Panel 1, pgs 1-58

AccessID	Gene	Functional Group	XPRESS Count	d0:d8 ratio	d0:d8 StdDev	Description
SW:KDGG_HUMAN	**DGKG**	41	1	10.54	0.00	SW:KDGG_HUMAN P49619 homo sapiens (human). diacylglycerol kinase, gamma (ec 2.7.1.107) (diglyceride kinase) (dgk-gamma) (dag kinase gamma). 5/2000 [MASS=88997]/Diacylglycerol kinase gamma, member of diacylglycerol kinase family, contains EF-hand motifs, zinc finger and ATP-binding site, converts diacylglycerol to phosphatidic acid in a phosphatidylserine-dependent manner, may regulate phospholipid turnover
GP:AB028980_1	**USP24**	32	1	9.55	0.00	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 24 /Member of the ubiquitin carboxyl-terminal hydrolase family 2 that contains a ubiquitin carboxyl-terminal hydrolases family 2 domain, has low similarity to a region of ubiquitin specific protease 9 X chromosome (human USP9X)
PIR2:S12444	**hypothetical/unknown**	45	1	7.89	0.00	PIR2:S12444 hypothetical protein 458 - human [MASS=49127]/human immunoglobulin lambda genes
GPN:AJ278775_1	**VL1**	45	1	7.61	0.00	immunoglobulin light chain variable region (human)
SW:AT2A_HUMAN	**ATP9A**	42	2	5.29	2.51	SW:AT2A_HUMAN O75110 homo sapiens (human). potential phospholipid-transporting atpase iia (ec 3.6.1.-) (fragment). 5/2000 [MASS=116933]/Member of the haloacid dehalogenase or epoxide hydrolase family, has moderate similarity to S. cerevisiae Neo1p, which is an ATPase whose overproduction confers neomycin resistance
GP:AJ002744_1	**GALNT7**	5, 19	1	4.00	0.00	GP:AJ002744_1 Homo sapiens mRNA for UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase 7. [MASS=75402]/UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 7, enzyme that functions in O-glycosylation and is specific for partially glycosylated substrates
GP:AF057145_1	ST14	32	1	3.98	0.00	(matriptase) (membrane- type serine protease 1) (mt-sp1)./Matriptase, a type 2 integral membrane serine protease, degrades extracellular matrix, activates hepatocyte growth factor (HGF) and urokinase plasminogen activator (PLAU), and may play a role in progression and metastasis of epithelial-derived cancers
SW:PA2M_HUMAN	PLA2G2A	19, 41	3	3.94	1.93	SW:PA2M_HUMAN P14555 homo sapiens (human). phospholipase a2, membrane associated precursor (ec 3.1.1.4) (phosphatidylcholine 2-acylhydrolase) (group ii phospholipase a2) (non-pancreatic secretory phosph [MASS=16083]/Group IIA phospholipase A2, a secreted member of the phospholipase A2 family that hydrolyzes the phospholipid sn-2 ester bond, plays roles in phospholipid metabolism, host defense, and inflammation; gene loss reported in a sporadic colorectal tumor
SW:RDC1_HUMAN	RDC1	41	4	3.86	1.24	SW:RDC1_HUMAN P25106 homo sapiens (human). g protein-coupled receptor rdc1 homolog. 7/1998 [MASS=41474]/Chemokine orphan receptor 1, protein with strong similarity to murine Rdc1, which is a member of the G protein-coupled receptor family and related to chemokine receptors of the CXC family, acts as a coreceptor for HIV strains that infect brain cells
SW:SFR7_HUMAN	SFRS7	25, 37, 38	2	3.66	0.49	SW:SFR7_HUMAN Q16629 homo sapiens (human). splicing factor, arginine/serine-rich 7 (splicing factor 9g8). 5/2000 [MASS=27367]/Splicing factor arginine serine rich 7, a splicing factor of the SR protein family containing an RNA binding domain (RBD) and a serine/arginine (SR) domain that is implicated in alternative pre-mRNA splicing
SW:LMG1_HUMAN	LAMC1	6, 16, 31	1	3.60	0.00	SW:LMG1_HUMAN P11047 homo sapiens (human). laminin gamma-1 chain precursor (laminin b2 chain). 7/1998 [MASS=177607]/Laminin C1, an extracellular matrix glycoprotein that may be involved in cell-matrix adhesion and the regulation of cell shape
SW:B3A2_HUMAN	SLC4A2	42	1	3.57	0.00	SW:B3A2_HUMAN P04920 homo sapiens (human). anion exchange protein 2 (non-erythroid band 3-like protein) (bnd3l). 10/1996 [MASS=136814]/Solute carrier family 4 member 2 (anion exchanger 2), a chloride and bicarbonate exchanger that may play a role in pH regulation, binds ankyrin and links the basolateral membrane to the cytoskeleton
GP:AK022587_1	FLJ12525	45	1	3.46	0.00	GP:AK022587_1 Homo sapiens cDNA FLJ12525 fis, clone NT2RM4000030, weakly similar to LAS1 PROTEIN; unnamed protein product. [MASS=83065]/Protein of unknown function, has a region of low similarity to a region of S. cerevisiae Las1p, which is involved in cell morphogenesis, cytoskeletal regulation, and bud formation
SW:NR54_HUMAN	NONO	25, 37, 38	2	3.38	1.09	SW:NR54_HUMAN Q15233 homo sapiens (human). 54 kda nuclear rna-binding protein (p54(nrb)) (p54nrb) (55 kda nuclear protein) (nmt55). 5/2000 [MASS=54232]/Non-POU-domain-containing octamer-binding nuclear protein, binds DNA and RNA, and implicated in transcription and pre-mRNA splicing; a fusion partner with TFE3 in papillary renal cell carcinoma
SW:GPDM_HUMAN	GPD2	5	1	3.30	0.00	SW:GPDM_HUMAN P43304 homo sapiens (human). glycerol-3-phosphate dehydrogenase, mitochondrial precursor (ec 1.1.99.5) (gpd-m) (gpdh-m). 5/2000 [MASS=80815]/Mitochondrial glycerol-3-phosphate dehydrogenase, component of the glycerol phosphate shuttle; mutation of the calcium binding domain in the corresponding gene has been found in a patient with type A diabetes
GP:AF002668_1	DEGS	16, 19, 41	1	3.29	0.00	GP:AF002668_1 Homo sapiens putative fatty acid desaturase MLD mRNA, complete cds; putative fatty acid desaturase. [MASS=37866]/Degenerative spermatocyte homolog (Drosophila), member of the membrane fatty acid desaturase family, regulates the biosynthesis of the epidermal growth factor receptor (EGFR)
PIR2:T08789	CDYL	45	1	3.26	0.00	PIR2:T08789 hypothetical protein DKFZp586C1622.1 - human (fragment) [MASS=16138]/Homo sapiens testis-specific chromodomain Y-like protein (CDYL) mRNA/Chromodomain protein Y chromosome-like, a ubiquitously-expressed autosomal protein with similarity to chromodomain-containing proteins located on the Y chromosome
SW:SR14_HUMAN	SRP14	36	2	3.24	0.14	SW:SR14_HUMAN P37108 homo sapiens (human). signal recognition particle 14 kda protein (srp14) (18 kda alu rna binding protein). 5/2000 [MASS=14544]/Signal recognition particle 14 kDa, heterodimer with SRP9 binds Alu-like RNAs, involved in the translocation of newly synthesized proteins across the rough endoplasmic reticulum membrane, may regulate expression and Alu transcript metabolism
SW:LAM1_HUMAN	LMNB1	11	1	3.22	0.00	SW:LAM1_HUMAN P20700 homo sapiens (human). lamin b1. 5/2000 [MASS=66277]/Lamin B1, present in the nuclear outer membrane, may be a structural member of the nuclear lamina, cleaved by proteases during apoptosis, targeted by autoantibodies in chronic fatigue syndrome

GP:AB006537_1	IL1RAP	31, 41	1	3.20	0.00	GP:AB006537_1 Homo sapiens mRNA for interleukin 1 receptor accessory protein, complete cds. [MASS=65418]/Interleukin-1 receptor accessory protein, a subunit of the interleukin-1 receptor complex, recruits IRAK to the receptor complex in an early stage of interleukin-1 signaling
GP:D63481_1	SCRIB	41	1	3.09	0.00	GP:D63481_1 Human mRNA for KIAA0147 gene, partial cds; The KIAA0147 gene product is related to adenylyl cyclase.. [MASS=166187]/Protein containing PDZ (DHR, GLGF) domains, which target signaling proteins to membranes, contains leucine rich repeats, which mediate protein-protein interactions
SW:H33_HUMAN	H3F3A	12	1	3.08	0.00	SW:H33_HUMAN P06351 homo sapiens (human), mus musculus (mouse), rattus norvegicus (rat), oryctolagus cuniculus (rabbit), gallus gallus (chicken), spisula solidissima (atlantic surf-clam), drosophila mel [MASS=15197]/H3 histone family 3A, a member of the H3 histone family of proteins involved in compaction of DNA into nucleosomes, a replacement histone; expression does not depend on DNA replication
SW:CAG4_HUMAN	SIAT4A	34	1	2.99	0.00	SW:CAG4_HUMAN Q11201 h cmp-n-acetylneuraminate-beta-galactosamide-alpha-2,3-sialyltransferase (ec 2.4.99.4) (beta-galactoside alpha-2,3-sialyltransferase) (alpha 2,3-st) (gal-nac6s) (gal-beta-1,3-galnac [MASS=39075]/Sialyltransferase 4A (beta-galactoside alpha-2,3-sialyltransferase), member of a sialyltransferase 4 family, catalyzes the transfer of NeuAc from CMP-NeuAc to asialo-fetuin
SW:K6PP_HUMAN	PFKP	5	1	2.96	0.00	SW:K6PP_HUMAN Q01813 homo sapiens (human). 6-phosphofructokinase, type c (ec 2.7.1.11) (phosphofructokinase 1) (phosphohexokinase) (phosphofructo-1-kinase isozyme c) (6-phosphofructokinase, platelet typ [MASS=85596]/Platelet-type phosphofructokinase, rate-limiting enzyme of glycolysis that catalyzes the formation of fructose 1,6-bisphosphate from fructose 6-phosphate and ATP; expression may be elevated upon malignant transformation
SW:LAMA_HUMAN	LMNA	11, 16	1	2.95	0.00	SW:LAMA_HUMAN P02545 homo sapiens (human). lamin a (70 kda lamin). 5/2000 [MASS=74139]/Lamin A, a structural protein of the nuclear lamina; mutations of the corresponding gene are associated with Emery-Dreifuss muscular dystrophy and partial lipodystrophies
SW:IF4E_HUMAN	EIF4E	35	1	2.94	0.00	SW:IF4E_HUMAN P06730 homo sapiens (human). eukaryotic translation initiation factor 4e (eif-4e) (eif4e) (mrna cap-binding protein) (eif-4f 25 kda subunit). 5/2000 [MASS=25097]/Eukaryotic translation initiation factor 4E, a subunit of eIF4F, a mRNA cap-binding protein involved in translation initiation, a target of insulin dependent signaling pathway, expression is upregulated in breast carcinomas
GP:AB000449_1	VRK1	34	2	2.94	1.64	GP:AB000449_1 Homo sapiens mRNA for VRK1, complete cds. [MASS=45476]/Vaccinia related kinase 1, nuclear serine/threonine kinase that phosphorylates acidic and basic protein substrates, may activate p53 and function in signal transduction, may regulate cellular proliferation, has similarity to vaccinia virus B1R kinase
SW:SBP1_HUMAN	SELENBP1	45	2	2.89	0.05	SW:SBP1_HUMAN Q13228 homo sapiens (human). selenium-binding protein 1. 5/2000 [MASS=52313]/Selenium binding protein 1, may have a role in negative regulation of cell growth; mouse Selenbp1 may play a role in mediating the anticarcinogenic effects of selenium
SW:LU_HUMAN	LU	6, 41	3	2.88	0.14	SW:LU_HUMAN P50895 homo sapiens (human). lutheran blood group glycoprotein precursor (b-cam cell surface glycoprotein) (auberger b antigen) (f8/g253 antigen). 11/1997 [MASS=67375]/Precursor of Lutheran blood group glycoprotein and B-CAM, laminin receptors and cell adhesion molecules, have a role in the blood-brain barrier, contribute to vasoocculsion in sickle cell disease and possibly tumorigenesis
SW:SORC_HUMAN	SRI	16, 26, 41, 42	2	2.86	2.11	SW:SORC_HUMAN P30626 homo sapiens (human). sorcin (22 kda protein) (cp-22) (v19). 11/1997 [MASS=21676]/Sorcin, an EF-hand calcium-binding protein, may be involved in multidrug resistance, a potential modulator of intracellular calcium levels through interaction with the ryanodine receptor
GP:AL023881_1	DECR1	26	1	2.78	0.00	peroxisomal 2,4-dienoyl-CoA reductase /2,4-dienoyl-CoA reductase, an auxiliary beta-oxidation enzyme of the mitochondrion that participates in the metabolism of unsaturated fatty enoyl-CoA esters with double bonds in both odd- and even-numbered positions
SW:COXG_HUMAN	COX6B	18	6	2.77	1.08	SW:COXG_HUMAN P14854 homo sapiens (human). cytochrome c oxidase polypeptide vib (ec 1.9.3.1) (aed). 11/1997 [MASS=10061]/Cytochrome c oxidase subunit VIb, a putative subunit of cytochrome C oxidase, which couples reduction of oxygen with proton translocation during oxidative phosphorylation
SW:FXR1_HUMAN	FXR1	16, 24	1	2.74	0.00	SW:FXR1_HUMAN P51114 homo sapiens (human). fragile x mental retardation syndrome related protein 1. 10/1996 [MASS=69692]/Fragile X mental retardation autosomal homolog 1, binds FMR1, associates with mRNPs and with 60S ribosomal subunits, may have a role in the ribosomal and RNA metabolism of neurons; identified as a scleroderma autoantigen processed during apoptosis
GP:AK024450_1	LOC89941	45	1	2.73	0.00	GP:AK024450_1 Homo sapiens mRNA for FLJ00042 protein, partial cds; For this clone, GeneMark analysis triggered an alert for spurious CDS split. The result of GeneMark analysis of the nucleotide sequence of this clone i. [MASS=48320]/Protein of unknown function, has a region of low similarity to aplysia Ras-related homolog B (human ARHB), which functions in actin cytoskeleton assembly and is the pharmacological target of certain anti-cancer drugs that inhibit cell growth
SW:PSS8_HUMAN	PRSS8	45	1	2.73	0.00	SW:PSS8_HUMAN Q16651 homo sapiens (human). prostasin precursor (ec 3.4.21.-). 7/1998 [MASS=36431]/Protease serine 8 (prostasin), a serine protease that plays a role in regulation of the amiloride-sensitive epithelial sodium channel, may act as a suppressor of invasive prostate and breast cancer, overexpressed in ovarian cancer cells
GP:AC005609_7	PCDHA4	6	1	2.70	0.00	GP:AC005609_7 Homo sapiens chromosome 5, BAC clone 203o13 (LBNL H155), complete sequence. [MASS=84896]/Protocadherin alpha 4, a member of a family of cadherin-like cell adhesion proteins that may have a role in forming neuronal connections in the brain
SW:NIPM_HUMAN	NDUFS5	18	2	2.69	0.02	SW:NIPM_HUMAN O43920 homo sapiens (human). nadh-ubiquinone oxidoreductase 15 kda subunit (ec 1.6.5.3) (ec 1.6.99.3) (complex i-15 kda) (ci-15 kda). 7/1999 [MASS=12386]/NADH dehydrogenase Fe-S protein 5 (15kD) (NADH-coenzyme Q reductase), putative subunit of NADH-ubiquinone oxidoreductase (complex I), a multiprotein complex that transports electrons from NADH to ubiquinone in the mitochondrial respiratory chain

SW:ATPQ_HUMAN	ATP5H	18	3	2.67	0.53	SW:ATPQ_HUMAN O75947 homo sapiens (human). atp synthase d chain, mitochondrial (ec 3.6.1.34). 5/2000 [MASS=18360]/Protein with high similarity to subunit d of the mitochondrial H(+)-ATP synthase (rat Atp5jd), which is part of a multisubunit enzyme that catalyzes the synthesis of ATP during oxidative phosphorylation
SW:PNL1_HUMAN	PNUTL1	11, 13	2	2.64	0.07	SW:PNL1_HUMAN Q99719 homo sapiens (human). peanut-like protein 1 (cell division control related protein 1) (cdcrel-1). 5/2000 [MASS=42777]/Peanut-like (CDCREL-1), member of the septin family of GTP-binding proteins, may be involved in vesicle targeting and fusion, may have a role in velo cardio facial or DiGeorge syndrome; PNUTL1 gene translocations are associated with acute myeloid leukemia
GP:AC004957_1	LOC222217	45	3	2.64	0.14	GP:AC004957_1 Homo sapiens PAC clone RP5-1093O17 from 7q11.23-q21, complete sequence; heterogeneous ribonuclear particle protein A1; similar to P49312 (PID:g1350822); H_DJ1093O17.1. [MASS=33911]
SW:ADDA_HUMAN	ADD1	11	1	2.64	0.00	SW:ADDA_HUMAN P35611 homo sapiens (human). erythrocyte adducin alpha subunit. 7/1998 [MASS=80971]/Adducin 1 alpha, a subunit of the membrane-skeletal adducin complex, may promote assembly of spectrin-actin complexes and regulate ion transport; mutations in the corresponding gene may be associated with hypertension
SW:Y017_HUMAN	SF3B3	25, 31, 37, 38	7	2.63	0.59	SW:Y017_HUMAN Q15393 homo sapiens (human). hypothetical protein kiaa0017. 5/2000 [MASS=44606]/ Homo sapiens mRNA for SAP 130 spliceosomal protein/Splicing factor 3b subunit 3, a component of the U2 snRNP-associated protein complex SF3b that plays a role in spliceosome assembly, interacts with STAGA and TFTC complexes implicated in DNA repair, chromatin modification, and transcription
SW:TPP1_HUMAN	CLN2	19, 32	1	2.62	0.00	SW:TPP1_HUMAN O14773 homo sapiens (human). tripeptidyl-peptidase i precursor (ec 3.4.14.9) (tpp-i) (tripeptidyl aminopeptidase) (lysosomal pepstatin insensitive protease) (lpic). 5/2000 [MASS=61229]/Tripeptidyl peptidase I (ceroid-lipofuscinosis neuronal 2), a lysosomal serine-type peptidase required for degradation of ATP synthase subunit c (ATP5G1 and ATP5G2); mutations in the corresponding gene cause late infantile neuronal ceroid lipofuscinosis
SW:PUR_HUMAN	PURA	15, 29	2	2.62	0.17	SW:PUR_HUMAN Q00577 homo sapiens (human). transcriptional activator protein pur-alpha (purine-rich single- stranded dna-binding protein alpha). 7/1998 [MASS=34911]/Purine rich element binding protein A, a single-stranded DNA-RNA binding protein implicated in the control of transcription and DNA replication; interacts with HIV Tat protein and JC virus T antigen to modulate host and viral gene expression
GP:AC004528_1	WDR18	45	1	2.62	0.00	GP:AC004528_1 Homo sapiens chromosome 19, cosmid R32184, complete sequence; Hypothetical human protein (partial CDS); CDS constructed from combination of BLASTX, EST matches and Xgrail predictions. N-terminus of protein likely encoded in flanking cosmid R29942. Pr [MASS=47306]/Protein containing four WD domains (WD-40 repeat), which may mediate protein-protein interactions, has a region of low similarity to a region of TATA box binding protein associated factor 2d 100 kD (human TAF5), which functions in transcription initiation
GP:AJ001258_1	NIPSNAP1	45	1	2.60	0.00	GP:AJ001258_1 Homo sapiens mRNA for NIPSNAP1 protein. [MASS=33324]/NIPSNAP C. elegans homolog 1, a member of the NIPSNAP family of proteins, may have a vesicle transport-related function
SW:ATCK_HUMAN	ATP2C1	16, 26, 42	2	2.59	0.30	SW:ATCK_HUMAN P98194 homo sapiens (human). calcium-transporting atpase 2c1 (ec 3.6.1.38) (atp-dependent ca2+ pump pmr1). 5/2000 [MASS=100606]/ATPase (Ca2+ transporting) type 2c member I, a a Ca2+-transporting P-type ATPase involved in Ca2+ homeostasis that may also may play a role in epidermal differentiation; mutations in the gene cause Hailey-Hailey disease, a blistering skin disease
SW:DD17_HUMAN	DDX17	25, 37	1	2.58	0.00	SW:DD17_HUMAN Q92841 homo sapiens (human). probable rna-dependent helicase p72 (dead-box protein p72) (dead box protein 17). 5/2000 [MASS=72371]/DEAD H box protein 17, a member of the DEAD box family of RNA-dependent ATPases and ATP-dependent RNA helicases, a component of an estrogen receptor alpha (ESR) transcriptional coactivator complex
GP:AF085361_1	MTCH2	45	5	2.58	0.98	GP:AF085361_1 Homo sapiens HSPC032 mRNA, complete cds. [MASS=33331]/mitochondrial carrier homolog 2 /Member of the mitochondrial carrier protein family of membrane transporters, has strong similarity to uncharacterized mouse Mtch2
SW:ADT3_HUMAN	SLC25A6	18, 42	1	2.57	0.00	SW:ADT3_HUMAN P12236 homo sapiens (human). adp,atp carrier protein, liver isoform t2 (adp/atp translocase 3) (adenine nucleotide translocator 3) (ant 3). 11/1995 [MASS=32866]/Solute carrier family 25 member 6 (adenine nucleotide translocator), member of the ADP/ATP translocase family
SW:GRBA_HUMAN	GRB10	16, 41	3	2.55	2.22	SW:GRBA_HUMAN Q13322 homo sapiens (human). growth factor receptor-bound protein 10 (grb10 adaptor protein) (insulin receptor binding protein grb-ir) (kiaa0207). 5/2000 [MASS=67231]/Growth factor receptor bound protein 10, an adaptor protein with PH and SH2 domains that binds to various receptor and cytosolic kinases and may mediate growth factor and Src family kinase signaling; variants may be associated with Russell-Silver Syndrome
SW:ADT2_HUMAN	SLC25A5	18, 42	8	2.53	1.17	SW:ADT2_HUMAN P05141 homo sapiens (human). adp,atp carrier protein, fibroblast isoform (adp/atp translocase 2) (adenine nucleotide translocator 2) (ant 2). 7/1999 [MASS=32895]/Solute carrier family 25 member 5 (adenine nucleotide translocator 2), may mediate the exchange of ADP and ATP between the cytosol and mitochondria, expression is altered in dilated cardiomyopathy
GP:AF161397_1	HPCL2	19	2	2.53	0.16	GP:AF161397_1 Homo sapiens HSPC279 mRNA, partial cds. [MASS=64199]/Homo sapiens mRNA for 2-hydroxyphytanoyl-CoA lyase; thiamine pyrophosphate dependent enzyme/2-Hydroxyphytanoyl-CoA lyase (peroxisomal 2-hydroxyphytanoyl-CoA lyase), catalyzes the thiamine pyrophosphate-dependent cleavage of C-C bonds during alpha-oxidation of 3-methyl-branched fatty acids to form formyl-CoA and 2-methyl-branched fatty aldehyde
SW:DHSA_HUMAN	SDHA	5, 18	5	2.48	0.32	SW:DHSA_HUMAN P31040 homo sapiens (human). succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial precursor (ec 1.3.5.1) (fp) (flavoprotein subunit of complex ii). 5/2000 [MASS=72692]/Succinate dehydrogenase complex subunit A (flavoprotein), transports electrons from succinate to ubiquinone in the TCA cycle and respiratory chain; gene mutation is associated with Leigh syndrome, which is a complex II respiratory chain deficiency

SW:ROU_HUMAN	HNRPU	25, 37	29	2.48	0.62	SW:ROU_HUMAN Q00839 homo sapiens (human). heterogenous nuclear ribonucleoprotein u (hnrnp u) (scaffold attachment factor a) (saf-a). 5/2000 [MASS=90479]/Heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A), binds RNA, binds EP300 in a complex that binds scaffold-matrix attachment regions of TOP1, involved in chromatin structure, apoptosis, and perhaps RNA processing and transcription
SW:ROA1_HUMAN	HNRPA1	24, 25, 37, 38	11	2.48	0.85	SW:ROA1_HUMAN P09651 homo sapiens (human). heterogeneous nuclear ribonucleoprotein a1 (helix-destabilizing protein) (single-strand binding protein) (hnrnp core protein a1). 11/1997 [MASS=38715]/Heterogeneous nuclear ribonucleoprotein A1, an RNA-binding protein involved in mRNA splicing and translational control, undergoes nucleocytoplasmic shuttling possibly for mRNA export and telomerase recruitment; an autoantigen in autoimmune disorders
SWN:POR3_HUMAN	VDAC3	42	6	2.48	0.55	SWN:POR3_HUMAN Q9y277 homo sapiens (human). voltage-dependent anion-selective channel protein 3 (vdac-3) (hvdac3) (outer mitochondrial membrane protein porin 3). 8/2001 [MASS=30659]/Voltage-dependent anion channel 3, may function as a voltage-gated pore of the outer mitochondrial membrane that binds hexokinase and glycerol kinase and transports adenine nucleotides
SW:RS2_HUMAN	RPS2	35	7	2.46	1.54	SW:RS2_HUMAN P15880 homo sapiens (human). 40s ribosomal protein s2 (s4) (llrep3 protein). 10/1996 [MASS=31324]/Ribosomal protein S2, a putative component of the small 40S ribosomal subunit, may bind RNA, upregulated in squamous cell carcinoma and in breast and colon tumors
SW:PPCM_HUMAN	PCK2	5, 18	6	2.45	1.09	SW:PPCM_HUMAN Q16822 homo sapiens (human). phosphoenolpyruvate carboxykinase, mitochondrial precursor [gtp] (ec 4.1.1.32) (phosphoenolpyruvate carboxylase) (pepck-m). 7/1999 [MASS=70637]/Phosphoenolpyruvate carboxykinase 2, catalyzes the formation of phosphoenolpyruvate by decarboxylation of oxaloacetate, rate-limiting step of gluconeogenesis
SW:UCRI_HUMAN	UQCRFS1	18	4	2.45	0.39	SW:UCRI_HUMAN P47985 homo sapiens (human). ubiquinol-cytochrome c reductase iron-sulfur subunit, mitochondrial precursor (ec 1.10.2.2) (rieske iron-sulfur protein) (risp). 7/1999 [MASS=29652]/Ubiquinol-cytochrome c reductase Rieske iron-sulfur polypeptide 1, a subunit of cytochrome bc1 complex, which transfers electron from ubiquinol to cytochrome c, located in the mitochondrion; deficient mitochondrial uptake may cause mitochondrial myopathy
SW:TOP1_HUMAN	TOP1	12	1	2.45	0.00	SW:TOP1_HUMAN P11387 homo sapiens (human). dna topoisomerase i (ec 5.99.1.2). 12/1998 [MASS=90754]/DNA topoisomerase I, a monomeric enzyme that relaxes supercoiled DNA and is mutated in camptothecin (CPT)-resistant human leukemia cell lines, a major self-antigen found in patients with systemic sclerosis
SW:THIL_HUMAN	ACAT1	18, 19	2	2.44	0.44	SW:THIL_HUMAN P24752 homo sapiens (human). acetyl-coa acetyltransferase, mitochondrial precursor (ec 2.3.1.9) (acetoacetyl-coa thiolase) (t2). 7/1999 [MASS=45200]/Acetyl-Coenzyme A acetyltransferase 1 (mitochondrial acetoacetyl-coenzyme A thiolase); mutations in the corresponding gene are associated with 3-ketothiolase deficiency
SW:IBP2_HUMAN	IGFBP2	41	6	2.43	0.38	SW:IBP2_HUMAN P18065 homo sapiens (human). insulin-like growth factor binding protein 2 precursor (igfbp-2) (ibp-2) (igf-binding protein 2). 12/1998 [MASS=35138]/Insulin like growth factor binding protein 2, binds to and modulates insulin-like growth factor activity, regulates cell proliferation, may be involved in apoptosis; associated with the malignant phenotype, may play a role in prostatic involution
GP:AF151809_1	CGI-51	45	1	2.42	0.00	GP:AF151809_1 Homo sapiens CGI-51 protein mRNA, complete cds. [MASS=52160]/similar to GASTRIN/CHOLECYSTOKININ TYPE BRECEPTOR (CCK-B RECEPTOR) (CCK-BR) (H. sapiens)/Protein of unknown function, has low similarity to uncharacterized C. elegans GOP-3
SW:RS20_HUMAN	RPS20	35	1	2.42	0.00	SW:RS20_HUMAN P17075 homo sapiens (human), and rattus norvegicus (rat). 40s ribosomal protein s20. 5/2000 [MASS=13373]/Ribosomal protein S20, a putative component of the small 40S ribosomal subunit, may play a role in apoptosis
SW:UCR2_HUMAN	UQCRC2	18	1	2.42	0.00	SW:UCR2_HUMAN P22695 homo sapiens (human). ubiquinol-cytochrome c reductase complex core protein 2 precursor (ec 1.10.2.2) (complex iii subunit ii). 7/1999 [MASS=48470]/Ubiquinol-cytochrome c reductase core protein II, a putative ubiquinol-cytochrome c reductase subunit of the mitochondrial cytochrome bc1 complex, likely to play a role in oxidative phosphorylation, may be involved in aerobic respiration
SW:TFPI_HUMAN	TFPI	45	1	2.40	0.00	SW:TFPI_HUMAN P10646 homo sapiens (human). tissue factor pathway inhibitor precursor (tfpi) (lipoprotein- associated coagulation inhibitor) (laci) (extrinsic pathway inhibitor) (epi). 12/1998 [MASS=35015]/Tissue factor pathway inhibitor, a Kunitz-type protease inhibitor that inhibits fibrin clot formation by directly inhibiting factor Xa and indirectly inhibiting the factor VIIa/tissue factor complex
SW:ATPA_HUMAN	ATP5A1	18, 42	8	2.38	0.42	SW:ATPA_HUMAN P25705 homo sapiens (human). atp synthase alpha chain, mitochondrial precursor (ec 3.6.1.34). 12/1998 [MASS=59751]/ATP synthase H+ transporting mitochondrial F1 complex alpha subunit isoform 1 cardiac muscle, part of the synthase enzymatic complex that catalyzes the synthesis of ATP during oxidative phosphorylation
SW:MAZ_HUMAN	MAZ	19, 29, 41	1	2.37	0.00	SW:MAZ_HUMAN P56270 homo sapiens (human). myc-associated zinc finger protein (mazi) (purine-binding transcription factor) (pur-1) (zf87) (zif87). 7/1999 [MASS=48608]/MYC-associated zinc finger protein (purine-binding transcription factor), functions both as a positive and a negative regulator of gene expression and may also have roles in initiating and terminating transcription
GP:AB018266_1	MATR3	11	4	2.37	0.25	GP:AB018266_1 Homo sapiens mRNA for KIAA0723 protein, complete cds. [MASS=94623]/Homo sapiens matrin 3 mRNA, complete cds/Matrin 3, an acidic protein that is a component of the nuclear matrix
SW:POR1_HUMAN	VDAC1	41, 42	28	2.36	0.34	SW:POR1_HUMAN P21796 homo sapiens (human). voltage-dependent anion-selective channel protein 1 (hvdac1) (outer mitochondrial membrane protein porin 1) (plasmalemmal porin) (porin 31hl) (porin 31hm). 5/2 [MASS=30641]/Voltage-dependent anion channel 1, mitochondrial outer membrane anion channel that mediates apoptotic signals from Bcl-2 (BCL2) and related proteins; deficiency of protein in skeletal muscle causes mitochondrial encephalomyopathy

SW:ETFA_HUMAN	ETFA	18, 19	1	2.36	0.00	SW:ETFA_HUMAN P13804 homo sapiens (human). electron transfer flavoprotein alpha-subunit precursor (alpha-etf). 5/2000 [MASS=35080]/Electron transfer flavoprotein alpha subunit, shuttles electrons between flavoprotein dehydrogenases of mitochondrial fatty acid metabolism and ubiquinone oxidoreductase, deficiency associated with Type II glutaricaciduria
GP:AF042284_1	SQRDL	45	3	2.36	0.51	GP:AF042284_1 Homo sapiens unknown mRNA; similar to fission yeast sulfide dehydrogenase. [MASS=49961]/CGI-44 protein (sulfide dehydrogenase like yeast), a putative oxidoreductase homolog of Schizosaccharomyces pombe hmt2
SW:UCRH_HUMAN	UQCRH	18	3	2.36	0.26	SW:UCRH_HUMAN P07919 homo sapiens (human). ubiquinol-cytochrome c reductase complex 11 kda protein precursor (ec 1.10.2.2) (mitochondrial hinge protein) (cytochrome c1, nonheme 11 kda protein) (complex [MASS=10755]/Ubiquinol-cytochrome c reductase hinge protein, hinges cytochrome c with cytochrome c1 in the mitochondrial respiratory chain, may function to accelerate apoptosis by enhancing cytochrome c release from the mitochondria
SW:U2AG_HUMAN	U2AF35	25, 37, 38	2	2.34	0.02	SW:U2AG_HUMAN Q01081 homo sapiens (human). splicing factor u2af 35 kda subunit (u2 auxiliary factor 35 kda subunit) (u2 snrnp auxiliary factor small subunit). 12/1998 [MASS=27872]/U2(RNU2) small nuclear RNA auxiliary factor 1, functions as a pre-mRNA splicing protein, involved in the functional recognition of the 3' splice site AG dinucleotide, interacts with ZNF265 protein involved in alternative splicing
SW:MIF_HUMAN	MIF	45	7	2.34	1.65	SW:MIF_HUMAN P14174 homo sapiens (human). macrophage migration inhibitory factor (mif) (glycosylation-inhibiting factor) (gif). 5/2000 [MASS=12345]/Macrophage migration inhibitory factor, an immunoregulatory cytokine involved in monocyte migration and chemotaxis, T cell activation, delayed type hypersensitivity, and the response to lipopolysaccharide, counteracts glucocorticoid suppression
GP:AK001714_1	FLJ10852	45	2	2.32	0.41	GP:AK001714_1 Homo sapiens cDNA FLJ10852 fis, clone NT2RP4001498, weakly similar to ANKYRIN REPEAT-CONTAINING PROTEIN AKR1; unnamed protein product. [MASS=54514]/Protein contains five ankyrin (Ank) repeats, which may mediate protein-protein interactions, and a DHHC-type zinc finger or NEW1 domain
SW:GST3_HUMAN	MGST3	19, 41	2	2.31	0.83	SW:GST3_HUMAN O14880 homo sapiens (human). microsomal glutathione s-transferase 3 (ec 2.5.1.18) (microsomal gst- 3) (microsomal gst-iii). 5/2000 [MASS=16516]/Microsomal glutathione S-transferase 3, a microsomal membrane protein that has glutathione-dependent transferase and peroxidase activities, member of a family that includes 5-lipoxygenase activating protein (ALOX5AP) and leukotriene-C4 synthase (LTC4S)
GP:AF151817_1	LOC51631	45	1	2.31	0.00	GP:AF151817_1 Homo sapiens CGI-59 protein mRNA, complete cds. [MASS=45695]/weakly similar to SPLICING FACTOR, ARGININE/SERINE-RICH 4/Member of the DUF259 protein of unknown function family, has strong similarity to uncharacterized human LUC7L
SW:RFA1_HUMAN	RPA1	14, 15, 29, 40	1	2.30	0.00	SW:RFA1_HUMAN P27694 homo sapiens (human). replication protein a 70 kda dna-binding subunit (rp-a) (rf-a) (replication factor-a protein 1) (single-stranded dna-binding protein). 11/1997 [MASS=68138]/Replication protein A1 (70 kDa), a DNA replication factor A subunit, has roles in DNA replication, recombination, repair, may contribute to latent virus reactivation, inactivated by anti-cancer drug adozelesin
SW:MDHM_HUMAN	MDH2	18	27	2.29	1.04	SW:MDHM_HUMAN P40926 homo sapiens (human). malate dehydrogenase, mitochondrial precursor (ec 1.1.1.37). 5/2000 [MASS=35531]/Mitochondrial malate dehydrogenase, part of the malate-aspartate shuttle where it putatively catalyzes the oxidation of malate to oxaloacetate
SW:ES1_HUMAN	C21orf33	45	4	2.28	0.84	SW:ES1_HUMAN P30042 homo sapiens (human). es1 protein homolog precursor (protein knp-i) (gt335). 5/2000 [MASS=28142]/Protein with similarity to zebrafish ES1 and E. coli SCRP-27A, highly expressed in skeletal muscle and heart
SW:Z142_HUMAN	ZNF142	45	1	2.28	0.00	SW:Z142_HUMAN P52746 homo sapiens (human). zinc finger protein 142 (kiaa0236) (ha4654). 5/2000 [MASS=187866]/Zinc finger protein 142, a putative transcription factor, member of the Kruppel zinc-finger protein family
SW:NB8M_HUMAN	NDUFB7	6, 18	2	2.27	0.65	SW:NB8M_HUMAN P17568 homo sapiens (human). nadh-ubiquinone oxidoreductase b18 subunit (ec 1.6.5.3) (ec 1.6.99.3) (complex i-b18) (ci-b18) (cell adhesion protein sqm1). 7/1998 [MASS=15648]/Subunit of the NADH-ubiquinone oxidoreductase (complex I), a multiprotein complex that transports electrons from NADH to ubiquinone, functions as a cell adhesion molecule with a role in metastasis, may have a role in drug transport
SW:DDX5_HUMAN	DDX5	16, 25, 37	1	2.27	0.00	SW:DDX5_HUMAN P17844 homo sapiens (human). probable rna-dependent helicase p68 (dead-box protein p68) (dead box protein 5). 7/1998 [MASS=69148]/DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 5 (RNA helicase 68kD), a ATP-dependent RNA helicase that has ATP-independent RNA renaturation activity and catalyses branch migration, binds estrogen receptor alpha and function as a transcriptional coactivator
GP:X92689_1	GALNAC-T3	26, 34, 41	3	2.26	0.17	GP:X92689_1 Homo sapiens mRNA for UDP-GalNAc:polypeptide N-acetylgalactosaminyl transferase (GalNAc-T3). [MASS=72638]/N-acetylgalactosaminyltranferase T3 (UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 3), enzyme that initiates O-glycosylation; elevated levels may be associated with differentiation of adenocarcinomas
GP:U96114_1	WWP2	45	1	2.25	0.00	GP:U96114_1 Homo sapiens Nedd-4-like ubiquitin-protein ligase WWP2 mRNA, complete cds; Nedd-4-like ubiquitin-protein ligase; WW domain-containing protein. [MASS=99070]/Atrophin 1 interacting protein 2, putative Nedd4-like ubiquitin ligase, may play a role in the ubiquitination and endocytosis of C1C 5 protein (CLCN5), may be involved in the ubiquitin-dependent degradation of LMP2A and Lyn
SW:DHSB_HUMAN	SDHB	5, 18	1	2.24	0.00	SW:DHSB_HUMAN P21912 homo sapiens (human). succinate dehydrogenase [ubiquinone] iron-sulfur protein, mitochondrial precursor (ec 1.3.5.1) (ip) (ip subunit of complex ii). 5/2000 [MASS=31629]/Succinate dehydrogenase complex iron sulfur subunit B, part of an enzyme complex that transports electrons from succinate to ubiquinone in the TCA cycle and aerobic respiratory chain, may be involved in familial pheochromocytoma
GP:AF146192_1	MRPS30	45	1	2.24	0.00	mitochondrial ribosomal protein S30; PAP protein; programmed cell death 9; bone marrow protein BM04/Mitochondrial ribosomal protein S30 (programmed cell death 9), a putative structural protein of the mitochondrial small 28S ribosomal subunit, may play a role in protein biosynthesis and apoptosis

SW:CYPM_HUMAN	PPIF	33	1	2.24	0.00	SW:CYPM_HUMAN P30405 homo sapiens (human). peptidyl-prolyl cis-trans isomerase, mitochondrial precursor (ec 5.2.1.8) (ppiase) (rotamase) (cyclophilin). 11/1997 [MASS=22040]/Peptidylprolyl isomerase F (Cyclophilin F), a putative mitochondrial protein that binds the immunosuppressant drug cyclosporin A
SW:UCR1_HUMAN	UQCRC1	18	8	2.24	0.43	SW:UCR1_HUMAN P31930 homo sapiens (human). ubiquinol-cytochrome c reductase complex core protein i precursor (ec 1.10.2.2). 7/1999 [MASS=52619]/Ubiquinol-cytochrome c reductase core protein I, a subunit of the ubiquinol-cytochrome c oxidoreductase component of the mitochondrial respiratory chain, may function as an electron transporter in aerobic respiration and oxidative phosphorylation
SW:CATA_HUMAN	CAT	10	3	2.24	0.12	SW:CATA_HUMAN P04040 homo sapiens (human). catalase (ec 1.11.1.6). 5/2000 [MASS=59756]/Catalase, a tetrameric hemoprotein that detoxifies H2O, part of the oxidative stress response, activity is altered in some forms of cancer and increased during septic shock; gene mutation causes acatalasemia
SW:MA32_HUMAN	C1QBP	45	9	2.23	0.22	SW:MA32_HUMAN Q07021 homo sapiens (human). complement component 1, q subcomponent binding protein, mitochondrial precursor (glycoprotein gc1qbp) (gc1q-r protein) (hyaluronan-binding protein 1) (pre-mrna [MASS=31362]/Complement component 1 q subcomponent binding protein, binds the globular heads of complement subcomponent C1q, interacts with a wide array of proteins, involved in regulation of complement activation, may be associated with sperm motility
GP:AF220049_1	MDS029	45	3	2.22	0.51	GP:AF220049_1 Homo sapiens uncharacterized hematopoietic stem/progenitor cells protein MDS029 mRNA, complete cds. [MASS=12199]/Protein of unknown function, has high similarity to a region of C. elegans KLP-17, which is a C-terminal motor kinesin that is involved in chromosome movement during early embryonic and germ line development
GP:AF150087_1	TIMM8A	36	1	2.22	0.00	mitochondrial import inner membrane translocase subunit tim8 b (deafness dystonia protein 2)/Translocase of inner mitochondrial membrane 8 (yeast) homolog A, member of a family of small zinc finger proteins, involved in mitochondrial protein import, may be involved in neurogenesis or X-inactivation; gene mutations cause Mohr Tranebjaerg syndrome
SW:NHPX_HUMAN	NHP2L1	7, 25, 37	2	2.21	0.20	SW:NHPX_HUMAN P55769 homo sapiens (human). nhp2/rs6 family protein yel026w homolog (high mobility group-like nuclear protein 2 homolog) (otk27). 5/2000 [MASS=14174]/Non-histone chromosome protein 2 (S. cerevisiae)-like 1, a member of a family of RNP-associated proteins, a component of the spliceosome and rRNA processing machinery, recognizes a shared stem-internal loop-stem structure in its RNA targets
SW:NRP_HUMAN	NRP1	16, 41	8	2.20	1.33	SW:NRP_HUMAN O14786 homo sapiens (human). neuropilin precursor (vascular endothelial cell growth factor 165 receptor). 5/2000 [MASS=103121]/Neuropilin 1, a receptor for VEGF (165) and the axonal chemorepellent Semaphorin III, involved in organogenesis, axon guidance and angiogenesis, may regulate cell proliferation and response to wounding, upregulated in neuroblastoma vascular endothelium
SW:TISB_HUMAN	BRF1	45	2	2.19	0.60	SW:TISB_HUMAN Q07352 homo sapiens (human). tis11b protein (butyrate response factor 1) (egf-response factor 1) (erf-1). 7/1999 [MASS=36314]/TATA box binding protein-associated factor RNA polymerase III C 90, a subunit of RNA polymerase III transcription factor TFIIIB that is required for transcription of genes encoding tRNA, 5S rRNA, and small nuclear RNAs
SW:RS16_HUMAN	RPS16	35	8	2.18	0.76	SW:RS16_HUMAN P17008 homo sapiens (human), and rattus norvegicus (rat). 40s ribosomal protein s16. 7/1999 [MASS=16314]/Ribosomal protein S16, putative component of the small 40S ribosomal subunit
SW:NUBM_HUMAN	NDUFV1	18	7	2.18	0.99	SW:NUBM_HUMAN P49821 homo sapiens (human). nadh-ubiquinone oxidoreductase 51 kda subunit precursor (ec 1.6.5.3) (ec 1.6.99.3) (complex i-51kd) (ci-51kd). 5/2000 [MASS=50956]/NADH dehydrogenase ubiquinone flavoprotein 1 (51 kDa), a subunit of NADH-ubiquinone oxidoreductase (Complex I); genetic variants are associated with mitochondrial complex I deficiency, leukodystrophy, and myoclonic epilepsy
SW:MSH3_HUMAN	MSH3	14	1	2.18	0.00	SW:MSH3_HUMAN P20585 homo sapien/Mismatch repair protein 3, dimerizes with MSH2 to form damaged-DNA recognition complex MutS beta, repairs short insertion-deletion loops (2-8 base pairs), may bind PCNA to effect repair, maintains stability of the genome and may suppress tumorss (human). dna mismatch repair protein msh3 (divergent upstream protein) (dup) (mismatch repair protein 1) (mrp1). 12/1998 [MASS=127384]
PIR2:A54601	HNRPD	25, 37, 39	9	2.17	0.65	PIR2:A54601 RNA-binding protein AUF1 - human [MASS=31200]/Heterogeneous nuclear ribonucleoprotein D (AU-rich element RNA-binding protein 1 37kD), an RNA and DNA-binding protein which binds to AU-rich elements in the 3' untranslated regions of mRNAs and mediates their degradation
GP:AC002540_1	SLC25A13	42	1	2.16	0.00	GP:AC002540_1 Human BAC clone GS1-25M2 from 7q21-q22, complete sequence; [MASS=25323]//Solute carrier family 25 member 13 (citrin), a calcium-dependent mitochondrial solute transporter that may play a role in urea cycle function; mutation of the corresponding gene result in neonatal:infantile and adult onset forms of type II citrullinemia
SW:ATPG_HUMAN	ATP5C1	18, 42	3	2.15	0.32	SW:ATPG_HUMAN P36542 homo sapiens (human). atp synthase gamma chain, mitochondrial precursor (ec 3.6.1.34). 5/2000 [MASS=32996]/ATP synthase H+ transporting mitochondrial F1 complex gamma 1, putative component of multisubunit enzyme that synthesizes ATP during oxidative phosphorylation, exists in tissue-specific alternative forms that are spliced in response to acidic conditions
GP:D26361_1	KIAA0042	45	1	2.15	0.00	GP:D26361_1 Human mRNA for KIAA0042 gene, complete cds. [MASS=186492]/EST/Protein containing two kinesin motor domains, which bind ATP and microtubules, and two forkhead associated (FHA) domains, which bind phosphopeptides, has a region of moderate similarity to a region of plus-end directed motor kinesin (C. elegans UNC-104)
SW:MA2B_HUMAN	MAN2B1	5, 34	1	2.14	0.00	SW:MA2B_HUMAN O00754 homo sapiens (human). lysosomal alpha-mannosidase precursor (ec 3.2.1.24) (mannosidase, alpha b) (lysosomal acid alpha-mannosidase) (laman). 5/2000 [MASS=113673]/Mannosidase alpha class 2B member 1, catalyzes the hydrolysis of alpha-mannoside linkages in glycoprotein catabolism, enzyme activity is inhibited by azafuranose analogs of mannose, deficiency is associated with alpha-mannosidosis

