cellular differentiation The LIM double zinc fin
- This CSRP3 gene encodes a member of the CSRP family of LIM domain proteins which may be involved in regulatory processes important for development and cellular differentiation The LIM double zinc fi
- The human Timeless protein interacts with both the circadian clock protein cryptochrome 2 and with the cell cycle checkpoint proteins Chk1 and the ATR ATRIP complex and plays an important role in the
- COPS2 is an essential component of the COP9 signalosome complex CSN a complex involved in various cellular and developmental processes The CSN complex is an essential regulator of the ubiquitin U
- TRIP10 is in FNBP1 family of proteins
- The activation of gene transcription is a multistep process that is triggered by factors that recognize transcriptional enhancer sites in DNA These factors work with co activators to direct transcrip
- ASPH is thought to play an important role in calcium homeostasis Alternative splicing of this gene results in five transcript variants which vary in protein translation the coding of catalytic domai
- ASH2L plays a role in hematopoiesis and is associated with some special kinds of leukemia The amount of ASH2L transcripts is extremely high in fetal liver testis and leukemia cell lines with erythr
- DXYS155E is a gene found in the pseudoautosomal region of the distal short arms of the X and Y chromosomes and appears to be ubiquitously expressed
- BRD2 is a mitogen activated kinase which localizes to the nucleus The gene maps to the major histocompatability complex MHC class II region on chromosome 6p21 3 but sequence comparison suggests tha
- BRD2 encodes a mitogen activated kinase which localizes to the nucleus BRD2 maps to the major histocompatability complex MHC class II region on chromosome 6p21 3 but sequence comparison suggests th
- PCGF4 regulates telomerase expression in MECs and plays a role in the development of human breast cancer
- CXorf6 is a protein predicted based on an ORF found in chromosome 14
- AF6 is a Ras target that regulates cell cell adhesions downstream of Ras activation It is fused with MLL in leukemias caused by t 6 11 translocations
- PAX9 is a member of the paired box PAX family of transcription factors Members of this gene family typically contain a paired box domain an octapeptide and a paired type homeodomain These genes
- The CCT chaperonin containing TCP 1 complex functions as a molecular chaperone in the eukaryotic cytosol CCT4 interacts with human cyclin E which has been implicated in positive control of the G1 S
- CCT4 is a subunit of a cytosolic hetero oligomeric chaperone that is known to be involved in the folding of actin and tubulin This protein is a member of the chaperonin family which includes Escheri
- ARID3B is a member of the ARID AT rich interaction domain family of DNA binding proteins The protein is homologous with two proteins that bind to the retinoblastoma gene product and also with the
- CORO1A forms homodimers It plays a role in the cross linking of F actin in the cell

- Polycomb group PcG of proteins form the multiprotein complexes that are important for the transcription repression of various genes involved in development and cell proliferation The protein encode
- M96 may be involved in the activation of MT metallothionein genes in response to heavy metal ions
- The function of Anti GTL3 has not yet been determined
- SAP30BP expressed as a fusion polypeptide with a fluorescent protein in the nucleus of HeLa cells SAP30BP induces cell death The interaction of SAP30BP with SAP30 in its conserved domain implies tha
- SAP30BP is a component of a histone deacetylase complex conserved among eukaryotic organisms This complex is active in deacetylating core histone octamers but inactive in deacetylating nucleosomal h
- SERTA is a transcriptional regulator that interacts with the PHD bromodomain of co repressors of Kruppel associated box KRAB mediated repression KRIP 1 TIF1beta and TIF1alpha as well as the co a
- In mouse recombining binding protein L RBP L is a transcription factor that binds to DNA sequences almost identical to that bound by the Notch receptor signalling pathway transcription factor RBP J
- FREQ is a member of the neuronal calcium sensor gene family which encode calcium binding proteins expressed predominantly in neurons The protein encoded by this gene regulates G protein coupled rece