GP:AK022590_1	FLJ12528	45	1	2.13	0.00	GP:AK022590_1 Homo sapiens cDNA FLJ12528 fis, clone NT2RM4000155, moderately similar to THREONYL-TRNA SYNTHETASE, CYTOPLASMIC (EC 6.1.1.3); unnamed protein product. [MASS=66372]/Protein containing a tRNA synthetase class II core domain (G, H, P, S and T), a TGS (ThrRS, GTPase, and SpoT) domain, and an anticodon binding domain, has moderate similarity to threonyl-tRNA synthetase (human TARS)/Protein containing a tRNA synthetase class II core domain (G, H, P, S and T), a TGS (ThrRS, GTPase, and SpoT) domain, and an anticodon binding domain, has moderate similarity to threonyl-tRNA synthetase (human TARS)
SW:MRP_HUMAN	CSRP3	16	21	2.13	0.55	SW:MRP_HUMAN P49006 homo sapiens (human). marcks-related protein (mac-marcks). 12/1998 [MASS=19398]/Cysteine- and glycine-rich protein 3, a zinc-finger LIM domain protein that is an essential regulator of cardiac muscle development, expression is decreased in chronic heart failure
SWN:NDR2_HUMAN	NDRG2	45	2	2.12	0.01	SWN:NDR2_HUMAN Q9un36 homo sapiens (human). ndrg2 protein (syld709613 protein). 8/2001 [MASS=39289]/N-myc downstream-regulated gene 2, a member of the Ndr family, which are involved in cell differentiation
SW:NTF2_HUMAN	NTF2	24	2	2.12	0.23	SW:NTF2_HUMAN P13662 homo sapiens (human), and rattus norvegicus (rat). nuclear transport factor 2 (ntf-2) (placental protein 15) (pp15). 7/1999 [MASS=14478]/Nuclear transport factor 2, cytosolic protein involved in nuclear import of proteins containing nuclear localization signals mediated by GDP-RAN and nucleoporins
SW:KC2B_HUMAN	CSNK2B	5, 18, 34, 41	2	2.11	0.18	SW:KC2B_HUMAN P13862 homo sapiens (human), mus musculus (mouse), rattus norvegicus (rat), bos taurus (bovine), sus scrofa (pig), oryctolagus cuniculus (rabbit), and gallus gallus (chicken). casein kinase [MASS=24942]/Casein kinase II beta subunit, regulatory subunit of casein kinase II (CK2), confers stability and specificity to CK2 catalytic subunits, may mediate formation of the tetrameric CK2 complex, and may be involved in heat stress response
GP:D21163_1	U5-116KD	25, 37, 38	1	2.11	0.00	GP:D21163_1 Human mRNA for KIAA0031 gene, complete cds; similar to human elongation factor 2 mRNA (HSEF2).. [MASS=109436]/U5 snRNP-specific protein 116 kD, a spliceosome component with GTPAse activity, plays a role in mRNA splicing and processing
SW:RU17_HUMAN	SNRP70	25, 37, 38	3	2.11	0.26	SW:RU17_HUMAN P08621 homo sapiens (human). u1 small nuclear ribonucleoprotein 70 kda (u1 snrnp 70 kda) (snrp70). 11/1995 [MASS=70081]/U1 small nuclear 70 kDa ribonucleoprotein, involved in pre mRNA splicing, acts as an autoantigen in systemic lupus erythematosus and mixed connective tissue disease
SW:CY1_HUMAN	CYC1	18	2	2.10	0.00	SW:CY1_HUMAN P08574 homo sapiens (human). cytochrome c1, heme protein precursor. 7/1999 [MASS=35390]/Cytochrome c1, a member of the cytochrome bc1 complex
SW:NUPM_HUMAN	NDUFA8	18	5	2.10	0.44	SW:NUPM_HUMAN P51970 homo sapiens (human). nadh-ubiquinone oxidoreductase 19 kda subunit (ec 1.6.5.3) (ec 1.6.99.3) (complex i-19kd) (ci-19kd) (complex i-pgiv) (ci-pgiv). 5/2000 [MASS=19974]/NADH dehydrogenase ubiquinone 1 alpha subcomplex 8 (19 kDa), a subunit of NADH-ubiquinone oxidoreductase (complex I), a multiprotein complex that transports electrons from NADH to ubiquinone
GP:AJ245620_1	CTL1	45	1	2.08	0.00	GP:AJ245620_1 Homo sapiens CTL1 gene. [MASS=73349]/CDW92 antigen; mutations in the corresponding gene may result in familial dysautonomia
SW:DDX6_HUMAN	DDX6	35	3	2.06	0.72	SW:DDX6_HUMAN P26196 homo sapiens (human). probable atp-dependent rna helicase p54 (oncogene rck) (dead box protein 6). 7/1998 [MASS=54418]/DEAD box protein 6, a member of the DEAD/H box ATP-dependent RNA helicase protein family, may be involved in cell proliferation, upregulated in colorectal adenocarcinoma and colonic adenoma; gene is translocated in a diffuse large B-cell lymphoma
SW:U2AF_HUMAN	U2AF65	25, 37, 38	1	2.05	0.00	SW:U2AF_HUMAN P26368 homo sapiens (human). splicing factor u2af 65 kda subunit (u2 auxiliary factor 65 kda subunit) (u2 snrnp auxiliary factor large subunit). 12/1998 [MASS=53501]/U2 small nuclear ribonucleoprotein auxiliary factor (65 kDa), a component of U2 small nucleoprotein auxiliary factor, which is necessary for mRNA splicing, binds to pre-mRNA
GP:AF043250_1	PLRG1	41	1	2.05	0.00	Homo sapiens pleiotropic regulator 1 (PLRG1) mRNA/Member of the WD repeat protein family, interacts with a nuclear protein kinase C-beta II isoenzyme that is involved in insulin signaling
SW:IDHP_HUMAN	IDH2	5, 18	7	2.04	0.65	SW:IDHP_HUMAN P48735 homo sapiens (human). isocitrate dehydrogenase [nadp], mitochondrial precursor (ec 1.1.1.42) (oxalosuccinate decarboxylase) (idh) (nadp+-specific icdh) (idp) (icd-m). 2/1996 [MASS=50948]/Isocitrate dehydrogenase 2 (NADP+) mitochondrial, catalyzes the oxidative decarboxylation of isocitrate to form alpha-ketoglutarate
GP:AK025822_1	FLJ22169	45	2	2.04	0.00	GP:AK025822_1 Homo sapiens cDNA: FLJ22169 fis, clone HRC00632; unnamed protein product. [MASS=74624]/EST/Protein of unknown function, has low similarity to a region of S. cerevisiae Apg9p, which is required for starvation-induced autophagy
SW:SPHM_HUMAN	SGSH	5, 26	1	2.03	0.00	SW:SPHM_HUMAN P51688 homo sapiens (human). n-sulphoglucosamine sulphohydrolase precursor (ec 3.10.1.1) (sulfoglucosamine sulfamidase) (sulphamidase). 5/2000 [MASS=56695]/N-sulfoglucosamine sulfohydrolase (sulfamidase), catalyzes the hydrolysis of the N-linked sulfate group from heparan sulfate; mutation of the corresponding gene causes the lysosomal storage disease Sanfilippo A syndrome (mucopolysaccharidosis type IIIA)
GP:AF242773_1	unknown	45	1	2.03	0.00	mesenchymal stem cell protein DSCD75
SWN:U123_HUMAN	PHF5A	45	1	2.03	0.00	SWN:U123_HUMAN Q9uh06 homo sapiens (human). hypothetical 12.4 kda protein bk223h9.2. 8/2001 [MASS=12405]/Member of the UPF0123 uncharacterized protein family, has very strong similarity to uncharacterized rat Loc192246
GP:AF007833_1	ZFP67	29	1	2.03	0.00	GP:AF007833_1 Homo sapiens kruppel-related zinc finger protein hcKrox mRNA, complete cds; zinc-finger transcription factor. [MASS=58218]/c-Krox, a zinc-finger domain-containing transcription factor that regulates transcription from the alpha 1(I) procollagen (COL1A1) and fibronectin (FN1) promoters, may play a role in regulating bone formation

SW:SMD2_HUMAN	SNRPD2	25, 37, 38	2	2.02	0.82	SW:SMD2_HUMAN P43330 homo sapiens (human). small nuclear ribonucleoprotein sm d2 (snrnp core protein d2) (sm-d2). 10/1996 [MASS=13527]/Small nuclear ribonucleoprotein D2 polypeptide, one of seven common core snRNP proteins involved in snRNP biogenesis and pre-mRNA splicing, autoantigen for anti-Sm antibodies produced by individuals with systemic lupus erythematosus
PIR2:B53737	SLC25A3	18, 42	21	2.02	0.42	PIR2:B53737 phosphate carrier protein precursor, mitochondrial, splice form B - human [MASS=39959]/Mitochondrial phosphate carrier (solute carrier family 25 member 3), catalyzes the transport of phosphate from the cytoplasm to the mitochondrial matrix for ATP synthesis during oxidative phosphorylation
SW:RL24_HUMAN	RPL24	35	6	2.02	0.10	SW:RL24_HUMAN P38663 homo sapiens (human), rattus norvegicus (rat), and bos taurus (bovine). 60s ribosomal protein l24 (l30). 5/2000 [MASS=17779]/Ribosomal protein L24, a putative component of the 60S ribosomal subunit
GP:AF277719_1	C(27)-3BETA-HSD	26	1	2.02	0.00	GP:AF277719_1 Homo sapiens 3 beta-hydroxy-delta 5-C27-steroid oxidoreductase mRNA, complete cds. [MASS=40930]/3 beta-hydroxy-delta 5-C27-steroid oxidoreductase, predicted to function in bile acid biosynthesis; variant form is associated with progressive intrahepatic cholestasis
SW:DRN2_HUMAN	DNASE2	25	3	2.01	0.42	SW:DRN2_HUMAN O00115 homo sapiens (human). deoxyribonuclease ii precursor (ec 3.1.22.1) (dnase ii) (acid dnase) (lysosomal dnase ii) (r31240_2). 7/1999 [MASS=39581]/Deoxyribonuclease II lysosomal, an acid-activated DNA nicking enzyme, may participate in DNA fragmentation during apoptosis, induces apoptotic chromosome condensation when transfected into cell lines
SW:RL40_HUMAN	UBA52	32, 34, 35	3	2.00	0.50	SW:RL40_HUMAN P14793 homo sapiens (human), rattus norvegicus (rat), and gallus gallus (chicken). 60s ribosomal protein l40 (cep52). 11/1997 [MASS=6181]/Ubiquitin A-52 residue ribosomal protein fusion product 1, protein consisting of ubiquitin at the N-terminus and ribosomal protein L40 at the C-terminus; the corresponding gene is upregulated in colon cancer but not in gastric cancer
GP:AL023805_1	PLCB4	19, 41	6	2.00	0.24	GP:AL023805_1 Human DNA sequence from clone RP4-811H13 on chromosome 20p12. Contains part of the PLCB4 gene for Phospholipase C beta 4, STSs, GSSs and a CpG island, complete sequence; combines with dJ1119D9.2.1 and .2 in Em:AL031652 to form isoforms 5 and 6; may a [MASS=61433]/1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase beta 4/Phospholipase C beta 4, member of a G protein-regulated family of phospholipases that hydrolyze phosphatidylinositol 4,5-bisphosphate to the second messengers inositol 1,4,5-trisphosphate and diacylglycerol
SW:CATH_HUMAN	CTSH	32	1	2.00	0.00	SW:CATH_HUMAN P09668 homo sapiens (human). cathepsin h precursor (ec 3.4.22.16). 7/1999 [MASS=37404]/Cathepsin H, a cysteine (thiol) protease, member of a family of lysosomal cysteine proteases involved in a variety of proteolytic processes, may serve as a marker of tumor progression in central nervous system and pancreatic neoplasms
SW:ETFB_HUMAN	ETFB	18, 19	2	1.99	0.48	SW:ETFB_HUMAN P38117 homo sapiens (human). electron transfer flavoprotein beta-subunit (beta-etf). 5/2000 [MASS=27844]/Electron transfer flavoprotein beta subunit, shuttles electrons between primary flavoprotein dehydrogenases involved in mitochondrial fatty acid metabolism and ubiquinone oxidoreductase; genetic variants are associated with type II glutaric acidemia
GP:AB046803_1	KIAA1583	45	6	1.99	0.11	GP:AB046803_1 Homo sapiens mRNA for KIAA1583 protein, partial cds; Start codon is not identified.. [MASS=46775]/ EST
GP:S69272_1	SERPINB6	45	5	1.99	0.08	GP:S69272_1 cytoplasmic antiproteinase=38 kda intracellular serine proteinase inhibitor [human, placenta, mRNA, 1465 nt]; 38 kda intracellular serine proteinase inhibitor; This sequence comes from Fig. 1; CAP. [MASS=42590]/Serine proteinase inhibitor clade B member 6 (placental thrombin inhibitor), member of the serine proteinase inhibitor (serpin) superfamily, may play roles in keratinocyte differentiation and platelet activat
SW:POR2_HUMAN	VDAC2	42	34	1.99	0.32	SW:POR2_HUMAN P45880 homo sapiens (human). voltage-dependent anion-selective channel protein 2 (hvdac2) (outer mitochondrial membrane protein porin 2). 5/2000 [MASS=38093]/Voltage-dependent anion channel 2, a voltage-gated pore of the outer mitochondrial membrane, may bind hexokinase
GP:AL035689_4	HINT3	45	1	1.98	0.00	GP:AL035689_4 Human DNA sequence from clone RP1-187J11 on chromosome 6q11.1-22.33. Contains the gene for a novel protein similar to S. pombe and S. cerevisiae predicted proteins, the gene for a novel protein similar to protein kinase C inhibitors, the 3' end of th [MASS=20361]/Member of the histidine triad (HIT) family
SW:GLYM_HUMAN	SHMT2	2	8	1.98	0.70	SW:GLYM_HUMAN P34897 homo sapiens (human). serine hydroxymethyltransferase, mitochondrial precursor (ec 2.1.2.1) (serine methylase) (glycine hydroxymethyltransferase) (shmt). 5/2000 [MASS=55993]/Serine hydroxymethyltransferase 2 (mitochondrial), a pyridoxal phosphate-dependent enzyme that catalyzes the conversion of serine and tetrahydrofolate to glycine and 5,10-methylenetetrahydrofolate, may play a role in glycine biosynthesis
GP:U28811_1	CFR-1	6, 36	14	1.97	0.53	Human cysteine-rich fibroblast growth factor receptor (CFR-1) mRNA/Golgi apparatus protein 1, a cysteine-rich membrane sialoglycoprotein that may be a receptor for fibroblast growth factor (FGF), may be involved in cell adhesion
SW:ECHA_HUMAN	HADHA	18, 19, 42	13	1.97	0.65	SW:ECHA_HUMAN P40939 homo sapiens (human). mitochondrial trifunctional enzyme alpha subunit precursor (tp-alpha) [includes: long-chain enoyl-coa hydratase (ec 4.2.1.17); long chain 3-hydroxyacyl-coa deh [MASS=82960]/Mitochondrial long-chain enoyl-CoA hydratase/3-hydroxyacyl-CoA dehydrogenase/3-ketoacyl-CoA thiolase alpha subunit, involved in fatty acid beta-oxidation, mutations are associated with trifuctional protein deficiency and Reye-like syndrome
PIR2:A49656	ZNF147	45	1	1.97	0.00	estrogen-responsive finger protein/Zinc finger protein 147, an estrogen-responsive zinc-finger transcription factor required for estrogen induced cell proliferation and may mediate estrogen action
GP:AB007867_1	PLXNB1	41	1	1.97	0.00	GP:AB007867_1 Homo sapiens KIAA0407 mRNA, complete cds. [MASS=232298]/Plexin B1 (plexin 5), a member of the plexin family of semaphorin receptors which are involved in axon guidance, receptor for semaphorin 4D (SEMA4D), functions in RAC and RHO signal transduction pathways and in actin cytoskeleton reorganization

SW:COX1_HUMAN	MTCO1	18	1	1.97	0.00	SW:COX1_HUMAN P00395 homo sapiens (human). cytochrome c oxidase polypeptide i (ec 1.9.3.1). 5/2000 [MASS=57041]/Mitochondrial cytochrome c oxidase subunit I, a subunit of complex IV of the mitochondrial respiratory chain; mutations in the corresponding gene may be associated with mitochondrial diseases and acquired idiopathic sideroblastic anemia
SW:MAOM_HUMAN	ME2	5, 19	2	1.96	0.04	SW:MAOM_HUMAN P23368 homo sapiens (human). nad-dependent malic enzyme, mitochondrial precursor (ec 1.1.1.38) (nad-me). 5/2000 [MASS=65444]/Malic enzyme 2, a NAD(+)-dependent mitochondrial form of malic enzyme, catalyzes the oxidative decarboxylation of malate to form pyruvate
SW:G732_HUMAN	TACSTD1	45	22	1.96	0.30	SW:G732_HUMAN P16422 homo sapiens major gastrointestinal tumor-associated protein ga733-2 precursor (epithelial cell surface antigen) (epithelial glycoprotein) (egp) (adenocarcinoma-associated antigen) [MASS=34920]/Tumor-associated calcium signal transducer 1 (Epithelial cell adhesion molecule), a surface glycoprotein that mediates homotypic calcium-independent cell adhesion, acts in pancreas morphogenesis, present on most carcinomas
SW:TDXM_HUMAN	PRDX3	10	4	1.96	0.16	SW:TDXM_HUMAN P30048 homo sapiens (human). mitochondrial thioredoxin-dependent peroxide reductase precursor (antioxidant protein 1) (aop-1) (mer5 protein homolog) (hbc189). 5/2000 [MASS=27693]/Peroxiredoxin 3, a mitochondrial antioxidant protein involved in oxygen and radical metabolism, has an antiapoptotic function, and inactivated by the apoptosis-inducing lectin abrin A
GP:U64791_1	GLG1	6, 36	1	1.95	0.00	GP:U64791_1 Human Golgi membrane sialoglycoprotein MG160 (GLG1) mRNA, complete cds; fibroblast growth factor. [MASS=134593]/Golgi apparatus protein 1, a cysteine-rich membrane sialoglycoprotein that may be a receptor for fibroblast growth factor (FGF), may be involved in cell adhesion
SW:COPA_HUMAN	COPA	43	15	1.95	3.01	SW:COPA_HUMAN P53621 homo sapiens (human). coatomer alpha subunit (alpha-coat protein) (alpha-cop) (hepcop) (hep-cop) [contains: xenin (xenopsin-related peptide); proxenin]. 5/2000 [MASS=138332]/ Coatomer protein complex subunit alpha, involved in transport between the endoplasmic reticulum and the Golgi apparatus, binds to RNA, N-terminal 25 amino acids may be cleaved to release the peptide xenin, which stimulates pancreatic secretion
SW:ITB1_HUMAN	ITGB1	6, 7, 41	5	1.94	0.58	SW:ITB1_HUMAN P05556 homo sapiens (human). fibronectin receptor beta subunit precursor (integrin beta-1) (cd29) (integrin vla-4 beta subunit). 7/1999 [MASS=88465]/Integrin beta 1, involved in extracellular matrix interactions and signal transduction, plays roles in cell adhesion, migration, proliferation and development, may be involved in tumor metastasis
SW:LYAG_HUMAN	GAA	5, 18	2	1.94	0.01	SW:LYAG_HUMAN P10253 homo sapiens (human). lysosomal alpha-glucosidase precursor (ec 3.2.1.20) (acid maltase). 5/2000 [MASS=105338]/Acid alpha-glucosidase, lysosomal alpha-glucosidase that hydrolyzes alpha(1->4) and alpha(1->6) linkages in glycogen during glycogen catabolism; heritable deficiency causes glycogenosis type II or Pompe disease
PIR2:S78046	RNASE6	25, 39	3	1.94	0.00	PIR2:S78046 ribonuclease 6 (EC 3.1.27.-) precursor - human [MASS=21941]/Ribonuclease k6, a ribonuclease of the ribonuclease A superfamily, possibly functions in host defense
SW:ANK1_HUMAN	ANK1	11	4	1.94	0.82	SW:ANK1_HUMAN P16157 homo sapiens (human). ankyrin 1 (erythrocyte ankyrin) (ankyrin r) (ankyrins 2.1 and 2.2). 5/2000 [MASS=206146]/Ankyrin 1, a cytoskeletal anchor protein that attaches cytoskeletal elements to the plasma membrane; alteration of the corresponding gene is associated with hereditary spherocytosis
GP:AK000501_1	P17.3	45	1	1.93	0.00	similar to neuronal protein 15.6/Protein of unknown function, has high similarity to uncharacterized mouse Np15.6
SW:ROA3_HUMAN	FBRNP	37	2	1.93	0.06	SW:ROA3_HUMAN P51991 homo sapiens (human). heterogeneous nuclear ribonucleoprotein a3 (hnrnp a3) (fbrnp) (d10s102). 7/1999 [MASS=39686]/Protein with similarity to heterogeneous ribonucleoproteins, contains RRM (RNA recognition motif) domains
PIR2:I55595	RNPC2	25, 37, 38	1	1.92	0.00	PIR2:I55595 splicing factor - human [MASS=58657]/Splicing factor CC1.3, a novel nuclear protein and putative member of the SR family of alternative splicing factors; target of autoantibodies from a patient with hepatocellular carcinoma
GP:AF154502_1	DPP7	45	2	1.90	0.01	Similar to dipeptidyl peptidase 7/Dipeptidyl peptidase 7 (quiescent cell proline dipeptidase), a serine protease that cleaves N-terminal Xaa-Pro dipeptides, member of a family of post proline cleaving exopeptidases, may play a role in inhibition of apoptosis in quiescent lymphocytes
GP:AF177344_1	FLJ10581	25, 37	1	1.89	0.00	GP:AF177344_1 Homo sapiens clone HC90 unknown mRNA. [MASS=30998]/ weakly similar to a methyltransferase/Member of the RNA methyltransferase family, which catalyze 2'-O-methylation of ribose groups in R
PIR2:T09073	SFRS2IP	16, 25, 38, 31	1	1.89	0.00	PIR2:T09073 splicing factor Sip1 - human [MASS=128875]/Splicing factor arginine serine rich 2 interacting protein, a SR domain family protein that interacts with the RNA polymerase II C-terminal domain and several splicing factors, is essential in mRNA splicing and possibly spliceosome A-complex formation
SW:CNBP_HUMAN	ZNF9	19, 29	2	1.87	0.27	SW:CNBP_HUMAN P20694 homo sapiens (human), and rattus norvegicus (rat). cellular nucleic acid binding protein (cnbp). 11/1997 [MASS=19463]/Zinc-finger protein that binds to sterol regulatory element (SRE) and may function in sterol-mediated repression of genes encoding the low density lipoprotein receptor and enzymes of the cholesterol biosynthetic pathway
SW:ECHB_HUMAN	HADHB	18, 19, 42	4	1.87	0.07	SW:ECHB_HUMAN P55084 homo sapiens (human). trifunctonal enzyme beta subunit, mitochondrial precursor (tp-beta) [includes: 3-ketoacyl-coa thiolase (ec 2.3.1.16) (acetyl-coa acyltransferase) (beta-ketothi [MASS=51294]/3-hydroxyacyl-CoA dehydrogenase, 3-ketoacyl-CoA thiolase trifunctional protein beta subunit, involved in fatty acid beta-oxidation; variants are associated with trifunctional protein deficiency, sudden infant death syndrome and liver failure
SW:NUAM_HUMAN	NDUFS1	18	1	1.87	0.00	SW:NUAM_HUMAN P28331 homo sapiens (human). nadh-ubiquinone oxidoreductase 75 kda subunit precursor (ec 1.6.5.3) (ec 1.6.99.3) (complex i-75kd) (ci-75kd). 7/1999 [MASS=79574]/NADH-dehydrogenase ubiquinone Fe-S protein 1 (75kD), a multiprotein complex that transports electrons from NADH to ubiquinone, present within the hydrophobic fraction of complex I; genetic variants are associated with mitochondrial complex I deficiency
PIR2:A55575	ANK3	11, 43	9	1.85	0.18	PIR2:A55575 ankyrin 3, long splice form - human [MASS=480403]/Ankyrin 3 (ankyrin G), may link integral membrane proteins to the cytoskeleton, may play a role in localizing sodium channels to the axonal initial segment and nodes of Ranvier, may play a role in vesicle transport

SWN:JAM1_HUMAN	JAM1	6	9	1.85	0.84	SWN:JAM1_HUMAN Q9y624 homo sapiens (human). junctional adhesion molecule precursor (jam) (platelet adhesion molecule 1) (pam-1) (platelet f11 receptor). 8/2001 [MASS=32583]/Junctional adhesion molecule 1, participates in platelet adhesion and aggregation and may play roles in intracellular signaling, the assembly of tight junctions, and the inflammatory response, may be involved in the pathogenesis of immune thrombocytopenia
SW:ASNS_HUMAN	ASNS	2	1	1.85	0.00	SW:ASNS_HUMAN P08243 homo sapiens (human). asparagine synthetase [glutamine-hydrolyzing] (ec 6.3.5.4) (glutamine-dependent asparagine synthetase) (ts11 cell cycle control protein). 2/1996 [MASS=64299]/Asparagine synthase, catalyzes ATP-dependent conversion of aspartate to asparagine using an amine group from glutamine or ammonia, expression is induced upon amino acid and glucose deprivation and induction increases cancer cell resistance to chemotherapy
SW:ADT1_HUMAN	SLC25A4	18, 42	2	1.84	0.94	SW:ADT1_HUMAN P12235 homo sapiens (human). adp,atp carrier protein, heart/skeletal muscle isoform t1 (adp/atp translocase 1) (adenine nucleotide translocator 1) (ant 1). 10/1994 [MASS=33064]/Solute carrier family 25 member 4, an ADP:ATP transporter that may act in mitochondrial genome stability, altered transport capacity due to autoimmune response leads to myocarditis and cardiomyopathy; mutation causes progressive external ophthalmoplegia
GP:AB043007_1	SDF2L1	45	2	1.84	0.06	GP:AB043007_1 Homo sapiens SDF2L1 mRNA for SDF2 like protein 1, complete cds. [MASS=23511]/Stromal cell-derived factor 2-like 1, a member of the protein-O-mannosyltransferase-rotated abdomen (pmt-rt) family, contains three MIR (protein mannosyltransferase, IP3R and RyR) domains and a C-terminal ER retention signal
SW:ADRO_HUMAN	FDXR	18, 19	1	1.82	0.00	SW:ADRO_HUMAN P22570 homo sapiens (human). nadph:adrenodoxin oxidoreductase precursor (ec 1.18.1.2) (adrenodoxin reductase) (ferredoxin-nadp(+) reductase). 7/1999 [MASS=53809]/Ferredoxin reductase, mitochondrial flavoprotein that mediates electron transport from NADPH to cytochrome P450scc
SW:DDX9_HUMAN	DDX9	45	2	1.82	0.00	SW:DDX9_HUMAN Q08211 homo sapiens (human). atp-dependent rna helicase a (nuclear dna helicase ii) (ndh ii) (dead box protein 9). 12/1998 [MASS=140877]/DEAD box protein 9 (RNA helicase A), ATP-dependent RNA and DNA helicase, involved in HIV replication and transcription, and retroviral mRNA nuclear export; present as an autoantigen in patients with systemic lupus erythematosus
GP:AB032903_1	LOC51292	10	1	1.81	0.00	GP:AB032903_1 Homo sapiens GMPR2 mRNA for guanosine monophosphate reductase isolog, complete cds. [MASS=37874]/Guanosine monophosphate reductase, enzyme with a predicted role in purine interconversion
SW:AGAL_HUMAN	GLA	5, 19	1	1.80	0.00	SW:BDH_HUMAN P06280 homo sapiens (human). alpha-galactosidase a precursor (ec 3.2.1.22) (melibiase) (alpha-d-galactoside galactohydrolase) (alpha-d-galactosidase a). 7/1998 [MASS=48767]/Alpha-galactosidase A (alpha-D-galactoside galactohydrolase), hydrolyzes glycosphingolipids to release alpha-D-galactosyl residues; mutation of the corresponding gene causes Fabry disease
SW:RB48_HUMAN	RBBP4	12, 34	1	1.80	0.00	SW:RB48_HUMAN Q09028 homo sapiens (human). chromatin assembly factor 1 p48 subunit (caf-1 p48 subunit) (retinoblastoma binding protein p48) (retinoblastoma-binding protein 4) (msi1 protein homolog). 12/ [MASS=47656]/Retinoblastoma binding protein 4, a nuclear protein that forms complexes with a variety of proteins including RB1, HDAC1, BRCA1, E2F, which function in histone acetylation, regulation of cell proliferation, or transcriptional repression
GP:AB039669_1	ALEX3	45	4	1.80	0.19	GP:AB039669_1 Homo sapiens mRNA for ALEX3, complete cds; similar to ALEX1 protein. [MASS=42501]/a novel human armadillo repeat containing protein/Arm proteins lost in epithelial cancers on chromosome X 3, a member of the ALEX protein family, contains a single armadillo-like (Arm) repeat and N-terminal hydrophobic residues that suggests it may be a membrane-associated protein
SW:RL44_HUMAN	RPL44	35	4	1.80	0.47	SW:RL44_HUMAN P09896 homo sapiens (human), rattus norvegicus (rat), mus musculus (mouse), and sus scrofa (pig). 60s ribosomal protein l44 (l36a). 7/1998 [MASS=12310]/Ribosomal protein L44, a component of the 60S ribosomal subunit; has very strong similarity to Rpl36a, which may be part of the peptidyl transferase center
GP:AF041483_1	H2AFY	12	1	1.80	0.00	GP:AF041483_1 Homo sapiens histone macroH2A1.2 mRNA, complete cds. [MASS=39601]/H2A histone family member Y, a histone H2A subtype containing a unique non-histone domain, involved in compaction of DNA into nucleosomes and X chromosome inactivation
SWN:ZH10_HUMAN	ZNF345	45	1	1.79	0.00	SWN:ZH10_HUMAN Q14585 homo sapiens (human). zinc finger protein hzf10. 8/2001 [MASS=55383]/Zinc finger protein 345, a Kruppel-related zinc protein
SW:RUXF_HUMAN	SNRPF	25, 37, 38	1	1.76	0.00	SW:RUXF_HUMAN Q15356 homo sapiens (human). small nuclear ribonucleoprotein f (snrnp-f) (sm protein f). 7/1999 [MASS=9725]/Sm protein F, a spliceosomal snRNA-associated Sm core protein that is involved in the biogenesis of the snRNPs; a target of autoantibodies in patients with the autoimmune disease systemic lupus erythematosus
GP:AF157317_1	LOC55829	45	1	1.76	0.00	GP:AF157317_1 Homo sapiens AD-015 protein mRNA, complete cds; protein x 0008. [MASS=22864]/ similar to mouse minor histocompatibility antigen precursor/Protein of unknown function
GP:AF161507_1	MRPL22	45	1	1.76	0.00	GP:AF161507_1 Homo sapiens HSPC158 mRNA, complete cds. [MASS=26192]/mitochondrial ribosomal protein L22/Mitochondrial ribosomal protein L22, a putative structural protein of the mitochondrial large 39S ribosomal subunit, may play a role in protein biosynthesis
SW:BDH_HUMAN	BDH	5	4	1.76	0.25	SW:BDH_HUMAN Q02338 homo sapiens (human). d-beta-hydroxybutyrate dehydrogenase precursor (ec 1.1.1.30) (bdh) (3-hydroxybutyrate dehydrogenase) (fragment). 12/1998 [MASS=38137]/D-beta-hydroxybutyrate dehydrogenase, a member of the short-chain alcohol dehydrogenase superfamily that requires phosphatidylcholine as an allosteric activator, involved carbohydrate and fatty acid metabolism
GP:AC003972_1	RENT1	25, 37, 39	1	1.74	0.00	GP:AC003972_1 Homo sapiens DNA from chromosome 19, cosmid R33485 containing pNORF1, complete sequence; human type 1 RNA helicase; DPS similarity to (U59323) type 1 RNA helicase pNORF1 [Homo sapiens]; Score. [MASS=123036]/regulator of nonsense transcripts 1 (nonsense mrna reducing factor 1) (norf1) (up-frameshift suppressor 1 homolog). 10/2001 [MASS=124345]

PIR2:A57099	PRKDC	14, 34, 40	13	1.74	0.27	PIR2:A57099 DNA-activated protein kinase, catalytic subunit - human [MASS=465428]/DNA-dependent protein kinase catalytic subunit, a DNA-binding protein kinase involved in DNA double-strand break repair and somatic recombination of antibody genes; absence of mouse Prkdc is associated with severe combined immunodeficiency
SW:DHB4_HUMAN	HSD17B4	19	12	1.74	0.52	SW:DHB4_HUMAN P51659 homo sapiens (human). estradiol 17 beta-dehydrogenase 4 (ec 1.1.1.62) (17-beta-hsd 4) (17-beta-hydroxysteroid dehydrogenase 4). 11/1997 [MASS=79686]/Type IV 17 beta-hydroxysteroid dehydrogenase, a peroxisomal multifunctional enzyme with estradiol 17 beta-dehydrogenase and D-3 hydroxyacyl CoA dehydratase activities, involved in steroid and bile acid metabolism
SW:BUB3_HUMAN	BUB3	7, 23	2	1.73	0.02	SW:BUB3_HUMAN O43684 homo sapiens (human). mitotic checkpoint protein bub3. 5/2000 [MASS=37155]/Budding uninhibited by benzimidazoles 3 homolog, involved in the mitotic spindle checkpoint, localization to unattached kinetochores suggests a role in detecting microtubule attachment, required for the localization of BUB1 and BUB1B to kinetochores
PIR2:I53799	KTN1	43	2	1.73	0.08	PIR2:I53799 CG1 protein - human [MASS=149611]/human kinectin/Kinectin, functions as a receptor for the microtubule-motor protein kinesin and plays a role in intracellular movement of organelles; mutations in the corresponding gene are associated with childhood papillary thyroid carcinoma
SW:ATCP_HUMAN	ATP2B1	42	21	1.73	0.61	SW:ATCP_HUMAN P20020 homo sapiens (human). calcium-transporting atpase plasma membrane, isoform 1b (ec 3.6.1.38) (calcium pump) (pmca1b). 5/2000 [MASS=134685]/ATPase Ca++ transporting plasma membrane 1, a member of the P type primary ion transport ATPase family, a housekeeping gene, alternatively spliced isoforms show differential tissue expression; candidate gene for hereditary hearing impairment
SW:CAN1_HUMAN	CAPN1	41	1	1.73	0.00	SW:CAN1_HUMAN P07384 homo sapiens (human). calpain 1, large [catalytic] subunit (ec 3.4.22.17) (calcium-activated neutral proteinase) (canp) (mu-type). 10/1996 [MASS=81890]/Calpain I, catalytic subunit of mu-calpain, a calcium-dependent cysteine (thiol) protease that requires micromolar concentrations of calcium in vitro
SW:PCB2_HUMAN	PCBP2	37	10	1.73	0.20	SW:PCB2_HUMAN Q15366 homo sapiens (human). poly(rc)-binding protein 2 (hnrnp-e2). 5/2000 [MASS=38580]/Poly(rC)-binding protein 2, poly(rC) and poly(U)-binding protein, involved in the translational regulation of poliovirus, papillomavirus, and hepatitis C virus transcripts
PIR2:JW0079	HNRPDL	25, 37	1	1.72	0.00	PIR2:JW0079 heterogeneous nuclear ribonucleoprotein homolog JKTBP [imported] - human [MASS=33589]/Heterogeneous nuclear ribonucleoprotein D-like, an RNA- and DNA-binding protein that may play a role in mRNA biogenesis
GP:AK024512_1	FLJ20859	45	1	1.71	0.00	GP:AK024512_1 Homo sapiens cDNA: FLJ20859 fis, clone ADKA01617; unnamed protein product. [MASS=50734]/ probable ATPase/ EST/Protein of unknown function, has low similarity to uncharacterized C. elegans F32A7.4
GP:AF214737_1	C9orf10	45	10	1.70	0.57	homo sapiens (human). protein c9orf10/EST/Protein of unknown function, has weak similarity to uncharacterized human KIAA1838
SW:GDIB_HUMAN	GDI2	43	2	1.70	0.01	SW:GDIB_HUMAN P50395 homo sapiens (human). rab gdp dissociation inhibitor beta (rab gdi beta) (gdi-2). 7/1998 [MASS=50664]/Guanosine diphosphate dissociation inhibitor 2, one of a family proteins that regulate GDP/GTP cycle and are involved in intracellular vesicular trafficking, associates with RAB1B, RAB5 and RAB6 and may play a role in their intracellular targeting
SW:IF2B_HUMAN	EIF2S2	35	2	1.70	0.48	SW:IF2B_HUMAN P20042 homo sapiens (human). eukaryotic translation initiation factor 2 beta subunit (eif-2-beta). 7/1999 [MASS=38400]/Eukaryotic translation initiation factor 2 subunit 2, the beta subunit of eIF2, a translation initiation factor, involved in the initiation of protein synthesis, binds GDP
PIR2:T42692	LOC221927	45	1	1.69	0.00	PIR2:T42692 hypothetical protein DKFZp434D0428.1 - human (fragment) [MASS=51316]
SW:R37A_HUMAN	RPL37A	35	2	1.69	0.23	SW:R37A_HUMAN P12751 homo sapiens (human), rattus norvegicus (rat), and mus musculus (mouse). 60s ribosomal protein l37a. 2/1996 [MASS=10144]/Ribosomal protein L37a, component of the large 60S ribosomal subunit
SW:P60_HUMAN	HSPD1	33	22	1.69	0.31	SW:P60_HUMAN P10809 homo sapiens (human). mitochondrial matrix protein p1 precursor (p60 lymphocyte protein) (60 kda chaperonin) (heat shock protein 60) (hsp-60) (protein cpn60) (groel protein) (hucha60 [MASS=61055]/Chaperonin 60, mitochondrial matrix protein induced by stress, component of the chaperonin complex that is implicated in mitochondrial protein folding and function, induced by inflammatory and immune responses, and implicated in coronary disease
SW:AOFA_HUMAN	MAOA	2, 26	15	1.68	0.50	(human). amine oxidase [flavin-containing] a (ec 1.4.3.4) (monoamine oxidase) (mao-a). 12/1998 [MASS=59682]/Monoamine oxidase A, an enzyme involved in degradation of amine neurotransmitters, may be associated with neuropsychiatric disorders, including impulsive aggression and panic disorder, and Parkinson disease
GP:AF111168_3	C14orf3	45	2	1.68	0.01	EST/Protein of unknown function, has moderate similarity to uncharacterized C. elegans C01G10.8
SW:DDX1_HUMAN	DDX1	16, 25, 35, 37	6	1.67	0.10	SW:DDX1_HUMAN Q92499 homo sapiens (human). dead box protein 1 (dead box protein-retinoblastoma) (dbp-rb). 5/2000 [MASS=82432]/DEAD box protein 1, a member of the DEAD-H box ATP-dependent RNA helicase protein family, plays a role in the processing of pre-mRNAs, may interact with CSTF2; corresponding gene is coamplified with MYC in some neuroblastoma and retinoblastoma cell lines
GP:AL035413_5	KIAA0090	45	1	1.67	0.00	GP:AL035413_5 Human DNA sequence from clone RP4-657E11 on chromosome 1p35.1-36.23 Contains 3' part of the CAPZB (capping protein (actin filament) muscle Z-line, beta) gene, genes for aldo-keto reductase family 7 (aflatoxin aldehyde reductase) members A2 (AKR7A2) a [MASS=95553]/ EST/Protein of unknown function
SW:FRIH_HUMAN	FTH1	26	7	1.67	0.26	SW:FRIH_HUMAN P02794 homo sapiens (human). ferritin heavy chain (ferritin h subunit). 7/1999 [MASS=21094]/Ferritin heavy polypeptide 1, a ferrioxidase involved in iron storage, heme biosynthesis, cell growth, oxidative stress response, and transcription, may play a role in iron transport, apoptosis, cell differentiation, and response to bacteria

SW:HCD2_HUMAN	HADH2	19	4	1.67	0.12	SW:HCD2_HUMAN Q99714 homo sapiens (human). 3-hydroxyacyl-coa dehydrogenase type ii (ec 1.1.1.35) (endoplasmic reticulum-associated amyloid beta-peptide binding protein) (short- chain type dehydrogenase/ [MASS=26923]/Hydroxyacyl-Coenzyme A dehydrogenase (type II), catalyzes the oxidation of steroids and alcohols, binds amyloid-beta protein; overexpressed and mediates neurotoxicity of Alzheimer's disease, mutation in the corresponding gene causes hyperinsulinism
GP:U17032_1	ARHGAP5	6, 41	1	1.66	0.00	GP:U17032_1 Human p190-B (p190-B) mRNA, complete cds; member of the Rho GAP family. [MASS=171569]/Rho GTPase activating protein 5/Rho GTPase-activating protein (GAP) 5, has GAP activity for ARHA, RAC1 and CDC42, which are ras-related GTP binding proteins of the rho subfamily; may be involved in the integrin receptor signaling pathway and in cell adhesion
SW:PTK7_HUMAN	PTK7	34, 41	9	1.66	0.30	SW:PTK7_HUMAN Q13308 homo sapiens (human). tyrosine-protein kinase-like 7 precursor (colon carcinoma kinase-4) (cck-4). 5/2000 [MASS=118260]/Protein tyrosine kinase 7 (colon carcinoma kinase-4), a glycosylated member of the receptor protein tyrosine kinase family that may be involved in tumorigenesis, likely to be catalytically inactive due to alterations within the RTK consensus sequences
SW:ROH1_HUMAN	HNRPH1	25, 37	4	1.66	0.22	SW:ROH1_HUMAN P31943 homo sapiens (human). heterogeneous nuclear ribonucleoprotein h (hnrnp h). 11/1997 [MASS=49229]/Heterogeneous nuclear ribonucleoprotein H1, a pre-mRNA splicing factor that is a component of a complex that mediates post-transcriptional processing of primary transcripts
GP:AF161494_1	MRPL15	45	3	1.66	0.06	GP:AF161494_1 Homo sapiens HSPC145 mRNA, complete cds. [MASS=33420]/mitochondrial ribosomal protein L15/Protein containing a ribosomal protein L15 family amino terminal domain, has a region of moderate similarity to a region of S. cerevisiae Mrpl10p, which is a mitochondrial ribosomal protein of the large subunit (YmL10)
SW:MCM4_HUMAN	MCM4	7, 15	3	1.65	0.14	SW:MCM4_HUMAN P33991 homo sapiens (human). dna replication licensing factor mcm4 (cdc21 homolog) (p1-cdc21). 5/2000 [MASS=96611]/Minichromosome maintenance deficient 4, forms a single stranded ATP-dependent DNA helicase with MCM6 and MCM7, may monitor sites of unreplicated DNA, displacement from replicated chromatin may ensure that DNA is only replicated once per cell cycle
SW:C1TC_HUMAN	MTHFD1	26	6	1.65	0.45	SW:C1TC_HUMAN P11586 h c-1-tetrahydrofolate synthase, cytoplasmic (c1-thf synthase) [includes: methylenetetrahydrofolate dehydrogenase (ec 1.5.1.5); methenyltetrahydrofolate cyclohydrolase (ec 3.5.4.9); [MASS=101428]/C1-Tetrahydrofolate synthase, a trifunctional enzyme with 10-formyltetrahydrofolate synthetase, 5,10-methenyltetrahydrofolate cyclohydrolase, and 5,10-methylenetetrahydrofolate dehydrogenase activities; mutation associated with risk of neural tube disease
SW:CUL2_HUMAN	CUL2	7, 23, 32	1	1.64	0.00	SW:CUL2_HUMAN Q13617 homo sapiens (human). cullin homolog 2 (cul-2). 12/1998 [MASS=86956]/Cullin 2, has E3 ubiquitin ligase activity when present in a complex containing von Hippel Lindau tumor suppressor (VHL)- elogin B (TCEB2)-elogin C (TCEB1); modification by ubiquitin-like protein NEDD8 may be important for VHL tumor suppressor function
SW:ROA0_HUMAN	HNRPA0	25, 37	2	1.64	0.40	SW:ROA0_HUMAN Q13151 homo sapiens (human). heterogeneous nuclear ribonucleoprotein a0 (hnrnp a0). 5/2000 [MASS=30841]/Heterogeneous nuclear ribonucleoprotein A0, has triplet repeats, two consensus sequence-type RNA-binding domains, and a glycine-rich auxiliary domain, found in low abundance hnRNP complexes
SW:RL14_HUMAN	RPL14	35	23	1.63	0.47	SW:RL14_HUMAN P50914 homo sapiens (human). 60s ribosomal protein l14 (cag-isl 7). 12/1998 [MASS=23158]/Ribosomal protein L14, a putative component of the large 60S ribosomal subunit; transcripts can contain either fixed or variable numbers of CAG triplet repeats depending on cell type
SW:RL17_HUMAN	RPL17	35	4	1.63	0.06	SW:RL17_HUMAN P18621 homo sapiens (human). 60s ribosomal protein l17 (l23). 5/2000 [MASS=21397]/Ribosomal protein L17, an RNA-binding structural component of the large 60S ribosomal subunit that plays a role in protein biosynthesis
SW:CISY_HUMAN	CS	5, 18	1	1.62	0.00	SW:CISY_HUMAN O75390 homo sapiens (human). citrate synthase, mitochondrial precursor (ec 4.1.3.7). 7/1999 [MASS=51706]/Citrate synthase, converts acetyl-CoA and oxaloacetate into citrate plus CoA in the tricarboxylic acid cycle
SW:DHA4_HUMAN	ALDH3A2	16, 19	2	1.62	0.67	SW:DHA4_HUMAN P51648 homo sapiens (human). fatty aldehyde dehydrogenase (ec 1.2.1.3) (aldehyde dehydrogenase, microsomal) (aldh class 3). 7/1999 [MASS=54848]/Aldehyde dehyrogenase 3 family member A2, catalyzes the oxidation of long chain fatty aldehydes and leukotrienes; mutation of the corresponding gene causes Sjogren Larsson syndrome, a disorder marked by mental retardation, spasticity, and ichthyosis
SW:HE47_HUMAN	BAT1	45	3	1.62	0.23	SW:HE47_HUMAN Q13838 homo sapiens (human). probable atp-dependent rna helicase p47. 11/1997 [MASS=48991]/HLA-B associated transcript 1, a putative DEAD/H box ATP-dependent RNA helicase, involved in immune response and may negatively regulate inflammation by repressing cytokine production; corresponding gene lies within the major histocompatibility complex
SW:RL12_HUMAN	RPL12	35	35	1.62	0.58	SW:RL12_HUMAN P30050 homo sapiens (human). 60s ribosomal protein l12. 7/1998 [MASS=17819]/Ribosomal protein L12, a likely RNA-binding structural component of the large 60S ribosomal subunit that plays a role in protein biosynthesis; autoantibodies to ribosomal protein L12 are associated with systemic lupus erythematosus
SW:CATB_HUMAN	CTSB	32	5	1.62	0.25	SW:CATB_HUMAN P07858 homo sapiens (human). cathepsin b precursor (ec 3.4.22.1) (cathepsin b1) (app secretase). 7/1998 [MASS=37808]/Cathepsin B, a cysteine (thiol) protease that degrades cartilage matrix proteins and other proteins, also cleaves APP; commonly overexpressed in tumors, and may be proapoptotic, but also facilitates tumor invasion
SW:RFA3_HUMAN	RPA3	7, 14, 15, 40	2	1.61	0.19	SW:RFA3_HUMAN P35244 homo sapiens (human). replication protein a 14 kda subunit (rp-a) (rf-a) (replication factor-a protein 3). 11/1997 [MASS=13569]/Replication protein A 3, a subunit of replication protein A, which is a single-stranded DNA-binding protein complex with roles in DNA replication, repair, and recombination

SW:PXF_HUMAN	PXF	19, 36	1	1.61	0.00	SW:PXF_HUMAN P40855 homo sapiens (human). peroxisomal farnesylated protein (33 kda housekeeping protein). 12/1998 [MASS=32807]/Peroxisomal farnesylated protein, peroxisomal protein that binds several peroxisomal membrane proteins (PMP), involved in early stages of PMP import and peroxisomal biogenesis; deficiency is associated with Zellweger syndrome complementation group J
PIR2:T46250	sialic acid-specific acetylesterase II	45	1	1.60	0.00	PIR2:T46250 hypothetical protein DKFZp761A051.1 - human (fragment) [MASS=58084]
GP:AF188611_1	HSPA5	33	1	1.60	0.00	GP:AF188611_1 Homo sapiens BiP protein (HSPA5) mRNA, partial cds; glucose-regulated protein (grp78). [MASS=70931]/Heat shock 70kD protein 5, chaperone and putative ATPase involved in protein folding in the endoplasmic reticulum, induced in the stress response; autoimmunity may be a factor in rheumatoid arthritis
GP:D89729_1	XPO1	24	1	1.60	0.00	GP:D89729_1 Homo sapiens mRNA for CRM1 protein, complete cds. [MASS=123386]/Exportin 1, a cell cycle-regulated nuclear export receptor, mediates NES containing protein export from the nucleus, also involved in nuclear export of HIV1 RNA, may be required for autophagy
SW:DLDH_HUMAN	DLD	5, 18	10	1.59	0.59	SW:DLDH_HUMAN P09622 homo sapiens (human). dihydrolipoamide dehydrogenase, mitochondrial precursor (ec 1.8.1.4). 5/2000 [MASS=54150]/Dihydrolipoamide dehydrogenase, E3 component of pyruvate dehydrogenase complex, also component of alpha-ketoglutarate dehydrogenase and branched-chain alpha-ketoacid dehydrogenase complexes and the glycine cleavage system
SW:AOFB_HUMAN	MAOB	2, 26	1	1.59	0.00	SW:AOFB_HUMAN P27338 homo sapiens (human). amine oxidase [flavin-containing] b (ec 1.4.3.4) (monoamine oxidase) (mao-b). 12/1998 [MASS=58763]/Monoamine oxidase B, an oxidase involved in the metabolism of various biologically important amines such as dopamine, requires covalently bound FAD as a cofactor, may play a role in aging and behavior
SW:C166_HUMAN	ALCAM	6, 41	8	1.58	0.27	SW:C166_HUMAN Q13740 homo sapiens (human). cd166 antigen precursor (activated leukocyte-cell adhesion molecule) (alcam). 7/1999 [MASS=65132]/Activated leukocyte cell adhesion molecule, an immunoglobulin superfamily member and ligand for CD6, involved in hematopoietic cell adhesion, may play a role in osteogenesis, marker for tumor progression in malignant melanoma
SW:EP1_HUMAN	NPC2	45	11	1.58	0.16	SW:EP1_HUMAN Q15668 homo sapiens (human), pan troglodytes (chimpanzee), and macaca fascicularis (crab eating macaque) (cynomolgus monkey). epididymal secretory protein e1 precursor (epi-1) (he1) (epidid [MASS=16570]/Neimann-Pick disease type C2 (epididymal secretory protein 1), putative lysosomal protein that may play a role in cholesterol transport; mutations of the corresponding gene cause Niemann-Pick type C2 disease
SW:PPT_HUMAN	PPT1	32, 34	7	1.57	0.39	SW:PPT_HUMAN P50897 homo sapiens (human). palmitoyl-protein thioesterase precursor (ec 3.1.2.22) (palmitoyl- protein hydrolase). 5/2000 [MASS=34193]/Palmitoyl-protein thioesterase (ceroid-lipofuscinosis, neuronal 1, infantile), catalyzes the hydrolysis of palmitate from S-acetylated cysteine residues, may be involved in apoptosis; gene mutation is detected in infantile neuronal ceroid lipofuscinosis
SW:PKBS_HUMAN	BZRP	19, 36	2	1.57	0.04	SW:PKBS_HUMAN P30536 homo sapiens (human). peripheral-type benzodiazepine receptor (pbr) (pkbs) (mitochondrial benzodiazepine receptor). 6/1994 [MASS=18779]/Benzodiazepine receptor (peripheral), involved in steroid biosynthesis, cell proliferation, and may contribute to mitochondrial biogenesis and inhibit oxygen radical induced apoptosis; expression, nuclear location may correlate to breast tumor progression
SW:APE1_HUMAN	APEX	14, 18, 29	13	1.57	0.38	SW:APE1_HUMAN P27695 homo sapiens (human). dna-(apurinic or apyrimidinic site) lyase (ec 4.2.99.18) (ap endonuclease 1) (apex nuclease) (apen) (ref-1 protein). 12/1998 [MASS=35423]/Apurinic/apyrimidinic endonuclease 1, multifunctional DNA repair enzyme that coordinates the repair of abasic sites and repair synthesis, acts as a transcription regulator; mutations may correlate with inclusion body myositis and colorectal tumorigenesis
SW:PCP_HUMAN	PRCP	45	1	1.57	0.00	SW:PCP_HUMAN P42785 homo sapiens (human). lysosomal pro-x carboxypeptidase precursor (ec 3.4.16.2) (prolylcarboxypeptidase) (prcp) (proline carboxypeptidase) (angiotensinase c) (lysosomal carboxypeptida [MASS=55800]/Prolylcarboxypeptidase (angiotensinase C), a serine carboxypeptidase that catalyzes the cleavage of C-terminal amino acid residues linked to proline; corresponding gene may be a candidate locus for essential hypertension
SW:PSS1_HUMAN	PAPSS1	25, 34	1	1.56	0.00	SW:PSS1_HUMAN P48651 homo sapiens (human). phosphatidylserine synthase i (serine-exchange enzyme i) (ec 2.7.8.-) (kiaa0024). 11/1997 [MASS=55528]/3'-phosphoadenosine 5'-phosphosulfate synthase 1, bifunctional polypeptide with ATP sulfurylase and adenosine 5'-phosphosulfate kinase activites, required for the synthesis of the sulfonate donor 3'-phosphoadenosine 5'-phosphosulfate
SW:GBI1_HUMAN	GNAI1	41	4	1.56	0.16	SW:GBI1_HUMAN P04898 homo sapiens (human), and bos taurus (bovine). guanine nucleotide-binding protein g(i), alpha-1 subunit (adenylate cyclase-inhibiting g alpha protein). 7/1999 [MASS=40230]/Guanine nucleotide binding protein alpha inhibiting activity polypeptide 1 (Gi alpha 1), pertussis toxin-sensitive heterotrimeric G protein subunit downregulated at the membrane by increased cholesterol, mediates adenylyl cyclase inhibition
SW:FXR2_HUMAN	FXR2	24	3	1.56	0.30	SW:FXR2_HUMAN P51116 homo sapiens (human). fragile x mental retardation syndrome related protein 2. 10/1996 [MASS=74128]/Fragile X mental retardation gene autosomal homolog 2, binds mRNA, forms homomers or heteromers with FMR1 and FXR1, associates with the 60S ribosomal subunit and with actively translating polyribosomes, shuttles between the cytoplasm and nucleolus
SW:SMD3_HUMAN	SNRPD3	25, 37, 38	1	1.55	0.00	SW:SMD3_HUMAN P43331 homo sapiens (human). small nuclear ribonucleoprotein sm d3 (snrnp core protein d3) (sm-d3). 10/1996 [MASS=13916]/Small nuclear ribonucleoprotein D3, part of a multimeric complex involved in biogenesis of snRNPs and mRNA splicing, interacts with the spinal muscular atrophy disease protein (SMN); autoantigen for antibodies associated with systemic lupus erythematosus

SW:MIC2_HUMAN	MIC2	6	11	1.55	0.30	SW:MIC2_HUMAN P14209 homo sapiens (human). t-cell surface glycoprotein e2 precursor (e2 antigen) (cd99) (mic2 protein) (12e7). 5/2000 [MASS=18848]/T-cell surface glycoprotein E2, a cell surface glycoprotein involved in T cell adhesion and apoptosis, activates MAP kinases, may be involved in Golgi-membrane transport, downregulated in EBV-associated Hodgkins disease
GP:U52111_2	RPL18A	45	27	1.54	0.43	GP:U52111_2 Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protei [MASS=20867]/ribosomal protein L18a/Ribosomal protein L18a, a component of the 60S ribosomal subunit that is likely to play a role in protein synthesis; murine Rpl18a may play a role in squamous cell carcinoma progression
SW:MAP4_HUMAN	MAP4	11	1	1.54	0.00	SW:MAP4_HUMAN P27816 homo sapiens (human). microtubule-associated protein 4. 6/1994 [MASS=121180]/Microtubule-associated protein 4, a microtubule-associated protein that stabilizes microtubules and may regulate microtubule dynamics during mitosis; target of a Poliovirus protease
SW:CAOP_HUMAN	ACOX1 or ACOX	18, 19	1	1.53	0.00	SW:CAOP_HUMAN Q15067 homo sapiens (human). acyl-coenzyme a oxidase, peroxisomal (ec 1.3.3.6) (palmitoyl-coa oxidase) (aox). 11/1997 [MASS=74502]/Peroxisomal acyl-coenzyme A oxidase, catalyzes the first step in very long chain fatty acid beta-oxidation, desaturates acyl-CoA to 2-trans-enoyl-CoA and produces hydrogen peroxide
SW:SMN1_HUMAN	SMN2	45	4	1.53	0.19	SW:SMN1_HUMAN Q16637 homo sapiens (human). survival motor neuron protein 1. 5/2000 [MASS=31849]/Survival of motor neuron 2 centromeric, involved in neuromuscular function and may be required for neurogenesis; deletion of the corresponding gene is associated with spinal muscular atrophy (SMA) and adult progressive muscular atrophy
SW:FBRL_HUMAN	FBL	37	1	1.53	0.00	SW:FBRL_HUMAN P22087 homo sapiens (human). fibrillarin (34 kda nucleolar scleroderma antigen). 7/1999 [MASS=33818]/Fibrillarin, a nucleolar RNA-binding protein that is involved in ribosomal RNA processing; recognized by antisera from patients with scleroderma autoimmune disease, systemic sclerosis, and other connective tissue diseases
SW:IF34_HUMAN	EIF3S4	35	1	1.53	0.00	SW:IF34_HUMAN O75821 homo sapiens (human). eukaryotic translation initiation factor 3 subunit 4 (eif-3 delta) (eif3 p44) (eif-3 rna-binding subunit) (eif3 p42). 5/2000 [MASS=35696]/Eukaryotic translation initiation factor 3 subunit 4 (delta 44kD), a component of the eIF-3 translation initiation complex which plays a role in formation of the 40S initiator complex containing methionyl-tRNA and 40S subunit, binds RNA
SW:RL10_HUMAN	RPL10	35	14	1.53	1.04	SW:RL10_HUMAN P27635 homo sapiens (human). 60s ribosomal protein l10 (qm protein) (tumor suppressor qm) (laminin receptor homolog). 5/2000 [MASS=24446]/Ribosomal protein L10, a component of the 60S ribosomal subunit; may be involved in the maintenance of the nontumorigenic phenotype in Wilms' microcell hybrid cells
SW:RO60_HUMAN	SSA2	28	2	1.53	0.01	SW:RO60_HUMAN P10155 homo sapiens (human). 60 kda ro protein (60 kda ribonucleoprotein ro) (rornp) (sjogren syndrome type a antigen (ss-a)). 2/1996 [MASS=60643]/Sjogren syndrome antigen A2, RNA-binding protein that is a component of ribonucleoprotein complexes in association with small cytoplasmic Y RNAs, an autoantigen in systemic rheumatic diseases such as lupus and Sjogren syndrome
SW:H105_HUMAN	HSP105B	10	1	1.53	0.00	SW:H105_HUMAN Q92598 homo sapiens (human). heat-shock protein 105 kda (heat shock 110 kda protein) (kiaa0201). 5/2000 [MASS=96865]/Heat shock protein (105 kDa), member of the high molecular weight family of heat shock proteins, expression is induced by heat shock and is increased in cancer cells
GP:AF013591_1	SUDD	7	2	1.53	0.02	GP:AF013591_1 Homo sapiens homolog of the Aspergillus nidulans sudD gene product mRNA, complete cds. [MASS=59117]/SudD (suppressor of bimD6 Aspergillus nidulans) homolog, a member of the SUDD family of proteins, has similarity to Aspergillus nidulans SUDD, which is a suppressor of the bimD6 chromosome-spindle attachment defect
SW:RS6_HUMAN	RPS6	35	5	1.52	0.13	SW:RS6_HUMAN P10660 homo sapiens (human), rattus norvegicus (rat), and mus musculus (mouse). 40s ribosomal protein s6 (phosphoprotein np33). 7/1998 [MASS=28681]/Ribosomal protein S6, structural component of the cytosolic small (40S) ribosomal subunit, functions in RNA binding and protein biosynthesis
SW:ROK_HUMAN	HNRPK	25, 37	6	1.51	0.30	SW:ROK_HUMAN Q07244 homo sapiens (human), and rattus norvegicus (rat). heterogeneous nuclear ribonucleoprotein k (hnrnp k) (dc-stretch binding protein) (csbp) (transformation upregulated nuclear protein [MASS=50976]/Heterogeneous nuclear ribonucleoprotein K, a transcription factor which binds to poly(C) of RNA and DNA and is involved in RNA processing, gene transcription and translational controls, may induce apoptosis and play a role in viral infection
GP:AK001207_1	PP199	45	1	1.51	0.00	GP:AK001207_1 Homo sapiens cDNA FLJ10345 fis, clone NT2RM2000984; unnamed protein product. [MASS=38193]
GPN:AF307137_1	EHD4	45	1	1.51	0.00	no_description_avail/Esp-15 homology domain-containing 4, may be involved in type VI collagen filament formation or stabilization, contains an N-terminal nucleotide-binding site, a bipartite nuclear localization signal, and a C-terminal EH protein-binding domain
SW:RL3L_HUMAN	RPL3L	35	11	1.51	0.24	SW:RL3L_HUMAN Q92901 homo sapiens (human). 60s ribosomal protein l3-like. 11/1997 [MASS=46165]/Ribosomal protein L3-like, a putative RNA-binding ribosome structural protein that plays a role in protein biosynthesis
SW:PTPF_HUMAN	LAR	6, 34, 41	5	1.50	0.35	SW:PTPF_HUMAN P10586 homo sapiens (human). lar protein precursor (leukocyte antigen related) (ec 3.1.3.48). 10/1994 [MASS=211845]/Protein tyrosine phosphatase receptor-type F (leukocyte common antigen related), regulates insulin receptor signaling and cell migration, inhibits tumor formation in nude mice
SW:NLTP_HUMAN	SCP2	19, 42	2	1.50	0.06	SW:NLTP_HUMAN P22307 homo sapiens (human). nonspecific lipid-transfer protein precursor (nsl-tp) (sterol carrier protein 2) (scp-2) (sterol carrier protein x) (scp-x) (scpx). 5/2000 [MASS=58994]/Sterol carrier protein 2, catalyzes the exchange of phospholipids between membranes, stimulates cholesterol metabolism and may regulate steroidogenesis; alternative form, SCPX, is a 3 oxoacyl CoA thiolase
SW:L130_HUMAN	LRPPRC	45	4	1.50	0.09	SW:L130_HUMAN P42704 homo sapiens (human). 130 kda leucine-rich protein (lrp 130) (gp130). 10/1996 [MASS=145201]/Leucine-rich PPR-motif containing, a leucine-rich protein associated with multiprotein complexes, binds mRNA and is likely involved in nuclear export of mRNA, may be involved in cytoskeletal organization

SW:RB13_HUMAN	RAB13	6, 21, 43	1	1.49	0.00	SW:RB13_HUMAN P51153 homo sapiens (human). ras-related protein rab-13. 12/1998 [MASS=22774]/Ras-related GTP-binding protein 13, a putative RAB small monomeric GTPase that is likely to play a role in intracellular protein trafficking and cell adhesion
GP:AK025859_1	FLJ22206	45	1	1.49	0.00	GP:AK025859_1 Homo sapiens cDNA: FLJ22206 fis, clone HRC01431; unnamed protein product. [MASS=49620]/Protein containing ten ankyrin (Ank) repeats, which may mediate protein-protein interactions, has moderate similarity to a region of ankyrin 3 (human ANK3, ankyrin G), which may link integral membrane proteins to the cytoskeleton
SW:RL18_HUMAN	RPL18	35	5	1.49	0.46	SW:RL18_HUMAN Q07020 homo sapiens (human). 60s ribosomal protein l18. 5/2000 [MASS=21503]/Ribosomal protein L18, a component of the large 60S ribosomal subunit, a negative regulator of double-stranded RNA-activated protein kinase (PKR) which is involved in control of protein synthesis initiation; gene expression increases in colon cancer
PIR2:T17219	SDFR1	45	4	1.48	0.37	PIR2:T17219 hypothetical protein DKFZp566H1924.1 - human (fragment) [MASS=32002]/Stromal cell derived factor receptor 1, contains an immunoglobulin domain
SW:MMSA_HUMAN	MMSDH	26	2	1.48	0.10	SW:MMSA_HUMAN Q02252 homo sapiens (human). methylmalonate-semialdehyde dehydrogenase [acylating] (ec 1.2.1.27) (mmsdh) (fragment). 12/1998 [MASS=46606]/Methylmalonate-semialdehyde dehydrogenase (2-methyl-3-oxopropanoate:NAD+ oxidoreductase (CoA-propanoylating)), a member of the aldehyde dehydrogenase superfamily; deficiency is associated with developmental delay
SW:G6PE_HUMAN	GDH	2	1	1.48	0.00	SW:G6PE_HUMAN O95479 homo sapiens (human). gdh/6pgl endoplasmic bifunctional protein precursor [includes: glucose 1-dehydrogenase (ec 1.1.1.47) (hexose-6-phosphate dehydrogenase); 6- phosphogluconolacto [MASS=88879]/Glutamate dehydrogenase, catalyzes the reversible deamination of L-glutamate into alpha-ketoglutarate, mitochondrial enzyme with role in neurotransmission; deficiency is associated with neurodegenerative disorders
SW:VAB2_HUMAN	ATP6B2	9, 16, 42	7	1.47	0.34	SW:VAB2_HUMAN P21281 homo sapiens (human). vacuolar atp synthase subunit b, brain isoform (ec 3.6.1.34) (endomembrane proton pump 58 kda subunit) (v-atpase b subunit) (ho57). 7/1999 [MASS=56517]/Vacuolar-type H(+)-ATPase (beta isoform 2), 56 kDa subunit of the ATPase catalytic domain which may assist in transepithelial H+ transport in the kidney, may effect vacuolar acidification, and may play a role in the polarization of osteoclasts
SWN:CNE3_HUMAN	CPN3	19, 43	28	1.47	0.27	SWN:CNE3_HUMAN O75131 homo sapiens (human). copine iii. 8/2001 [MASS=60131]/Copine III, a member of the copine family of phospholipid binding proteins, contains C2 and integrin A domains, may play a role in membrane trafficking, displays protein kinase activity, however, it does not contain a traditional kinase catalytic domain
GP:AB018313_1	VPS39	45	1	1.47	0.00	GP:AB018313_1 Homo sapiens mRNA for KIAA0770 protein, partial cds. [MASS=83943]/Vam6-Vps39-like, contains a citron homology (CNH) domain and a clathrin heavy chain repeat domain, forms homooligomers and may act as a tethering or docking factor that promotes lysosome clustering and fusion
GP:D87453_1	MRPS27	45	2	1.47	0.17	GP:D87453_1 Human mRNA for KIAA0264 gene, partial cds. [MASS=47798]/Protein of unknown function
GP:U16406_1	HIV	45	1	1.47	0.00	GP:U16406_1 Human immunodeficiency virus type 1 patient I01, clone D, envelope glycoprotein (env) gene, V3 region, partial cds. [MASS=10815]
SWN:Z272_HUMAN	ZNF272	45	1	1.47	0.00	SWN:Z272_HUMAN Q14592 homo sapiens (human). zinc finger protein 272 (zinc finger protein hzf8) (fragment). 8/2001 [MASS=19678]/Zinc finger protein 272, a protein that contains tandem zinc fingers, may be involved in hemopoiesis
SW:PYR1_HUMAN	CAD	25	6	1.47	0.46	SW:PYR1_HUMAN P27708 homo sapiens (human). cad protein [includes: glutamine-dependent carbamoyl-phosphate synthase (ec 6.3.5.5); aspartate carbamoyltransferase (ec 2.1.3.2); dihydroorotase (ec 3.5.2.3)] [MASS=242917]/Carbamoylphosphate synthetase 2-aspartate transcarbamylase-dihydroorotase, a trifunctional enzyme that catalyzes the first three steps of pyrimidine biosynthesis
SW:MAPB_HUMAN	MAP1B	11	4	1.47	0.30	SW:MAPB_HUMAN P46821 homo sapiens (human). microtubule-associated protein 1b [contains: map1 light chain lc1]. 7/1999 [MASS=270620]/MAP1B
SW:TPMN_HUMAN	TPM4	11	6	1.47	0.30	SW:TPMN_HUMAN P12324 homo sapiens (human). tropomyosin, cytoskeletal type (tm30-nm). 7/1999 [MASS=29033]/Tropomyosin 4, a member of a family of actin filament binding proteins involved in a variety of cytoskeletal-related functions; fusion of the gene with ALK has been seen in inflammatory myofibroblastic tumors
SW:CAS_HUMAN	CSE1L	24, 36	3	1.46	0.18	SW:CAS_HUMAN P55060 homo sapiens (human). cellular apoptosis susceptibility protein. 11/1997 [MASS=110314]/CSE1 chromosome segregation 1-like (yeast), importin-alpha nuclear export receptor, functions in toxin and TNF resistance and apoptosis, may regulate cell proliferation; corresponding gene is amplified in breast and colon carcinoma cell lines
SW:OBRG_HUMAN	LEPR	18, 41	1	1.46	0.00	SW:OBRG_HUMAN O15243 homo sapiens (human). leptin receptor gene-related protein (ob-r gene related protein) (ob- rgrp). 7/1999 [MASS=14254]/Leptin receptor, member of the gp130 (IL6ST) cytokine-receptor family, signals through the JAK/STAT cascade and functions in regulation of appetite, body fat, bone formation, and reproduction; mutations in the gene cause obesity and pituitary dysfunction
SW:KU86_HUMAN	XRCC5	12, 14, 40	6	1.46	0.36	SW:KU86_HUMAN P13010 h atp-dependent dna helicase ii, 80 kda subunit (lupus ku autoantigen protein p86) (ku86) (ku80) (86 kda subunit of ku antigen) (thyroid- lupus autoantigen) (tlaa) (ctc box binding [MASS=82573]/X-ray repair complementing defective repair in Chinese hamster cells 5, binds ds-DNA free ends, binds Ku70 (G22P1) to regulate DNA-PK, involved in DNA repair, V(D)J recombination, cell adhesion, and enzyme activation, may play a role in tumor progression
SW:ATNB_HUMAN	ATP1B1	42	23	1.46	0.36	SW:ATNB_HUMAN P05026 homo sapiens (human). sodium/potassium-transporting atpase beta-1 chain (sodium/potassium-dependent atpase beta-1 subunit). 7/1999 [MASS=35061]/Beta 1 subunit of Na+:K+-ATPase, a putative sodium:potassium-exchanging ATPase

SW:ACPM_HUMAN	NDUFAB1	18	3	1.46	0.23	SW:ACPM_HUMAN O14561 homo sapiens (human). acyl carrier protein, mitochondrial precursor (acp) (nadh-ubiquinone oxidoreductase 9.6 kda subunit) (ec 1.6.5.3) (ec 1.6.99.3) (ci-sdap). 5/2000 [MASS=14806]/NADH-ubiquinone oxidoreductase subunit of alpha-beta subcomplex 1 (8 kD), a probable acyl carrier component of the multiprotein complex that transports electrons from NADH to ubiquinone, present within the hydrophobic fraction of complex I
GP:AF037448_1	NSAP1	24, 25, 37, 38	4	1.45	0.22	GP:AF037448_1 Homo sapiens RRM RNA binding protein Gry-rbp (GRY-RBP) mRNA, complete cds; RRM RNA binding protein; Glycine, arginine and tyrosine-rich at C-terminus. [MASS=69633]/NS1 associated protein 1, component of the ApoB mRNA editosome involved in apolipoprotein B (APOB) mRNA editing, may bind RNA, may play a role in the regulation of mRNA splicing or transport from the nucleus
GP:AF149418_1	SLC4A4	42	1	1.45	0.00	GP:AF149418_1 Oryctolagus cuniculus duodenal sodium bicarbonate cotransport protein NBC1 mRNA, complete cds; transmembrane protein; belongs to the functional superfamily of HCO3- transporters; similar to human and mouse pancreatic NBC1 proteins. [MASS=121427]/Solute carrier family 4 (sodium bicarbonate cotransporter) member 4, acts in cellular pH regulation and maintenance of cornea and lens transparency and intraocular pressure; mutations cause proximal renal tubular acidosis with ocular abnormalities
SW:TXTP_HUMAN	SLC25A1	42	2	1.45	0.00	SW:TXTP_HUMAN P53007 homo sapiens (human). tricarboxylate transport protein precursor (citrate transport protein) (ctp) (tricarboxylate carrier protein). 5/2000 [MASS=34085]/Solute carrier family 25 (mitochondrial carrier citrate transporter) member 1, a putative mitochondrial membrane citrate transporter; gene is localized to a region deleted in DiGeorge:velocardiofacial syndromes
SW:PRTP_HUMAN	PPGB	32	2	1.45	0.04	SW:PRTP_HUMAN P10619 homo sapiens (human). lysosomal protective protein precursor (ec 3.4.16.5) (cathepsin a) (carboxypeptidase c). 12/1998 [MASS=54496]/Protective protein for beta-galactosidase (cathepsin A), has serine carboxypeptidase activity, forms a complex with beta galactosidase (GLB1) and neuraminidase (NEU1), facilitates NEU1 transport and activation; genetic mutation leads to galactosialidosis
SW:KCRU_HUMAN	CKMT1	18	6	1.45	0.16	SW:KCRU_HUMAN P12532 homo sapiens (human). creatine kinase, ubiquitous mitochondrial precursor (ec 2.7.3.2) (u- mtck) (mia-ck) (acidic-type mitochondrial creatine kinase). 7/1999 [MASS=47037]/Mitochondrial creatine kinase 1 (ubiquitous), mitochondrial isoform that has a probable role in the phosphocreatine shuttle, plays a role in energy pathways; inactivation is involved in anthracycline cardiotoxicity
SW:GST1_HUMAN	MGST1	10	13	1.45	0.34	SW:GST1_HUMAN P10620 homo sapiens (human). microsomal glutathione s-transferase 1 (ec 2.5.1.18) (microsomal gst- 1). 5/2000 [MASS=17599]/Microsomal glutathione S-transferase 1, may play a role in protection against oxidative stress
SW:RSP4_HUMAN	LAMR1	6, 35, 41	7	1.44	0.05	SW:RSP4_HUMAN P08865 homo sapiens (human). 40s ribosomal protein sa (p40) (34/67 kda laminin receptor) (colon carcinoma laminin-binding protein) (nem/1chd4). 5/2000 [MASS=32854]/Laminin receptor 1, a ribosomal protein of the small 40S ribosomal subunit, plays a role in cancer cell and basement membrane glycoprotein laminin interactions during tumor invasion and metastasis, expression correlates with cancer cell aggressiveness
GP:U85625_1	RNASE6PL	25, 39	3	1.44	0.04	GP:U85625_1 Homo sapiens ribonuclease 6 precursor, mRNA, complete cds. [MASS=29481]/Ribonuclease 6 precursor, a putative ribonuclease that plays a role in the negative regulation of proliferation, may be involved in senescence, may be a class II tumor suppressor, downregulated in ovarian cancer and in ovarian cancer cell lines
GP:AB033078_1	SGPL1	19, 41	2	1.44	0.06	GP:AB033078_1 Homo sapiens mRNA for KIAA1252 protein, partial cds; Start codon is not identified.. [MASS=64962]/Protein with strong similarity to sphingosine phosphate lyase 1 (mouse Sgpl1), which is a member of the carbon-carbon lyase subclass of aldehyde-lyases that catalyzes cleavage of sphingosine phosphate and is involved in proliferative signal transduction
GP:AL096857_1	hypothetical protein	45	2	1.44	0.15	GP:AL096857_1 Novel human mRNA from chromosome 1, which has similarities to BAT2 genes. [MASS=295830]
SW:GBLP_HUMAN	GNB2L1	41	13	1.44	0.51	SW:GBLP_HUMAN P25388 homo sapiens (human), mus musculus (mouse), rattus norvegicus (rat), sus scrofa (pig), and gallus gallus guanine nucleotide-binding protein beta subunit-like protein 12.3 (p205) (re [MASS=35077]/Guanine nucleotide binding protein beta 2 related sequence 1, protein kinase C (PKC) anchoring system subunit, homologous to G protein beta subunits, deficit is associated with impaired activation of PKC in the aging brain, contributing to Alzheimers
SW:IF39_HUMAN	EIF3S9	35	5	1.44	0.20	SW:IF39_HUMAN P55884 homo sapiens (human). eukaryotic translation initiation factor 3 subunit 9 (eif-3 eta) (eif3 p116) (eif3 p110). 5/2000 [MASS=92492]/Eukaryotic translation initiation factor 3 subunit (EIF3 subunit eta), the 116 kDa subunit of the EIF3 complex that plays a role in protein synthesis initiation
SW:RL2A_HUMAN	RPL27A	35	7	1.44	0.56	SW:RL2A_HUMAN P46776 homo sapiens (human). 60s ribosomal protein l27a. 5/2000 [MASS=16430]/Ribosomal protein L27a, component of the large 60S ribosomal subunit; gene is abnormally expressed in colorectal carcinomas
SW:AAC1_HUMAN	ACTN1	11	12	1.44	1.22	SW:AAC1_HUMAN P12814 homo sapiens (human). alpha-actinin 1, cytoskeletal isoform (f-actin cross linking protein). 11/1997 [MASS=102974]/Alpha-actinin isoform 1, a non-muscle cell actin-binding protein that interacts with collagen (human COL17A1) and functions in actin filament stabilization, may play a role in cell shape control
PIR2:T02673	HNRPR	25, 37	3	1.43	0.18	no_description_avail/Heterogeneous nuclear ribonucleoprotein R, a putative pre-mRNA processing protein that contains three RNA recognition domains and an RGG domain, interacts with survival motor neuron protein and is an autoantigen in autoimmune disease
SW:CTOG_HUMAN	KIAA0097	20, 23	4	1.43	0.10	SW:CTOG_HUMAN Q14008 homo sapiens (human). ch-tog protein (colonic and hepatic tumor over-expressed protein) (kiaa0097). 5/2000 [MASS=225509]/Microtubule-associated protein that promotes rapid plus end microtubule assembly necessary for mitotic spindle assembly

SW:PPOL_HUMAN	ADPRT	10, 12, 14, 29, 34	2	1.43	0.42	SW:PPOL_HUMAN P09874 homo sapiens (human). poly [adp-ribose] polymerase (ec 2.4.2.30) (parp) (adprt) (nad(+) adp-ribosyltransferase) (poly[adp-ribose] synthetase). 11/1997 [MASS=112953]/ADP-ribosyltransferase, catalyzes formation of ADP ribose polymers attached to proteins using NAD(+) as substrate in response to DNA damage, modulates chromatin structure and plays a role in DNA repair and apoptosis
GP:AF157325_1	EPLIN	45	5	1.43	0.39	GP:AF157325_1 Homo sapiens sterol regulatory element binding protein 3 (SREBP3) mRNA, complete cds. [MASS=51277]/Epithelial protein lost in neoplasm, a component of actin cytoskeleton, exists as alternative splice forms alpha and beta, and contributes to cell growth regulation; downregulation of EPLIN alpha may promote cancer progression
GP:AF177377_1	EML4	45	1	1.43	0.00	GP:AF177377_1 Homo sapiens cytoplasmic protein mRNA, complete cds; 120kDa; strongly overexpressed during mitosis. [MASS=108903]/Restrictedly overexpressed proliferation-associated protein, a cytoplasmic protein containing WD repeats and a serine protease motif, highly expressed only during mitosis
GP:AK022722_1	FLJ12660	45	1	1.43	0.00	GP:AK022722_1 Homo sapiens cDNA FLJ12660 fis, clone NT2RM4002174, moderately similar to MRP PROTEIN; unnamed protein product. [MASS=31130]/Protein of unknown function, has high similarity to uncharacterized C. albicans Orf6.5982p
PIR2:I38026	TRAF4	41	2	1.43	0.18	PIR2:I38026 MLN 62 protein - human [MASS=53444]/TNF receptor-associated factor 4, a member of a family of proteins that interact with the cytoplasmic domain of TNF receptors, plays a role in apoptosis, may function in TNF-related signal transduction associated with breast cancer
SW:AOPP_HUMAN	PRDX5	10	4	1.43	0.25	SW:AOPP_HUMAN P30044 homo sapiens (human). putative peroxisomal antioxidant enzyme (liver tissue 2d-page spot 71b). 12/1998 [MASS=16864]/Peroxiredoxin 5, catalyzes the reduction of hydrogen peroxide through Cys sulfhydryl group oxidation and reduction by thioredoxin, may be involved in oxidative stress and inflammatory responses, may contribute to tendon degeneration during aging
SW:SYN_HUMAN	NARS	2, 35, 37	4	1.42	0.19	SW:SYN_HUMAN O43776 homo sapiens (human). asparaginyl-trna synthetase, cytoplasmic (ec 6.1.1.22) (asparagine-- trna ligase) (asnrs). 5/2000 [MASS=62943]/Asparaginyl-tRNA synthetase, a class II aminoacyl tRNA synthetase, aminoacylates its cognate tRNAs with asparagine for protein biosynthesis, acts as an autoantigen in patients with inflammatory myopathy in interstitial lung disease
SW:OCRL_HUMAN	OCRL	16, 19, 41	2	1.42	1.00	SW:OCRL_HUMAN Q01968 homo sapiens (human). lowe's oculocerebrorenal syndrome protein. 7/1998 [MASS=111485]/Oculocerebrorenal syndrome of Lowe, phosphatidylinositol-4,5-bisphosphate 5-phosphatase, may play a role in intracellular protein trafficking; mutation of the corresponding gene causes Lowe oculocerebrorenal syndrome
GP:U52426_1	STIM1	45	5	1.42	0.34	GP:U52426_1 Homo sapiens GOK (STIM1) mRNA, complete cds. [MASS=77492]/Stromal interaction molecule 1, a protein involved in both positive and negative control of cell proliferation; loss of expression is associated with rhabdomyosarcoma and may be involved in Beckwith Wiedemann syndrome
SW:MCP_HUMAN	MCP	44	3	1.42	0.95	SW:MCP_HUMAN P15529 homo sapiens (human). membrane cofactor protein precursor (cd46 antigen) (trophoblast leucocyte common antigen) (tlx). 5/2000 [MASS=42248]/Membrane cofactor protein (CD46), a cofactor for factor I-mediated cleavage of C3B and C4B, a T-cell coactivator with signal transduction properties, and a receptor for viruses and bacteria, protects host cells against complement-mediated cytolysis
GP:AF035959_1	PPAP2C	19	1	1.42	0.00	GP:AF035959_1 Homo sapiens type-2 phosphatidic acid phosphatase-gamma (PAP2-g) mRNA, complete cds; phosphatidate phosphohydrolase; phospholipid phosphatase. [MASS=32574]/Phosphatidic acid phosphatase 2c, hydrolyzes phospholipids, may play a role in signal transduction
GP:AF055016_1	CLLD6	45	2	1.41	0.64	GP:AF055016_1 Homo sapiens clone 24774 unknown mRNA, partial cds. [MASS=23711]/Protein containing a SPRY (SPla and RYanodine Receptor) domain, has high similarity to uncharacterized C. elegans F18H3.1
GP:S82470_1	LENG4	45	4	1.41	0.09	GP:S82470_1 BB1=malignant cell expression-enhanced gene/tumor progression-enhanced gene [human, UM-UC-9 bladder carcinoma cell line, mRNA, 1897 nt]; malignant cell expression-enhanced gene/tumor progression-enhanced gene; This sequence comes from Fig. 4A. [MASS=38164]/Member of the membrane bound O-acyl transferase (MBOAT) family, which are found in acyltransferase enzymes
GPN:AF305686_1	NJMU-R1	45	2	1.41	0.03	no_description_avail/Protein of unknown function
SW:THIO_HUMAN	TXN	41	1	1.41	0.00	SW:THIO_HUMAN P10599 homo sapiens (human). thioredoxin (atl-derived factor) (adf) (surface associated sulphydryl protein) (sasp). 7/1998 [MASS=11606]/Thioredoxin, has dithiol-disulfide oxidoreductase activity and is upregulated in activated monocytes and in established dividing cell lines, promotes neutrophil migration
SW:ROM_HUMAN	HNRPM	36	2	1.41	0.23	SW:ROM_HUMAN P52272 homo sapiens (human). heterogeneous nuclear ribonucleoprotein m (hnrnp m). 10/1996 [MASS=77469]/Heterogeneous nuclear ribonucleoprotein M, initiates recycling of internalized immature thyroglobulin for further processing through the Golgi back to the apical membrane
SW:EFTU_HUMAN	TUFM	35	8	1.41	0.11	SW:EFTU_HUMAN P49411 homo sapiens (human). elongation factor tu, mitochondrial precursor (p43). 12/1998 [MASS=49542]/Tu translation elongation factor (mitochondrial), a putative translation elongation factor, may be involved in protein biosynthesis, upregulated in some tumors
SW:EBI2_HUMAN	EBI2	41, 44	1	1.40	0.00	SW:EBI2_HUMAN P32249 homo sapiens (human). ebv-induced g protein-coupled receptor 2 (ebi2). 7/1998 [MASS=41224]/Epstein-Barr virus induced gene 2, a lymphocyte specific G protein-coupled receptor that may mediate the effects of Epstein-Barr virus on B lymphocytes
GP:AK000512_1	C1orf27	45	1	1.40	0.00	GP:AK000512_1 Homo sapiens cDNA FLJ20505 fis, clone KAT09459; unnamed protein product. [MASS=37773]/Protein of unknown function
SW:RL30_HUMAN	RPL30	45	27	1.40	0.25	SW:RL30_HUMAN P04645 homo sapiens (human), rattus norvegicus (rat), and mus musculus (mouse). 60s ribosomal protein l30. 2/1995 [MASS=12653]/Ribosomal protein L30, a putative component of the large 60S ribosomal subunit
SW:LONM_HUMAN	PRSS15	32	4	1.40	0.68	SW:LONM_HUMAN P36776 homo sapiens (human). mitochondrial lon protease homolog precursor (ec 3.4.21.-). 11/1995 [MASS=106467]/Protease serine 15, an ATP-dependent mitochondrial peptidase that binds single-stranded DNA and may play a role in the regulation of mitochondrial DNA replication and gene expression