- CNOT3 is a protein component of CCR4 NOT protein complex Yeast CCR NOT is a global regulator of RNA polymerase II transcription It is comprised of yeast NOT1 to NOT5 yeast CCR4 and additional prot
- Located on chromosome 4 the RIPX encodes a protein with unknown function
- C14orf101 is a protein predicted based on an ORF found in chromosome 14
- MANSC1 located on chromosome 12 encodes a protein whose function is not yet defined
- The MGC4618 is a hypothetical protein found in Chromosome 4
- The MGC4618 is a hypothetical protein found in Chromosome 4
- COLQ encodes the subunit of a collagen like molecule associated with acetylcholinesterase in skeletal muscle Each molecule is composed of three identical subunits Each subunit contains a proline ric
- Human ESP1 CRP2 protein has two LIM domains and each shares 35 1 and 77 or 79 identical residues with human cysteine rich protein CRP and rat CRIP respectively Northern blot analysis of ESP1 CR
- ENO1 is one of three enolase isoenzymes found in mammals it encodes alpha enolase a homodimeric soluble enzyme and also encodes a shorter monomeric structural lens protein tau crystallin The two
- ENO1 encodes one of three enolase isoenzymes found in mammals it encodes alpha enolase a homodimeric soluble enzyme and also encodes a shorter monomeric structural lens protein tau crystallin The
- LIM proteins named for LIN11 ISL1 and MEC3 are defined by the possession of a highly conserved double zinc finger motif called the LIM domain FHL1 may play an important role during the early st
- The ELK4 gene is a member of the Ets family of transcription factors and of the ternary complex factor TCF subfamily Proteins of the TCF subfamily form a ternary complex by binding to the the serum
- NFKB1 MIM 164011 or NFKB2 MIM 164012 is bound to REL MIM 164910 RELA MIM 164014 or RELB MIM 604758 to form the NFKB complex The NFKB complex is inhibited by I kappa B proteins NFKBIA MI
- POU2F2 is a member of the POU family and is predominantly expressed in B cells in activated T cells and in the nervous system
- Located on chromosome 19 ZFP36 encodes a protein that is involved in controlling pro inflammatory cytokines
- Focal adhesions are actin rich structures that enable cells to adhere to the extracellular matrix and at which protein complexes involved in signal transduction assemble Zyxin is a zinc binding phosp
- HOXB7 belongs to the homeobox family The homeobox genes encode a highly conserved family of transcription factors that play an important role in morphogenesis in all multicellular organisms Mammals
- NSEP1 is a cell cycle stage specific transcription factor important for cell proliferation NSEP1 encodes a protein that correlates with P glycoprotein expression in human breast carcinoma
- Part of the d4 family of zinc finger proteins DPF1 has been localized on chromosome 19
- WDR39 is a member of the WD40 family of proteins WDR39 specifically interacts with WT1 both in vitro and in vivo This interaction results in a decrease in transcriptional activation mediated by WT1
- PCGF3 contains a C3HC4 type RING finger which is a motif known to be involved in protein protein interactions The specific function of this protein has not yet been determined
- PCGF3 encodes a protein that contains a C3HC4 type RING finger which is a motif known to be involved in protein protein interactions The specific function of this protein has not yet been determined
- ARIH2 might act as an E3 ubiquitin protein ligase or as part of E3 complex which accepts ubiquitin from specific E2 ubiquitin conjugating enzymes such as UBE2L3 UBCM4 and then transfers it to subs
- HEXIM1 expression is induced by hexamethylene bis acetamide in vascular smooth muscle cells The function of this protein is not yet known
- TRIM10 is a member of the tripartite motif TRIM family The TRIM motif includes three zinc binding domains a RING a B box type 1 and a B box type 2 and a coiled coil region This protein localize
- CBX1 is the component of heterochromatin CBX1 recognizes and binds histone H3 tails methylated at Lys 9 leading to epigenetic repression CBX1 interaction with lamin B receptor LBR can contribut