SWN:ARVC_HUMAN	ARVCF	6	4	1.40	0.33	SWN:ARVC_HUMAN O00192 homo sapiens (human). armadillo repeat protein deleted in velo-cardio-facial syndrome. 8/2001 [MASS=104642]/Armadillo repeat gene deleted in velocardiofacial syndrome, binds cadherins and may play a role in cell adhesion at the adherens junction; hemizygosity of the corresponding gene is associated with velocardiofacial syndrome
GP:AB000095_1	SPINT1	45	7	1.39	0.22	no_description_avail/Serine protease inhibitor (Kunitz type 1), a Kunitz type serine protease inhibitor that may inhibit hepatocyte growth factor activator (HGFAC), involved in the progression of hepatocellular carcinoma, downregulated in colorectal adenocarcinomas
SW:SAP3_HUMAN	GM2A	19	3	1.39	0.14	SW:SAP3_HUMAN P17900 homo sapiens (human). ganglioside gm2 activator precursor (cerebroside sulfate activator protein) (shingolipid activator protein 3) (sap-3). 7/1999 [MASS=20822]/GM2 ganglioside activator protein, binds glycolipids and is a cofactor for GM2 ganglioside hydrolysis by beta hexosaminidase A, activates phospholipase D, and inhibits platelet activating factor; mutation of the gene causes GM2-gangliosidosis variant AB
SW:UTX_HUMAN	UTX	17	1	1.39	0.00	SW:UTX_HUMAN O15550 homo sapiens (human). ubiquitously transcribed x chromosome tetratricopeptide repeat protein (ubiquitously transcribed tpr protein on the x chromosome). 7/1999 [MASS=154232]/Protein that has very strong similarity to murine Utx, which contains tetratricopeptide repeats and is widely transcribed; corresponding gene is found on X chromosomes and escapes X-inactivation
PIR2:T13159	E1B-AP5	24, 25, 37	3	1.38	0.41	PIR2:T13159 E1B-55kDa-associated protein - human [MASS=95810]/E1B-55kDa-associated protein 5, a heterogeneous nuclear ribonucleoprotein involved in nucleocytoplasmic transport of adenovirus and cellular mRNAs, binds adenovirus early 1B (E1B-55 kD) protein and may regulate viral oncogenic transformation
SW:R10A_HUMAN	RPL10A	16, 35	1	1.38	0.00	SW:R10A_HUMAN P53025 homo sapiens (human). 60s ribosomal protein l10a (csa-19). 10/1996 [MASS=24859]/Ribosomal protein L10a, a component of the large 60S ribosomal subunit; expression in the thymus is downregulated by cyclosporin-A
GP:D87116_1	MAP2K3	10, 34, 41	3	1.38	0.17	GP:D87116_1 Human mRNA for MAP kinase kinase 3b ,complete cds; MKK3b. [MASS=39318]/Mitogen activated protein kinase kinase 3, phosphorylates MAP kinase p38, involved in stress and inflammatory responses, senescence, and apoptosis, also has roles in ischemic kidney injury, and H. influenzae infection
SW:HEPS_HUMAN	HPN	45	2	1.38	0.65	SW:HEPS_HUMAN P05981 homo sapiens (human). serine protease hepsin (ec 3.4.21.-) (transmembrane protease, serine 1). 11/1997 [MASS=45011]/Hepsin, a transmembrane serine protease implicated in cell growth control and initiation of blood coagulation; overexpressed in prostate and ovarian tumors
SW:R27A_HUMAN	RPS27A	35	3	1.38	0.38	SW:R27A_HUMAN P14798 homo sapiens (human), and cavia porcellus (guinea pig). 40s ribosomal protein s27a. 5/2000 [MASS=9418]/Ribosomal protein S27a, component of the small ribosomal subunit, consists of ubiquitin at the N-terminus and ribosomal protein S27a at the C-terminus; overexpressed in colon and renal cancers
SW:ROF_HUMAN	HNRPF	25, 37	3	1.37	0.10	SW:ROF_HUMAN P52597 homo sapiens (human). heterogeneous nuclear ribonucleoprotein f (hnrnp f). 11/1997 [MASS=45672]/Heterogeneous nuclear ribonucleoprotein F, an RNA binding protein which contains quasi-RRMs (RNA recognition motifs) and plays a role in pre-mRNA splicing
GP:AC007055_5	unknown	45	1	1.37	0.00	GP:AC007055_5 Homo sapiens chromosome 14 clone BAC 201F1 map 14q24.3, complete sequence; unknown; This gene is predicted by Genscan and supported by ESTs AA836348 and AI077817. The closes. [MASS=35283]
GP:AF030291_1	MCG4	45	3	1.37	0.38	no_description_avail/Zinc-finger protein-like 1, a putative transcription regulator with zinc-finger-like domains and leucine-zipper-like motifs, expressed strongly (and perhaps exclusively) in the exocrine (but not the endocrine) pancreas
GP:AF059524_1	RTN3	45	3	1.37	0.05	no_description_avail/Reticulon 3, member of the reticulon (neuroendocrine-specific, NSP) family of proteins that associate with the endoplasmic reticulum, most highly expressed in brain
GP:AJ131186_1	NMP200	45	1	1.37	0.00	GP:AJ131186_1 Homo sapiens mRNA for nuclear matrix protein NMP200; related to splicing factor PRP19. [MASS=55181]/Protein containing six WD domains (WD-40 repeats), which may mediate protein-protein interactions, has weak similarity to non-snRNP spliceosome component (S. cerevisiae Prp19p), which is involved in mitotic recombination and gene conversion
PIR2:T12456	LOC152502	45	4	1.37	0.08	PIR2:T12456 hypothetical protein DKFZp564M2423.1 - human [MASS=42427]
SW:RBP2_HUMAN	RANBP2	45	3	1.37	0.58	SW:RBP2_HUMAN P49792 homo sapiens (human). ran-binding protein 2 (nuclear pore complex protein nup358) (nucleoporin nup358) (358 kda nucleoporin) (p270). 5/2000 [MASS=358218]/RAN binding protein 2, binds RAN-GTP at the cytoplasmic face of nuclear pores, also functions as a chaperone for red and green opsin molecules
SW:TM21_HUMAN	TMP21	43	3	1.37	0.60	SW:TM21_HUMAN P49755 homo sapiens (human). transmembrane protein tmp21 precursor (s31iii125) (s31i125). 12/1998 [MASS=24976]/Transmembrane protein Mr 21,000, involved in biosynthetic protein transport from the ER to Golgi, regulates Rac-GTP levels through interaction with beta 2-chimaerin (CHN2); corresponding gene is located in the AD3 region mutated in Alzheimer's Disease
GP:AB020880_1	SART3	37	5	1.37	0.17	GP:AB020880_1 Homo sapiens mRNA for squamous cell carcinoma antigen SART-3, complete cds; squamous cell carcinoma antigen recognized by T cells. [MASS=109935]/Squamous cell carcinoma antigen recognized by T-cells 3, a snRNA binding protein that functions in spliceosome reassembly, acts as a tumor antigen recognized by cytotoxic T lymphocytes, may be a target for immunotherapy in a number of cancers
SW:IVD_HUMAN	IVD	2	1	1.37	0.00	SW:IVD_HUMAN P26440 homo sapiens (human). isovaleryl-coa dehydrogenase precursor (ec 1.3.99.10) (ivd). 7/1998 [MASS=46319]/Mitochondrial isovaleryl-CoA dehydrogenase, catalyzes the conversion of isovaleryl-CoA to 3-methylcrotonyl-CoA in leucine metabolism; deficiency causes isovaleric acidemia
SW:KG3B_HUMAN	GSK3B	5, 18, 41	1	1.36	0.00	SW:KG3B_HUMAN P49841 homo sapiens (human). glycogen synthase kinase-3 beta (ec 2.7.1.37) (gsk-3 beta). 7/1999 [MASS=46768]/Glycogen synthase kinase-3 beta, a serine threonine protein kinase that phosphorylates several cytoplasmic and nuclear proteins, involved in embryonic development, and may hyperphosporylate tau (MAPT) in

SW:SERA_HUMAN	PHGDH	2, 16	44	1.36	0.41	SW:SERA_HUMAN O43175 homo sapiens (human). d-3-phosphoglycerate dehydrogenase (ec 1.1.1.95) (pgdh). 7/1999 [MASS=56665]/3-phosphoglycerate dehydrogenase, enzyme that catalyzes the first step of serine biosynthesis which is the oxidation of 3-phosphoglycerate to 3-phosphohydroxypyruvate; mutation of the corresponding gene causes microcephaly, retardation, and seizures
SW:ECH1_HUMAN	ECH1	18, 19	28	1.36	0.24	SW:ECH1_HUMAN Q13011 homo sapiens (human). delta3,5-delta2,4-dienoyl-coa isomerase precursor (ec 5.3.3.-). 7/1999 [MASS=35994]/Enoyl Coenzyme A hydratase 1 (peroxisomal), putative enzyme that may play a role in peroxisomal beta-oxidation
GP:AB046774_1	KIAA1554	45	1	1.36	0.00	GP:AB046774_1 Homo sapiens mRNA for KIAA1554 protein, partial cds; Start codon is not identified.. [MASS=150426]/Protein containing a C3HC4 type (RING) zinc finger, which may mediate protein-protein interactions
GP:AF239727_1	MRPL39	45	1	1.36	0.00	no_description_avail/Protein of unknown function, has low similarity to a region of threonyl-tRNA synthetases
GP:AJ011129_1	LOC64148	45	2	1.36	0.16	GP:AJ011129_1 Homo sapiens mRNA for 17kD fetal brain protein; ORF1. [MASS=17218]/Member of the SCP-like extracellular protein family, has moderate similarity to a region of S. cerevisiae Pry3p, which shows daughter-specific expression and may have a role in mating efficiency
GP:U97519_1	PODXL	45	1	1.36	0.00	GP:U97519_1 Homo sapiens podocalyxin-like protein mRNA, complete cds. [MASS=55596]/Podocalyxin like, a transmembrane sialomucin that is an L selectin ligand and important for lymphocyte adhesion and homing
GP:AB037108_1	TPRA40	19	2	1.36	0.09	GP:AB037108_1 Homo sapiens mRNA for seven transmembrane domain orphan receptor, complete cds; seven transmembrane domain containing protein. [MASS=41090]/Protein with strong similarity to murine Tpra40, which is a seven transmembrane domain protein expressed in 3T3 adipocytes, and that has elevated expression in epididymal fat of genetically diabetic and obese mice
SW:GL6S_HUMAN	GNS	5	5	1.36	0.20	SW:GL6S_HUMAN P15586 homo sapiens (human). n-acetylglucosamine-6-sulfatase precursor (ec 3.1.6.14) (g6s) (glucosamine-6-sulfatase). 7/1998 [MASS=62082]/N-acetylglucosamine-6-sulfate sulfatase, an enzyme that hydrolyzes sulfate groups from glycosaminoglycans and is involved in the catabolism of heparan sulfate and keratan sulfate; deficiency causes Sanfilippo disease type D
GP:AB002377_1	KIAA0379	45	4	1.35	0.17	no_description_avail/Protein containing many ankyrin (Ank) repeats, which may mediate protein-protein interactions, has low similarity to a region of ankyrin (rat Ank3), which binds Na+/K+-ATPase and links integral membrane proteins to the cytoskeleton
GP:AF078860_1	MRPL42	45	2	1.35	0.14	GP:AF078860_1 Homo sapiens PTD007 mRNA, complete cds. [MASS=16661]/Mitochondrial ribosomal protein L42, component of the large ribosomal subunit
GP:AK000325_1	FLJ20318	45	2	1.35	0.22	GP:AK000325_1 Homo sapiens cDNA FLJ20318 fis, clone HEP08704; unnamed protein product. [MASS=62816]/Protein of unknown function
PIR2:T08787	TES	45	1	1.35	0.00	PIR2:T08787 probable testin DKFZp586B2022.1 - human (fragment) [MASS=15593]/Protein containing three LIM domains, has a region of low similarity to a region of four and a half LIM domains 2 (human FHL2), which is a apoptosis and transcription regulator that is downregulated in rhabdomyosarcoma cell lines
SW:Y041_HUMAN	CENTB2	45	1	1.35	0.00	SW:Y041_HUMAN Q15057 homo sapiens (human). hypothetical protein kiaa0041 (fragment). 7/1999 [MASS=71243]/Centaurin beta 2, a GTPase activating protein for ARF6, stimulated by phosphatidic acid and PIP2, and acts in the cell periphery to affect the actin cytoskeleton
GPN:AF191298_1	VPS35	43	7	1.35	0.49	Homo sapiens, vacuolar protein sorting 35/Maternal-embryonic 3, may be a component of the sorting machinery required for vesicle to Golgi retrieval
PIR2:S33377	CKAP4	43	5	1.35	0.22	PIR2:S33377 P63 protein - human [MASS=65793]/Cytoskeleton-associated protein 4, type II membrane protein of the endoplasmic reticulum, binds to microtubules and links them to the endoplasmic reticulum, promotes tubulin polymerization and endoplasmic reticulum reorganization
GP:AK001521_1	DIP13B	41	4	1.35	0.12	GP:AK001521_1 Homo sapiens cDNA FLJ10659 fis, clone NT2RP2006071; unnamed protein product. [MASS=36277]/Protein with unknown function, has high similarity to a region of APPL, an adaptor protein with a PH domain, a PTB domain and a leucine zipper motif, and which binds to AKT2 and PI3 kinase catalytic subunit p110alpha
SW:RLA0_HUMAN	RPLP0	35	14	1.35	0.20	SW:RLA0_HUMAN P05388 homo sapiens (human). 60s acidic ribosomal protein p0 (l10e). 5/2000 [MASS=34274]/Ribosomal protein P0, acidic phosphoprotein component of the large 60S ribosomal subunit; shows increased expression in hepatocellular and colon carcinomas
GP:AB032179_1	EHM2	11	1	1.35	0.00	GP:AB032179_1 Homo sapiens EHM2 mRNA, complete cds; similar to mouse Ehm2. [MASS=58628]/Protein containing two FERM (Band 4.1) family domains, which link cytoplasmic proteins to membranes, has low similarity to myosin regulatory light chain interacting protein (human MIR), which may be linked to mental retardation
SW:OGT1_HUMAN	OGT	26, 34, 41	1	1.34	0.00	SW:OGT1_HUMAN O15294 homo sapiens (human). udp-n-acetylglucosamine--peptide n-acetylglucosaminyltransferase 100 kda subunit (ec 2.4.1.-) (o-glcnac transferase p100 subunit). 5/2000 [MASS=103012]/O-linked N-acetylglucosamine transferase (UDP-N-acetylglucosamine:polypeptide-N-acetylglucosaminyltransferase), enzyme that functions in O-glycosylation, may be involved in insulin secretion and glucose homeostasis, may play a role in signal transduction
PIR2:T08769	KIAA0747	45	8	1.34	0.14	PIR2:T08769 hypothetical protein DKFZp586K011.1 - human (fragment) [MASS=81441]/Protein with strong similarity to rat Mbc2, which localizes to microsomes and plasma membranes and is expressed ubiquitously
GP:AJ001714_1	myo9a	11	1	1.34	0.00	GP:AJ001714_1 Homo sapiens mRNA for myosin-IXA. [MASS=90079]/Myosin IXA, a member of the unconventional myosin family that contains a GTPase activating protein (GAP) domain; the corresponding gene is a candidate for Bardet Biedl syndrome, characterized by mental retardation, obesity, and retinitis pigmentosa
SW:HMG1_HUMAN	HMG1	12, 40	3	1.33	0.21	SW:HMG1_HUMAN P09429 homo sapiens (human). high mobility group protein hmg1 (hmg-1). 5/2000 [MASS=24763]/High-mobility group (nonhistone chromosomal) protein 1, induces DNA bending, binds damaged DNA, activates and represses transcription, involved in the DNA damage response and V(D)J recombination, may be a target for therapeutic intervention of sepsis

GP:U85946_1	SEC10L1	43	5	1.33	0.11	GP:U85946_1 Homo sapiens brain secretory protein hSec10p (HSEC10) mRNA, complete cds; similar to S. cerevisiae Sec10p. [MASS=81853]/SEC10 (S. cerevisiae)-like 1, a component of the exocyst complex, involved in the synthesis and delivery of secretory proteins in epithelial cells, involved in the development of epithelial cysts and tubules
GPN:AF293383_1	ABCF1	35	1	1.33	0.00	ATP-binding cassette subfamily F member 1, a member of the ATP-binding cassette family that does not contain a transmembrane domain and may play a role in translation
SW:RS11_HUMAN	RPS11	35	8	1.33	0.07	SW:RS11_HUMAN P04643 homo sapiens (human), rattus norvegicus (rat), and mus musculus (mouse). 40s ribosomal protein s11. 5/2000 [MASS=18431]/Ribosomal protein S11, putative component of the small 40S ribosomal subunit
PIR2:I59405	TCEB2	29, 31, 32	2	1.32	0.00	PIR2:I59405 RNA polymerase II transcription factor SIII p18 subunit - human [MASS=13133]/Transcription elongation factor B (SIII) polypeptide 2, a subunit of the elongin complex that facilitates RNA polymerase II elongation, component of a ubiquitin ligase complex that stabilizes and enhances the tumor suppressor action of the VHL protein
SW:ERF1_HUMAN	ETF1	35	1	1.32	0.00	SW:ERF1_HUMAN P46055 homo sapiens (human), mesocricetus auratus (golden hamster), and oryctolagus cuniculus (rabbit). eukaryotic peptide chain release factor subunit 1 (erf1) (tb3-1) (c11 protein). 5/20 [MASS=49031]/ Eukaryotic translation termination factor 1, an RNA binding translation release factor involved in translation termination, expression is increased in H. pylori infected gastric cancer cells; may be candidate gene for certain malignant myeloid diseases
SW:RL5_HUMAN	RPL5	35	7	1.32	0.51	SW:RL5_HUMAN P46777 homo sapiens (human). 60s ribosomal protein l5. 7/1999 [MASS=34317]/Ribosomal protein L5, a putative component of the 60S ribosomal subunit, binds 5S rRNA, undergoes nuclear export, may play a role in rev-mediated HIV-1 RNA nucleocytoplasmic transport; expression is altered in colorectal cancer and astrocytomas
SW:DDXY_HUMAN	DBY	16	2	1.32	0.05	SW:DDXY_HUMAN O15523 homo sapiens (human). dead box protein 3, y-chromosomal. 7/1999 [MASS=73095]/DEAD/H box polypeptide Y chromosome, a putative ATP-dependent RNA helicase, plays a role in spermatogenesis; deletion of the corresponding gene is associated with male infertility
SW:SAP_HUMAN	PSAP	19, 42	14	1.31	0.91	SW:SAP_HUMAN P07602 h proactivator polypeptide precursor [contains: saposin a (protein a); saposin b (sphingolipid activator protein 1) (sap-1) (dispersin) (sulfatide/gm1 activator); saposin c (co-beta- [MASS=58113]/Prosaposin, precursor of saposins A, B, C, and D which transport gangliosides and activate sphingolipid hydrolysis, stimulates neurite growth and inhibits apoptosis; variants are associated with metachromatic leukodystrophy and Gaucher disease
PIR2:JC5938	Txnl	18, 34, 41	2	1.31	0.01	PIR2:JC5938 thioredoxin-like protein - human [MASS=32251]/Thioredoxin-like 32, a thioredoxin related protein that has thioredoxin-like reducing activity
SW:D3D2_HUMAN	DCI	18, 19	3	1.31	0.20	SW:D3D2_HUMAN P42126 homo sapiens (human). 3,2-trans-enoyl-coa isomerase, mitochondrial precursor (ec 5.3.3.8) (dodecenoyl-coa delta-isomerase). 7/1999 [MASS=32816]/Dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenzyme A isomerase), catalyzes the isomerization of 3-cis and 3-trans enoyl CoA esters to 2-trans enoyl CoA esters, functions in mitochondrial beta-oxidation of unsaturated fatty acids
GP:AF161380_1	Mrpl38	45	1	1.31	0.00	GP:AF161380_1 Homo sapiens HSPC262 mRNA, partial cds. [MASS=20619]
SW:DDX3_HUMAN	DDX3	45	14	1.31	0.36	SW:DDX3_HUMAN O00571 homo sapiens (human). dead box protein 3 (helicase-like protein 2) (hlp2) (dead box, x isoform). 7/1999 [MASS=73243]/DEAD box protein 3, a member of the DEAD/H box ATP-dependent RNA helicase protein family, interacts with Hepatitis C virus core protein; corresponding gene is found on X chromosomes and escapes X-inactivation
GP:AF144700_1	TIMM13A	36	5	1.31	0.20	SW:I13A_HUMAN Q9uhl8 homo sapiens (human), mus musculus (mouse), and rattus norvegicus (rat). mitochondrial import inner membrane translocase subunit tim13 a. 10/2001 [MASS=10458]/Translocase of the mitochondrial inner membrane 13, a mitochondrial translocase subunit that oligomerizes with DDP1 (human TIMM8A) and mediates the translocation of the Tim23 (human TIM23) precursor across the outer mitochondrial membrane
SW:DHE3_HUMAN	GLUD1	2	8	1.31	0.24	SW:DHE3_HUMAN P00367 homo sapiens (human). glutamate dehydrogenase 1 precursor (ec 1.4.1.3) (gdh). 5/2000 [MASS=61398]/Glutamate dehydrogenase, catalyzes the reversible deamination of L-glutamate into alpha-ketoglutarate, mitochondrial enzyme with role in neurotransmission; deficiency is associated with neurodegenerative disorders
SW:P2BA_HUMAN	PPP3CA	7, 29, 34, 41	3	1.30	0.16	SW:P2BA_HUMAN Q08209 homo sapiens (human). serine/threonine protein phosphatase 2b catalytic subunit, alpha isoform (ec 3.1.3.16) (calmodulin-dependent calcineurin a subunit, alpha isoform) (cam-prp cat [MASS=58688]/Calcineurin A alpha, catalytic subunit of calcium/calmodulin regulated protein phosphatase, regulates activity of transcription factors involved in signal transduction and growth control
SW:RCC_HUMAN	CHC1	7, 12, 24	2	1.30	0.00	SW:RCC_HUMAN P18754 homo sapiens (human). regulator of chromosome condensation (cell cycle regulatory protein). 7/1999 [MASS=44969]/Regulator of chromosome condensation 1, a chromatin-binding protein that functions as a guanine nucleotide exchange factor for RAN, plays roles in nucleocytoplasmic transport, mitotic spindle formation, and nuclear envelope assembly
SW:CPT1_HUMAN	CPT1A	18, 19	1	1.30	0.00	SW:CPT1_HUMAN P50416 homo sapiens (human). carnitine o-palmitoyltransferase i, mitochondrial liver isoform (ec 2.3.1.21) (cpt i) (cpti-l). 7/1999 [MASS=88429]/Liver carnitine palmitoyltransferase I, enzyme of long-chain fatty acid beta-oxidation pathway; mutations in the corresponding gene are associated with carnitine palmitoyltransferase I deficiency
GP:AB020694_1	KIAA0887	45	2	1.30	0.00	GP:AB020694_1 Homo sapiens mRNA for KIAA0887 protein, partial cds. [MASS=52421]/Protein containing a UBX domain, which are found in ubiquitin regulatory proteins
GP:U47924_19	C3f	45	2	1.30	0.07	GP:U47924_19 Human chromosome 12p13 sequence, complete sequence; similar to S. cerevisiae ORF YOR175c, encoded by GenBank Accession Number Z75083. [MASS=44122]/Member of the membrane bound O-acyl transferase (MBOAT) family, which are found in acyltransferase enzymes, has strong similarity to uncharacterized mouse Grcc3f
GP:AB037857_1	PTGFRN	41	10	1.30	0.21	GP:AB037857_1 Homo sapiens mRNA for KIAA1436 protein, partial cds; Start codon is not identified.. [MASS=102996]/Prostaglandin F2 alpha receptor regulatory protein, a putative transmembrane glycoprotein that copurifies with and negatively regulates the prostaglandin F2 alpha receptor by inhibiting ligand-binding

SW:RL23_HUMAN	RPL23	35	10	1.30	0.27	SW:RL23_HUMAN P23131 homo sapiens (human), rattus norvegicus (rat), and sus scrofa (pig). 60s ribosomal protein l23 (l17). 7/1999 [MASS=14865]/Ribosomal protein L23, a putative large ribosomal subunit component that is likely to play a role in protein biosynthesis
SW:RS21_HUMAN	RPS21	35	3	1.30	0.29	SW:RS21_HUMAN P35265 homo sapiens (human), and sus scrofa (pig). 40s ribosomal protein s21. 5/2000 [MASS=9111]/Ribosomal protein S21, component of the small 40S ribosomal subunit
SWN:DUSC_HUMAN	DUSP12	34	3	1.30	0.17	SWN:DUSC_HUMAN Q9uni6 homo sapiens (human). dual specificity protein phosphatase 12 (ec 3.1.3.48) (ec 3.1.3.16) (dual-specificity tyrosine phosphatase yvh1). 8/2001 [MASS=37687]/Dual specificity phosphatase 12, binds zinc via a zinc-finger motif in the carboxyl terminus, may play a role in cell growth; genetic variants may be associated with cancer susceptibility
SW:AR34_HUMAN	ARPC2	8, 11	2	1.29	0.38	SW:AR34_HUMAN O15144 homo sapiens (human). arp2/3 complex 34 kda subunit (p34-arc). 7/1998 [MASS=34333]/Actin related protein 2/3 complex subunit 2, component of the Arp2/3 complex, which is involved in assembly of the actin cytoskeleton, interacts directly with ARPC4, possibly as an early intermediate in Arp2/3 complex formation
PIR2:I37405	GALNT1	26, 34	4	1.29	0.30	PIR2:I37405 polypeptide N-acetylgalactosaminyltransferase (EC 2.4.1.41) - human [MASS=64733]/N-acetylgalactosaminyltransferase T1, enzyme that initiates O-glycosylation; inhibition affects the sensitivity of tumors cells to immune killer cells
SW:BCR_HUMAN	BCR	10, 34, 41	1	1.29	0.00	SW:BCR_HUMAN P11274 homo sapiens (human). breakpoint cluster region protein (ec 2.7.1.-). 7/1999 [MASS=142806]/Breakpoint cluster region, GTPase-activating protein for p21rac with serine/threonine kinase activity; translocation of the corresponding gene is associated with Philadelphia chromosome-positive chronic myeloid leukemia
GP:AF005888_1	NOC4	45	3	1.29	0.16	GP:AF005888_1 Homo sapiens COX4AL mRNA, complete cds. [MASS=23773]/Neighbor of COX4, ubiquitously expressed, contains potential binding sites for Sp1 and NRF-2/GABP
GP:AF116347_1	SMBP	45	5	1.29	0.23	SW:T9S3_HUMAN Q9hd45 homo sapiens (human). transmembrane 9 superfamily protein member 3 precursor (sm-11044 binding protein) (ep70-p-iso). 10/2001 [MASS=67888]/SM-11044 binding protein, member of the transmembrane protein 9 superfamily, a predicted integral membrane protein which has functional ligand binding properties
GPN:AL449244_1	Hypothetical protein PP2447	45	1	1.29	0.00	GPN:AK017745_1 Mus musculus 8 days embryo whole body cDNA, RIKEN full-length enriched library, clone:5730502D15:homolog to human DJ402G11.4 (NOVEL PROTEIN SIMILAR TO C. ELEGANS F38A5.2 (ISOFORM 2)) (FRAGMENT), full insert sequence; data source:SPTR, source key:Q9UG [MASS=46538]
GP:AF020202_1	UNC13	41	3	1.29	0.09	GP:AF020202_1 Homo sapiens Munc13 mRNA, complete cds; contains C2 domains; similar to R. norvegicus Munc13-2 encoded by GenBank Accession Number U24071. [MASS=180684]/UNC13 (C. elegans)-like, a diacylglycerol receptor that may function in a PKC-independent, diacylglycerol-activated signaling pathway that induces apoptosis, may be involved in renal cell injury in hyperglycemia
SW:TCPQ_HUMAN	CCT8	33	3	1.29	0.06	SW:TCPQ_HUMAN P50990 homo sapiens (human). t-complex protein 1, theta subunit (tcp-1-theta) (cct-theta) (kiaa0002). 5/2000 [MASS=59635]/Protein with very strong similarity to murine Mm.17989, which is the theta subunit of the cytosolic chaperonin containing TCP-1 that assists in the proper folding of tubulin, actin and centractin
SW:SODC_HUMAN	SOD1	10	5	1.29	0.18	SW:SODC_HUMAN P00441 homo sapiens (human). superoxide dismutase [cu-zn] (ec 1.15.1.1). 5/2000 [MASS=15805]/Copper zinc superoxide dismutase, an enzyme that catalyzes the dismutation of the superoxide radical to molecular oxygen and hydrogen peroxide; mutations are associated with some cases of familial amyotrophic lateral sclerosis
SW:ATC2_HUMAN	ATP2B2	6, 16, 42	9	1.28	0.35	SW:ATC2_HUMAN P16615 h sarcoplasmic/endoplasmic reticulum calcium atpase isoform 2 (ec 3.6.1.38) (calcium pump 2) (serca2) (sr ca(2+)-atpase 2) (calcium- transporting atpase sarcoplasmic reticulum type, [MASS=114757]/Sarcoplasmic reticulum Ca2+-ATPase 2 (slow twitch muscle, cardiac, and nonmuscle form), pumps calcium from the cytoplasm to the ER; reduced activity in the heart is implicated in dilated cardiomyopathy and gene mutations are associated with Darier disease
SW:UBCI_HUMAN	UBE2I	32, 34	2	1.28	0.02	SW:UBCI_HUMAN P50550 homo sapiens (human), mus musculus (mouse), and xenopus laevis (african clawed frog). ubiquitin-conjugating enzyme e2-18 kda (ec 6.3.2.19) (ubiquitin-protein ligase) (ubiquitin carr [MASS=18007]/Ubiquitin-conjugating enzyme E2I, member of the ubiquitin-conjugating enzyme family that catalyzes the ubiquitination of cellular proteins and marks them for degradation, may play roles in cell cycle progression and repair of TOP1-mediated DNA damage
SW:KAPA_HUMAN	PRKACA	16, 34, 41	2	1.28	0.55	SW:KAPA_HUMAN P17612 homo sapiens (human). camp-dependent protein kinase, alpha-catalytic subunit (ec 2.7.1.37) (pka c-alpha). 5/2000 [MASS=40458]/Catalytic subunit C alpha of cAMP-dependent protein kinase, plays a role in transcriptional regulation and may mediate suppression of apoptosis, may also serve as a tumor biomarker; alternative form C alpha 2 may play a role in sperm development
GP:AB037855_1	KIAA1434	45	1	1.28	0.00	GP:AB037855_1 Homo sapiens mRNA for KIAA1434 protein, partial cds; Start codon is not identified.. [MASS=76634]/Member of the glycerophosphoryl diester phosphodiesterase family, which are involved in lipid metabolism, contains a starch binding domain, which are found in glycosyl hydrolases, has low similarity to uncharacterized C. elegans T05H10.7
PIR2:T08729	DKFZp566H073	45	2	1.28	0.00	PIR2:T08729 RING zinc finger protein homolog DKFZp566H073.1 - human (fragment) [MASS=35718]/Protein containing a C3HC4 type (RING) zinc finger and a PA (protease associated) domain, has a region of moderate similarity to a region of RING finger protein 12 (mouse Rnf12), which is a corepressor of LIM that binds to LIM domains
SW:ACON_HUMAN	ACO2	5, 18	1	1.27	0.00	SW:ACON_HUMAN Q99798 homo sapiens (human). aconitate hydratase, mitochondrial precursor (ec 4.2.1.3) (citrate hydro-lyase) (aconitase). 5/2000 [MASS=85425]/Aconitase 2 mitochondrial (aconitate hydratase), catalyzes the conversion of citrate to cis-aconitate in the tricarboxylic acid cycle, may be involved in iron homeostasis; deficiency may be associated with lifelong exercise intolerence

GP:AK000330_1	FLJ20323	45	1	1.27	0.00	GP:AK000330_1 Homo sapiens cDNA FLJ20323 fis, clone HEP09648; unnamed protein product. [MASS=64016]/Protein containing three WD domains (WD-40 repeats), which likely mediate protein-protein interactions
SW:GBB1_HUMAN	GNB1	41	27	1.27	0.26	SW:GBB1_HUMAN P04901 homo sapiens (human), mus musculus (mouse), bos taurus (bovine), and canis familiaris (dog). guanine nucleotide-binding protein g(i)/g(s)/g(t) beta subunit 1 (transducin beta chain [MASS=37377]/Guanine nucleotide binding protein (G protein) beta 1, a component of heterotrimeric G protein complexes, plays a role in signal transduction
SW:MDHC_HUMAN	MDH1	18	4	1.27	0.10	SW:MDHC_HUMAN P40925 homo sapiens (human). malate dehydrogenase, cytoplasmic (ec 1.1.1.37). 5/2000 [MASS=36295]/Cytosolic malate dehydrogenase, part of the malate-aspartate shuttle where it putatively catalyzes the reduction of oxaloacetate to malate
GP:AF022728_1	DTNB	11	1	1.27	0.00	GP:AF022728_1 Homo sapiens beta-dystrobrevin (BDTN) mRNA, complete cds; member of the dystrophin gene family. [MASS=71356]/Beta-dystrobrevin, a member of the dystrobrevin subfamily within the dystrophin family of proteins, part of the syntrophin-associated protein complex
SW:CD81_HUMAN	CD81	6	2	1.27	0.06	SW:CD81_HUMAN P18582 homo sapiens (human), and pan troglodytes (chimpanzee). cd81 antigen (26 kda cell surface protein tapa-1). 5/2000 [MASS=25809]/CD81 antigen, member of the transmembrane 4 superfamily (TM4SF) that regulates lymphoma cell growth, may be involved in cell motility and the defense response, associates with integrins in the plasma membrane
SW:THIK_HUMAN	ACAA1	18, 19	15	1.26	0.25	SW:THIK_HUMAN P09110 homo sapiens (human). 3-ketoacyl-coa thiolase, peroxisomal precursor (ec 2.3.1.16) (beta-ketothiolase) (acetyl-coa acyltransferase) (peroxisomal 3-oxoacyl- coa thiolase). 7/1999 [MASS=44292]/Peroxisomal 3-oxoacyl-coenzyme A thiolase (peroxisomal 3-ketoacyl-Coenzyme A thiolase), functions in peroxisomal beta-oxidation of fatty acids, deficiency is associated with rhizomelic chondrodysplasia punctata (RCDP)
GP:AC005788_1	XPTP	45	4	1.26	0.20	GP:AC005788_1 Homo sapiens chromosome 19, cosmid R26652, complete sequence; protein tyrosine phosphatase sigma. [MASS=157056]
GP:AB028128_1	DPM3	5, 34	2	1.25	0.51	GP:AB028128_1 Homo sapiens DPM3 mRNA for dolichol-phosphate-mannose synthase, complete cds. [MASS=10080]/Dolichyl-phosphate mannosyltransferase subunit 3 (prostin 1), part of a complex that produces mannosyl donors for glycoconjugate biosynthesis, stabilizes DPM1 and is stabilized by DPM2; expression is associated with a lack of invasive potential in tumors
SW:SR09_HUMAN	SRP9	35, 36	7	1.25	0.29	SW:SR09_HUMAN P49458 homo sapiens (human). signal recognition particle 9 kda protein (srp9). 12/1998 [MASS=9981]/Signal recognition particle 9 kDa, a subunit of the signal recognition particle that forms the Alu RNA-binding protein and binds to Alu RNA with SRP14, involved in translocation of newly synthesized proteins across the membrane of the rough ER
SWN:SYFB_HUMAN	FRSB	2, 25, 35, 37	4	1.25	0.44	SWN:SYFB_HUMAN Q9nsd9 homo sapiens (human). phenylalanyl-trna synthetase beta chain (ec 6.1.1.20) (phenylalanine--trna ligase beta chain) (phers) (protein hspc173). 8/2001 [MASS=66130]/Phenylalanyl-tRNA synthetase beta-subunit, regulatory subunit that forms heterodimers with the catalytic alpha subunit (FARSL), involved in protein synthesis, may play a role in tumorigenic events
GP:AB046829_1	KIAA1609	45	1	1.25	0.00	GP:AB046829_1 Homo sapiens mRNA for KIAA1609 protein, partial cds; Start codon is not identified.. [MASS=52735]/Protein of unknown function
SW:PTPA_HUMAN	PPP2R4	45	2	1.25	0.01	SW:PTPA_HUMAN P18433 homo sapiens (human). protein-tyrosine phosphatase alpha precursor (ec 3.1.3.48) (r-ptp- alpha). 5/2000 [MASS=90600]/Phosphotyrosyl phosphatase activator, regulatory subunit of protein phosphatase 2A, involved in cell cycle control and may protect against oxidative DNA damage
SWN:UNRI_HUMAN	UNRIP	45	4	1.25	0.20	SWN:UNRI_HUMAN Q9y3f4 homo sapiens (human). unr-interacting protein (wd-40 repeat protein pt-wd). 8/2001 [MASS=38438]/Unr-interacting protein, has WD domain, interacts with unr (NR1H2) protein and may function in the transforming growth receptor signaling pathway; upregulated in breast cancer and may contribute to tumor progression
GPN:AF279372_1	ITPK1	41	3	1.25	0.11	GP:BC018192_1 Homo sapiens, inositol 1,3,4-triphosphate 5/6 kinase, clone MGC:21491 IMAGE:3867269, mRNA, complete cds. [MASS=45621]/Inositol 1,3,4-triphosphate 5-6 kinase, phosphorylates Ins(1,3,4)P3 to form Ins(1,3,4,5)P4 and Ins(1,3,4,6)P4, regulates inositol phosphate metabolism; variant form phosphorylates Ins(3,4,5,6)P4 to yield Ins(1,3,4,5,6)P5
SW:TRA2_HUMAN	TRAF2	41	2	1.25	0.26	SW:TRA2_HUMAN Q12933 homo sapiens (human). tnf receptor associated factor 2 (traf2) (tumor necrosis factor type 2 receptor associated protein 3). 5/2000 [MASS=55794]/TNF receptor-associated factor 2, interacts with and mediates tumor necrosis factor signaling through activation of NF-kappaB cascade, functions as an apoptosis inhibitor
GP:AF034544_1	DHCR7	19	6	1.25	0.30	GP:AF034544_1 Homo sapiens delta7-sterol reductase mRNA, complete cds; D7SR. [MASS=54516]/7-dehydrocholesterol reductase, catalyzes the reduction of the C7-C8 (delta 7) double bond of 7-dehydrocholesterol in the last step of cholesterol biosynthesis; mutations in the corresponding gene are associated with Smith-Lemli-Opitz
SW:NPL1_HUMAN	NAP1L1	7, 12, 15	1	1.24	0.00	SW:NPL1_HUMAN P55209 homo sapiens (human). nucleosome assembly protein 1-like 1 (nap-1 related protein). 10/1996 [MASS=45374]/Nucleosome assembly protein 1-like 1, member of the NAP/SET protein family, binds histones H2A and H2B, a histone chaperone that mediates assembly of nucleosomes, complex with histone acetyltransferase coactivator p300 (EP300) may stimulate transcription
SW:PI52_HUMAN	PIP5K2A	19, 41	1	1.24	0.00	SW:PI52_HUMAN P48426 homo sapiens (human). phosphatidylinositol-4-phosphate 5-kinase type ii alpha (ec 2.7.1.68) (pip5kii-alpha) (1-phosphatidylinositol-4-phosphate kinase) (ptdins(4)p-5-kinase b isofor [MASS=46193]/Phosphatidylinositol-4-phosphate 5-kinase type II, alpha, a member of a family of kinases responsible for the synthesis of PtdIns(4,5)P2

SW:DYL1_HUMAN	PIN	11, 16, 26	10	1.24	0.34	SW:DYL1_HUMAN Q15701 homo sapiens (human), mus musculus (mouse), rattus norvegicus (rat), and oryctolagus cuniculus (rabbit). dynein light chain 1, cytoplasmic (protein inhibitor of neuronal nitric oxid [MASS=10366]/Dynein cytoplasmic light polypeptide (protein inhibitor of nitric oxide synthase), a component of the cytoplasmic dynein motor complex, inhibits neuronal nitric oxide synthase (NOS1), regulates the proapoptotic activity of BCL2-interacting protein BCL2L11
GPN:AB014729_1	SMAP1	45	2	1.24	0.01	GP:AB014729_1 Homo sapiens mRNA for SMAP-1, complete cds; tetratricopeptide repeat(TPR motif). [MASS=101675]/Protein containing two putative arf GTPase activation (GAP) domains, which have C-4 class zinc fingers, has a region of moderate similarity to a region of centaurin-alpha (human CENTA1), which is a PtdIns(3,4,5)P3-binding protein
GPN:AL136131_4	MRPS18A	45	1	1.24	0.00	GPN:AL136131_4 Human DNA sequence from clone RP1-261G23 on chromosome 6p12.2-21.1 Contains ESTs, STSs, GSSs and CpG islands. Contains the KIAA0110 gene, two novel genes, a novel pseudogene similar to OPA-interacting protein (OIP1), a putative novel gene, and the VE [MASS=22184]/Mitochondrial ribosomal protein S18A, component of the small (28S) ribosomal subunit of mitochondria
PIR2:T42646	KIAA0731	45	2	1.24	0.00	PIR2:T42646 hypothetical protein DKFZp727K171.1 - human (fragment) [MASS=64691]/Protein of unknown function, has a region of moderate similarity to a region of Sjogren syndrome antigen B (human SSB), which is an RNA-binding protein that regulates translation and is associated with Sjogren syndrome and systemic lupus erythematosus
SW:COPD_HUMAN	ARCN1	45	2	1.24	0.07	SW:COPD_HUMAN P48444 homo sapiens (human). coatomer delta subunit (delta-coat protein) (delta-cop) (archain). 11/1997 [MASS=57210]/Archain 1, a putative structural protein that is ubiquitously expressed and may play a role in intracellular protein trafficking
GP:AF257077_1	EIF2B3	35	2	1.24	0.11	GP:AF257077_1 Homo sapiens eukaryotic translation initiation factor EIF2B subunit 3 (EIF2B3) mRNA, complete cds; eukaryotic translation initiation factor EIF2Bgamma; guanine nucleotide exchange factor. [MASS=50240]/Eukaryotic translation initiation factor 2B gamma subunit, has a putative role in the initiation of protein synthesis; acts as a cofactor for hepatitis C virus IRES-mediated translation
SW:ODPX_HUMAN	PDX1	5	3	1.24	0.16	SW:ODPX_HUMAN O00330 homo sapiens (human). pyruvate dehydrogenase protein x component, mitochondrial precursor (dihydrolipoamide dehydrogenase-binding protein of pyruvate dehydrogenase complex) (e3-bind [MASS=54138]/Dihydrolipoamide dehydrogenase-binding protein (protein X), lipoyl-containing component of the pyruvate dehydrogenase complex, anchors the dihydrolipoamide dehydrogenase (E3) to the dihydrolipoamide transacetylase (E2) core, deficiency causes disease
GP:AB033767_1	C20orf3	45	1	1.23	0.00	GP:AB033767_1 Homo sapiens BSCv mRNA, partial cds; brain-selective and closely mapped on the counter allele of CMAP in cystatin cluster. [MASS=47746]/Member of the strictosidine synthase family, which catalyze the condensation of tryptamine with secologanin to form strictosidine, has low similarity to uncharacterized C. elegans F57C2.5
SWN:PM5P_HUMAN	PM5	45	4	1.23	0.27	SWN:PM5P_HUMAN Q15155 homo sapiens (human). protein pm5 precursor. 8/2001 [MASS=134321]/Protein of unknown function, has low similarity to uncharacterized C. elegans C02E11.1
SWN:TALI_HUMAN	TLN	45	1	1.23	0.00	SWN:TALI_HUMAN Q9y490 homo sapiens (human). talin. 8/2001 [MASS=269718]/Talin 1, a component of focal adhesion sites, links integrins to the actin cytoskeleleton, binds phospholipids, and mediates other interactions at the cytoplasmic face of cell/matrix contacts, important for cell spreading and motility
SW:PCB1_HUMAN	PCBP1	37	20	1.23	0.19	SW:PCB1_HUMAN Q15365 homo sapiens (human). poly(rc)-binding protein 1 (hnrnp-e1) (nucleic acid binding protein sub2.3) (alpha-cp1). 5/2000 [MASS=37526]/Poly(rC)-binding protein 1, contains KH RNA-binding domains, binds poly(rC) RNA, acts as a translational repressor and plays a role in mRNA stability
SW:IF2G_HUMAN	EIF2S3	35	22	1.23	0.22	SW:IF2G_HUMAN P41091 homo sapiens (human). eukaryotic translation initiation factor 2 gamma subunit (eif-2- gamma). 5/2000 [MASS=50978]/Eukaryotic initiation factor 2G, gamma subunit of the heterotrimeric GTP binding protein involved in recruitment of Met-tRNAi to the 40S ribosomal subunit, activity is regulated by herpes simplex virus type 1 gamma 34.5 and by the cellular GADD34 proteins
SW:IF37_HUMAN	EIF3S7	35	6	1.23	0.32	SW:IF37_HUMAN O15371 homo sapiens (human). eukaryotic translation initiation factor 3 subunit 7 (eif-3 zeta) (eif3 p66). 5/2000 [MASS=63973]/Eukaryotic translation initiation factor 3 subunit 7, mRNA-binding subunit of the tranlation initiation factor 3 complex, which mediates dissociation of 80S ribosomes and stabilizes initiator Met-tRNAi binding to 40S subunits
SW:RL4_HUMAN	RPL4	35	17	1.23	0.33	SW:RL4_HUMAN P36578 homo sapiens (human). 60s ribosomal protein l4 (l1). 12/1998 [MASS=47759]/Ribosomal protein L4, a putative component of the large 60S ribosomal subunit, may bind RNA
SW:RS17_HUMAN	RPS17	35	6	1.23	0.24	SW:RS17_HUMAN P08708 homo sapiens (human). 40s ribosomal protein s17. 8/1992 [MASS=15419]/Ribosomal protein S17, component of the small 40S ribosomal subunit
SW:RS3A_HUMAN	RPS3A	35	13	1.23	0.20	SW:RS3A_HUMAN P49241 homo sapiens (human), and felis silvestris catus (cat). 40s ribosomal protein s3a. 5/2000 [MASS=29814]/Ribosomal protein S3A (v fos transformation effector), component of the 40S ribosomal subunit, may play roles in apoptosis, cell growth and protein biosynthesis
GP:AB020723_1	KIAA0916	7	1	1.23	0.00	GP:AB020723_1 Homo sapiens mRNA for KIAA0916 protein, partial cds; k06582 cDNA clone for KIAA0916 has a nucleotide substitution at the position 1955 (C- T; nonsense mutation) of the sequence of KIAA0916.. [MASS=134896]/Protein associated with Myc, a putative transcriptional regulator that binds the Myc oncoprotein (human Myc) and may regulate Myc activated transcription, binds and inhibits adenylyl cyclase types I (ADCY1) and V (ADCY6)
SW:ODB2_HUMAN	DBT	2	1	1.23	0.00	SW:ODB2_HUMAN P11182 homo sapiens (human). lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex, mitochondrial precursor (ec 2.3.1.-) (e2) (dihydrolipoamide branch [MASS=53487]/Dihydrolipoamide branched chain transacylase E2, a subunit of the branched-chain alpha-ketoacid dehydrogenase complex; mutation of the corresponding gene causes type II maple syrup urine disease (branched chain alpha ketoaciduria)

SW:INSR_HUMAN	INSR	5, 18, 34, 41	2	1.22	0.02	SW:INSR_HUMAN P06213 homo sapiens (human). insulin receptor precursor (ec 2.7.1.112) (ir). 5/2000 [MASS=156281]/Insulin receptor, a transmembrane receptor protein tyrosine kinase involved in carbohydrate metabolism, energy pathways, and cell growth; gene mutation is associated with insulin-resistant diabetes mellitus and leprechaunism
SW:PAB1_HUMAN	PABPC1	24, 25, 35, 39	13	1.22	0.44	SW:PAB1_HUMAN P11940 homo sapiens (human). polyadenylate-binding protein 1 (poly(a) binding protein 1) (pabp 1). 7/1998 [MASS=70671]/Poly(A)-binding protein cytoplasmic 1, binds to poly(A) tails of mRNA and plays roles in regulating mRNA stability and translation, also implicated in mRNA transport from the nucleus to the cytoplasm
GP:AF084523_1	CREG	16, 29	1	1.22	0.00	GP:AF084523_1 Homo sapiens cellular repressor of E1A-stimulated genes CREG mRNA, complete cds. [MASS=24075]/Repressor of transcriptional activation and transformation by the adenovirus E1A protein, binds the general transcription factor TBP and the tumor suppressor pRb (RB1), involved in transcriptional control of cell growth and differentiation
SW:HS9B_HUMAN	HSPCB	10, 33	10	1.22	0.52	SW:HS9B_HUMAN P08238 homo sapiens (human). heat shock protein hsp 90-beta (hsp 84) (hsp 90). 5/2000 [MASS=83163]/Heat shock 90kD protein 1 beta, involved in regulation of both cytochrome c-dependent apoptosis and antiapoptosis via the Akt/PKB (AKT1) serine-threonine kinase, elevated expression is reported in patients with active systemic lupus erythematosus (SLE)
SW:EF12_HUMAN	EEF1A2	35	6	1.22	0.11	SW:EF12_HUMAN Q05639 homo sapiens (human). elongation factor 1-alpha 2 (ef-1-alpha-2) (statin s1). 12/1998 [MASS=50470]/Eukaryotic translation elongation factor 1 alpha 2, a putative translation elongation factor, upregulated in an estrogen receptor-expressing breast carcinoma cell line; mutation in mouse Eef1a2 causes the multiple-defect wasted phenotype
GP:D87684_1	UBXD2	32	6	1.22	0.16	GP:D87684_1 Homo sapiens mRNA for KIAA0242 protein, partial cds; Start codon is not identified. ha03111 cDNA clone for KIAA0242 has a 94-bp deletion at the region from 573 to 666 of the sequence of KIAA0242; similar to a C.elegans ZK353.8 protein (S44655). [MASS=59094]/Protein containing a UBX domain, which are found in ubiquitin regulatory proteins, has low similarity to uncharacterized C. elegans ZK353.8
SW:NDK6_HUMAN	NME2	25	1	1.22	0.00	SW:NDK6_HUMAN O60361 homo sapiens (human). putative nucleoside diphosphate kinase (ec 2.7.4.6) (ndk) (ndp kinase). 12/1998 [MASS=15529]/Nucleoside diphosphate kinase B, a transcription factor and endodeoxyribonuclease that binds to the Myc promoter, may function in DNA repair, may suppress metastasis in some tumors, displays reduced expression in breast carcinoma cells
SW:LMB2_HUMAN	LAMB2	6	2	1.22	0.15	SW:LMB2_HUMAN P55268 homo sapiens (human). laminin beta-2 chain precursor (s-laminin). 7/1999 [MASS=196080]/Laminin beta 2 (s-laminin), a basement membrane protein that forms a heterotrimer with other laminin proteins, mediates cell-matrix adhesion, cell migration, and possibly wound healing; lower expression is associated with Walker Warburg Syndrome
SW:GLCM_HUMAN	GBA	5, 19	2	1.21	0.09	SW:GLCM_HUMAN P04062 homo sapiens (human). glucosylceramidase precursor (ec 3.2.1.45) (beta-glucocerebrosidase) (acid beta-glucosidase) (d-glucosyl-n-acylsphingosine glucohydrolase) (alglucerase) (imigl [MASS=59697]/Acid beta glucosidase (beta-glucocerebrosidase), a lysosomal membrane protein that hydrolyzes glucosylceramide and glucosylsphingosine, may play a role in epidermal differentiation; mutations in the corresponding gene cause Gaucher's disease
SW:ER60_HUMAN	ERP60	24, 41	17	1.21	0.54	SW:ER60_HUMAN P30101 homo sapiens (human). probable protein disulfide isomerase er-60 precursor (ec 5.3.4.1) (erp60) (58 kda microsomal protein) (p58) (grp58) (erp57). 7/1998 [MASS=56782]/Glucose regulated 58kDa protein, acts as a protein disulfide isomerase and possibly a protease, involved in folding and maturation of N-linked glycoproteins and MHC class I antigen processing; identified as a sperm antigen in immunological infertility
GP:AB018790_1	LOC244373	45	1	1.21	0.00	GP:AB018790_1 Homo sapiens gene, complete cds, similar to Caenorhabditis elegans C42C1.9 gene sequence; similar to Caenorhabditis elegans C42C1.9 gene sequence in GenBank Accession Number AF043695. [MASS=37840]
GP:AF271388_1	CMAS	45	3	1.21	0.16	GP:AF271388_1 Homo sapiens CMP-N-acetylneuraminic acid synthase mRNA, complete cds. [MASS=48379]/Protein with strong similarity to cytidine monophospho-N-acetylneuraminic acid synthetase (mouse Cmas), which generates the activated sugar nucleotide CMP-N-acetylneuraminic acid for use by sialyltransferases, member of the cytidylyltransferase
GP:AK002135_1	FLJ11273	45	1	1.21	0.00	GP:AK002135_1 Homo sapiens cDNA FLJ11273 fis, clone PLACE1009338; unnamed protein product. [MASS=31113]/Protein of unknown function, has high similarity to uncharacterized human MGC5576
GP:AF000560_1	TIP20	29	2	1.21	0.57	GP:AF000560_1 Homo sapiens TTF-I interacting peptide 20 mRNA, partial cds; TIP20; Transcription Termination Factor I Interacting Peptide 20. [MASS=40770]/TTF-I interacting peptide 20, a protein that contains a putative nucleic acid-binding C2H2 type zinc finger domain
SW:A2HS_HUMAN	AHSG	16	4	1.21	0.13	SW:A2HS_HUMAN P02765 homo sapiens (human). alpha-2-hs-glycoprotein precursor (fetuin) (alpha-2-z-globulin). 5/2000 [MASS=39325]/Alpha 2-HS-glycoprotein, inhibits insulin receptor (INSR) tyrosine kinase activity and may play roles in bone metabolism, monocyte recruitment, cell death, cell adhesion, and the immune response; genotype may be associated with osteoporosis and stature
SW:AATM_HUMAN	GOT2	2	4	1.21	0.02	SW:AATM_HUMAN P00505 homo sapiens (human). aspartate aminotransferase, mitochondrial precursor (ec 2.6.1.1) (transaminase a) (glutamate oxaloacetate transaminase-2). 7/1999 [MASS=47476]/Mitochondrial aspartate aminotransferase (glutamic oxaloacetic transaminase), catalyzes the reversible transfer of the amino group from aspartate to 2-oxoglutarate to form oxaloacetate and glutamate
SW:TRSR_HUMAN	TFRC	26, 42	2	1.20	0.12	SW:TRSR_HUMAN P02786 homo sapiens (human). transferrin receptor protein (tr) (antigen cd71) (t9) (p90). 7/1999 [MASS=84901]/Transferrin receptor, binds and internalizes the iron carrier transferrin, involved in iron homeostasis, important for neurologic development and likely erythropoiesis, expression is deregulated in anemia, hemochromatosis, and Friedreich's ataxia

SW:IPYR_HUMAN	PP	26, 27	1	1.20	0.00	SW:IPYR_HUMAN Q15181 homo sapiens (human). inorganic pyrophosphatase (ec 3.6.1.1) (pyrophosphate phosphohydrolase) (ppase). 5/2000 [MASS=32660]/Inorganic pyrophosphatase, catalyzes the hydrolysis of pyrophosphate to inorganic phosphate
GP:AB038995_1	LOC51762	45	1	1.20	0.00	GP:AB038995_1 Homo sapiens mRNA for RAB-8b protein, complete cds. [MASS=23584]/Member of the Ras superfamily of GTP-binding proteins, has very strong similarity to rat Rn.10995 (Rab8b), which is a member of the Rab family of small GTP binding proteins
GP:AK001050_1	FLJ10188	45	1	1.20	0.00	GP:AK001050_1 Homo sapiens cDNA FLJ10188 fis, clone HEMBA1004693; unnamed protein product. [MASS=30704]/Protein of unknown function
GP:AK024781_1	FLJ21128	45	2	1.20	0.05	GP:AK024781_1 Homo sapiens cDNA: FLJ21128 fis, clone CAS06258; unnamed protein product. [MASS=56106]/Member of the YjeF-related protein N-terminus containing family, has weak similarity to uncharacterized C. albicans Orf6.
SW:2ABA_HUMAN	PPP2R2A	45	2	1.20	0.03	SW:2ABA_HUMAN Q00007 h serine/threonine protein phosphatase 2a, 55 kda regulatory subunit b, alpha isoform (pp2a, subunit b, b-alpha isoform) (pp2a, subunit b, b55-alpha isoform) (pp2a, subunit b, pr55- [MASS=51692]/Protein phosphatase 2 regulatory subunit B alpha isoform, determines the substrate affinity and regulates the kinetics of protein phosphatase 2, expression is decreased in the hippocampus of Alzheimer's disease patients
SW:VAB1_HUMAN	ATP6B1	42	2	1.20	0.08	SW:VAB1_HUMAN P15313 homo sapiens (human). vacuolar atp synthase subunit b, kidney isoform (ec 3.6.1.34) (endomembrane proton pump 58 kda subunit) (v-atpase b subunit). 5/2000 [MASS=56980]/Vacuolar H+-ATPase proton pump (B1 kidney isoform of the B subunit), mediates distal nephron acid secretion and the interaction between V-ATPase and F-actin; variants are associated with renal tubular acidosis accompanied with sensorineural deafness
GP:AB002313_1	PLXNB	41	12	1.20	0.40	GP:AB002313_1 Human mRNA for KIAA0315 gene, partial cds. [MASS=205412]/Plexin B2, putative semaphorin receptor that may be involved in mediating cell guidance
SW:RS14_HUMAN	RPS14	35	3	1.20	0.12	SW:RS14_HUMAN P06366 homo sapiens (human), and cricetulus griseus (chinese hamster). 40s ribosomal protein s14. 8/1992 [MASS=16273]/Ribosomal protein S14, a putative component of the small 40S ribosomal subunit, may play a role in protein biosynthesis, may bind RNA, upregulated in prostate carcinoma cell lines
SW:EPA7_HUMAN	EPHA7	34, 41	2	1.19	0.14	SW:EPA7_HUMAN Q15375 homo sapiens (human). ephrin type-a receptor 7 precursor (ec 2.7.1.112) (tyrosine-protein kinase receptor ehk-3) (eph homology kinase-3) (receptor protein- tyrosine kinase hek11). 5 [MASS=112097]/ Ephrin type A receptor 7, an Eph-related receptor tyrosine kinase, interacts with the PDZ domain of the Ras binding protein AF6 (MLLT4), may be involved in cell signaling
SW:CYP4_HUMAN	PPID	31, 33	1	1.19	0.00	SW:CYP4_HUMAN Q08752 homo sapiens (human). 40 kda peptidyl-prolyl cis-trans isomerase (ec 5.2.1.8) (ppiase) (rotamase) (cyclophilin-40) (cyp-40) (cyclophilin-related protein). 5/2000 [MASS=40764]/Petidylprolyl isomerase D, cyclosporin A and HSPCA -binding peptidylprolyl isomerase, part of steroid receptor and mitochondrial permeability transition pore complexes, may regulate protein trafficking, steroid receptor signal transduction, and apoptosis
GP:AK022956_1	TBLR1	45	1	1.19	0.00	GP:AK022956_1 Homo sapiens cDNA FLJ12894 fis, clone NT2RP2004170, moderately similar to Homo sapiens mRNA for transducin (beta) like 1 protein; unnamed protein product. [MASS=55569]/Protein with strong similarity to transducin (beta)-like 1 (human TBL1), which binds histone H3 and is part of the SMRT corepressor complex and may be involved in vision and hearing, contains eight WD domains (WD-40 repeats)
PIR2:S55474	LLGL2	45	1	1.19	0.00	PIR2:S55474 Human giant larvae homolog - human [MASS=112908]/Protein with high similarity to lethal giant larvae (Drosophila) homolog 1 (human LLGL1), which is a nonmuscle myosin II heavy chain-associating cytoskeletal protein that may be linked to Smith-Magenis Syndrome, contains three WD domains (WD-40 repeats)
SW:1A01_HUMAN	HLAA	45	4	1.19	0.02	SW:1A01_HUMAN P30443 homo sapiens (human). hla class i histocompatibility antigen, a-1 alpha chain precursor. 5/2000 [MASS=40846]/Major histocompatibility complex class I-A, binds antigenic peptides, associates with beta 2-microglobulin (B2M) to form a complex that contributes to self-recognition by cytotoxic T lymphocytes
SW:GAL1_HUMAN	GALK1	5	1	1.19	0.00	SW:GAL1_HUMAN P51570 homo sapiens (human). galactokinase 1 (ec 2.7.1.6). 5/2000 [MASS=42272]/Galactokinase 1, an essential enzyme for galactose metabolism, catalyzes the ATP-dependent phosphorylation of galactose to produce galactose-1-phosphate, deficiency leads to cataract formation
PIR2:T00387	CLASP1	7, 23	1	1.18	0.00	PIR2:T00387 KIAA0622 protein - human (fragment) [MASS=141604]/CLIP-associating protein 1 (Mast), a microtubule-associated protein with a putative role in centrosome separation and organization of the bipolar mitotic spindle
SW:COXS_HUMAN	COX17	18, 42	1	1.18	0.00	SW:COXS_HUMAN Q14061 homo sapiens (human). cytochrome c oxidase copper chaperone. 7/1999 [MASS=6784]/Cytochrome c oxidase assembly protein 17, a putative copper binding protein, may function to transport copper to mitochondria for assembly into cytochrome oxidase complex; mutation does not appear to be a common cause of COX deficiency disorders
SW:GBI2_HUMAN	GNAI2	16, 41	1	1.18	0.00	SW:GBI2_HUMAN P04899 homo sapiens (human). guanine nucleotide-binding protein g(i), alpha-2 subunit (adenylate cyclase-inhibiting g alpha protein). 12/1998 [MASS=40320]/G protein alpha subunit i2, a component of pertussis toxin sensitive heterotrimeric G protein complexes that transduces signals to effectors and inhibits adenylyl cyclase; mutations in the gene are associated with tachycardia and endocrine tumors
SW:RS3_HUMAN	RPS3	45	5	1.18	0.40	SW:RS3_HUMAN P23396 homo sapiens (human). 40s ribosomal protein s3. 2/1996 [MASS=26688]/Ribosomal protein S3, a putative component of the small 40S ribosomal subunit, has DNA endonuclease activity, endonuclease activity is absent in Xeroderma pigmentosum group D patients, expression is increased in colorectal cancer
SW:VATG_HUMAN	ATP6G1	45	1	1.18	0.00	SW:VATG_HUMAN O75348 homo sapiens (human). vacuolar atp synthase subunit g (ec 3.6.1.34) (v-atpase 13 kda subunit) (vacuolar h(+)-atpase subunit g) (vacuolar atp synthase subunit m16). 5/2000 [MASS=13758]/Member of the vacuolar (H+)-ATPase G subunit family, which may couple ATP degradation to H+ translocation, has high similarity to uncharacterized human ATP6G2

SW:CATD_HUMAN	CTSD	32	17	1.18	0.28	SW:CATD_HUMAN P07339 homo sapiens (human). cathepsin d precursor (ec 3.4.23.5). 2/1996 [MASS=44552]/Cathepsin D, a lysosomal aspartyl protease that is induced by estrogen and degrades intracellular and endocytosed proteins, a positive mediator of apoptosis; abnormal expression observed in tumor cell proliferation and metastasis
PIR2:T00361	KIAA0678	10	3	1.18	0.16	PIR2:T00361 hypothetical protein KIAA0678 - human (fragment) [MASS=114535]/Protein containing a DnaJ domain, which are part of chaperone (protein folding) system that mediates interaction with heat shock proteins, has moderate similarity to a region of C. elegans rme-8, which is required for some types of endocytosis
SW:MYSO_HUMAN	MYH10	10	4	1.18	0.49	SW:MYSO_HUMAN P35580 homo sapiens (human). myosin heavy chain, nonmuscle type b (cellular myosin heavy chain, type b) (nmmhc-b). 12/1998 [MASS=228939]/Myosin heavy chain 10 (non-muscle), a putative ATP- and actin-binding motor protein; expression of an alternative splice form is coincident with neuronal cell differentiation
SW:RS29_HUMAN	RPS29	11, 35	1	1.17	0.00	SW:RS29_HUMAN P30054 homo sapiens (human), mus musculus (mouse), rattus norvegicus (rat), and bos taurus (bovine). 40s ribosomal protein s29. 5/2000 [MASS=6546]Ribosomal protein S29, a component of the small 40S ribosomal subunit, contains a zinc finger-like motif, enhances activity of the tumor suppressor Krev-1 (RAP1A)
SW:PEBP_HUMAN	PBP	11, 16, 19, 26	2	1.17	0.15	SW:PEBP_HUMAN P30086 homo sapiens (human). phosphatidylethanolamine-binding protein (pebp) (neuropolypeptide h3). 7/1999 [MASS=20926]/Phosphatidylethanolamine-binding protein, binds GTP, may regulate cAMP accumulation, enhance acetylcholine synthesis, and play a role in organizing phospholipids in the myelin sheath
GP:AB033011_1	KIAA1185	45	7	1.17	0.22	GP:AB033011_1 Homo sapiens mRNA for KIAA1185 protein, partial cds; Start codon is not identified.. [MASS=44499]/Protein containing a leucine rich repeat, which mediates protein-protein interactions, has a region of low similarity to a region of phenylalanyl-tRNA synthetase beta-subunit (human PheHB), which is involved in protein synthesis and possibly tumurigenesis
GP:AF151062_1	LIP5 LYST-interacting protein	45	8	1.17	0.25	GP:AF151062_1 Homo sapiens HSPC228 mRNA, complete cds. [MASS=33677]
SW:HEXB_HUMAN	HEXB	45	6	1.17	0.22	SW:HEXB_HUMAN P07686 homo sapiens (human). beta-hexosaminidase beta chain precursor (ec 3.2.1.52) (n-acetyl-beta-glucosaminidase) (beta-n-acetylhexosaminidase) (hexosaminidase a). 5/2000 [MASS=63111]/Hexosaminidase B beta polypeptide, a subunit of a lysosomal enzyme that hydrolyzes the ganglioside GM2; mutations in the gene cause Sandhoff disease, a lysosomal stroage disorder
GP:AB019435_1	P125	43	3	1.17	0.10	GP:AB019435_1 Homo sapiens mRNA for putative phospholipase, complete cds; putative. [MASS=111076]/Sec23-interacting protein p125, a proline rich protein containing a phospholipase motif, binds to the COPII vesicle coat protein Sec23p (mouse Sec23a), may play a role in protein transport between the endoplasmic reticulum and Golgi
GP:AF195951_1	SRP68	36	2	1.17	0.00	GP:AF195951_1 Homo sapiens signal recognition particle 68 mRNA, complete cds; SRP68; subunit of signal recognition particle. [MASS=70242]/Signal recognition particle 68kD, a component of the signal recognition particle complex involved in targeting nascent proteins to the ER; corresponding gene maps to a tumor suppression locus associated with breast, esophageal, and ovarian cancers
GP:AB006572_1	RMP	29	1	1.17	0.00	GP:AB006572_1 Homo sapiens RMP mRNA for RPB5 meidating protein, complete cds. [MASS=56764]/RPB5-mediating protein, binds to and negatively regulates the function of RNA polymerase II subunit 5 (POLR2E), inhibits transcriptional activation by hepatitis B virus X protein; marker for Reed Sternberg cells in Hodgkin disease
GP:U97276_1	Q6	7	1	1.17	0.00	GP:U97276_1 Homo sapiens quiescin (Q6) mRNA, complete cds, alternatively spliced; alternatively spliced; probable sulfhydryl oxidase; thioredoxin superfamily member. [MASS=82578]/Quiescin Q6, a quiescence-inducible protein that contains 9 quiescin homology zones and has similarity to thioredoxins and S. cerevisiae Erv1p and sulfhydryl oxidases, may play a role in the induction of quiencence
SW:ODPA_HUMAN	PDHA1	5	3	1.17	0.41	SW:ODPA_HUMAN P08559 homo sapiens (human). pyruvate dehydrogenase e1 component alpha subunit, somatic form, mitochondrial precursor (ec 1.2.4.1) (pdhe1-a type i). 7/1999 [MASS=43296]/E1 alpha subunit of pyruvate dehydrogenase complex, somatic form, oxidatively decarboxylates pyruvate to acetyl-CoA; mutation of the corresponding gene causes the majority of pyruvate dehydrogenase deficiencies
SW:GNT2_HUMAN	MGAT2	5, 34	1	1.16	0.00	SW:GNT2_HUMAN Q10469 h alpha-1,6-mannosyl-glycoprotein beta-1,2-n- acetylglucosaminyltransferase (ec 2.4.1.143) (n-glycosyl- oligosaccharide-glycoprotein n-acetylglucosaminyltransferase ii) (beta-1,2-n- [MASS=51550]/UDP-N-acetylglucosamine: alpha-6-D-mannoside-beta-1,2- N-acetylglucosaminyltransferase II, catalyzes the conversion of oligomannose to complex N-glycans; activity is reduced or absent in type II congenital disorders of glycosylation
GP:AF039689_1	STUB1	32, 33	4	1.16	0.13	GP:AF039689_1 Homo sapiens antigen NY-CO-7 (NY-CO-7) mRNA, complete cds; TPR domain protein. [MASS=34791]/STUB1
SW:RAB7_HUMAN	RAB7	21, 43	1	1.16	0.00	SW:RAB7_HUMAN P51149 homo sapiens (human). ras-related protein rab-7. 7/1998 [MASS=23490]/Ras-related GTP-binding protein 7, a member of the rab family of proteins that is involved in vesicle transport, membrane fusion, and vacuole formation; implicated in Chediak Higashi Syndrome
SW:NPC1_HUMAN	NPC1	19, 42	1	1.16	0.00	SW:NPC1_HUMAN O15118 homo sapiens (human). niemann-pick c1 protein precursor. 5/2000 [MASS=142149]/Niemann-Pick disease type C1, a lysosomal sterol transporter involved in cholesterol metabolism; mutation of the corresponding gene causes Niemann-Pick type C1 disease and mutation of mouse Npc1 causes a disease like Niemann-Pick type C1 disease
PIR2:JE0334	RUVBL1	16, 20, 29, 40	3	1.16	0.14	PIR2:JE0334 nuclear matrix protein NMP 238 - human [MASS=50228]/RuvB like 1, a member of the TIP49 family of proteins, a nuclear protein which contains ATPase-helicase motifs, may interact with the transactivation domain of c-myc (MYC)
GP:AL451015_9	unknown	45	1	1.16	0.00	GP:AL451015_9 Neurospora crassa DNA linkage group V BAC clone B13O20; weak similarity to g-alpha interacting protein, homo sapiens, SWISSPROT:GAIP_HUMAN contains EST gb:AW708419, AW708418, AI330099, AI330098. [MASS=16236]

SW:IF2A_HUMAN	EIF2S1	35	1	1.16	0.00	SW:IF2A_HUMAN P05198 homo sapiens (human). eukaryotic translation initiation factor 2 alpha subunit (eif-2- alpha). 7/1999 [MASS=35981]/Eukaryotic translation initiation factor 2 subunit 1 (alpha subunit of eIF2), a translation initiation factor, involved in translational regulation, inhibited by phosphorylation
GP:AF308601_1	NOTCH2	16	2	1.16	0.06	GP:AF308601_1 Homo sapiens NOTCH 2 (N2) mRNA, complete cds. [MASS=265404]/Notch (Drosophila) homolog 2, a transcriptional co-activator of the Notch family of receptors, interacts with MAML1, functions in apoptosis induction and possibly in skeletal development, constitutive activation may contribute to neoplastic transformation
SW:MCM3_HUMAN	MCM3	15	1	1.16	0.00	SW:MCM3_HUMAN P25205 homo sapiens (human). dna replication licensing factor mcm3 (dna polymerase alpha holoenzyme-associated protein p1) (rlf beta subunit) (p102 protein) (p1-mcm3). 5/2000 [MASS=90952]/Minichromosome maintenance deficient 3, associates with the DNA polymerase alpha-primase complex, involved in the initiation of DNA replication, selectively degraded during apoptosis
SW:DESP_HUMAN	DSP	6, 11, 16	7	1.15	0.13	SW:DESP_HUMAN P15924 homo sapiens (human). desmoplakin i and ii (dpi and dpii) (fragment). 5/2000 [MASS=201359]/Desmoplakin, a desmosomal plaque protein involved in cell adhesion and tumor migration, cleaved by caspases during desmosomal disruption associated with keratinocyte apoptosis; gene mutation is associated with hereditary palmoplantar keratoderma
GPN:AF196479_1	tRNA 2,2-dimethylguanosine-26 methyltransferase	45	1	1.15	0.00	SW:TRM1_HUMAN Q9nxh9 homo sapiens (human). probable n2,n2-dimethylguanosine trna methyltransferase (ec 2.1.1.32) (trna(guanine-26,n2-n2) methyltransferase) (trna 2,2- dimethylguanosine-26 methyltransfer [MASS=72234]
SW:COPP_HUMAN	COPB2	43	5	1.15	0.22	SW:COPP_HUMAN P35606 homo sapiens (human). coatomer beta' subunit (beta'-coat protein) (beta'-cop) (p102). 12/1998 [MASS=102356]/Coatomer protein (COP) complex subunit beta 2 (COP beta prime), part of a Golgi coatomer complex that comprises the coat of non-clathrin coated vesicles, likely to play a role in exocytosis
GP:AL096767_2	SBF1	41	1	1.15	0.00	GP:AL096767_2 Human DNA sequence from clone 579N16 on chromosome 22. Contains the 3' part of the gene for KIAA0685, the SBF1 gene for SET binding factor 1, a novel gene, ESTs, an STS, GSSs and three putative CpG islands, complete sequence; owing to approximately 7 [MASS=182476]/SET binding factor 1, a pseudo phosphatase that is inactive as a phosphatase and may act as a competitive inhibitor of other protein phosphatases, regulates cellular growth and may have a role in signal transduction
SW:NTC1_HUMAN	NOTCH1	41	1	1.15	0.00	SW:NTC1_HUMAN P46531 homo sapiens (human). neurogenic locus notch protein homolog 1 precursor (translocation-associated notch protein tan-1) (fragment). 2/1996 [MASS=260649]/Notch homolog 1, a transcriptional regulator involved in different types of cell proliferation and differentiation (especially blood cells), may play a role in cell cycle control; gene translocation is associated with T-cell leukemia
GP:AB015631_1	TMEM4	45	10	1.14	0.17	GP:AB015631_1 Homo sapiens mRNA for type II membrane protein, complete cds, clone:HP10390. [MASS=20652]/Transmembrane protein 4, a putative type II membrane protein
GP:AB018270_1	MYO1D	45	4	1.14	0.11	GP:AB018270_1 Homo sapiens mRNA for KIAA0727 protein, partial cds. [MASS=78790]/Protein containing two IQ calmodulin-binding motifs and a myosin head (motor domain), has very strong similarity to a region of rat Myo1c, which is an unconventional Class I myosin heavy chain that binds calmodulin and may be involved in neurogenesis
GP:AF155658_1	HSPC117	45	5	1.14	0.27	GP:AF155658_1 Homo sapiens putative 55 kDa protein mRNA, complete cds. [MASS=55003]/Member of the uncharacterized protein family UPF0027, has high similarity to uncharacterized C. elegans F16A11.2
GP:AK001718_1	FLJ10856	45	2	1.14	0.09	GP:AK001718_1 Homo sapiens cDNA FLJ10856 fis, clone NT2RP4001547; unnamed protein product. [MASS=40684]/Protein with moderate similarity to S. cerevisiae Cdc50p, which is a protein that functions in cell cycle control, transcription regulation from the Pol II promoter, and is associated with a cell-division-cycle (CDC) phenotype when mutated
PIR2:T00345	KIAA0590	45	1	1.14	0.00	PIR2:T00345 hypothetical protein KIAA0590 - human [MASS=165197]/Protein containing two WD domains (WD-40 repeats), which may mediate protein-protein interactions, has low similarity to C. elegans CHE-11, which is required for normal cilial development, dauer larva formation, and chemotaxis
GPN:AB047847_1	COPG2	43	5	1.14	0.06	no_description_avail/Coatomer protein complex subunit gamma 2, putative intracellular transporter that may be involved in non-selective vesicle transport
SW:SR19_HUMAN	SRP19	36	1	1.14	0.00	SW:SR19_HUMAN P09132 homo sapiens (human). signal recognition particle 19 kda protein (srp19). 10/1996 [MASS=16156]/Signal recognition particle 19 kDa, a signal recognition particle subunit that binds to 7SL RNA and mediates SRP54 binding to the SRP RNA, may be involved in translocation of newly synthesized proteins across the membrane of the rough ER
SW:FRAP_HUMAN	FRAP1	7, 14, 40	1	1.13	0.00	SW:FRAP_HUMAN P42345 homo sapiens (human). fkbp-rapamycin associated protein (frap) (rapamycin target protein). 7/1999 [MASS=288892]/FK506 binding protein 12-rapamycin associated protein 1, serine/threonine and 1-phosphatidylinositol 4-kinase, regulates translation, cell cycle and p53 (TP53) -dependent apoptosis; altered expression is associated with recurrent prostate tumors
SW:PHB_HUMAN	PHB	45	1	1.13	0.00	SW:PHB_HUMAN P35232 homo sapiens (human). prohibitin. 12/1998 [MASS=29804]/Prohibitin, mitochondrial suppressor of cell proliferation that binds to Rb family members RB1 , RBL1 , and RBL2 , represses E2F-induced transcription; gene is mutated in sporadic breast cancer and expression is elevated in endometrial adenocarcinoma
SW:RS25_HUMAN	RPS25	35	4	1.13	0.24	SW:RS25_HUMAN P25111 homo sapiens (human), and rattus norvegicus (rat). 40s ribosomal protein s25. 10/1993 [MASS=13742]/Ribosomal protein S25, a putative RNA-binding component of the small 40S ribosomal subunit that may play a role in protein biosynthesis
SW:PDI_HUMAN	P4HB	34	3	1.13	0.01	SW:PDI_HUMAN P07237 homo sapiens (human). protein disulfide isomerase precursor (pdi) (ec 5.3.4.1) (prolyl 4-hydroxylase beta subunit) (cellular thyroid hormone binding protein) (p55). 5/2000 [MASS=57116]/Procollagen-proline 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase) beta polypeptide (protein disulfide isomerase- thyroid hormone binding protein p55), acts as a protein folding catalyst and promotes protein solubility

SW:HYEP_HUMAN	EPHX1	26	6	1.13	0.03	SW:HYEP_HUMAN P07099 homo sapiens (human). epoxide hydrolase (ec 3.3.2.3) (microsomal epoxide hydrolase) (epoxide hydratase). 10/1996 [MASS=52949]/Microsomal epoxide hydrolase, hydrates reactive epoxides to form dihydrodiols, detoxifies cytochrome p450-generated epoxides from the metabolism of xenobiotics; polymorphisms of the gene may affect risk of cancer, lung disease, and preeclampsia
SW:CBS_HUMAN	CBS	2	1	1.13	0.00	SW:CBS_HUMAN P35520 homo sapiens (human). cystathionine beta-synthase (ec 4.2.1.22) (serine sulfhydrase) (beta-thionase). 10/2001 [MASS=60455]/Cystathionine beta-synthase, catalyzes condensation of serine and homocysteine to form cystathionine, thereby removing toxic homocysteine; deficiency causes homocystinuria with associated vascular disease
SW:NSF_HUMAN	NSF	21, 43	6	1.12	0.16	SW:NSF_HUMAN P46459 homo sapiens (human). vesicular-fusion protein nsf (n-ethylmaleimide-sensitive fusion protein) (nem-sensitive fusion protein). 12/1998 [MASS=82654]/N-ethylmaleimide-sensitive factor, an ATPase involved in membrane fusion during exocytosis
SW:FLRE_HUMAN	BLVRB	18, 26	3	1.12	0.12	SW:FLRE_HUMAN P30043 homo sapiens (human). flavin reductase (ec 1.6.99.1) (fr) (nadph-dependent diaphorase) (nadph-flavin reductase) (flr) (biliverdin reductase b) (ec 1.3.1.24) (bvr-b) (biliverdin-ix b [MASS=21988]/Biliverdin-IX beta reductase (NADPH-flavin reductase), catalyzes the conversion of biliverdin-IX beta to bilirubin-IX beta, the major heme catabolite produced during early fetal development; also has NAD(P)H-linked flavin reductase activity
PIR2:T50639	GPSN2	45	5	1.12	0.09	PIR2:T50639 synaptic glycoprotein SC2, spliced variant [imported] - human [MASS=36061]/Member of the 3-oxo-5-alpha-steroid 4-dehydrogenase family, which are involved in dihydrotestosterone biosynthesis
SW:ATHL_HUMAN	ATP12A	42	7	1.12	0.11	SW:ATHL_HUMAN P54707 homo sapiens (human). potassium-transporting atpase alpha-like chain (ec 3.6.1.36) (proton pump) (non-gastric h+/k+ atpase alpha subunit). 5/2000 [MASS=115511]/Alpha subunit of non-gastric H,K ATPase, the catalytic subunit of the non-gastric nongastric hydrogen:potassium-exchanging ATPase, likely mediates Na+,K+ exchange, activity is pH dependent and sensitive to inhibition by ouabain and vanadate
SW:143Z_HUMAN	YWHAZ	41	4	1.12	0.63	SW:143Z_HUMAN P29312 homo sapiens (human), and bos taurus (bovine). 14-3-3 protein zeta/delta (protein kinase c inhibitor protein-1) (kcip-1) (factor activating exoenzyme s) (fas). 7/1999 [MASS=27745]/14-3-3 zeta, mediates various signal transduction pathways, including inhibition of protein kinase C and activation of inositol polyphosphate 5-phosphatase, phospholipase A2 activity is questionable; may be associated with Alzheimer's disease
SW:E2BE_HUMAN	EIF2B5	35	1	1.12	0.00	SW:E2BE_HUMAN Q13144 homo sapiens (human). translation initiation factor eif-2b epsilon subunit (eif-2b gdp-gtp exchange factor) (fragment). 7/1999 [MASS=72237]/Translation initiation factor 2B subunit 5 (epsilon, 82kD), putative guanyl-nucleotide exchange factor component of the translation initiation factor 2B complex, predicted to mediate the exchange of GDP bound to translation initiation factor eIF2 for GTP
SW:RL9_HUMAN	RPL9	35	8	1.12	0.30	SW:RL9_HUMAN P32969 homo sapiens (human). 60s ribosomal protein l9. 5/2000 [MASS=21863]/Ribosomal protein L9, putative component of the large 60S ribosomal subunit
SW:RS5_HUMAN	RPS5	35	19	1.12	0.89	SW:RS5_HUMAN P46782 homo sapiens (human). 40s ribosomal protein s5. 5/2000 [MASS=22777]/Ribosomal protein S5, a component of the 40S ribosomal subunit; gene expression is altered in colorectal carcinoma cells
PIR2:G02520	PLEC1	11	7	1.12	0.19	PIR2:G02520 plectin - human [MASS=518488]/Plectin 1, a member of the plakin family that crosslinks the cytoskeleton and the plasma membrane in hemidesmosomes and focal contacts; mutation of the corresponding gene causes muscular dystrophy with epidermolysis bullosa simplex (MDEBS)
SW:NPM_HUMAN	NPM1	25, 37	3	1.11	0.14	SW:NPM_HUMAN P06748 homo sapiens (human). nucleophosmin (npm) (nucleolar phosphoprotein b23) (numatrin) (nucleolar protein no38). 5/2000 [MASS=32575]/Nucleophosmin (numatrin), a nucleic acid-binding phosphoprotein involved in apoptosis, abundant in tumor cells; gene fusion with anaplastic lymphoma kinase (ALK) is detected in non-Hodgkin's lymphoma and fusion with MLF1 is seen in acute myeloid leukemia
SW:HBP_HUMAN	HDLBP	19, 42	3	1.11	0.27	SW:HBP_HUMAN Q00341 homo sapiens (human). high density lipoprotein binding protein (hdl-binding protein). 12/1998 [MASS=141440]/High density lipoprotein binding protein, binds and inhibits cleavage of the 3' UTR of vitellogenin mRNA, binds and promotes nuclear export of tRNA, binds high density lipoproteins and may have roles in cholesterol metabolism and atherogenesis
GP:AB040882_1	KIAA1449	45	1	1.11	0.00	GP:AB040882_1 Homo sapiens mRNA for KIAA1449 protein, partial cds; Start codon is not identified.. [MASS=68085]/Protein containing six WD domains (WD-40 repeats), which may mediate protein-protein interactions, has a region of low similarity to a region of platelet-activating factor acetylhydrolase isoform 1b alpha subunit (45kD) (human PAFAH1B1)
GP:AF151069_1	RPML2	45	4	1.11	0.04	GP:AF151069_1 Homo sapiens HSPC235 mRNA, complete cds. [MASS=40152]/Mitochondrial ribosomal protein L37, putative component of the large subunit (39S) of the mitochondrial ribosome
GP:AF226045_1	MRPS22	45	1	1.11	0.00	GP:AF226045_1 Homo sapiens GK002 (GK002) mRNA, complete cds. [MASS=41280]/Mitochondrial ribosomal protein S22, a putative component of the mitochondrial small 28S ribosomal subunit
GP:D42085_1	KIAA0095	45	1	1.11	0.00	GP:D42085_1 Human mRNA for KIAA0095 gene, complete cds; KIAA0095 gene is related to S.cerevisiae NIC96 gene.. [MASS=93488]/Protein with low similarity to S. cerevisiae Nic96p, which is a nuclear pore protein (nucleoporin) that acts in a complex with S. cerevisiae Nsp1p, Nup57p, and Nup49p
GP:AB011126_1	FBP17	41	1	1.11	0.00	GP:AB011126_1 Homo sapiens mRNA for KIAA0554 protein, partial cds. [MASS=77448]/Formin binding protein 17, contains a Src homology 3 (SH3) domain and a Fes/CIP4 homology domain, binds SNX2 and may mediate the assembly of protein signaling complexes; gene is a fusion partner with MLL in acute myelogeneous leukemia
GP:AF132939_1	LOC51067	35	1	1.11	0.00	GP:AF132939_1 Homo sapiens CGI-04 protein mRNA, complete cds. [MASS=53063]/Member of the class I tryptophanyl and tyrosyl (W and Y) tRNA synthetase family, has low similarity to tyrosyl-tRNA synthetase mitochondrial (S. cerevisiae Msy1p), which is involved in tyrosyl-tRNA aminoacylation