- USF1 encodes a member of the basic helix loop helix leucine zipper family and can function as a cellular transcription factor The encoded protein can activate transcription through pyrimidine rich i
- ZNF237 is a candidate transcription factor
- VPS24 encodes a protein that acts in the sorting of transmembrane proteins into lysosomes vacuoles via the multivesicular body MVB pathway This protein along with other soluble coiled coil contain
- The protein encoded by the TRIM68 gene contains a RING finger domain a motif present in a variety of functionally distinct proteins and known to be involved in protein protein and protein DNA interac
- RRN3 is RNA polymerase I specific transcription initiation factor Phosphorylation of RRN3 by MAPK cascades links cell signaling with the control of gene expression namely results in rRNA synthesis i
- In mammals growth dependent regulation of RNA polymerase I Pol I transcription is mediated by RRN3 an essential initiation factor It interacts with Pol I in the absence of template DNA augments
- ZA20D3 is a zinc finger protein located on chromosome 15
- The association of hMI ER1 with Sp1 represents a novel mechanism for the negative regulation of Sp1 target promoters Results demonstrate that alternate use of a facultative intron regulates the subce
- TFB2M is a S adenosyl L methionine dependent methyltransferase which specifically dimethylates mitochondrial 12S rRNA at the conserved stem loop It is also required for basal transcription of mitocho
- SMARCA2 is a member of the SWI SNF family of proteins and is highly similar to the brahma protein of Drosophila Members of this family have helicase and ATPase activities and are thought to regulate
- The function of ZNF498 remains unknown The protein bears some similarity to zinc finger proteins which are involved in DNA binding and protein protein interactions Alternative splicing results in t
- VAX1 is a homeo domain containing protein from a class of homeobox transcription factors which are conserved in vertebrates It may play an important role in the development of anterior ventral forebr
- LOC390874 is a new protein with unknown function
- LOC390874 is a new protein with unknown function
- Inhibition of NFkappa B activity by the hepatitis C virus core protein might be related to its physical interaction with and interrupted nuclear localization of IKKbeta Increased nuclear factor kappa
- FHL2 is a member of LIM proteins that contain a highly conserved double zinc finger motif called the LIM domain
- SMARCA3 HLTF is a member of the SWI SNF family Members of this family have helicase and ATPase activities and are thought to regulate transcription of certain genes by altering the chromatin struct
- The function remains unknown Western blots using two different antibodies against two unique regions of this protein target confirm the same apparent molecular weight in our tests
- TBC1D10B which belongs to the TBC1 domain family member 10B was experimentally validated as a Hela cell nuclei protein currently with unknown function TBC rabGAP domain containing microvillar pr
- LARP2 encodes a protein containing domains found in the La related protein of Drosophila melanogaster La motif containing proteins are thought to be RNA binding proteins where the La motif and adjac
- KLHL25 is also known as ENC2 It is a BTB POZ KELCH domain protein
- The transcription of genes from mitochondrial DNA requires a mitochondrial RNA polymerase and a DNA binding transcription factor Transcription factor B1 TFB1M is a part of this transcription comple
- The function of the C14orf266 gene has not yet been determined
- TRIM17 encodes a protein that is a member of the tripartite motif TRIM family The TRIM motif includes three zinc binding domains a RING a B box type 1 and a B box type 2 and a coiled coil region
- TRIM17 is a member of the tripartite motif TRIM family The TRIM motif includes three zinc binding domains a RING a B box type 1 and a B box type 2 and a coiled coil region The protein localizes
- EPLIN is a cytoskeleton associated protein that inhibits actin filament depolymerization and cross links filaments in bundles EPLIN is a cytoskeleton associated protein that inhibits actin filament d
- The protein encoded by RNF141 contains a RING finger a motif known to be involved in protein DNA and protein protein interactions Abundant expression of this gene was found in the testicular tissue