SW:IF38_HUMAN	EIF3S8	35	5	1.11	0.32	SW:IF38_HUMAN Q99613 homo sapiens (human). eukaryotic translation initiation factor 3 subunit 8 (eif3 p110). 5/2000 [MASS=105344]/Translation initiation factor 3 subunit 8, 110 kDa eIF3 subunit that recruits translation initiation factor 1 (human SUI1) to 40S ribosomes, interacts with viral internal ribosome entry sites, and may be involved in seminoma development
SW:RL3_HUMAN	RPL3	35	2	1.11	0.01	SW:RL3_HUMAN P39023 homo sapiens (human). 60s ribosomal protein l3 (hiv-1 tar rna binding protein b) (tarbp-b). 5/2000 [MASS=45978]/Ribosomal protein L3, component of the large 60S ribosomal subunit; overexpressed in rapidly dividing cells
SW:TBA1_HUMAN	TUBA1	11	36	1.11	0.28	SW:TBA1_HUMAN P04687 homo sapiens (human). tubulin alpha-1 chain, brain-specific. 7/1999 [MASS=50158]/Alpha-tubulin, a member of a family of structural proteins that polymerize to form microtubules
GP:U40572_1	SNTB2	9	3	1.11	0.12	GP:U40572_1 Human beta2-syntrophin (SNT B2) mRNA, complete cds; contains two pleckstrin homology domains and a domain related to both the tumor discs-large protein and the zonula occludens protein; dystrophin-binding intracellular membrane cytoskeletal protein. [MASS=57950]/Syntrophin beta 2, a membrane-associated protein that binds to dystrophin (DMD) and utrophin-dystrophin related protein (UTRN), may link proteins to the actin cytoskeleton
PIR2:T14762	ACE2	32, 34	1	1.10	0.00	PIR2:T14762 hypothetical protein DKFZp434A014.1 - human (fragment) [MASS=92341]/Member of the angiotensin-converting enzyme family of dipeptidyl carboxydipeptidases
SW:UBPA_HUMAN	USP10	32, 34	1	1.10	0.00	SW:UBPA_HUMAN Q14694 homo sapiens (human). ubiquitin carboxyl-terminal hydrolase 10 (ec 3.1.2.15) (ubiquitin thiolesterase 10) (ubiquitin-specific processing protease 10) (deubiquitinating enzyme 10) (k [MASS=87134]/Ubiquitin specific protease 10, a member of the ubiquitin-specific cysteine (thiol) protease family, cleaves ubiquitin from ubiquitin-conjugated protein substrates, activity is inhibited upon association with Ras-GAP SH3 domain binding protein
SWN:UBPF_HUMAN	USP15	32, 34	3	1.10	0.11	SWN:UBPF_HUMAN Q9y4e8 homo sapiens (human). ubiquitin carboxyl-terminal hydrolase 15 (ec 3.1.2.15) (ubiquitin thiolesterase 15) (ubiquitin-specific processing protease 15) (deubiquitinating enzyme 15) (f [MASS=108965]/Ubiquitin-specific protease 15, a member of the ubiquitin-specific cysteine (thiol) protease family, cleaves ubiquitin from ubiquitin-conjugated protein substrates, may play a role in growth regulation
SW:SYI_HUMAN	IARS	2, 35, 37	9	1.10	0.16	SW:SYI_HUMAN P41252 homo sapiens (human). isoleucyl-trna synthetase, cytoplasmic (ec 6.1.1.5) (isoleucine--trna ligase) (ilers) (irs). 7/1999 [MASS=144959]/Isoleucine-tRNA synthetase, a class I aminoacyl tRNA synthetase, aminoacylates isoleucyl-tRNA with isoleucine for protein biosynthesis, acts as an autoantigen in some autoimmune diseases
GP:AB011163_1	KIF1B	45	1	1.10	0.00	GP:AB011163_1 Homo sapiens mRNA for KIAA0591 protein, partial cds. [MASS=151594]/Kinesin family member 1B, a putative motor protein involved in synaptic vesicle transnport; mutation of the gene underlies Charcot-Marie-Tooth type 2A peripheral neuropathy
GP:AF272357_1	NPDC1	45	2	1.10	0.01	GP:AF272357_1 Homo sapiens NPDC1-like protein (NPDC1) mRNA, complete cds; similar to mouse NPDC1. [MASS=34507]/Protein of unknown function, has a region of low similarity to a region of C. elegans CAB-1, which is a component of a neuronal transmission pathway that affects defecation and locomotion
SW:KNLC_HUMAN	KLC	45	1	1.10	0.00	SW:KNLC_HUMAN Q07866 homo sapiens (human). kinesin light chain (klc). 10/1996 [MASS=64786]/Kinesin light chain, member of a family of microtubule-associated motor proteins that function in intracellular transport and mitosis; has very strong similarity to murine Klc1, which is abundantly expressed in the axons of sciatic nerve
SW:AP50_HUMAN	AP2M1	43	3	1.10	0.08	SW:AP50_HUMAN P20172 homo sapiens clathrin coat assembly protein ap50 (clathrin coat associated protein ap50) (plasma membrane adaptor ap-2 50 kda protein) (ha2 50 kda subunit) (clathrin assembly protei [MASS=49655]/Medium chain subunit of the clathrin associated protein complex AP2, involved in vesicle transport, endocytosis, and required for V-ATPase complex activity
SW:ATCS_HUMAN	ATP2B4	42	6	1.10	0.21	SW:ATCS_HUMAN P23634 homo sapiens (human). calcium-transporting atpase plasma membrane, isoform 4 (ec 3.6.1.38) (calcium pump) (pmca4). 5/2000 [MASS=133931]/ATPase Ca++ transporting plasma membrane 4, a calcium pump that regulates levels of cytosolic free Ca2+, binds calmodulin
PIR1:JC5394	DJ-1	41	7	1.10	0.32	PIR1:JC5394 DJ-1 protein - human [MASS=19847]/RNA-binding protein regulatory subunit, a putative oncogene that may regulate the androgen receptor, play a role in RAS protein signal transduction, and is predicted to play a role in fertilization
SW:TF1B_HUMAN	TIF1B	29	4	1.10	0.26	SW:TF1B_HUMAN Q13263 homo sapiens (human). transcription intermediary factor 1-beta (nuclear corepressor kap-1) (krab-associated protein 1). 7/1999 [MASS=88550]/KRAB associated protein 1, a member of the transcriptional intermediary factor 1 (TIF1) gene family, acts as a transcriptional corepressor to silence heterochromatin, and as a co-activator in association with HP1-type chromodomain-containing proteins
SW:FAAH_HUMAN	FAAH	19	3	1.10	0.22	SW:FAAH_HUMAN O00519 homo sapiens (human). fatty-acid amide hydrolase (ec 3.1.-.-) (oleamide hydrolase). 5/2000 [MASS=63038]/Fatty acid amide hydrolase, degrades neuromodulatory fatty acid amides, including anandamide, predicted to have a role in a wide variety of physiologic efffects such as voluntary movement, pain, sleep, and fertility, may have a role in Parkinson disease
SW:PP1A_HUMAN	PPP1CA	7, 23, 34	2	1.09	0.03	SW:PP1A_HUMAN P08129 homo sapiens (human), mus musculus (mouse), rattus norvegicus (rat), and oryctolagus cuniculus (rabbit). serine/threonine protein phosphatase pp1-alpha 1 catalytic subunit (ec 3.1.3 [MASS=37512]/Protein phosphatase 1 catalytic subunit alpha isoform, plays roles in diverse cellular signal transduction processes that involve protein dephosphorylation, regulates of cell growth and apoptosis and may be a tumor suppressor
SW:KPY1_HUMAN	PKM2	5, 18	19	1.09	0.24	SW:KPY1_HUMAN P14618 homo sapiens (human). pyruvate kinase, m1 isozyme (ec 2.7.1.40) (pyruvate kinase muscle isozyme) (cytosolic thyroid hormone-binding protein) (cthbp) (thbp1). 12/1998 [MASS=57747]/Pyruvate kinase muscle (pyruvate kinase 3), glycolytic enzyme that converts phosphoenolpyruvate to pyruvate with phosphorylation of ADP to ATP, exists as M1 and M2 alternative forms, may have roles in viral transformation and cell differentiation

SW:CRTC_HUMAN	CALR	24, 29	21	1.09	0.26	SW:CRTC_HUMAN P27797 homo sapiens (human). calreticulin precursor (crp55) (calregulin) (hacbp) (erp60) (52 kda ribonucleoprotein autoantigen ro/ss-a). 7/1998 [MASS=48142]/Calreticulin, an ER-resident Ca2+-binding protein and lectin-binding chaperone involved in protein folding, Ca2+ homeostasis, cell adhesion, and integrin signaling; anti-angiogenic fragment, vasostatin, is a potential anti-cancer agent
GP:AF032922_1	UNC-18C	21, 43	2	1.09	0.03	GP:AF032922_1 Homo sapiens syntaxin 4 binding protein UNC-18c (UNC-18c) mRNA, complete cds. [MASS=67764]/Syntaxin binding protein 3, binds syntaxin 4 (STX4), predicted to be involved in vesicle transport and docking and in neurotransmitter release
SW:STB2_HUMAN	STXBP2	21, 43	4	1.09	0.34	SW:STB2_HUMAN Q15833 homo sapiens (human). syntaxin binding protein 2 (unc-18 homolog 2) (unc-18b). 5/2000 [MASS=66439]/Syntaxin-binding protein 2, a member of the Sec1 family of proteins involved in synaptic transmission and secretion, may be involved in intracellular vesicular transport
SW:A4_HUMAN	APP	10, 26, 41	5	1.09	0.19	SW:A4_HUMAN P05067 homo sapiens (human). alzheimer's disease amyloid a4 protein precursor (protease nexin-ii) (pn-ii) (appi) [contains: beta-amyloid protein (beta-app) (a-beta)]. 5/2000 [MASS=86943]/Amyloid beta (A4) precursor protein, cell surface protease inhibitor that reduces copper, deposits of proteolytic peptide products are found in Alzheimer's disease and Down syndrome brains, deficiency is associated with early-onset Alzheimer's disease
GP:AL049795_2	LOC200081	45	2	1.09	0.06	GP:AL049795_2 Human DNA sequence from clone RP4-622L5 on chromosome 1p34.2-36.11. Contains the gene for importin alpha 7 (karyopherin), up to six novel genes and the 5' end of the EIF3S2 gene for eukaryotic translation initiation factor 3 beta. Contains ESTs, STSs [MASS=41648]
PIR2:T12544	TBL2	45	1	1.09	0.00	SW:TBL2_HUMAN Q9y4p3 homo sapiens (human). transducin beta-like 2 protein (ws beta-transducin repeats protein) (ws-betatrp). 10/2001 [MASS=49798]/Protein containing five WD domains (WD-40 repeat), which may mediate protein-protein interactions, has weak similarity to human CIAO1, which interacts with and inhibits Wilms tumor suppressor protein (human WT1) transactivation activity
GP:AF151858_1	LOC50999	43	2	1.09	0.01	GP:AF151858_1 Homo sapiens CGI-100 protein mRNA, complete cds. [MASS=26005]/Protein with high similarity to T1-ST2 receptor binding protein (human IL1RL1LG), which binds to the T1/ST2 receptor (human IL1RL1), member of the emp24 family, which are involved in protein transport from endoplasmic reticulum to Golgi
GP:AK022871_1	TOLLIP	41	4	1.09	0.03	GP:AK022871_1 Homo sapiens cDNA FLJ12809 fis, clone NT2RP2002408, highly similar to Homo sapiens mRNA for TOLLIP protein; unnamed protein product. [MASS=22813]/Tollip, mediates interleukin-1 receptor signaling through interaction with serine/threonine kinase IRAK, inhibits the activity of IRAK1, inhibits lipopolysaccharide-induced activation of macrophages and TLR2 and TLR4 induced activation of NF-KB
SW:EF2_HUMAN	EEF2	35	39	1.09	0.20	SW:EF2_HUMAN P13639 homo sapiens (human). elongation factor 2 (ef-2). 12/1998 [MASS=95338]/Translation elongation factor 2, member of the superfamily of GTP hydrolases, binds ribosomes, catalyzes the translocation step of peptide elongation in protein biosynthesis, target of ADP-ribosylation by diphteria toxin and Pseudomonas exotoxin
SW:P4HA_HUMAN	P4HA1	34	3	1.09	0.11	SW:P4HA_HUMAN P13674 homo sapiens (human). prolyl 4-hydroxylase alpha subunit precursor (ec 1.14.11.2). 11/1997 [MASS=61049]/Proline 4-hydroxylase alpha polypeptide I, catalyzes the hydroxylation of proline to form 4-hydroxyproline in collagens in an oxygen-dependent manner, plays an essential role in collagen synthesis
GP:AF203687_1	PREB	29	2	1.09	0.06	SWN:PREB_HUMAN Q9hcu5 homo sapiens (human). prolactin regulatory element-binding protein. 3/2002 [MASS=45502]/Prolactin regulatory element binding protein, transcriptional activator, member of the WD-repeat protein family, may have a role in development; chromosomal location of the gene makes this a candidate for the gene mutated in partial trisomy 2p syndrome
GP:AF113123_1	DCXR	5	2	1.09	0.01	GP:AF113123_1 Homo sapiens carbonyl reductase mRNA, complete cds; CR. [MASS=25913]/Protein with high similarity to murine Cbr2, carbonyl reductase, which is involved in differentiation of adipocytes from adipoblasts, member of the glucose/ribitol dehydrogenase family
PIR2:T00363	KIAA0674	33, 34	2	1.08	0.12	PIR2:T00363 hypothetical protein KIAA0674 - human (fragment) [MASS=135179]/Member of the FKBP-type peptidyl-prolyl cis-trans isomerase family
PIR2:T47172	CORO1C or CRNN4	23, 41	5	1.08	0.38	PIR2:T47172 hypothetical protein DKFZp762H186.1 - human (fragment) [MASS=55769]/Coronin actin-binding protein 1C, a member of the coronin-like protein family, has five WD repeats and a coiled-coil motif, a putative actin binding protein that may play a role in mitosis, cytokinesis, cell motility, signal transduction, and phagocytosis
SW:CPT2_HUMAN	CPT2	18, 19, 42	1	1.08	0.00	SW:CPT2_HUMAN P23786 homo sapiens (human). carnitine o-palmitoyltransferase ii, mitochondrial precursor (ec 2.3.1.21) (cpt ii). 5/2000 [MASS=73777]/Carnitine palmitoyltransferase II, a mitochondrial long-chain fatty acid oxidation enzyme; mutations are associated with a lipid metabolism disorder that includes recurrent myopathy with progressive rhabdomyolysis, muscle weakness and myoglobinuria
SW:RAC1_HUMAN	RAC1	10, 11, 16, 34, 41	18	1.08	0.53	SW:RAC1_HUMAN P15154 homo sapiens (human), mus musculus (mouse), and canis familiaris (dog). ras-related c3 botulinum toxin substrate 1 (p21-rac1) (ras-like protein tc25). 12/1998 [MASS=21450]/Ras-related C3 botulinum toxin substrate 1, a monomeric GTPase of the Rho family, involved in transducing signals that regulate proliferation, apoptosis, cytoskeletal organization, and response to oxidative stress, contributes to tumor cell invasiveness
PIR2:T46254	RAGD	45	2	1.08	0.07	PIR2:T46254 hypothetical protein DKFZp761H171.1 - human [MASS=28611]/Protein with high similarity to S. cerevisiae Gtr2p, which is a putative small GTPase involved in nucleocytoplasmic transport
SW:DSR3_HUMAN	DSCR3	45	4	1.08	0.12	SW:DSR3_HUMAN O14972 homo sapiens (human). down syndrome critical region protein 3. 5/2000 [MASS=33010]/Down syndrome criticial region gene 3, a ubiquitously expressed protein; the corresponding gene is located in the Down syndrome critical region of chromosome 21
SW:SKP1_HUMAN	SKP1	45	3	1.08	0.12	SW:SKP1_HUMAN P34991 homo sapiens (human), and cavia porcellus (guinea pig). cyclin a/cdk2-associated protein p19 (rna polymerase ii elongation factor-like protein) (organ of corti protein 2) (ocp-ii pr [MASS=18527]/S-phase kinase-associated protein 1A (p19A), component of Cbf3 kinetochore and SCF (Skp1p-cullin-F-box) complexes which target many cell cycle dependent proteins for ubiquitin-dependent degradation, deregulation may lead to tumorigenesis

SW:TBB1_HUMAN	TUBB1	45	22	1.08	0.36	SW:TBB1_HUMAN P07437 homo sapiens (human). tubulin beta-1 chain. 7/1999 [MASS=49759]/Protein with high similarity to beta-2 tubulin (rat Tubb2), which plays a role in the response to wounding and possibly in axonal outgrowth and regeneration, member of the tubulin-FtzA family, which are involved in polymer formation
SW:IF4G_HUMAN	EIF4G1	35	2	1.08	0.39	SW:IF4G_HUMAN Q04637 homo sapiens (human). eukaryotic translation initiation factor 4 gamma (eif-4-gamma) (eif- 4g) (eif4g) (p220). 7/1999 [MASS=153361]/Eukaryotic translation initiation factor 4 gamma 1, gamma subunit of eIF4, functions in translation initiation, binds RNA and forms a bridge between the mRNA cap and polyA tail, cleaved during apoptosis and poliovirus infection
SW:OXYB_HUMAN	OSBP	19	3	1.08	0.26	SW:OXYB_HUMAN P22059 homo sapiens (human). oxysterol-binding protein. 11/1995 [MASS=89421]/Oxysterol binding protein, member of a family of intracellular lipid receptors, contains a pleckstrin domain and an oxysterol binding domain, binds oxysterols, may play a role in the regulation of cholesterol metabolism and oxysterol-induced cell death
SW:ERB2_HUMAN	ERBB2	7, 16, 34, 41	5	1.07	0.09	SW:ERB2_HUMAN P04626 homo sapiens (human). receptor protein-tyrosine kinase erbb-2 precursor (ec 2.7.1.112) (p185erbb2) (neu proto-oncogene) (c-erbb-2) (tyrosine kinase-type cell surface receptor her2) [MASS=137910]/Avian erythroblastosis oncogene B 2, a receptor tyrosine kinase and most oncopotent member of the EGF receptor family, heterodimerizes with other EGFRs; overexpression contributes to growth, metastasis and chemoresistance of epithelial-derived tumors
SW:HXK1_HUMAN	HK1	5, 18	5	1.07	0.11	SW:HXK1_HUMAN P19367 homo sapiens (human). hexokinase, type i (ec 2.7.1.1) (hk i) (brain form hexokinase). 12/1998 [MASS=102503]/Hexokinase Type I (ATP:D-hexose 6-phosphotransferase), catalyzes ATP-dependent conversion of glucose to glucose 6 phosphate in glycolysis, deficiency may lead to non-spherocytic hemolytic anemia
SW:ARF6_HUMAN	ARF6	11, 43	2	1.07	0.05	SW:ARF6_HUMAN P26438 homo sapiens (human), mus musculus (mouse), and rattus norvegicus (rat). adp-ribosylation factor 6. 12/1998 [MASS=19951]/ADP-ribosylation factor 6, GTP-binding protein that stimulates cholera toxin activity and is involved in endocytosis, exocytosis, membrane trafficking, and possibly regulation of glucose transport
GP:AK001243_1	FLJ10381	45	1	1.07	0.00	GP:AK001243_1 Homo sapiens cDNA FLJ10381 fis, clone NT2RM2002055; unnamed protein product. [MASS=49582]/Protein of unknown function
GPN:AB040462_1	RTN4	45	1	1.07	0.00	SWN:RTN4_HUMAN Q9nqc3 homo sapiens (human). reticulon 4 (neurite outgrowth inhibitor) (nogo protein) (foocen) (neuroendocrine-specific protein)(nsp) (neuroendocrine specific protein c homolog) (rtn-x) ([MASS=129931]/Reticulon 4, ligand for RTN4R, inhibits axon regeneration in adult CNS but not PNS, yet peptide derivative NEP1-40 acts as an antagonist and promotes axonal regeneration and may have therapeutic potential
PIR2:T46272	DKFZP564L0864	45	1	1.07	0.00	PIR2:T46272 hypothetical protein DKFZp564L0864.1 - human (fragment) [MASS=20191]/Protein with high similarity to uncharacterized mouse Hiat1
SW:COPB_HUMAN	COPB	43	1	1.07	0.00	SW:COPB_HUMAN P53618 homo sapiens (human). coatomer beta subunit (beta-coat protein) (beta-cop) (fragment). 11/1997 [MASS=33444]/Coatomer protein beta, component of non-clathrin-coated vesicles essential for membrane trafficking, binds to HIV-1 Nef protein
SWN:SNX3_HUMAN	SNX3	43	1	1.07	0.00	SWN:SNX3_HUMAN O60493 homo sapiens (human). sorting nexin 3 (sdp3 protein). 8/2001 [MASS=18762]/Sorting nexin 3, involved in intracellular protein trafficking
SW:RS8_HUMAN	RPS8	35	9	1.07	0.56	SW:RS8_HUMAN P09058 homo sapiens (human), rattus norvegicus (rat), and mus musculus (mouse). 40s ribosomal protein s8. 2/1996 [MASS=24074]/Ribosomal protein S8, component of the small 40S ribosomal subunit
GP:AF260566_1	HGS	41, 43	1	1.06	0.00	GP:AF260566_1 Homo sapiens hepatocyte growth factor-regulated tyrosine kinase substrate HRS isoform 2 (HRS) mRNA, complete cds. [MASS=76362]/Hepatocyte growth factor regulated tyrosine kinase substrate, zinc-finger protein with ATPase activity, tyrosine phosphorylated upon growth factor stimulation, involved in endosome trafficking and mediates FOS transcription via cytokine signaling
SW:IMB2_HUMAN	KPNB2	24, 36	1	1.06	0.00	SW:IMB2_HUMAN Q92973 homo sapiens (human). importin beta-2 subunit (karyopherin beta-2 subunit) (transportin) (m9 region interaction protein) (mip). 5/2000 [MASS=101310]/Transportin (karyopherin beta 2), a component of the nuclear pore complex, mediates the import of HNRPA1 by binding the M9 nuclear localization sequence, also binds nuclear Ran GTP and nucleoporin Nup153; may mediate mRNA transport
GP:AF126782_1	RETSDR1	19, 26	8	1.06	0.21	GP:AF126782_1 Homo sapiens retinal short-chain dehydrogenase/reductase retSDR4 mRNA, complete cds. [MASS=32268]/Short-chain dehydrogenase-reductase 1, catalyzes the NADPH-dependent reduction of all-trans-retinal to retinol, may play a role in visual system phototransduction; the corresponding gene is deleted in many neuroblastoma cell lines with MYCN amplification
SW:HEMZ_HUMAN	FECH	18, 26	8	1.06	0.19	SW:HEMZ_HUMAN P22830 homo sapiens (human). ferrochelatase precursor (ec 4.99.1.1) (protoheme ferro-lyase) (heme synthetase). 12/1998 [MASS=47834]/Ferrochelatase (protoheme ferrochelatase), catalyzes the final step in the heme biosynthetic pathway by inserting ferrous iron into protoporphyrin IX to form heme; reduced activity and mutations in the corresponding gene are associated with protoporphyria
GP:AC005154_1	MGC3077	45	2	1.06	0.00	GP:AC005154_1/Protein of unknown function, has moderate similarity to uncharacterized C. elegans C44B7.7
GP:AF137372_1	RAB18	45	2	1.06	0.01	GP:AF137372_1 Homo sapiens ras-related protein RAB18 mRNA, complete cds. MASS=22977]/Ras-related GTP-binding protein 18, putative GTP binding protein and GTPase, may be involved in vesicle transport and may play a role in inflammation
GP:X87832_1	PLXNA1	45	1	1.06	0.00	GP:X87832_1 Homo sapiens mRNA for partial NOV/plexin-A1 protein. [MASS=194818]/Plexin A1, acts as a coreceptor with neuropilin (NRP1) for semaphorins, which are signaling molecules controlling cell repulsion
SW:ANXA_HUMAN	ANXA10	45	8	1.06	0.12	SW:ANXA_HUMAN P50995 homo sapiens (human). annexin xi (calcyclin-associated annexin 50) (cap-50) (56 kda autoantigen). 5/2000 [MASS=54390]/Annexin A10, a liver-specific member of the annexin family of calcium-dependent phospholipid-binding proteins that typically have a role in inositol phosphate metabolism; downregulation correlates with high grade and high stage hepatocellular carcinoma

SW:YCE7_HUMAN	Hypothetical protein CGI-147	45	1	1.06	0.00	SW:YCE7_HUMAN Q9y3e5 homo sapiens (human). hypothetical protein cgi-147. 5/2000 [MASS=19194]
PIR2:I53171	H-SP1	43	1	1.06	0.00	PIR2:I53171 pantophysin - human [MASS=28565]/Synaptophysin-like protein (pantophysin), a protein that has similarity to the synaptic vesicle protein synaptophysin (SYP), may play a role in vesicle transport
SW:FASA_HUMAN	TNFSF6	41	1	1.06	0.00	SW:FASA_HUMAN P25445 homo sapiens (human). fasl receptor precursor (apoptosis-mediating surface antigen fas) (apo-1 antigen) (cd95 antigen). 11/1997 [MASS=37732]/Apoptosis antigen ligand 1, a tumor necrosis factor alpha related cytokine that binds Fas and induces apoptosis, plays important roles in immune system development, immune response and tumorigenesis, may be a prognostic tumor marker
SW:FK38_HUMAN	FKBP8	41	3	1.06	0.31	SW:FK38_HUMAN Q14318 homo sapiens (human). 38 kda fk-506 binding protein homolog (fkbpr38). 5/2000 [MASS=38408]/FK506 binding protein, member of a subclass of immunophilins, contains tetratricopeptide repeat and a consensus leucine zipper domains
SW:PSD4_HUMAN	PSMD4	32	5	1.06	0.29	SW:PSD4_HUMAN P55036 homo sapiens (human). 26s proteasome regulatory subunit s5a (multiubiquitin chain binding protein) (antisecretory factor-1) (af) (asf). 12/1998 [MASS=40737]/Proteasome 26S subunit non ATPase 4, an antisecretory factor that is a subunit of the 26S proteasome and may bind to multiubiquitinated proteins; inhibits intestinal fluid secretion induced by cholera toxin
SWN:PSA7_HUMAN	PSMA7	32	4	1.06	0.22	SWN:PSA7_HUMAN O14818 homo sapiens (human). proteasome subunit alpha type 7 (ec 3.4.99.46) (proteasome subunit rc6-1) (proteasome subunit xapc7). 8/2001 [MASS=27887]/Proteasome (prosome, macropain) subunit (alpha type) 7, a subunit of the 20S core proteasome, a target of hepatitis B virus X protein; may be involved in pathogenesis of pancreatic cancer
SW:ODPB_HUMAN	PDHB	5, 18	1	1.05	0.00	SW:ODPB_HUMAN P11177 homo sapiens (human). pyruvate dehydrogenase e1 component beta subunit, mitochondrial precursor (ec 1.2.4.1) (pdhe1-b). 7/1999 [MASS=39219]/E1 beta subunit of pyruvate dehydrogenase complex, oxidatively decarboxylates pyruvate to acetyl-CoA
SW:PTN1_HUMAN	PTPN1	34, 41	3	1.05	0.15	SW:PTN1_HUMAN P18031 homo sapiens (human). protein-tyrosine phosphatase 1b (ec 3.1.3.48) (ptp-1b). 7/1999 [MASS=49967]/Protein tyrosine phosphatase non-receptor type I, likely involved in the negative regulation of insulin receptor signaling, may be associated with type II diabetes and obesity
GP:AJ245621_1	CTL2	45	17	1.05	0.27	GP:AJ245621_1 Homo sapiens CTL2 gene. [MASS=80138]/Protein of unknown function, has high similarity to uncharacterized mouse 2210409B01Rik
GP:Z74021_1	RPS17L4	45	7	1.05	0.21	GP:Z74021_1 Human DNA sequence from clone SC22CB-1E7 on chromosome 22 Contains the RPS17L4 gene for Ribosomal protein S17-like 4, exons 1 and 2 of the SLC5A1 gene for solute carrier family 5 (sodium/glucose cotransporter) member 1 (High Affinity Sodium-Glucose C [MASS=15602]
GPN:AF060511_1	LOC112473	45	1	1.05	0.00	GPN:AF060511_1 Homo sapiens clone 016b10 My016 protein mRNA, complete cds.[MASS=10117]
PIR2:PH0268	EPPK1	45	3	1.05	0.01	PIR2:PH0268 epidermal autoantigen 450K (clone pE450-C/D) - human (fragment) [MASS=73263]/Epiplakin 1, a member of the plakin family of proteins that bind to cytoplasmic intermediate filaments; autoantigens to the protein are present in patients with a subepidermal blistering disease that resembles bullous pemphigoid
GP:U81006_1	TM9SF2	42	3	1.05	0.06	GP:U81006_1 Human p76 mRNA, complete cds; predicted molecular weight is 76kD; contains nine potential membrane spanning domains; similar to yeast p24a precursor protein encoded by GenBank Accession Number X67316. [MASS=75776]/Transmembrane 9 superfamily member 2, an endosomal protein with membrane spanning domains, may be a channel or transporter of small molecules
SW:EF1G_HUMAN	EEF1G	35	7	1.05	0.15	SW:EF1G_HUMAN P26641 homo sapiens (human). elongation factor 1-gamma (ef-1-gamma). 5/2000 [MASS=50119]/Eukaryotic elongation factor 1 gamma, a likely translation elongation factor 1 (EF-1) complex component that binds cytoplasmic cysteinyl-tRNA synthetase and possibly EF-1 beta; overexpression in gastric carcinoma correlates with vascular permeation
GP:D88435_1	GAK	7	2	1.05	0.04	GP:D88435_1 Homo sapiens mRNA for HsGAK, complete cds. [MASS=143165]/Cyclin G-associated kinase, a putative serine/threonine protein kinase that shares homology with tensin and auxilin, may play a role in cell cycle regulation
SW:KCCD_HUMAN	CAMK2D	34, 41	3	1.04	0.01	SW:KCCD_HUMAN Q13557 homo sapiens (human). calcium/calmodulin-dependent protein kinase type ii delta chain (cam-kinase ii delta chain) (ec 2.7.1.123) (camk-ii, delta subunit) (fragment). 5/2000 [MASS=12846]/Calcium/calmodulin-dependent protein kinase II delta, member of the multifunctional CAMKII family involved in Ca2+ regulated processes; alternative form delta 3 is specifically upregulated in the myocardium of patients with heart failure
SW:KRCB_HUMAN	AKT2	34, 41	1	1.04	0.00	SW:KRCB_HUMAN P31751 homo sapiens (human). rac-beta serine/threonine kinase (ec 2.7.1.-) (rac-pk-beta) (akt2 kinase). 11/1995 [MASS=55769]/v-akt murine thymoma viral oncogene homolog 2, protein kinase that is activated by mitogens and survival factors, may regulate cell proliferation and apoptosis, overexpression is associated with ovarian, breast and pancreatic cancers
GP:AB002310_1	UREB1	32, 34	3	1.04	0.06	GP:AB002310_1 Human mRNA for KIAA0312 gene, partial cds. [MASS=209315]/Protein containing a HECT domain, which may confer ubiquitin-protein ligase activity, has high similarity to a region of S. cerevisiae Tom1p, which is a protein required for the G2/M transition
SW:KAP2_HUMAN	PRKAR2A	16, 41	2	1.04	0.57	SW:KAP2_HUMAN P13861 homo sapiens (human). camp-dependent protein kinase type ii-alpha regulatory chain. 5/2000 [MASS=45387]/cAMP-dependent Protein kinase A regulatory subunit alpha (type II), binds A-kinase anchoring proteins to mediate holoenzyme localization and plays important roles in sperm motility and in trophoblast cell differentiation

GP:AK025520_1	GOCAP1	45	3	1.04	0.22	GP:AK025520_1 Homo sapiens cDNA: FLJ21867 fis, clone HEP02419; unnamed protein product. [MASS=60579]/Protein with strong similarity to peripheral benzodiazepine receptor associated protein 7 (mouse Pap7), which binds peripheral-type benzodiazepine receptor (Bzrp) and functions in regulation of steroidogenesis, contains an acyl CoA binding domain
PIR2:T46333	macrothioredoxin	45	1	1.04	0.00	PIR2:T46333 hypothetical protein DKFZp434J1813.1 - human (fragment) [MASS=53778]
SW:LEGU_HUMAN	LGMN	45	8	1.04	0.16	SW:LEGU_HUMAN Q99538 homo sapiens (human). legumain precursor (ec 3.4.22.34) (asparaginyl endopeptidase). 12/1998 [MASS=49411]/Protease cysteine 1 (legumain), a lysosomal cysteine endopeptidase that hydrolyzes asparaginyl bonds, inhibits osteoclast differentiation, may play a role in antigen processing for MHC class II presentation
GP:AC006378_1	BET1	43	1	1.04	0.00	GP:AC006378_1 Homo sapiens BAC clone RP11-455I9 from 7q21.2-q22, complete sequence; match to AAB62941.1 (PID:2253426); H_NH0455I09.1. [MASS=13289]/S. cerevisiae Bet1 homolog, may be involved in ER to Golgi transport
SW:ATN1_HUMAN	ATP1A1	42	54	1.04	0.22	SW:ATN1_HUMAN P05023 homo sapiens (human). sodium/potassium-transporting atpase alpha-1 chain precursor (ec 3.6.1.37) (sodium pump) (na+/k+ atpase). 7/1999 [MASS=112896]/Alpha 1 subunit of the Na+-K+-transporting ATPase, required for active transport of sodium in the kidney and other tissues, may function in blood pressure regulation; mutations may be associated with essential hypertension and diabetic neuropathy
GP:AF077032_1	FLJ10578	36	5	1.04	0.27	GP:AF077032_1 Homo sapiens sec61 homolog mRNA, complete cds. [MASS=52480]/Sec61 alpha form 2, a protein with high similarity to S. cerevisiae Sec61p, which is a component of the Sec61p-Sss1p-Sbh1p complex involved in protein translocation into the endoplasmic reticulum, member of the SecY protein family of protein translocators
PIR2:S52920	ADAM10	34	9	1.04	0.18	PIR2:S52920 disintegrin (EC 3.4.24.-) - human (fragment) [MASS=54380]/A disintegrin and metalloproteinase domain 10, an ADAM family disintegrin domain-containing zinc metalloprotease, acts in ectodomain proteolysis of membrane proteins, cleaves cellular prion protein (PRNP), acts as an alpha secretase on APP
SW:CYPH_HUMAN	PPIA	33	15	1.04	0.29	SW:CYPH_HUMAN P05092 homo sapiens (human), cercopithecus aethiops (green monkey) (grivet), macaca mulatta (rhesus macaque), and papio anubis peptidyl-prolyl cis-trans isomerase a (ec 5.2.1.8) (ppiase) ([MASS=17881]/Peptidylprolyl isomerase A (cyclophilin A), mediates immunosuppressant action of cyclosporin A by inhibiting calcineurin phosphatase activity, has nuclease activity, binds to transcription factors, incorporates into HIV-1 virions and regulates infectivity
GP:AB002387_1	MYO6	11	34	1.04	0.35	GP:AB002387_1 Human mRNA for KIAA0389 gene, complete cds. [MASS=148714]/Myosin VI, an unconventional myosin motor protein, may function in membrane trafficking in the secretory and endocytic pathways; mutations in the corresponding gene are associated with deafness
GP:AF020797_1	HSMU1B	36, 43	1	1.03	0.00	GP:AF020797_1 Homo sapiens AP-mu chain family member mu1B (HSMU1B) mRNA, complete cds. [MASS=48108]/Adaptor-related protein complex 1 mu 2 subunit, involved in protein sorting
SW:MPRD_HUMAN	M6PR	36, 43	1	1.03	0.00	SW:MPRD_HUMAN P20645 homo sapiens (human). cation-dependent mannose-6-phosphate receptor precursor (cd man-6-p receptor) (cd-mpr) (46 kda mannose 6-phosphate receptor) (mpr 46). 5/2000 [MASS=30993]/Cation-dependent mannose-6-phosphate receptor, involved in intracellular sorting and transport of acid hydrolases, transports lysosomal enzymes
PIR2:A57017	ABCE1	25, 39	5	1.03	0.03	PIR2:A57017 RNase L inhibitor - human [MASS=67559]/Ribonuclease L inhibitor, inhibits the nuclease activity and 2-5A binding ability of RNase L, may be induced by HIV-1 to inhibit the 2-5A/RNase L pathway, can inhibit the antiviral activity of interferon when overexpressed
GP:AK002163_1	FLJ11301	45	1	1.03	0.00	GP:AK002163_1 Homo sapiens cDNA FLJ11301 fis, clone PLACE1009908, weakly similar to HYPOTHETICAL GTP-BINDING PROTEIN IN SEH1-PRP20 INTERGENIC REGION; unnamed protein product. [MASS=73142]/Member of an uncharacterized GTPase family, has moderate similarity to yeast YGL099W, which is required for normal growth, morphology, mating, and sporulation
PIR2:T00050	DDEF2	45	1	1.03	0.00	PIR2:T00050 hypothetical protein KIAA0400 - human [MASS=111651]/Development and differentiation enhancing factor 2 (Pyk2 C terminus-associated protein), phosphatidylinositol-4,5-bisphosphate-dependent ARF GTPase activator, binds Src kinases and PYK2 (PTK2B), inhibits paxillin (PXN) recruitment to focal adhesions
SW:ACTY_HUMAN	ACTR1B	45	1	1.03	0.00	SW:ACTY_HUMAN P42025 homo sapiens (human). beta-centractin. 7/1999 [MASS=42293]/Beta centractin, a member of the centractin family of actin-related proteins, a subunit of the dynactin complex which functions in the cytoplasmic dynein-driven organelle movement along microtubules
GP:AF288687_1	CGI-152	42	3	1.03	0.07	GP:AF288687_1 Homo sapiens CGI-152 protein mRNA, complete cds. [MASS=121110]/Member of the haloacid dehalogenase or epoxide hydrolase family and the E1-E2 (P-type) ATPase family, which are cation transporters, has moderate similarity to S. cerevisiae Spf1p, which functions in cell wall organization and xenobiotic response
SW:CLC3_HUMAN	CLCN3	42	1	1.03	0.00	SW:CLC3_HUMAN P51790 homo sapiens (human). chloride channel protein 3 (clc-3). 7/1998 [MASS=84793]/Chloride channel 3, chloride channel of the voltage-gated family, plays a role in chloride transport, may be responsible for outwardly rectifying chloride currents, regulated by calcium/calmodulin dependent protein kinase II (CAMK2A), binds to SLC9A3R1
PIR2:G02390	MDC15	6	6	1.03	0.12	PIR2:G02390 disintegrin-like metalloproteinase MDC15 (EC 3.4.24.-) - human [MASS=87719]/Metargidin, member of the ADAM family of disintegrin domain-containing zinc metalloproteases, interacts specifically with the alphavbeta3 integrin, upregulated in atherosclerotic lesions and increased expression occurs during atrial fibrillation
GP:AJ131612_1	Slc25a10	5, 18, 42	1	1.02	0.00	GP:AJ131612_1 Homo sapiens dic gene, exons 1-11. [MASS=31325]/Solute carrier family 25 member 10 (dicarboxylate carrier), a putative dicarboxylic acid transporter predicted to reside in the inner mitochondrial membrane, may be involved in gluconeogenesis
GP:AF132941_1	LOC51068	25, 35, 39	1	1.02	0.00	GP:AF132941_1 Homo sapiens CGI-07 protein mRNA, complete cds. [MASS=57585]/Protein with moderate similarity to S. cerevisiae Nmd3p, which is a protein involved in the nuclear export of 60S ribosomal subunits

GP:AB037819_1	RRBP1	16, 35, 36	7	1.02	0.13	GP:AB037819_1 Homo sapiens mRNA for KIAA1398 protein, partial cds; Start codon is not identified.. [MASS=170212]/Ribosome binding protein 1, a putative ribosome receptor, may play a role in protein biosynthesis, appears to be involved in cardiac development, may play a role in cardiac remodeling in heart failure
SW:TDX1_HUMAN	PRDX1	10, 16	2	1.02	0.01	SW:TDX1_HUMAN P32119 homo sapiens (human). thioredoxin peroxidase 1 (thioredoxin-dependent peroxide reductase 1) (thiol-specific antioxidant protein) (tsa) (prp) (natural killer cell enhancing factor b) [MASS=21892]/Peroxiredoxin 1, oxidative stress-inducible antioxidant protein with peroxidase activity, may have anticytotoxic and antiapoptotic activity and may have a role in cell proliferation
GP:AF129332_1	MUM2	45	1	1.02	0.00	GP:AF129332_1 Homo sapiens MUM2 (MUM2) gene, complete cds; similar to Saccharomyces cerevisiae bet5. [MASS=16832]/Protein with low similarity to S. cerevisiae Bet5p, which is a subunit of both the Transport Protein Particle I complex involved in vesicular transport from endoplasmic reticulum to Golgi and the Transport Protein Particle II involved in Golgi trafficking
GP:AK022763_1	MRPL44	45	2	1.02	0.20	GP:BC012058_1 Homo sapiens, hypothetical protein FLJ12701, clone MGC:19885 IMAGE:4554033, mRNA, complete cds. [MASS=37535]/Protein containing a double-stranded RNA binding domain
GPN:AL109804_12	KIAA1271	45	2	1.02	0.27	GP:AB033097_1 Homo sapiens mRNA for KIAA1271 protein, partial cds; Start codon is not identified.. [MASS=56670]/Protein of unknown function
PIR2:T17237	DKFZP434P106	45	1	1.02	0.00	PIR2:T17237 hypothetical protein DKFZp434P106.1 - human (fragment) [MASS=28268]/Protein of unknown function, has high similarity to uncharacterized mouse 6330583M11Rik
SW:ANX6_HUMAN	ANXA6	45	3	1.02	0.02	SW:ANX6_HUMAN P08133 homo sapiens (human). annexin vi (lipocortin vi) (p68) (p70) (protein iii) (chromobindin 20) (67 kda calelectrin) (calphobindin-ii) (cpb-ii). 5/2000 [MASS=75742]/Annexin VI, member of the annexin family of calcium-dependent phospholipid binding proteins that shift between soluble and membrane associated states; involved in the budding of clathrin coated pits and may play a role in tumor suppression
SW:DOPD_HUMAN	DDT	26	1	1.02	0.00	SW:DOPD_HUMAN P30046 homo sapiens (human). d-dopachrome tautomerase (phenylpyruvate tautomerase ii). 5/2000 [MASS=12581]/D-dopachrome tautomerase, a tyrosinase-related zinc metalloenzyme that catalyzes the conversion of D-dopachrome to 5,6-dihydroxyindole in the melanin biosynthetic pathway, specifically expressed in melanin-producing cells, and is a melanoma tumor antigen
SW:SPCN_HUMAN	SPTAN1	11	2	1.02	0.35	SW:SPCN_HUMAN Q13813 homo sapiens (human). spectrin alpha chain, brain (spectrin, non-erythroid alpha chain) (fodrin alpha chain) (sptan1). 11/1997 [MASS=284282]/Non-erythroid alpha-spectrin 1 (alpha-fodrin), a member of a family of actin crosslinking proteins of the membrane-associated cytoskeleton, binds calcium, cleaved during apoptosis, acts as an autoantigen in the development of Sjogren syndrome
SW:TCPD_HUMAN	CCT4	7, 29, 33	4	1.01	0.17	SW:TCPD_HUMAN P50991 homo sapiens (human). t-complex protein 1, delta subunit (tcp-1-delta) (cct-delta) (stimulator of tar rna binding). 5/2000 [MASS=57839]/Chaperonin containing T-complex 1 subunit 4 (delta), part of a cytosolic hexadecamer structure involved in ATP-dependent folding of actin, tubulin and other proteins
SW:ENOA_HUMAN	ENO1	5, 18, 29	3	1.01	0.08	SW:ENOA_HUMAN P06733 homo sapiens (human). alpha enolase (ec 4.2.1.11) (2-phospho-d-glycerate hydro-lyase) (non-neural enolase) (nne) (phosphopyruvate hydratase). 7/1998 [MASS=47038]/Enolase 1 (alpha enolase), converts 2-phospho-D-glycerate to phosphoenolpyruvate in glycolysis, an autoantigen in multiple autoimmune diseases, shorter alternative form c-myc promoter binding protein (MPB1) is a transcriptional repressor
GP:U41806_1	SQSTM1	32, 41	4	1.01	0.21	GP:U41806_1 Human EBI3-associated protein p60 mRNA, complete cds; EBI3-associated protein. [MASS=47602]/Sequestosome 1 (ubiquitin-binding protein p62), a ubiquitin-binding protein with a zinc finger-like motif, a G protein-binding region and a PEST motif, interacts with several signal transduction pathways, may be involved in endosome to lysosome transport
SW:RINI_HUMAN	RNH	25, 39	1	1.01	0.00	SW:RINI_HUMAN P13489 homo sapiens (human). placental ribonuclease inhibitor (ribonuclease/angiogenin inhibitor) (rai) (ri). 12/1998 [MASS=49842]/Ribonuclease and angiogenin inhibitor, tightly binds and inhibits alkaline and neutral ribonucleases and angiogenin, functions in mRNA degradation and inhibition of HT-29 human colon adenocarcinoma cell binding to angiogenin (ANG)
SW:SYK_HUMAN	KARS	2, 35, 37	7	1.01	0.18	SW:SYK_HUMAN Q15046 homo sapiens (human). lysyl-trna synthetase (ec 6.1.1.6) (lysine--trna ligase) (lysrs) (kiaa0070). 7/1998 [MASS=68034]/Lysyl-tRNA synthetase, a class II aminoacyl tRNA synthetase, aminoacylates its cognate tRNAs with lysine for protein biosynthesis, packaged into HIV virions, exists as cytoplasmic and mitochondrial alternative forms
GP:AK023618_1	NDRG3	45	2	1.01	0.10	GP:AK023618_1 Homo sapiens cDNA FLJ13556 fis, clone PLACE1007705, moderately similar to Mus musculus mRNA for Ndr1 related protein Ndr3; unnamed protein product. [MASS=31484]/Protein with high similarity to human NDRG1, which is induced by nickel, homocysteine, 2-mercaptoethanol, and tunicamycin and is induced during colon carcinoma cell line differentiation
SW:TBA4_HUMAN	TUBA4	45	25	1.01	0.25	SW:TBA4_HUMAN P05215 homo sapiens (human), macaca fascicularis (crab eating macaque) (cynomolgus monkey), and mus musculus (mouse). tubulin alpha-4 chain. 7/1999 [MASS=49924]/Member of the tubulin-FtzA family, which are involved in polymer formation, has strong similarity to a region of mouse Tuba6, which is a structural protein that polymerizes to form microtubules
SW:IEFS_HUMAN	STIP1	42	5	1.01	0.17	SW:IEFS_HUMAN P31948 homo sapiens (human). transformation-sensitive protein ief ssp 3521. 10/1996 [MASS=62639]/Stress-induced phosphoprotein 1, a cochaperone that inhibits protein folding and may stabilize a heat shock protein complex on the lysosomal membrane, contains nine TPR (tetratricopeptide repeat) domains, which may mediate protein-protein interactions
SW:SRD6_HUMAN	PGRMC2	41	1	1.01	0.00	SW:SRD6_HUMAN O15173 homo sapiens (human). steroid receptor protein dg6. 5/2000 [MASS=23818]/Progesterone receptor membrane component 2, putative transmembrane steroid hormone receptor, preferentially expressed in placenta

GP:AF112214_1	RPL13	35	1	1.01	0.00	GP:AF112214_1 Homo sapiens ribosomal protein L13 mRNA, complete cds; RPL13. [MASS=19917]/Ribosomal protein L13, putative component of the 60S ribosomal subunit, expressed at higher levels in benign breast lesions than in carcinomas
SW:PON2_HUMAN	PON2	26	1	1.01	0.00	SW:PON2_HUMAN Q15165 homo sapiens (human). serum paraoxonase/arylesterase 2 (ec 3.1.1.2) (ec 3.1.8.1) (pon 2) (serum aryldiakylphosphatase 2) (a-esterase 2) (aromatic esterase 2). 7/1999 [MASS=39398]/Paraoxonase 2 (arylesterase 2), an antioxidant that protects low density lipoprotein against peroxidation, member of a family of proteins that hydrolyze toxic organophosphates; gene mutations are associated with an increased risk of coronary heart disease
SW:G19P_HUMAN	PRKCSH	5	3	1.01	0.47	SW:G19P_HUMAN P14314 homo sapiens (human). protein kinase c substrate, 80 kda protein, heavy chain (pkcsh) (80k-h protein). 7/1999 [MASS=59296]/Protein kinase C substrate 80K-H, acidic protein that is phosphorylated by type I and II protein kinase C, may play a role in fibroblast growth factor and Ras signal transduction, may be a receptor for advanced glycation end products
SW:DIAC_HUMAN	CTBS	5, 32	1	1.00	0.00	SW:DIAC_HUMAN Q01459 homo sapiens (human). di-n-acetylchitobiase precursor (ec 3.2.1.-). 7/1999 [MASS=43760]/Chitobiase (di-N-acetylchitobiase), a lysosomal glycosidase involved in the degradation of asparagine-linked glycoproteins
SW:KPB1_HUMAN	PHKA1	5, 18	3	1.00	0.09	SW:KPB1_HUMAN P46020 homo sapiens (human). phosphorylase b kinase alpha regulatory chain, skeletal muscle isoform (phosphorylase kinase alpha m subunit). 2/1996 [MASS=137338]/Phosphorylase kinase regulatory subunit alpha-1 (muscle), which phosphorylates and thereby activates muscle-specific glycogen phosphorylase (PYGM); mutations in the corresponding gene are associated with muscle glycogenosis, a glycogen storage disease
SW:TPIS_HUMAN	TPI1	5, 16, 18	9	1.00	0.18	SW:TPIS_HUMAN P00938 homo sapiens (human), and pan troglodytes (chimpanzee). triosephosphate isomerase (ec 5.3.1.1) (tim). 7/1998 [MASS=26538]/Triosephosphate isomerase 1, catalyzes the reversible interconversion of glyceraldehyde 3-phosphate and dihydroxyacetone phosphate in glycolysis; variant forms cause hemolytic anemia and neurodegeneration; variant form is an antigen on melanoma cells
GP:AB020697_1	DDX30	45	1	1.00	0.00	GP:AB020697_1 Homo sapiens mRNA for KIAA0890 protein, complete cds. [MASS=133938]/Protein containing two helicase conserved C-terminal domains and four double-stranded RNA binding domains, 6), has a region of low similarity to a region of S. pombe Cdc28p, which is an ATP-dependent RNA helicase involved in cell cycle progression
GP:AK022827_1	FLJ12765	45	1	1.00	0.00	GP:AK022827_1 Homo sapiens cDNA FLJ12765 fis, clone NT2RP2001511, moderately similar to Homo sapiens putative RNA-binding protein Q99 mRNA; unnamed protein product. [MASS=97330]/Protein with high similarity to C. elegans ALG-1, which is a piwi-related protein involved in the production of stRNA (small temporal RNA) of LIN-4, contains a PAZ (Piwi, Argonaut and Zwille) domain, which may mediate protein-protein interactions
GP:U25756_1	Ki nuclear autoantigen	45	1	1.00	0.00	GP:U25756_1 Human Ki nuclear autoantigen gene, partial cds; region of similarity to Ki nuclear autoantigen mRNA sequence, GenBank Accession Number U11292. [MASS=6323]
SW:CYTC_HUMAN	CST3	45	2	1.00	0.03	SW:CYTC_HUMAN P01034 homo sapiens (human). cystatin c precursor (neuroendocrine basic polypeptide) (gamma-trace) (post-gamma-globulin). 5/2000 [MASS=15799]/Cystatin C, a cysteine protease inhibitor regulated by TGFB1, may have roles in vascular remodeling and disease; mutations in the gene cause hereditary cystatin C amyloid angiopathy, in which amyloid aggregates form in the brain
GP:AC006942_1	ADTAA	43	5	1.00	0.28	GP:AC006942_1 Homo sapiens chromosome 19, cosmid R31181, complete sequence CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-A LARGE CHAIN); Non- consensussplice junction found at position 18996. [MASS=90046]/Adaptor-related protein complex 2 alpha 1 subunit, component of the clathrin adaptor complex, involved in vesicle transport
SW:CD59_HUMAN	CD59	41	8	1.00	0.26	SW:CD59_HUMAN P13987 homo sapiens (human). cd59 glycoprotein precursor (membrane attack complex inhibition factor) (macif) (mac-inhibitory protein) (mac-ip) (mem43 antigen) (protectin) (membrane inhibit [MASS=14177]/CD59 antigen (protectin), plasma membrane-secreted protein, inhibits formation of the membrane attack complex and protects against complement-mediated cell lysis, acts as a T-cell co-activator, may contribute to tumor cell escape from immune surveillance
SW:RL32_HUMAN	RPL32	35	7	1.00	0.12	SW:RL32_HUMAN P02433 homo sapiens (human), mus musculus (mouse), and rattus norvegicus (rat). 60s ribosomal protein l32. 6/1994 [MASS=15729]/Ribosomal protein L32, an RNA-binding structural component of the large 60S ribosomal subunit that is likely to play a role in protein biosynthesis
SW:TPP2_HUMAN	TPP2	32	5	1.00	0.14	SW:TPP2_HUMAN P29144 homo sapiens (human). tripeptidyl-peptidase ii (ec 3.4.14.10) (tpp ii) (tripeptidyl aminopeptidase). 11/1997 [MASS=138449]/Tripeptidyl peptidase II, a serine exopeptidase that may provide an alternative, non-proteasomal mechanism for protein turnover, participates in the apoptotic pathway activated by Shigella, upregulated in Burkitt's lymphoma cells overexpressing MYC
SW:ARP2_HUMAN	ACTR2	8, 11, 34	5	0.99	0.15	SW:ARP2_HUMAN O15142 homo sapiens (human). actin-like protein 2. 7/1999 [MASS=44761]/Actin-related protein 2 homolog, a component of the Arp2/3 protein complex, which is involved in actin filament nucleation and polymerization, may form the nucleation interface with the pointed end of the actin filament
SW:TERA_HUMAN	VCP	7, 43	41	0.99	0.20	SW:TERA_HUMAN P55072 homo sapiens (human). transitional endoplasmic reticulum atpase (ter atpase) (15s mg(2+)-atpase p97 subunit) (valosin containing protein) (vcp) [contains: valosin]. 7/1999 [MASS=89322]/Valosin-containing protein, a putative clathrin-binding ATPase involved in cell cycle control, ubiquitin-dependent protein degradation, and JAK-STAT signaling, may be involved in DNA repair via BRCA1, may be involved in receptor-mediated endocytosis
SW:EFA5_HUMAN	EFNA5	6, 41	1	0.99	0.00	SW:EFA5_HUMAN P52803 homo sapiens (human). ephrin-a5 precursor (eph-related receptor tyrosine kinase ligand 7) (lerk-7) (al-1). 5/2000 [MASS=26297]/Ephrin A5, a ligand of Eph-related receptor tyrosine kinases that is attached to the membrane via glycosylphosphatidylinositol linkage and is developmentally regulated in the brain, and may play a role during neurogenesis

SW:PUR6_HUMAN	PAICS	25, 26	7	0.99	0.09	SW:PUR6_HUMAN P22234 homo sapiens (human). multifunctional protein ade2 [includes: phosphoribosylaminoimidazole-succinocarboxamide synthase (ec 6.3.2.6) (saicar synthetase); phosphoribosylaminoimidazol [MASS=47079]/SAICAR (phosphoribosylaminoimidazole-succinocarboxamide) synthetase and AIR (phosphoribosylaminoimidazole) carboxylase, a bifunctional protein required for de novo purine biosynthesis
SW:ASAH_HUMAN	ASAH	16, 19	1	0.99	0.00	SW:ASAH_HUMAN Q13510 homo sapiens (human). acid ceramidase precursor (ec 3.5.1.23) (acylsphingosine deacylase) (n-acylsphingosine amidohydrolase) (ac) (putative 32 kda heart protein) (php32). 5/2000 [MASS=44650]/N-acylsphingosine amidohydrolase (acid ceramidase), catalyzes hydrolysis of ceramide to sphingosine and free fatty acid, inhibits apoptosis, upregulated in prostate cancer, deficiency is associated with Farber disease
GP:AB014555_1	HIP12	45	1	0.99	0.00	GP:AB014555_1 Homo sapiens mRNA for KIAA0655 protein, partial cds. [MASS=120902]/Huntingtin interacting protein 1 related protein, putative actin-binding protein predicted to be involved in actin polymerization, interacts with HIP1 but not Huntingtin (HD)
GP:AB037773_1	KIAA1352	45	8	0.99	0.20	GP:AB037773_1 Homo sapiens mRNA for KIAA1352 protein, partial cds; Start codon is not identified.. [MASS=138362]/
PIR2:I52882	RCD-8	45	2	0.99	0.02	PIR2:I52882 autoantigen - human [MASS=131858]/Protein of unknown function
PIR2:T46375	DKFZp434D1319	45	1	0.99	0.00	PIR2:T46375 hypothetical protein DKFZp434D1319.1 - human [MASS=49166]
SW:ADB1_HUMAN	AP1B1	43	20	0.99	0.27	SW:ADB1_HUMAN Q10567 homo sapiens (human). beta-adaptin 1 (plasma membrane adaptor ha2/ap2 adaptin beta subunit) (clathrin assembly protein complex 2 beta large chain) (ap105a). 7/1999 [MASS=104607]/Adaptor-related protein complex 1 beta 1, likely participates in clathrin-coated vesicle endocytosis and intracellular receptor transport; loss is associated with meningioma tumors
SW:TCPA_HUMAN	CCT1	33	8	0.99	0.36	SW:TCPA_HUMAN P17987 homo sapiens (human). t-complex protein 1, alpha subunit (tcp-1-alpha) (cct-alpha). 5/2000 [MASS=60344]/T-complex 1, subunit of the cytosolic chaperonin containing TCP-1 (CCT), may assist in the proper folding of tubulin, and may be involved in the response to chemical stressors
SW:PRS4_HUMAN	PSMC1	32	12	0.99	0.17	SW:PRS4_HUMAN Q03527 homo sapiens (human). 26s protease regulatory subunit 4 (p26s4). 12/1998 [MASS=49185]/Proteasome 26S subunit ATPase 1, an ATPase subunit of the 26S proteasome multicatalytic protease complex, may play a role in ubiquitin-dependent protein degradation, interacts with the papilloma virus oncoprotein E7
SW:HS9A_HUMAN	HSPCA	31	7	0.99	0.41	SW:HS9A_HUMAN P07900 homo sapiens (human). heat shock protein hsp 90-alpha (hsp 86). 5/2000 [MASS=84543]/Heat shock 90kD protein 1 alpha, a molecular chaperone that mediates protein folding, activates MAPK1, MAPK3, and caspase, may regulate a G protein-coupled receptor signaling pathway, may promote the proliferation of breast cancer cells
SW:RAPA_HUMAN	RAP1A	7, 41	1	0.98	0.00	SW:RAPA_HUMAN P10113 homo sapiens (human), rattus norvegicus (rat), and bos taurus (bovine). ras-related protein rap-1a (c21kg) (krev-1 protein) (gtp-binding protein smg-p21a) (g-22k). 12/1998 [MASS=20987]/RAP1A member of RAS oncogene family (Ras-related protein 1a), a member of the Ras superfamily of low molecular weight GTPases that is involved in cell cycle control and negative regulation of cellular proliferation, acts as a tumor suppressor
SW:RAN_HUMAN	RAN	7, 15, 23, 24, 41	3	0.98	0.04	SW:RAN_HUMAN P17080 homo sapiens (human). gtp-binding nuclear protein ran (tc4). 12/1998 [MASS=24354]/RAN, member of the ras family of GTP binding proteins, couples completion of DNA synthesis to mitosis and induces mitotic spindle formation, involved in nuclear transport of RNA and proteins, interacts with polyglutamate repeats of the androgen receptor
SW:DYNA_HUMAN	DCTN1	4, 7, 23	1	0.98	0.00	SW:DYNA_HUMAN Q14203 homo sapiens (human). dynactin, 150 kda isoform (150 kda dynein-associated polypeptide) (dp-150) (dap-150) (p150-glued) (p135) (fragment). 5/2000 [MASS=140784]/Dynactin 1 ((p150, Glued (Drosophila) homolog), microtubule associated protein, interacts with HsEg5 (KNSL1), may play a role in cell division, level is reduced in apoptotic cells
SW:LYN_HUMAN	LYN	34, 41	2	0.98	0.02	SW:LYN_HUMAN P07948 homo sapiens (human). tyrosine-protein kinase lyn (ec 2.7.1.112). 5/2000 [MASS=58443]/ protein tyrosine kinase, a non-receptor tyrosine kinase important in cytokine receptor- and IgE receptor-mediated signal transduction, regulates cell adhesion and apoptosis, plays a role in platelet activation and inflammatory responses
SW:CAZ2_HUMAN	CAPZA2	11, 31	1	0.98	0.00	SW:CAZ2_HUMAN P47755 homo sapiens (human). f-actin capping protein alpha-2 subunit (capz). 12/1998 [MASS=32949]/Capping protein Z-line (alpha 2), subunit of an actin-binding protein that may play a role in cell motility; corresponding gene is amplified in malignant gliomas and may be involved in tumorigenesis
GP:AB037728_1	KIAA1307	45	2	0.98	0.03	GP:AB037728_1 Homo sapiens mRNA for KIAA1307 protein, partial cds; Start codon is not identified.. [MASS=186192]/Protein containing two putative zinc finger in N-recognition domains
GP:AJ293573_1	CEZANNE	45	1	0.98	0.00	GP:AJ293573_1 Homo sapiens mRNA for zinc finger protein Cezanne (CEZANNE gene). [MASS=94401]/of unknown function, has a region of low similarity to a region of tumor necrosis factor alpha-induced protein 3 (mouse Tnfaip3), which is a cytoplasmic protein that blocks NF-kappaB activation and inhibits Tnf -induced apoptosis and necrosis
GP:AK025999_1	E2-230K	45	1	0.98	0.00	GP:AK025999_1 Homo sapiens cDNA: FLJ22346 fis, clone HRC06158; unnamed protein product. [MASS=81877]/Member of the ubiquitin-conjugating enzyme (E2) family, which catalyze the covalent attachment of ubiquitin to target proteins, has a region of moderate similarity to a region of mouse Birc6, which is a ubiquitin-conjugating enzyme
PIR2:G01447	C5ORF8	45	3	0.98	0.04	PIR2:G01447 GP36b glycoprotein - human [MASS=40229]/Protein of unknown function, has moderate similarity to a region of human LMAN1, which is a mannose-binding lectin involved in the traffic of glycoproteins between endoplasmic reticulum and the Golgi apparatus, and associated with a coagulation disorder
SW:SP02_HUMAN	DLG3	45	1	0.98	0.00	SW:SP02_HUMAN Q92796 homo sapiens (human). presynaptic protein sap102 (synapse-associated protein 102) (neuroendocrine-dlg) (ne-dlg). 5/2000 [MASS=90344]/Discs large (Drosophila) homolog 3 (neuroendocrine-dlg), putative guanylate kinase, inhibits cell proliferation, acts in neuronal cell adhesion, may facilitate neoplasm development or progression; corresponding gene is upregulated in ovarian carcinomas
SW:SPC1_HUMAN	KIAA0102	45	3	0.98	0.03	SW:SPC1_HUMAN Q15005 homo sapiens (human). microsomal signal peptidase 25 kda subunit (ec 3.4.-.-) (spc25) (kiaa0102). 5/2000 [MASS=25003]/Protein of unknown function

SW:TGT_HUMAN	TGT	45	6	0.98	0.19	SW:TGT_HUMAN P54578 homo sapiens (human). queuine trna-ribosyltransferase (ec 2.4.2.29) (trna-guanine transglycosylase) (guanine insertion enzyme). 5/2000 [MASS=55938]/tRNA-guanine transglycosylase, catalyses the exchange of queuine for guanine in the first position of the anticodon of tRNAs for asparagine, aspartic acid, histidine and tyrosine
SW:VE1_HPV14	E1	44	1	0.98	0.00	SW:VE1_HPV14 P36721 human papillomavirus type 14. replication protein e1. 7/1998 [MASS=69302]/ATP-DEPENDENT DNA HELICASE REQUIRED FOR INITIATION OF VIRAL DNA REPLICATION. IT FORMS A COMPLEX WITH THE VIRAL E2 PROTEIN. THE E1-E2 COMPLEX BINDS TO THE REPLICATION ORIGIN WHICH CONTAINS BINDING SITES FOR BOTH PROTEINS
SWN:SU12_HUMAN	GC20	35	4	0.98	0.06	SWN:SU12_HUMAN Q9unq9 homo sapiens (human). protein translation factor sui1 homolog a121. 8/2001 [MASS=12745]/Translation factor sui1 homolog, a translation initiation factor, plays a role in initiating translation, may modulate translation initiation during periods of cell stress such as UV-induced and endoplasmic reticulum stress
SW:C211_HUMAN	PTTG1IP	24	2	0.98	0.03	SW:C211_HUMAN P53801 homo sapiens (human). putative surface glycoprotein c21orf1 precursor (c21orf3). 7/1999 [MASS=20324]/Pituitary tumor-transforming gene 1 interacting protein, binds to pituitary tumor-transforming gene (PTTG1) and may promote nuclear translocation of PPTG1 to the nucleus
SW:DREB_HUMAN	DBN1	11	1	0.98	0.00	SW:DREB_HUMAN Q16643 homo sapiens (human). drebrin e. 7/1998 [MASS=71425]/Drebrin 1, developmentally regulated actin-binding protein expressed in brain, levels are reduced in Altzheimer's patients
SW:K6PL_HUMAN	PFKL	5, 18	8	0.97	0.17	SW:K6PL_HUMAN P17858 homo sapiens (human). 6-phosphofructokinase, liver type (ec 2.7.1.11) (phosphofructokinase 1) (phosphohexokinase) (phosphofructo-1-kinase isozyme b). 10/1996 [MASS=85148]/Liver phosphofructokinase, catalyses the phosphorylation of fructose-6-phosphate to fructose-1,6-bisphosphate in glycolysis, deficiency is linked to glycogenosis type VII while overexpression may lead to the cognitive diabilites of Down's syndrome
SW:PRO1_HUMAN	PFN1	11, 41	4	0.97	0.39	SW:PRO1_HUMAN P07737 homo sapiens (human). profilin i. 12/1998 [MASS=14923]/Profilin I, a protein that regulates actin polymerization in response to extracellular signals and may suppress breast cancer cell tumorigenicity
SW:MK01_HUMAN	MAPK1	10, 34, 41, 42	1	0.97	0.00	SW:MK01_HUMAN P28482 homo sapiens (human). mitogen-activated protein kinase 1 (ec 2.7.1.-) (extracellular signal-regulated kinase 2) (erk2) (mitogen-activated protein kinase 2) (map kinase 2) (mapk 2) [MASS=41390]/Mitogen-activated protein kinase 1, a serine-threonine kinase effector of the RAS-MAP kinase pathway, translocates to the nucleus to mediate transcription when activated, involved in the regulation of cell growth, differentiation, migration and apoptosis
GP:AK023834_1	FLJ13772	45	1	0.97	0.00	GP:AK023834_1 Homo sapiens cDNA FLJ13772 fis, clone PLACE4000300; unnamed protein product. [MASS=72580]/Protein of unknown function
PIR2:T47160	RAB14	45	6	0.97	0.25	PIR2:T47160 hypothetical protein DKFZp762K0911.1 - human [MASS=23897]/Ras-related GTP-binding protein 14, putative GTP binding protein and GTPase, induced in lung fibroblasts in response to endothelin treatment
SW:LYII_HUMAN	CD36L2	45	2	0.97	0.07	SW:LYII_HUMAN Q14108 homo sapiens (human). lysosome membrane protein ii (limp ii) (85 kda lysosomal membrane sialoglycoprotein) (lgp85) (cd36 antigen-like 2). 7/1998 [MASS=54159]/Lysosomal integral membrane protein II, a lysosomal membrane sialoglycoprotein with similarity to CD36 antigen
GP:AF092130_1	MADHIP	41	1	0.97	0.00	GP:AF092130_1 Homo sapiens GTP-binding protein Sara mRNA, complete cds. [MASS=22410]/Mothers against decapentaplegic homolog interacting protein receptor activation anchor (Smad anchor for receptor activation), an early endosomal protein involved in activin- and TGF beta-mediated Smad activation, binds phosphatidylinositol 3-phosphate
PIR2:S29815	P2RY4	41	1	0.97	0.00	PIR2:S29815 N-ras upstream protein NRU - human [MASS=88885]/Pyrimidinergic receptor P2Y4, a G protein-coupled nucleotide receptor activated by UTP and ATP and insensitive to inhibition by suramin, signals through stimulation of phosphoinositide hydrolysis and elevation of intracellular calcium
SW:PRCI_HUMAN	PSMA6	32	12	0.97	0.27	SW:PRCI_HUMAN P34062 homo sapiens (human), and rattus norvegicus (rat). proteasome iota chain (ec 3.4.99.46) (macropain iota chain) (multicatalytic endopeptidase complex iota chain) (27 kda prosomal pro [MASS=27399]/Proteasome subunit alpha type 6, a member of the alpha type prosomal gene family, part of a multicatalytic protease complex involved in cellular protein degradation; also binds RNA specifically
SW:ICLN_HUMAN	CLNS1A	42	1	0.96	0.00	SW:ICLN_HUMAN P54105 homo sapiens (human). chloride conductance regulatory protein icln (chloride channel, nucleotide sensitive 1a) (chloride ion current inducer protein) (clci) (reticulocyte picln). 12 [MASS=26215]/Chloride channel nucleotide-sensitive 1A, a putative chloride channel regulator, binds beta-actin, may regulate chloride transport and cell volume (especially in young red blood cells), may play a role in aqueous humor formation in the eye
PIR2:I38176	RAGA	41	1	0.96	0.00	PIR2:I38176 ras-related GTPase rag, splice form A [imported] - human [MASS=36566]/Ras-related GTP binding protein, a GTP-binding protein that lacks GTPase activity, interacts with RAGC (GTR2), RAGD, and the adenovirus 14.7 kDa E3 protein, may be part of the tumor necrosis factor alpha (TNF) signaling pathway
SW:IF5A_HUMAN	EIF5A	35	4	0.96	0.06	SW:IF5A_HUMAN P10159 homo sapiens (human). initiation factor 5a (eif-5a) (eif-4d) (rev binding factor). 5/2000 [MASS=16701]/Eukaryotic initiation factor 5A, a translation initiation factor, also an HIV-1 transactivator protein Rev cofactor that exports viral mRNA from the nucleus
SW:RM03_HUMAN	MRPL3	35	1	0.96	0.00	SW:RM03_HUMAN P09001 homo sapiens (human). mitochondrial 60s ribosomal protein l3. 8/1992 [MASS=38633]/Mitochondrial ribosomal protein L3, a likely component of the large mitochondrial 60S ribosomal subunit, may be involved in mRNA binding to the ribosome, can interact with the 3' UTR of hepatitis C; elevated levels are associated with hepatocarcinoma
SW:TCPH_HUMAN	CCT7	7, 33	2	0.95	0.10	SW:TCPH_HUMAN Q99832 homo sapiens (human). t-complex protein 1, eta subunit (tcp-1-eta) (cct-eta) (hiv-1 nef interacting protein). 7/1998 [MASS=59367]/Chaperonin containing T-complex polypeptide-1 (TCP1) subunit 7, the eta subunit of the chaperonin containing complex (CCT), plays a role in protein folding and in the response to chemical stress, may be required for proper folding of cyclin E

SW:APP2_HUMAN	APLP2	7, 16, 41	2	0.95	0.08	SW:APP2_HUMAN Q06481 homo sapiens (human). amyloid-like protein 2 precursor (amyloid protein homolog) (apph) (cdei-box binding protein) (cdebp). 5/2000 [MASS=86956]/Amyloid precursor-like protein 2, a nuclear protein whcih may contribute to neurogenesis and cell cycle control
SW:RHOA_HUMAN	ARHA	7, 11, 41	37	0.95	0.25	SW:RHOA_HUMAN P06749 homo sapiens (human), and bos taurus (bovine). transforming protein rhoa (h12). 7/1998 [MASS=21768]/Ras homolog gene family member A, monomeric GTPase of the Rho family that mediates cell surface receptor and integrin signaling, induces actin stress fiber and focal adhesion formation, activity may contribute to cellular transformation and tumor invasion
PIR2:T46270	FLNB	11, 41	12	0.95	0.39	PIR2:T46270 hypothetical protein DKFZp564N1563.1 - human (fragment) [MASS=77321]/Filamin B (beta, actin-binding protein-278), may be involved in actin cytoskeleton organization through interaction with the cytoplasmic domain of glycoprotein Ib alpha (GP1BA) and mediation of thyrotropin-induced actin microfilament disruption
SW:SYV_HUMAN	VARS2	1, 35, 37	4	0.95	0.14	SW:SYV_HUMAN P26640 homo sapiens (human). valyl-trna synthetase (ec 6.1.1.9) (valine--trna ligase) (valrs). 2/1996 [MASS=140377]/Valyl-tRNA synthetase 2, a putative class I tRNA sythetase, predicted to function in aminoacylation of valyl tRNAs for protein biosynthesis
GP:AB032993_1	GRIPAP1	45	1	0.95	0.00	GP:AB032993_1 Homo sapiens mRNA for KIAA1167 protein, partial cds; Start codon is not identified.; hj01786 cDNA clone for KIAA1167 has 1412-bp and 708-bp insertions (may be introns) after the positions 850 and 2258 of the sequence of KIAA1167, respectively.. [MASS=95259]/Protein of unknown function/Protein of unknown function
GP:AJ245820_1	psk-1	45	1	0.95	0.00	GP:AJ245820_1 Homo sapiens mRNA for type I transmembrane receptor (psk-1 gene). [MASS=92455]/Protein with high similarity to murine Sez6, which is expressed in the brain and may play a role in seizure, contains five sushi or short consensus repeat domains, which are found in complement and adhesion proteins, and an extracellular CUB domain
GPN:AL512750_1	FLJ11127	45	1	0.95	0.00	GP:BC011524_1 Homo sapiens, Similar to hypothetical protein, clone MGC:8793 IMAGE:3872837, mRNA, complete cds. [MASS=42196]/Protein of unknown function, has moderate similarity to uncharacterized human LOC90268
GP:D87930_1	PPP1R12A	41	3	0.95	0.13	GP:D87930_1 Homo sapiens mRNA for myosin phosphatase target subunit 1 (MYPT1); MYPT1. [MASS=115281]/Myosin phosphatase target subunit 1, a signal transducer that is involved in Rho-mediated regulation of myosin light chain dephosphorylation, may function in muscle contraction
SW:IMD2_HUMAN	IMPDH2	25	8	0.95	0.32	SW:IMD2_HUMAN P12268 homo sapiens (human). inosine-5'-monophosphate dehydrogenase 2 (ec 1.1.1.205) (imp dehydrogenase 2) (impdh-ii) (impd 2). 5/2000 [MASS=55805]/Inosine monophosphate dehydrogenase type 2, catalyzes the oxidation of inosine monophosphate to xanthosine monophosphate in GTP biosynthesis, required for T cell activation, a target for immunosuppressive and anticancer chemotherapy
SW:ODO1_HUMAN	OGDH	5, 18	9	0.94	0.18	SW:ODO1_HUMAN Q02218 homo sapiens (human). 2-oxoglutarate dehydrogenase e1 component, mitochondrial precursor (ec 1.2.4.2) (alpha-ketoglutarate dehydrogenase). 7/1999 [MASS=113475]/2-Oxoglutarate dehydrogenase (alpha-ketoglutarate dehydrogenase), E1 component of the complex that converts alpha-ketoglutarate to succinyl coenzyme A in the Krebs cycle; deficiency has been observed in Alzheimer and Parkinson disease
SW:SYQ_HUMAN	QARS	2, 25, 35, 37	2	0.94	0.20	SW:SYQ_HUMAN P47897 homo sapiens (human). glutaminyl-trna synthetase (ec 6.1.1.18) (glutamine--trna ligase) (glnrs). 5/2000 [MASS=87799]/Glutaminyl-tRNA synthetase, aminoacylates cognate tRNAs with glutamine for protein biosynthesis, also suppresses FAS (TNFRSF6)-mediated apoptosis by inhibiting ASK1 (MAP3K5) kinase activity, contains N-terminal appended and C-terminal catalytic domains
GP:AC005067_2	NPD007	45	2	0.94	0.17	GP:AC005067_2 Homo sapiens BAC clone CTB-122E10 from 7q11.23-q21.1, complete sequence; Supported by Human EST H08032.1 (NID:g872854), mouse EST AA870042.1 (NID:g2965487), and genscan; H_RG122E10.2b. [MASS=39202]/Member of the rhomboid family of integral membrane proteins
GP:AF226054_1	GK001	45	2	0.94	0.01	GP:AF226054_1 Homo sapiens GK001 (GK001) mRNA, complete cds. [MASS=55816]/Protein of unknown function, has moderate similarity to uncharacterized C. elegans ZK1058.4
PIR2:T47174	CORO1B	45	3	0.94	0.18	PIR2:T47174 hypothetical protein DKFZp762I166.1 - human (fragment) [MASS=31436]/Protein with high similarity to coronin 1a (human CORO1A), which is an actin-binding protein that binds to phagocyte oxidases and may transport them to the phagosome membrane, contains three WD domains (WD-40 repeat)
SW:S23A_HUMAN	SEC23A	43	5	0.94	0.18	SW:S23A_HUMAN Q15436 homo sapiens (human). protein transport protein sec23 homolog isoform a. 11/1997 [MASS=86147]/Sec23 homolog A, a putative intracellular transporter that plays a role in protein trafficking, interacts with SEC24B and SEC24C
GP:AK022853_1	NTT73	42	1	0.94	0.00	GP:AK022853_1 Homo sapiens cDNA FLJ12791 fis, clone NT2RP2001991, highly similar to SODIUM- AND CHLORIDE-DEPENDENT TRANSPORTER NTT73; unnamed protein product. [MASS=32264]/Orphan transporter V7-3, a member of the sodium:neurotransmitter symporter family with an unknown substrate specificity, predominantly expressed in neuronal tissues
SWN:E2BD_HUMAN	DKFZP586J0119	35	2	0.94	0.19	SWN:E2BD_HUMAN Q9ui10 homo sapiens (human). translation initiation factor eif-2b delta subunit (eif-2b gdp-gtp exchange factor). 8/2001 [MASS=57599]/Protein with strong similarity to eukaryotic translation initiation factor 2B delta subunit (rat Eif2b), which is a guanine nucleotide-exchange factor subunit of eIF-2B that mediates inhibition of eIF-2B, member of the initiation factor 2 subunit family
SW:CYPB_HUMAN	PPIB	33	15	0.94	0.20	SW:CYPB_HUMAN P23284 homo sapiens (human). peptidyl-prolyl cis-trans isomerase b precursor (ec 5.2.1.8) (ppiase) (rotamase) (cyclophilin b) (s-cyclophilin) (scylp) (cyp-s1). 7/1999 [MASS=22742]/Cyclophilin B, a peptidyl prolyl cis-trans isomerase that binds to and is inhibited by the immunosuppressive drug cyclosporin A, plays a role in protein folding, binds to the human immunodeficiency virus type I Gag polyprotein

SW:ACTB_HUMAN	ACTB	11	32	0.94	0.59	SW:ACTB_HUMAN P02570 homo sapiens (human), mus musculus (mouse), rattus norvegicus (rat), bos taurus (bovine), ovis aries (sheep), equus caballus (horse), trichosurus vulpecula (brush-tailed possum), an [MASS=41737]/Beta actin, a non-muscle cell actin that is the site of action for cytochalasin B effects on cell motility and also inhibits phospholipase D activity; mutation of the gene is associated with neutrophil dysfunction and recurrent infections
SW:DHAG_HUMAN	ALDH9A1	5	1	0.94	0.00	SW:DHAG_HUMAN P49189 homo sapiens (human). aldehyde dehydrogenase, e3 isozyme (ec 1.2.1.3) (gamma-aminobutyraldehyde dehydrogenase) (ec 1.2.1.19) (r-aminobutyraldehyde dehydrogenase). 5/2000 [MASS=53533]/Gamma-aminobutyraldehyde dehydrogenase (aldehyde dehydrogenase 9, subfamily A1), member of NAD(P)(+)-dependent aldehyde dehydrogenase family, catalyzes the dehydrogenation of gamma-aminobutyraldehyde, may regulate carnitine biosynthesis
SW:PGK1_HUMAN	PGK1	5, 18	16	0.93	0.18	SW:PGK1_HUMAN P00558 homo sapiens (human). phosphoglycerate kinase 1 (ec 2.7.2.3) (primer recognition protein 2) (prp 2). 7/1999 [MASS=44597]/Phosphoglycerate kinase 1, catalyzes conversion of 1,3-diphosphoglycerate to 3-phosphoglycerate in glycolysis, forming one molecule of ATP; PGK1 gene transcription is induced by hypoxia and mutation is associated with non-spherocytic hemolytic anemia
GPN:AB025194_1	HD-PTP	34, 41	1	0.93	0.00	GP:AB025194_1 Homo sapiens mRNA for protein tyrosine phosphatase HD-PTP, complete cds. [MASS=178974]/Member of the protein-tyrosine phosphatase family, has a region of strong similarity to a region of protein tyrosine phosphatase TD14 (rat Ptpn23), which is a putative tyrosine phosphatase that associates with cytoplasmic vesicles when overexpressed
GP:AC005545_2	AP3D1	26, 43	2	0.93	0.18	GP:AC005545_2 Homo sapiens chromosome 19, cosmid R26634, complete sequence; vesicle coat component, similar to alpha and gamma adaptins. [MASS=121170]/Adaptor-related protein complex 3 delta 1 subunit, a component of the AP-3 complex, involved in intracellular vesicle transport
SW:CST1_HUMAN	CSTF1	25, 37	1	0.93	0.00	SW:CST1_HUMAN Q05048 homo sapiens (human). cleavage stimulation factor, 50 kda subunit (cstf 50 kda subunit) (cf-1 50 kda subunit). 7/1998 [MASS=48358]/Cleavage stimulation factor subunit 1, the 50 kDa subunit of the cleavage stimulation factor complex required for pre-mRNA polyadenylation and 3'-end cleavage, interacts with BARD1 and the C-terminal domain of the RNA polymerase II large subunit
SWN:STX8_HUMAN	STX8	21, 23, 42, 43	1	0.93	0.00	SWN:STX8_HUMAN Q9unk0 homo sapiens (human). syntaxin 8. 8/2001 [MASS=26907]/Syntaxin 8, member of the soluble NSF attachment protein receptor (SNARE) family, plays a role in endosome trafficking, may mediate vesicle docking and fusion, may regulate CFTR -mediated chloride currents
GP:AK021647_1	MPPE1	45	1	0.93	0.00	GP:AK021647_1 Homo sapiens cDNA FLJ11585 fis, clone HEMBA1003692; unnamed protein product. [MASS=16310]/Metallophosphoesterase 1, a putative transmembrane phosphoesterase expressed only in brain
SW:EF1B_HUMAN	EEF1B1	45	3	0.93	0.05	SW:EF1B_HUMAN P24534 homo sapiens (human). elongation factor 1-beta (ef-1-beta). 6/1994 [MASS=24633]/Eukaryotic translation elongation factor 1 beta 2, putative component of the eukaryotic translation elongation complex
SW:PPAL_HUMAN	ACP2	45	1	0.93	0.00	SW:PPAL_HUMAN P11117 homo sapiens (human). lysosomal acid phosphatase precursor (ec 3.1.3.2) (lap). 12/1992 [MASS=48344]/Lysosomal acid phosphatase, a tartrate-inhibitable lysosomal enzyme; mice lacking Acp2 are more susceptible to seizures
PIR2:S69890	MIG2	7	2	0.93	0.03	PIR2:S69890 mitogen inducible gene mig-2 - human [MASS=81993]/Mitogen inducible 2, a mitogen-induced protein that may be involved in cell cycle control and cell proliferation
SW:GDE_HUMAN	AGL	5, 18	18	0.92	0.22	SW:GDE_HUMAN P35573 homo sapiens (human). glycogen debranching enzyme (glycogen debrancher) [includes: 4-alpha-glucanotransferase (ec 2.4.1.25) (oligo-1,4-1,4-glucantransferase); amylo-1,6-glucosidase [MASS=172497]/Glycogen debranching enzyme, (amylo-1,6-glucosidase 4-alpha-glucanotransferase), catalyzes glycantransferase and glucosidase activities required for glycogen degradation; mutations and dysregulation are associated with type III glycogen storage diseases
SW:SYEP_HUMAN	EPRS	2, 35, 37	23	0.92	0.84	SW:SYEP_HUMAN P07814 homo sapiens (human). multifunctional aminoacyl-trna synthetase [includes: glutamyl-trna synthetase (ec 6.1.1.17) (glutamate--trna ligase); prolyl-trna synthetase (ec 6.1.1.15) (pro [MASS=163026]/Glutamyl-prolyl-tRNA synthetase, a bifunctional enzyme with two functionally separable domains, one that aminoacylates prolyl-tRNA with proline and another that is believed to aminoacylate glutamyl-tRNA with glutamate for protein biosynthesis
GP:AF151793_1	AIP1	11, 41	8	0.92	0.09	GP:AF151793_1 Homo sapiens ALG-2 interacting protein 1 (AIP1) mRNA, complete cds. [MASS=96079]/Protein with very strong similarity to murine Mm.28049, which interacts with the activin type IIA receptor and signaling molecule Smad3, has very strong similarity to rat Rn.29998, which is a synaptic scaffolding protein, contains PDZ and WW domains
SW:UTRO_HUMAN	UTRN	11, 16	7	0.92	0.24	SW:UTRO_HUMAN P46939 homo sapiens (human). utrophin (dystrophin-related protein 1) (drp1) (drp). 7/1999 [MASS=394494]/Utrophin, a membrane-associated protein that interacts with cytoskeletal proteins, associated with muscle and neuromuscular junction development and cell adhesion, may partially compensate for dystrophin (DMD) deficiency in Duchenne's muscular dystrophy
GPN:AF130092_1	KIAA1049	45	4	0.92	0.08	GP:AF130092_1 Homo sapiens clone FLB9715 PRO2620 mRNA, complete cds; predicted protein of HQ2620. [MASS=53655]/Protein of unknown function, has low similarity to uncharacterized S. pombe Spac1142.01p
SW:CN37_HUMAN	CNP	45	14	0.92	0.15	SW:CN37_HUMAN P09543 homo sapiens (human). 2',3'-cyclic nucleotide 3'-phosphodiesterase (ec 3.1.4.37) (cnp) (cnpase). 5/2000 [MASS=47579]/2'3'-Cyclic nucleotide 3' phosphodiesterase, a myelin-associated phosphodiesterase that is involved in regulation of central nervous system myelination
SW:ACTZ_HUMAN	ACTR1A	43	7	0.92	0.04	SW:ACTZ_HUMAN P42024 homo sapiens (human), mus musculus (mouse), and canis familiaris (dog). alpha-centractin (centractin) (centrosome-associated actin homolog) (actin-rpv) (arp1). 7/1999 [MASS=42614]/Actin-related protein 1, a component of the dynactin complex involved in transport along microtubules, associates with centrophilin NUMA1 at nuclear envelope breakdown, expression is significantly reduced in Down syndrome fetal brain

GP:AF284422_1	LOC56996	42	1	0.92	0.00	GP:AF284422_1 Homo sapiens cation-chloride cotransporter-interacting protein mRNA, complete cds; cation-chloride cotransporter family; CIP1; 96.2 kDa; predicted to contain 12 transmembrane domains and cytoplasmic N-and C-termini. [MASS=96171]/Cation-chloride cotransporter-interacting protein 1, inhibits Na+-K+-Cl- cotransporter 1-mediated transport activity, may modulate cation-chloride cotransporter activity or kinetics through heterodimer formation
SW:MOT4_HUMAN	SLC16A3	42	1	0.92	0.00	SW:MOT4_HUMAN O15374 homo sapiens (human). monocarboxylate transporter 4 (mct 4). 5/2000 [MASS=54022]/Monocarboxylate transporter, member of a family of proton-linked monocarboxylate transporters, may transport monocarboxylates such as lactate across the plasma membrane
GP:AC002306_1	EDG4	41	1	0.92	0.00	GP:AC002306_1 Homo sapiens DNA from chromosome 19-cosmid R33799, genomic sequence, complete sequence; hypothetical human G-protein coupled receptor on 19p; hypothetical human protein with BLASTX similarity to G protein-coupled receptor Rec1.3 [Mus musculus],(U4823 [MASS=39084]/Endothelial differentiation lysophosphatidic acid (LPA) G protein-coupled receptor 4, activated by saturated and unsaturated LPA, elevates intracellular Ca2+ and cAMP levels, activates MAP kinase, may mediate LPA-induced tumor growth in ovarian cancer
SW:GBB2_HUMAN	GNB2	41	23	0.92	0.22	SW:GBB2_HUMAN P11016 homo sapiens (human). guanine nucleotide-binding protein g(i)/g(s)/g(t) beta subunit 2 (transducin beta chain 2). 5/2000 [MASS=37331]/Guanine nucleotide binding protein beta 2, component of heterotrimeric G protein complexes that transduce signals from G protein-coupled receptors to intracellular effectors, complex with Ggamma mediates inhibition of N- and PQ-type calcium channels
GP:Y18206_1	PPP1R6	36	1	0.92	0.00	GP:Y18206_1 Homo sapiens mRNA for protein phosphatase 1 (PPP1R6). [MASS=32559]/Protein phosphatase 1 regulatory 6, glycogen targeting subunit of protein phosphatase 1, functions in glycogen metabolism in muscle
SW:TCPG_HUMAN	CCT3	33	7	0.92	0.12	SW:TCPG_HUMAN P49368 homo sapiens (human). t-complex protein 1, gamma subunit (tcp-1-gamma) (cct-gamma). 12/1998 [MASS=60331]/Cytosolic chaperonin containing TCP-1 (CCT) gamma subunit, may act as a chaperonin and assist in the proper folding of tubulin, actin, and centractin
SW:143T_HUMAN	YWHAQ	7, 41, 43	3	0.91	0.05	SW:143T_HUMAN P27348 homo sapiens (human). 14-3-3 protein tau (14-3-3 protein theta) (14-3-3 protein t-cell) (hs1 protein). 11/1997 [MASS=27764]/14-3-3 theta (14-3-3 tau in T-cells), may modulate T-cell signaling and cytokine expression through interaction with and inhibition of protein kinase C and phosphatidylinositol 3-kinase, may promote cell survival during amyotrophic lateral sclerosis (ALS)
GP:AB006534_1	SPINT2	7, 41	1	0.91	0.00	GP:AB006534_1 Homo sapiens mRNA for hepatocyte growth factor activator inhibitor type 2, complete cds. [MASS=28169]/Serine protease inhibitor Kunitz type 2 (bikunin), inhibits hepatocyte growth factor activator (HGFAC) and serine proteases involved in coagulation and fibrinolysis, overexpressed in pancreatic cancer, may play roles in urolithiasis and glioma progression
SW:ITA5_HUMAN	ITGA5	6, 41	2	0.91	0.03	SW:ITA5_HUMAN P08648 homo sapiens (human). integrin alpha-5 precursor (fibronectin receptor alpha subunit) (integrin alpha-f) (vla-5) (cd49e). 7/1999 [MASS=114508]/Integrin alpha 5, acts as a receptor for fibronectin, mediates binding of the cell to the extracellular matrix, involved in cell migration and trophoblast invasion; upregulation is associated with metastatic melanomas and carcinomas
GP:U66669_1	HIBCH	2, 19	1	0.91	0.00	GP:U66669_1 Homo sapiens 3-hydroxyisobutyryl-coenzyme A hydrolase mRNA, complete cds. [MASS=42908]/Beta-hydroxyisobutyryl-coenzyme A hydrolase, enzyme that hydrolyzes 3-hydroxyisobutyryl CoA, an intermediate of valine catabolism
SW:KIME_HUMAN	MVK	19, 34	1	0.91	0.00	SW:KIME_HUMAN Q03426 homo sapiens (human). mevalonate kinase (ec 2.7.1.36) (mk). 7/1999 [MASS=42451]/Mevalonate kinase (mevalonic aciduria), a peroxisomal enzyme involved in isoprenoid and cholesterol biosynthesis; mutations in the corresponding gene cause mevalonic aciduria, hyperimmunoglobulinemia D and periodic fever syndrome
GP:AB015798_1	HSJ2	10, 33	1	0.91	0.00	GP:AB015798_1 Homo sapiens HSJ2 mRNA for DnaJ homolog, complete cds; DnaJ homologue HSJ2a. [MASS=36087]/DnaJ homolog subfamily A member 1, heat shock protein, expressed in many tissues
SW:BTF3_HUMAN	BTF3	29	1	0.91	0.00	SW:BTF3_HUMAN P20290 homo sapiens (human). transcription factor btf3 (rna polymerase b transcription factor 3). 12/1998 [MASS=22168]/Basic transcription factor 3, a general transcription factor that forms a stable complex with RNA polymerase II and is required for transcriptional initiation by RNA polymerase II, and may be a substrate for protein kinase CK2 (CSNK2B)
SW:TBB2_HUMAN	TUBB2	11	30	0.91	0.31	SW:TBB2_HUMAN P05217 homo sapiens (human). tubulin beta-2 chain. 7/1999 [MASS=49831]/Tubulin beta 2, a member of the tubulin family of structural proteins that polymerizes to form microtubules, soluble form binds nuclear envelope, may serve as a marker for prostate adenocarcinoma
SW:RHOG_HUMAN	ARHG	7, 41	5	0.90	0.29	SW:RHOG_HUMAN P35238 homo sapiens (human), and cricetus cricetus (black-bellied hamster). rho-related gtp-binding protein rhog. 11/1995 [MASS=21309]/Aplysia ras-related homolog G (RhoG), a Ras-related GTP-binding protein of the rho-subfamily which regulates reorganization of the actin cytoskeleton and may be involved in the regulation of cholesterol excretion in patients with Tangier disease
SW:TCPB_HUMAN	CCT2	7, 33	5	0.90	0.26	SW:TCPB_HUMAN P78371 homo sapiens (human). t-complex protein 1, beta subunit (tcp-1-beta) (cct-beta). 7/1999 [MASS=57488]/Chaperonin containing T-complex polypeptide-1 (TCP1) subunit 2, the beta subunit of the chaperonin containing complex (CCT), plays a role in the folding of cytosolic proteins, may be required for the proper folding of cyclin E
SW:G25B_HUMAN	CDC42	7, 23, 34, 41, 43	13	0.90	0.13	SW:G25B_HUMAN P21181 homo sapiens (human), mus musculus (mouse), and bos taurus (bovine). g25k gtp-binding protein, brain isoform (gp) (cdc42 homolog). 12/1998 [MASS=21311]/Cell division cycle 42 (GTP binding protein 25kD), Rho GTPase involved in actin cytoskeleton organization, cell migration, cell cycle progression and apoptosis, downregulated in fibroblasts and macrophages from patients with Tangiers disease