- RNF141 contains a RING finger a motif known to be involved in protein DNA and protein protein interactions Abundant expression of this gene was found in the testicular tissue of fertile men but was
- PER3 is a member of the Period family of genes and is expressed in a circadian pattern in the suprachiasmatic nucleus the primary circadian pacemaker in the mammalian brain Genes in this family enco
- C21orf18 located on chromosome 21 is predicted to encode for a hypothetical protein
- SUV420H1 is a protein that contains a SET domain SET domains appear to be protein protein interaction domains that mediate interactions with a family of proteins that display similarity with dual spe
- BTBD5 is a transcription factor containing BTB POZ domain
- TRMT1 is a tRNA m 2 2 G 26 dimethyltransferase
- Decapping is a key step in general and regulated mRNA decay The protein encoded by this gene is a decapping enzyme This protein and another decapping enzyme form a decapping complex which interacts
- TIP120A functions as a negative regulator of SCF E3 ubiquitin ligases and may modulate other cullin ligases in a similar fashion
- METTL3 is the 70 kDa subunit of MT A which is part of N6 adenosine methyltransferase This enzyme is involved in the posttranscriptional methylation of internal adenosine residues in eukaryotic mRNAs
- The ZA20D1 gene encodes an enzyme that cleaves ubiquitin from proteins This gene has the ability to down regulate NF kappa B which plays a pivotal role in inflammatory processes through induction of
- CBX8 is one of the proteins homolog to the Polycomb group PcG proteins They assemble to form large multiprotein complexes involved in gene silencing Evidence suggests that PcG complexes are hetero
- EGLN1 has a role in the regulation of hypoxia inducible factor It is not affected by overexpression or downregulation of HIF 2alpha
- The function of the Anti BTBD14B gene has not yet been determined
- C16orf44 is an open reading frame 44 found in chromosome 16
- RIN3 biochemically characterized as the stimulator and stabilizer for GTP Rab5 plays an important role in the transport pathway from plasma membrane to early endosomes
- KCNIP4 encodes a member of the family of voltage gated potassium Kv channel interacting proteins KCNIPs which belong to the recoverin branch of the EF hand superfamily Members of the KCNIP famil
- KVNIP4 is a member of the family of voltage gated potassium Kv channel interacting proteins KCNIPs which belong to the recoverin branch of the EF hand superfamily Members of the KCNIP family are
- cDNA sequence was generated by The National Institutes of Health Mammalian Gene Collection MGC Program
- The function of LAS1L has not been determined
- The function of LAS1L has not been determined
- The protein encoded by RNF135 contains a RING finger domain a motif present in a variety of functionally distinct proteins and known to be involved in protein protein and protein DNA interactions Th
- ZNF289 is a candidate transcription factor
- PSIP1 encodes a multidomain adaptor protein that interacts with the nuclear import apparatus lentiviral IN proteins and chromatin by means of an NLS an IBD and additional chromatin interacting domai
- PSIP1 is a transcriptional coactivator It also acts as an adaptor to coordinate pre mRNA splicing and transcriptional activation of class II genes
- KLHL13 contains 6 Kelch repeats and 1 BTB POZ domain

The function of this protein remains unknown

- DKFZP781I1119 is a member of mesoderm induction early response 1 family
- RCOR2 may act as a component of a corepressor complex that represses transcription
- CREB3L2 is a member of the old astrocyte specifically induced substance OASIS DNA binding and basic leucine zipper dimerization bZIP family of transcription factors which includes CREB3 MIM 6064
- KLHL14 is a member of the KLHL family
- MID1 is a member of the tripartite motif TRIM family also known as the RING B box coiled coil RBCC subgroup of RING finger proteins The TRIM motif includes three zinc binding domains a RING
- MEIS2 encodes a homeobox protein belonging to the TALE three amino acid loop extension family of homeodomain containing proteins TALE homeobox proteins are highly conserved transcription regulato

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