SW:VPP1_HUMAN	ATP6N1	36, 42	3	0.90	0.19	SW:VPP1_HUMAN Q93050 homo sapiens (human). clathrin-coated vesicle/synaptic vesicle proton pump 116 kda subunit (ec 3.6.1.34) (vacuolar proton pump subunit 1). 12/1998 [MASS=95751]/ATPase (H+ transporting lysosomal (vacuolar proton pump) noncatalytic accessory protein 1A (110/116 kDa), a component of a multisubunit enzyme which couples ATP hydrolysis to proton translocation
SW:UB5A_HUMAN	UBE2D1	32, 34	2	0.90	0.01	SW:UB5A_HUMAN P51668 homo sapiens (human). ubiquitin-conjugating enzyme e2-17 kda 1 (ec 6.3.2.19) (ubiquitin- protein ligase) (ubiquitin carrier protein) (e2(17)kb 1). 12/1998 [MASS=16602]/Ubiquitin-conjugating enzyme E2D1, member of the ubiquitin-conjugating enzyme subfamily that catalyzes the ubiquitination of cellular proteins and marks them for degradation, acts with the ubiquitin protein ligase E6AP (UBE3A) to ubiquitinate p53 (TP53)
GP:AF250859_1	MGAT1.2	45	1	0.90	0.00	GP:AF250859_1 Homo sapiens UDP-GlcNAc:a-3-D-mannoside b1,2-N-acetylglucosaminyltransferase I.2 (MGAT1.2) mRNA, partial cds; glycosyltransferase; similar to b1,2-N-acetylglucosaminyltransferase I; GnTI.2. [MASS=65499]/O-linked mannose beta1,2-N-acetylglucosaminyltransferase, has specific activity for alpha-linked terminal Man residues and is predicted to be involved in glycoprotein metabolism
SW:ROH2_HUMAN	HNRPH2	45	1	0.90	0.00	SW:ROH2_HUMAN P55795 homo sapiens (human). heterogeneous nuclear ribonucleoprotein h' (hnrnp h') (ftp-3). 11/1997 [MASS=49264]/Heterogeneous nuclear ribonucleoprotein H2, a putative heterogeneous nuclear ribonucleoprotein that contains three repeats that resemble the RNA recognition motif (RRM)
GP:AF004563_1	STXBP1	21, 43	4	0.89	0.26	GP:AF004563_1 Homo sapiens hUNC18b alternatively-spliced mRNA, complete cds; alternatively-spliced; similar to rat n-Sec1. [MASS=68736]/Syntaxin-binding protein 1, binds syntaxins, may be involved in synaptic vesicle exocytosis
GP:AF128536_1	PACSIN2	11, 43	4	0.89	0.45	GP:AF128536_1 Homo sapiens cytoplasmic phosphoprotein PACSIN2 mRNA, complete cds; related to PACSIN1; contains CDC15 N-terminal domain, 3 EH domain-binding NPF motifs, and a C-terminal SH3 domain. [MASS=55905]/Protein kinase C and casein kinase substrate in neurons 2, member of the PACSIN family of cytoplasmic adapter proteins, may function to organize the actin cytoskeleton and regulate vesicular traffic
GP:AF236056_1	GP73	45	3	0.89	0.04	GP:AF236056_1 Homo sapiens golgi membrane protein GP73 mRNA, complete cds. [MASS=45202]/Golgi phosphoprotein 2, an integral membrane Golgi protein that is epithelial cell-specific in healthy liver, upregulated in hepatocytes in both nonviral- and viral-associated liver disease including adult giant-cell hepatitis
GP:AF284574_1	NIT2	45	1	0.89	0.00	GP:AF284574_1 Homo sapiens Nit protein 2 (NIT2) mRNA, complete cds; Nit2; similar to the Nit domains of Caenorhabditis elegans NitFhit and Drosophila melanogaster NitFhit. [MASS=30608]/NIT2
GP:AK022868_1	FLJ12806	45	1	0.89	0.00	GP:AK022868_1 Homo sapiens cDNA FLJ12806 fis, clone NT2RP2002235; unnamed protein product. [MASS=34951]/Protein of unknown function
PIR2:T46298	FLJ14362	45	1	0.89	0.00	PIR2:T46298 hypothetical protein DKFZp434I1110.1 - human (fragment) [MASS=18088]
SW:FA5_HUMAN	F5	45	1	0.89	0.00	SW:FA5_HUMAN P12259 homo sapiens (human). coagulation factor v precursor (activated protein c cofactor). 11/1997 [MASS=251701]/Coagulation factor V, a cofactor in the prothrombinase complex that plays a role in the regulation of blood coagulation; alterations of corresponding gene are associated with activated protein C (APC) resistance, parahemophilia, and thrombosis
SW:SR72_HUMAN	SRP72	45	1	0.89	0.00	SW:SR72_HUMAN O76094 homo sapiens (human). signal recognition particle 72 kda protein (srp72). 12/1998 [MASS=74475]/Signal recognition particle 72, a ribonucleoprotein that undergoes cleavage by caspase during apoptosis; protein is an autoantigen in patients with dermatomyositis and systemic lupus erythematosus
SW:VATX_HUMAN	ATP6D	42	2	0.89	0.03	SW:VATX_HUMAN Q02547 homo sapiens (human). vacuolar atp synthase subunit ac39 (ec 3.6.1.34) (v-atpase ac39 subunit) (32 kda accessory protein) (p39). 11/1997 [MASS=31704]/Vacuolar H+-ATPase proton pump (subunit D), an accessory subunit in the peripheral catalytic V1 complex, may be involved in coupling ATP hydrolysis (V1 complex) and proton transport (V0 complex)
GP:AB002382_1	CTNND1	6, 11, 41	18	0.88	0.31	GP:AB002382_1 Human mRNA for KIAA0384 gene, complete cds. [MASS=104952]/Catenin delta 1, a member of the catenin family of cadherin-binding proteins that link cadherins to the cytoskeleton, acts in cell signaling, plays a role in cell migration, loss of expression is correlated with bladder, colorectal and other cancer
GP:AB009398_1	PSMD13	32, 34	5	0.88	0.24	GP:AB009398_1 Homo sapiens mRNA for 26S proteasome subunit p40.5, complete cds. [MASS=42945]/Proteasome (prosome, macropain) 26S subunit (non-ATPase, 13), a subunit of the PA700 regulatory complex of the 26S proteasome
PIR2:T46412	NEDD4	26, 29, 32, 34, 42	1	0.88	0.00	PIR2:T46412 ubiquitin--protein ligase (EC 6.3.2.19) NEDD4 - human (fragment) [MASS=95283]/Neural cell precursor expressed developmentally downregulated 4, ubiquitin-protein ligase with multiple WW domains, binds to and reduces the activity of epithelial sodium channels, may play a role in neural differentiation, regulated by kinase SGK
GP:AF044670_1	VAP33	21, 31, 43	2	0.88	0.24	GP:AF044670_1 Homo sapiens 33 kDa Vamp-associated protein (VAP33) mRNA, complete cds; VAP-33. [MASS=27318]/Vesicle-associated membrane protein (VAMP)-associated protein A, binds v-SNAREs, t-SNAREs, VAPB, and VAMP, predicted to be involved in vesicle transport and fusion
PIR2:B55053	SCYE1	2, 35, 41	9	0.88	0.07	PIR2:B55053 endothelial monocyte-activating protein II precursor - human [MASS=34254]/Endothelial monocyte activating polypeptide II, a proinflammatory cytokine that interacts with ATP synthase and inhibits endothelial cell growth, released during apoptosis, may sensitize tumors to killing by tumor necrosis factor alpha (TNF)
GP:AB037856_1	FENS-1	45	3	0.88	0.16	GP:AB037856_1 Homo sapiens mRNA for KIAA1435 protein, partial cds; Start codon is not identified.. [MASS=46908]/Protein containing two FYVE zinc finger domains, which bind phosphatidylinositol 3-phosphate, and 12 WD domains (WD-40 repeats), has a region of low similarity to a region of F-box/WD-repeat protein (C. elegans LIN-23), which regulates cell proliferation
GP:AK022499_1	FLJ00365	45	1	0.88	0.00	GP:AK022499_1 Homo sapiens cDNA FLJ12437 fis, clone NT2RM1000118, weakly similar to CALCINEURIN B SUBUNIT; unnamed protein product. [MASS=26041]

SW:EF1D_HUMAN	EEF1D	45	2	0.88	0.01	SW:EF1D_HUMAN P29692 homo sapiens (human). elongation factor 1-delta (ef-1-delta). 6/1994 [MASS=31221]/Eukaryotic translation elongation factor 1 delta, a guanine nucleotide exchange protein that gets hyperphosphorylated in cells infected with herpesviruses, binds HIV-1 protein Tat and causes a reduction of host mRNA translation efficiency
GP:AF087020_1	PZR	41	12	0.88	0.08	GP:AF087020_1 Homo sapiens protein zero related protein (PZR) mRNA, complete cds; immunoglobulin superfamily member. [MASS=29082]/Myelin protein zero-like 1, a member of the immunoglobulin superfamily that is a concanavalin A (ConA) receptor, mediates ConA and c-Src (SRC) signaling, may be a plasma membrane anchor for SHP-2 (PTPN11) type I, contains two ITIM motifs
SW:RL8_HUMAN	RPL8	35	4	0.88	0.57	SW:RL8_HUMAN P25120 homo sapiens (human), rattus norvegicus (rat), and mus musculus (mouse). 60s ribosomal protein l8. 5/2000 [MASS=28025]/Ribosomal protein L8, putative component of the large 60S ribosomal subunit
GP:D38048_1	PSMB7	32	1	0.88	0.00	GP:D38048_1 Human mRNA for proteasome subunit z, complete cds. [MASS=29965]/Proteasome (prosome, macropain) subunit beta 7, a subunit of the 26S proteasome, replaced by PSMB10 upon interferon gamma (IFNG) stimulation
SW:PRC8_HUMAN	PSMA3	32	2	0.88	0.06	SW:PRC8_HUMAN P25788 homo sapiens (human). proteasome component c8 (ec 3.4.99.46) (macropain subunit c8) (multicatalytic endopeptidase complex subunit c8). 12/1998 [MASS=28302]/Proteasome subunit alpha type 3, the C8 subunit of the 20S core proteasome, which is a multicatalytic proteinase complex involved in cellular protein degradation; expression is increased in skeletal muscle of slim AIDS patients
SW:KCRB_HUMAN	CKB	18	3	0.88	0.26	SW:KCRB_HUMAN P12277 homo sapiens (human). creatine kinase, b chain (ec 2.7.3.2) (b-ck). 7/1999 [MASS=42644]/Brain creatine kinase, involved in energy homeostasis, expression is elevated in some forms of cancer; CK-MB is a dimer of subunits CKM and CKB, and is an important serum marker for acute myocardial infarction
SW:ANX7_HUMAN	ANXA7	21, 42	4	0.87	0.02	SW:ANX7_HUMAN P20073 homo sapiens (human). annexin vii (synexin). 5/2000 [MASS=50316]/Annexin A7 (synexin), a calcium-dependent GTPase that acts as a voltage-dependent calcium channel, interaction with galectin 3 (LGALS3) suggests roles in apoptosis and exocytosis, may function as a tumor suppressor
SW:SYM_HUMAN	MARS	2, 35, 37	9	0.87	0.18	SW:SYM_HUMAN P56192 homo sapiens (human). methionyl-trna synthetase (ec 6.1.1.10) (methionine--trna ligase) (metrs). 12/1998 [MASS=101129]/Methionine-tRNA synthetase, putative tRNA synthetase that is predicted to aminoacylate its cognate tRNAs with methionine for protein biosynthesis, required for rRNA synthesis in the nucleolus
PIR2:T08753	E46L	45	2	0.87	0.13	PIR2:T08753 hypothetical protein DKFZp586H2219.1 - human [MASS=53489]/Protein of unknown function, has strong similarity to uncharacterized rat Sca10
GP:AF124145_1	AMFR	41	1	0.87	0.00	GP:AF124145_1 Homo sapiens autocrine motility factor receptor (AMFR) mRNA, complete cds. [MASS=73022]/Autocrine motility factor receptor, a cell surface transmembrane glycoprotein involved in cell motility signaling and metastasis, acts as a ubiqiuitin ligase involved in protein degradation, associated with tumor progression in various carcinomas
SW:SERC_HUMAN	PSA	2	2	0.87	0.15	SW:SERC_HUMAN Q9y617 homo sapiens (human). phosphoserine aminotransferase (ec 2.6.1.52) (psat). 5/2000 [MASS=35189]/Member of the aminotransferases class-V family of pyridoxal-phosphate-dependent enzymes, has moderate similarity to S. cerevisiae Ser1p, which is a 3-phosphoserine transaminase involved in synthesis of serine from 3-phosphoglycerate
SW:GPS1_HUMAN	GPS1	7, 34, 41	4	0.86	0.12	SW:GPS1_HUMAN Q13098 homo sapiens (human). g protein pathway suppressor 1 (gps1 protein) (mfh protein). 11/1997 [MASS=53372]/G protein pathway suppressor 1, suppressor of G protein and MAP kinase-mediated signaling pathways
SW:ENOB_HUMAN	ENO3	5, 18	4	0.86	0.13	SW:ENOB_HUMAN P13929 homo sapiens (human). beta enolase (ec 4.2.1.11) (2-phospho-d-glycerate hydro-lyase) (skeletal muscle enolase) (mse). 7/1998 [MASS=46856]/Enolase 3 (muscle-specific enolase, beta enolase), a putative enolase which catalyzes the conversion of 2-phospho-D-glycerate to phosphoenolpyruvate in muscle glycolysis, deficiency is associated with exercise intolerance and myalgias
SW:MPRI_HUMAN	IGF2R	36, 41, 43	76	0.86	0.21	SW:MPRI_HUMAN P11717 homo sapiens (human). cation-independent mannose-6-phosphate receptor precursor (ci man-6-p receptor) (ci-mpr) (insulin-like growth factor ii receptor) (300 kda mannose 6-phosphate [MASS=274309]/Insulin-like growth factor II receptor, functions in transport of mannose 6-phosphate-containing lysosomal enzymes and IGF-II maturation and clearance, mediates granzyme B-induced apoptosis, putative tumor suppressor
SW:HIP_HUMAN	ST13	29, 33	5	0.86	0.10	SW:HIP_HUMAN P50502 homo sapiens (human). hsc70-interacting protein (progesterone receptor-associated p48 protein) (putative tumor suppressor st13). 5/2000 [MASS=41332]/Suppression of tumorigenicity 13 (Hsp70-interacting protein), acts as an Hsc70 cochaperone, contains tetratricopeptide repeats, participates in protein complex assembly, heat shock response, and lysosomal transport; downregulated in colorectal carcinoma
SW:DNJ2_HUMAN	DNAJA1	10, 33	1	0.86	0.00	SW:DNJ2_HUMAN P31689 homo sapiens (human). dnaj protein homolog 2 (hsj-2). 7/1999 [MASS=44868]/DnaJ homolog subfamily A member 1, heat shock protein, expressed in many tissues
SW:ADB_HUMAN	AP2B1	43	5	0.86	0.14	SW:ADB_HUMAN P21851 homo sapiens (human), rattus norvegicus (rat), and bos taurus (bovine). beta-adaptin (plasma membrane adaptor ha2/ap2 adaptin beta subunit) (clathrin assembly protein complex 2 beta [MASS=104553]/Adaptor-related protein complex 2 beta 1 subunit, a large subunit of the AP2 adaptor complex, involved in clathrin coat assembly at the plasma membrane; may bind to the transmembrane envelope protein of HIV-1 and HTLV retroviruses
PIR1:I38908	DDB1	14	2	0.86	0.03	SW:DDB1_HUMAN Q16531 h dna damage binding protein 1 (damage-specific dna binding protein 1) (ddb p127 subunit) (ddba) (uv-damaged dna-binding protein 1) (uv-ddb 1) (xeroderma pigmentosum group e complem [MASS=126968]/Damage-specific DNA-binding protein 1, larger subunit of a complex that recognizes and binds damaged DNA and stimulates repair, not essential for DNA repair; deficiencies are associated with xeroderma pigmentosum complementation group E

GP:AF144074_1	G2AN	5	3	0.86	0.05	GP:AF144074_1 Homo sapiens glucosidase II alpha subunit mRNA, complete cds; similar to sequences encoded by GenBank Accession Numbers D42041 and U92793. [MASS=109438]/Alpha glucosidase II (alpha neutral subunit), trims alpha(1,3)-linked glucose from Glc(3)Man(9)GlcNAc(2) structures, localizes to the endoplasmic
SW:G3P2_HUMAN	GAPD	5, 14, 18	2	0.85	0.01	SW:G3P2_HUMAN P04406 homo sapiens (human). glyceraldehyde 3-phosphate dehydrogenase, liver (ec 1.2.1.12). 7/1999 [MASS=35922]/Glyceraldehyde-3-phosphate dehydrogenase, catalyzes reversible oxidation and phosphorylation of glyceraldehyde-3-phosphate to 1,3-diphosphoglycerate in glycolysis, involved in apoptosis, may play a role in neurodegeneration in diseases like Alzheimer's
SW:KPC1_HUMAN	PRKCB1	34, 41	1	0.85	0.00	SW:KPC1_HUMAN P05771 homo sapiens (human). protein kinase c, beta-i type (ec 2.7.1.-) (pkc-beta-1). 7/1999 [MASS=76839]/Protein kinase C beta 1, conventional PKC expressed as beta I and beta II forms, beta II mediates G2/M phase transition, mitotic nuclear envelope breakdown, neutrophil NADPH oxidase assembly; rat Prkcb1 activity is enhanced in diabetes mellitus
GP:U45976_1	PICALM	31, 43	1	0.85	0.00	GP:U45976_1 Human clathrin assembly protein lymphoid myeloid leukemia (CALM) mRNA, complete cds. [MASS=70695]/Phosphatidylinositol binding clathrin assembly protein, binds to clathrin heavy chain (CLTC) and plays a role in coated pit internalization; rearrangements in the corresponding gene are associated with acute lymphoblastic and acute myeloid leukemias
SWN:P23_HUMAN	p23	19, 41	2	0.85	0.01	SWN:P23_HUMAN Q15185 homo sapiens (human). telomerase-binding protein p23 (hsp90 co-chaperone) (progesterone receptor complex p23). 8/2001 [MASS=18697]/Inactive progesterone receptor (23kD), cochaperone with prostaglandin E synthase activity that is a component of the unstimulated progesterone receptor complex and that enhances receptor complex formation through interactions with Hsp90 (HSPCA)
SW:ABP2_HUMAN	FLNA	11, 41	11	0.85	0.11	SW:ABP2_HUMAN P21333 homo sapiens (human). endothelial actin-binding protein (abp-280) (nonmuscle filamin) (filamin 1). 11/1997 [MASS=280761]/Filamin A (alpha), an actin crosslinking phosphoprotein involved in actin cytoskeletal organization, signal transduction, and mechanical stimulus response, may contribute to cell adhesion; genetic mutations are associated with periventricular heterotopia
GP:AB037807_1	KIAA1386	45	1	0.85	0.00	GP:AB037807_1 Homo sapiens mRNA for KIAA1386 protein, partial cds; Start codon is not identified.. [MASS=135444]/Protein containing ankyrin repeats, an IBR domain, which are found in zinc finger proteins, and a C3HC4 type (RING) zinc finger, which may mediate protein-protein interactions
SW:PRC2_HUMAN	PSMA1	32	4	0.85	0.05	SW:PRC2_HUMAN P25786 homo sapiens (human). proteasome component c2 (ec 3.4.99.46) (macropain subunit c2) (proteasome nu chain) (multicatalytic endopeptidase complex subunit c2) (30 kda prosomal protein) [MASS=29556]/Alpha type 1 proteasome (prosome, macropain) subunit , a component of a multicatalytic proteinase complex that is involved in cellular protein degradation
SW:G6PI_HUMAN	GPI	5	2	0.85	0.01	SW:G6PI_HUMAN P06744 homo sapiens (human). glucose-6-phosphate isomerase (gpi) (ec 5.3.1.9) (phosphoglucose isomerase) (pgi) (phosphohexose isomerase) (phi) (neuroleukin) (nlk). 5/2000 [MASS=63189]/Glucose phosphate isomerase, plays a role in glycolysis and gluconeogenesis, tumor-secreted form (neuroleukin) acts as an autocrine factor to stimulate motility, invasion and metastasis of cancer cells; deficiency is associated with hemolytic anemia
SW:CALX_HUMAN	CANX	33, 36, 43	4	0.84	0.04	SW:CALX_HUMAN P27824 homo sapiens (human). calnexin precursor (major histocompatibility complex class i antigen-binding protein p88) (p90) (ip90). 11/1995 [MASS=67568]/Calnexin, a calcium and lectin binding protein that functions as a chaperone in the endoplasmic reticulum, involved in protein folding and secretion, mediates retention of misfolded proteins in the endoplasmic reticulum
SW:ER53_HUMAN	LMAN1	33, 36, 43	2	0.84	0.00	SW:ER53_HUMAN P49257 homo sapiens (human). ergic-53 protein precursor (er-golgi intermediate compartment 53 kda protein) (gp58) (mr60) (lectin, mannose-binding 1). 7/1998 [MASS=57563]/Mannose-binding lectin 1, involved in the traffic of glycoproteins between endoplasmic reticulum and the Golgi apparatus; mutations of the corresponding gene is associated with combined factor V and VIII coagulation deficiency
SW:SYR_HUMAN	RARS	2, 35, 37	7	0.84	0.08	SW:SYR_HUMAN P54136 homo sapiens (human). arginyl-trna synthetase (ec 6.1.1.19) (arginine--trna ligase) (args). 5/2000 [MASS=74977]/Arginyl-tRNA synthetase, aminoacylates its cognate tRNAs with arginine for protein biosynthesis
GP:AF068297_1	HDCMD45P	45	2	0.84	0.14	GP:AF068297_1 Homo sapiens HDCMD45P mRNA, partial cds. [MASS=17895]
PIR2:JC6524	PSMD11	32	3	0.84	0.08	PIR2:JC6524 26S proteasome regulatory complex chain p44.5 - human [MASS=47464]/Subunit 9 of the 26S proteasome (proteasome 26S subunit non-ATPase 11), a non-ATPase subunit of the 19S regulatory unit of the 26S proteasome complex, confers ATP dependency to the 26S proteasome, which mediates ubiquitin-dependent protein degradation
SW:ENPL_HUMAN	TRA1	10	5	0.84	0.11	SW:ENPL_HUMAN P14625 homo sapiens (human). endoplasmin precursor (94 kda glucose-regulated protein) (grp94) (gp96 homolog) (tumor rejection antigen 1). 10/1996 [MASS=92469]/Tumor rejection antigen 1, a putative molecular chaperone that may play roles in protein folding, cytoprotection, the immune response, and the heat shock and stress responses; vaccination with TRA1 elicits immune responses to cancer
GP:U59435_1	PA2G4	7	7	0.84	0.18	GP:U59435_1 Human cell cycle protein p38-2G4 homolog (hG4-1) mRNA, complete cds. [MASS=43813]/Proliferation associated 2G4, interacts with the juxtamembrane domain of ERBB3, dissociates from ERBB3 and translocates from the cytoplasm to the nucleus following treatment with heregulin
GP:AB002323_1	DNCH1	7, 23	8	0.83	0.29	GP:AB002323_1 Human mRNA for KIAA0325 gene, partial cds. [MASS=238445]/Dynein cytoplasmic heavy chain 1, a member of a family of dynein ATPases that function as motor proteins, plays a role in mitotic spindle formation
PIR2:T03842	SKB1	7, 23	5	0.83	0.18	PIR2:T03842 fission yeast Skb1 protein homolog - human [MASS=72786]/Protein arginine methyltransferase 5, methylates target proteins on arginine residues, may inhibit mitosis
SW:ITA6_HUMAN	ITGA6	6, 41	3	0.83	0.04	SW:ITA6_HUMAN P23229 homo sapiens (human). integrin alpha-6 precursor (vla-6) (cd49f). 5/2000 [MASS=119462]/Integrin alpha 6, a laminin receptor and component of hemidesmosomes, participates in the maintenance of epidermal integrity; gene mutations are responsible for epidermolysis bullosa and overexpression is correlated with carcinoma invasiveness

SW:SRC_HUMAN	SRC	34, 41	1	0.83	0.00	SW:SRC_HUMAN P12931 homo sapiens (human). proto-oncogene tyrosine-protein kinase src (ec 2.7.1.112) (p60-src) (c-src). 5/2000 [MASS=59704]/V-src avian sarcoma viral oncogene homolog (Schmidt-Ruppin A-2), tyrosine kinase involved in cell proliferation, cell adhesion, and cytoskeletal organization, implicated in the progression of colon cancer and certain breast tumors
SWN:ENT1_HUMAN	ENT1	25, 42	1	0.83	0.00	SWN:ENT1_HUMAN Q99808 homo sapiens (human). equilibrative nucleoside transporter 1 (equilibrative nitrobenzylmercaptopurine riboside-sensitive nucleoside transporter) (equilibrative nbmpr-sensitive nucle [MASS=50088]/Solute carrier family 29 member 1 (equilibrative nucleoside transporter 1), functions in the transport of physiologic nucleosides and chemotherapeutic nucleoside analog drugs, inhibited by nitrobenzylthioinosine, dipyridamole, and dilazep
SW:SYA_HUMAN	AARS	2, 25, 35, 37	1	0.83	0.00	SW:SYA_HUMAN P49588 homo sapiens (human). alanyl-trna synthetase (ec 6.1.1.7) (alanine--trna ligase) (alars). 7/1998 [MASS=106801]/Alanyl-tRNA synthetase, aminoacylates its cognate tRNA with alanine for protein biosynthesis, acts as an autoantigen in patients with polymyositis
GP:AF293335_1	KIAA1967	45	2	0.83	0.01	GP:AF293335_1 Homo sapiens p30 DBC mRNA, complete cds; putative protein from MH0802201. [MASS=30451]
GP:AK000303_1	FLJ20296	45	3	0.83	0.03	GP:AK000303_1 Homo sapiens cDNA FLJ20296 fis, clone HEP05890; unnamed protein product. [MASS=36853]/Protein of unknown function
GPN:AF193795_1	VPS29	45	2	0.83	0.04	PIR2:JC7515 vesicle protein sorting 29 protein - human [MASS=20506]/Vacuolar sorting protein 29, putative transporter that may play a role in retrograde transport from endosomes to the trans-Golgi network
PIR2:T46292	BAG3	45	1	0.83	0.00	PIR2:T46292 hypothetical protein DKFZp434E0610.1 - human (fragment) [MASS=65841]/BCL2-associated athanogene 3, interacts with the Hsc70 ATPase domain to regulate its chaperone activity, interacts with BCL2 to modulate cellular antiapoptosis , and participates in the EGF signaling pathway
GP:D31886_1	RAB3GAP	43	3	0.83	0.11	GP:D31886_1 Human mRNA for KIAA0066 gene, partial cds. [MASS=110524]/RAB3 GTPase-activating protein, GTPase-activating protein specific for lipid-modified members of the Rab3 subfamily, may influence calcium-dependent exocytosis of synaptic vesicles
SW:DRS1_HUMAN	PECI	19	9	0.83	0.22	SW:DRS1_HUMAN O75521 homo sapiens (human). dbi-related protein 1 (drs-1). 5/2000 [MASS=40151]/Peroxisomal D3,D2-enoyl-CoA isomerase, catalyzes the isomerization of 3-cis-octenoyl-CoA to 2-trans-octenoyl-CoAm, a step in the beta oxidation of fatty acids in peroxisomes
SW:ITMA_HUMAN	ITM2A	16	1	0.83	0.00	SW:ITMA_HUMAN O43736 homo sapiens (human). integral membrane protein 2a (e25 protein). 5/2000 [MASS=29741]/Integral membrane protein 2, a putative type II integral membrane protein with a leucine zipper motif
SW:SC13_HUMAN	SEC13L1	45	3	0.82	0.02	SW:SC13_HUMAN P55735 homo sapiens (human). sec13-related protein. 7/1998 [MASS=35569]/SEC13 (S. cerevisiae)-like 1, a serine- and threonine-rich WD40 repeat-containing protein that plays a role in protein transport from the endoplasmic reticulum to the Golgi
GP:U70735_1	MOV34-34KD	41	1	0.82	0.00	GP:U70735_1 Homo sapiens 34 kDa Mov34 homolog mRNA, complete cds; similar to Mov34. [MASS=33576]/COP9 subunit 6, putative translation initiation factor and a subunit of COP9 signalosome, which mediates p53 (human TP53) degradation, may be involved in G2-M phase transition of cell cycle
SW:BASI_HUMAN	BSG	41	2	0.82	0.00	SW:BASI_HUMAN P35613 homo sapiens (human). basigin precursor (leukocyte activation antigen m6) (collagenase stimulatory factor) (extracellular matrix metalloproteinase inducer) (emmprin) (5f7) (cd147 an [MASS=29221]/Basigin (OK blood group), a cyclophilin receptor of the immunoglobulin family, enhances cancer progression by increasing the production and activation of MMP2 and enhances infectivity of HIV 1 virions
SW:PRC5_HUMAN	PSC5	32	2	0.82	0.03	SW:PRC5_HUMAN P20618 homo sapiens (human). proteasome component c5 (ec 3.4.99.46) (macropain subunit c5) (proteasome gamma chain) (multicatalytic endopeptidase complex subunit c5). 11/1997 [MASS=26489]/Proteasome subunit alpha type 5 (ZETA), component of the 20S catalytic core proteasome that is involved in cellular protein degradation, has ribonuclease activity
PIR2:S71460	PRPS1	25	2	0.82	0.12	PIR2:S71460 ribose-phosphate pyrophosphokinase (EC 2.7.6.1) 39K regulatory chain - human [MASS=39480]/Phosphoribosyl pyrophosphate (PRPP) synthetase 1, generates PRPP, which is required for de novo purine and pyrimdine biosynthesis; mutations causing superactivity are associated with gout and neurological impairment
SW:ARS1_HUMAN	ASNA1	24	1	0.82	0.00	SW:ARS1_HUMAN O43681 homo sapiens (human). arsenical pump-driving atpase (ec 3.6.1.-) (arsenite-translocating atpase) (arsenical resistance atpase) (arsa) (asna-i). 5/2000 [MASS=38793]/Arsenite transporter ATP-binding homolog 1, a soluble putative arsenite transporter with similarity to bacterial arsA that has ATPase activity, may function in nucleocytoplasmic transport of a nucleolar component, and is stimulated by arsenite
SW:LCB2_HUMAN	SPTLC2	19	1	0.82	0.00	SW:LCB2_HUMAN O15270 homo sapiens (human). serine palmitoyltransferase 2 (ec 2.3.1.50) (long chain base biosynthesis protein 2) (lcb 2) (serine-palmitoyl-coa transferase 2) (spt 2) (kiaa0526). 5/2000 [MASS=62924]/Serine palmitoyltransferase long chain base subunit 2, member of the aminolevulinate synthase superfamily, catalyzes the first step in ceramide formation, involved in epidermal cell response to UV exposure and in leukemia cell ectopside-induced apoptosis
SW:DYN2_HUMAN	DNM2	7, 23, 43	1	0.81	0.00	SW:DYN2_HUMAN P50570 homo sapiens (human). dynamin 2. 10/1996 [MASS=98018]/Dynamin II, member of a family of 100-kD guanosine triphosphatases, regulates budding of endocytic vesicles at the plasma membrane and may function in the formation of transport vesicles at the trans-Golgi
SW:Y253_HUMAN	NCSTN	32, 41	2	0.81	0.05	SW:Y253_HUMAN Q92542 homo sapiens (human). hypothetical protein kiaa0253 (fragment). 7/1998 [MASS=78280]/Nicastrin, a transmembrane glycoprotein that may be required for the assembly and transport of presenilin complex that processes amyloid precursor protein (APP), may play a role in notch signaling and abnormal APP processing in Alzheimer disease

GP:AC003956_1	Acetolactate synthase	45	5	0.81	0.28	GP:AC003956_1 Homo sapiens DNA from chromosome 19, cosmid R34078, complete sequence; human homolog of acetolactate synthase; DPS similarity to Accession: gi|1730288 (U61263) acetolactate synthase homolog [Homo sapiens. [MASS=67868]
GP:U06631_1	H326	45	2	0.81	0.07	GP:U06631_1 Human (H326) mRNA, complete cds; homologous to mouse gene PC326:GenBank Accession Number M95564. [MASS=66385]/Protein containing seven WD domains (WD-40 repeats), which may mediate protein-protein interactions, has a region of low similarity to a region of breakpoint cluster region protein uterine leiomyoma 2 (human BCRP2), which may have a housekeeping function
SW:ME18_HUMAN	ZNF144	45	1	0.81	0.00	SW:ME18_HUMAN P35227 homo sapiens (human). dna-binding protein mel-18 (zinc finger protein 144). 11/1995 [MASS=37788]/Zinc finger protein 144, member of the Drosophila polycomb gene group, contains a helix-loop-helix like structure and a proline and serine-rich region, putative transcription factor that may be involved in hematopoiesis
GP:AJ131245_1	SEC24B	43	1	0.81	0.00	GP:AJ131245_1 Homo sapiens mRNA for Sec24 protein (Sec24B isoform). [MASS=137789]/SEC24 related gene family member B, a member of the SEC24 family of vesicle trafficking proteins, interacts with SEC23A, predicted to be localized to COPII-coated vesicles and to be involved in the export of proteins from the endoplasmic reticulum
SW:PRSC_HUMAN	PSMD7	32	2	0.81	0.00	SW:PRSC_HUMAN P51665 homo sapiens (human). 26s proteasome regulatory subunit s12 (proteasome subunit p40) (mov34 protein). 11/1997 [MASS=37060]/Proteasome (prosome, macropain) 26S subunit non-ATPase 7, a putative regulatory subunit of the 26S proteasome; mutation of the mouse Psdm7 gene results in recessive embryonic lethality
SW:PSD1_HUMAN	PSMD1	32	11	0.81	0.20	SW:PSD1_HUMAN Q99460 homo sapiens (human). 26s proteasome regulatory subunit s1 (p112). 12/1998 [MASS=105866]/Proteasome (prosome, macropain) 26S subunit (non-ATPase,1), a regulatory subunit of the 26S proteasome
SW:AMD2_HUMAN	AMPD2	25	1	0.81	0.00	SW:AMD2_HUMAN Q01433 homo sapiens (human). amp deaminase 2 (ec 3.5.4.6) (amp deaminase isoform l). 11/1997 [MASS=88198]/Adenosine monophosphate deaminase 2 (isoform L), catalyzes the deamination of adenosine monophosphate to form inosine monophosphate in purine nucleotide metabolism
SW:LCFA_HUMAN	FACL1	19	14	0.81	0.13	SW:LCFA_HUMAN P41215 homo sapiens (human). long-chain-fatty-acid--coa ligase 1 (ec 6.2.1.3) (long-chain acyl-coa synthetase 1) (lacs 1) (palmitoyl-coa ligase). 10/1996 [MASS=78348]/Long chain fatty acid-Coenzyme A ligase (palmitoyl-CoA ligase), a member of the long chain acyl-CoA synthetase family required for lipid synthesis and fatty acid degradation
SW:EZRI_HUMAN	VIL2	6, 11, 36	1	0.80	0.00	SW:EZRI_HUMAN P15311 homo sapiens (human). ezrin (p81) (cytovillin) (villin-2). 12/1998 [MASS=69268]/Villin 2 (ezrin), a member of the band 4.1 superfamily, links the cytoskeleton to the plasma membrane and thereby regulates cell adhesion and cortical morphogenesis, may play a role in rheumatoid arthritis and retinal degeneration
GP:AF151867_1	INTEGRAL TYPE I PROTEIN	45	2	0.80	0.07	GP:AF151867_1 Homo sapiens CGI-109 protein mRNA, complete cds. [MASS=24354
GPN:AB041832_1	WBP11	45	1	0.80	0.00	1 Homo sapiens mRNA for nuclear protein containing a WW domain (Npw38), complete cds. [MASS=30472]/Npw38-binding protein, interacts with the WW domain of Npw38 (PQBP1), binds poly(rG) and G-rich single-stranded DNA, interacts with nuclear or perinuclear filaments and may play a role in regulation of pre-mRNA processing
SW:PSD2_HUMAN	PSMD2	32	1	0.80	0.00	SW:PSD2_HUMAN Q13200 homo sapiens (human). 26s proteasome regulatory subunit s2 (p97) (tumor necrosis factor type 1 receptor associated protein 2) (55.11 protein). 7/1999 [MASS=100200]/Proteasome 26S non-ATPase subunit 2, a subunit of the 26S proteasome, likely involved in ubiquitin-dependent proteolysis, binds the type 1 tumor necrosis factor receptor (TNFRSF1A) and may function in TNFR signaling
SW:PUR8_HUMAN	ADSL	25	2	0.80	0.00	SW:PUR8_HUMAN P30566 homo sapiens (human). adenylosuccinate lyase (ec 4.3.2.2) (adenylosuccinase) (asl) (asase). 5/2000 [MASS=54889]/Adenylosuccinate lyase, catalyzes two steps in adenosine monophosphate biosynthesis; deficiency is associated with psychomotor retardation, epilepsy, and autism
SW:CTNB_HUMAN	CTNNB1	6, 11, 29, 41	19	0.79	0.26	SW:CTNB_HUMAN P35222 homo sapiens (human). beta-catenin. 2/1996 [MASS=85497]/Beta catenin, links cadherins to the cytoskeleton, may act as a component of the Wnt signal transduction pathway transmitting nuclear signals via a complex with LEF1 and TCF transcription factors; mutations in the gene are associated with various cancers
SW:CC4H_HUMAN	LRBA	45	1	0.79	0.00	SW:CC4H_HUMAN P50851 homo sapiens (human). cdc4-like protein (fragment). 7/1998 [MASS=213599]/Lipopolysaccharide-responsive and beige-like anchor, a putative protein-binding protein that contains WD-like repeats and a BEACH (BEige And CHS) domain, may play a role in vesicle transport
SW:G100_HUMAN	ADRM1	45	4	0.79	0.06	SW:G100_HUMAN Q16186 homo sapiens (human). 110 kda cell membrane glycoprotein. 11/1997 [MASS=42167]/Cell membrane glycoprotein 110 kDa, putative integral plasma membrane glycoprotein, putative tumor antigen and is expressed on human gastric carcinoma cells; upregulated in response to IFNgamma (IFNG)
SW:LMO6_HUMAN	LMO6	45	1	0.79	0.00	SW:LMO6_HUMAN O43900 homo sapiens (human). lim-only protein 6 (triple lim domain protein 6). 12/1998 [MASS=46098]/LIM domain only 6, a member of the LIM family of proteins which are involved in regulating development, protein-protein interactions and perhaps binding to nucleic acids, contains three LIM domains
SW:ATHA_HUMAN	ATP4A	42	2	0.79	0.08	SW:ATHA_HUMAN P20648 homo sapiens (human). potassium-transporting atpase alpha chain (ec 3.6.1.36) (proton pump) (gastric h+/k+ atpase alpha subunit). 5/2000 [MASS=114091]/H+/K+ transporting ATPase alpha polypeptide, a putative gastric heterodimeric proton pump responsible for acidification of the stomach lumen
SW:PRCD_HUMAN	PSMB6	32	1	0.79	0.00	SW:PRCD_HUMAN P28072 homo sapiens (human). proteasome delta chain precursor (ec 3.4.99.46) (macropain delta chain) (multicatalytic endopeptidase complex delta chain) (proteasome subunit y). 5/2000 [MASS=25316]/Proteasome (prosome, macropain) subunit beta 6 (proteasome delta), putative endopeptidase down-regulated by interferon gamma, may be involved in proteolysis and peptidolysis
GP:AB008567_1	SPTBN2	11	4	0.79	0.03	GP:AB008567_1 Homo sapiens mRNA for beta-spectrin III, complete cds. [MASS=271295]/Beta III spectrin, member of a family of actin-cross linking proteins of the membrane-associated cytoskeleton, associates with Golgi and cytoplasmic vesicles

GPN:AF239156_1	PDF1A	45	1	0.79	0.00	GPN:AF239156_1 Homo sapiens peptide deformylase-like protein mRNA, complete cds; huPD. [MASS=27013]/
SW:P2AA_HUMAN	PPP2CA	7, 34, 41	7	0.78	0.11	SW:P2AA_HUMAN P05323 homo sapiens (human), oryctolagus cuniculus (rabbit), sus scrofa (pig), and bos taurus (bovine). serine/threonine protein phosphatase 2a, catalytic subunit, alpha isoform (ec 3.1.3. [MASS=35594]/Protein phosphatase 2 catalytic subunit alpha, a catalytic subunit of protein phosphatase 2A involved in regulating diverse cellular processes via protein phosphorylation
SW:FKB1_HUMAN	FKBP1A	7, 33, 41	2	0.78	0.00	SW:FKB1_HUMAN P20071 homo sapiens (human), and oryctolagus cuniculus (rabbit). fk506-binding protein (fkbp-12) (peptidyl-prolyl cis-trans isomerase) (ec 5.2.1.8) (ppiase) (rotamase) (immunophilin fkbp12 [MASS=11820]/FK506-binding protein 1A, peptidyl prolyl cis-trans isomerase, modulates the Ca2+-release activity of ryanodine receptors, complex with FK506 inhibits calcineurin-dependent lymphokine gene transcription and mediates FK506 immunosuppressive activity
GP:AF306723_1	JUP	6, 11, 29	1	0.78	0.00	GP:BC000441_1 Homo sapiens, junction plakoglobin, clone MGC:8404 IMAGE:2820715, mRNA, complete cds. [MASS=81727]/Junction plakoglobin (gamma catenin), links cell-cell adhesion molecules with the cytoskeleton, involved in desmosome organization, cell adhesion, cell prolifiration, apoptosis; loss of heterozygosity is associated with breast and ovarian tumors
GP:AB011145_1	ERp44	45	9	0.78	0.13	GP:AB011145_1 Homo sapiens mRNA for KIAA0573 protein, partial cds. [MASS=51859]/Member of the thioredoxin family, which are small enzymes involved in redox reactions, has low similarity to S. cerevisiae Pdi1p, which is a protein disulfide isomerase and oxidoreductase
SW:GC5L_HUMAN	GCN5L1	45	1	0.78	0.00	SW:GC5L_HUMAN P78537 homo sapiens (human). gcn5-like protein 1 (rt14 protein). 7/1999 [MASS=14311]/General control of amino acid synthesis-like 1 (yeast), a widely expressed protein that may be a transcriptional activator
GP:AF091079_1	YKT6	43	1	0.78	0.00	GP:AF091079_1 Homo sapiens clone 560 SNARE protein Ykt6 mRNA, partial cds. [MASS=21607]/Homolog of S. cerevisiae Ykt6p, which is a v-SNARE required for ER to Golgi transport, likely involved in trafficking proteins from the ER to the Golgi
SW:CLH1_HUMAN	CLTC	43	49	0.78	0.44	SW:CLH1_HUMAN Q00610 homo sapiens (human). clathrin heavy chain 1 (clh-17) (kiaa0034). 5/2000 [MASS=191615]/Clathrin heavy polypetide c, involved in endocytosis, may bind to endocytic proteins through an LLDLD consensus sequence, interacts with huntingtin interacting protein 1 (HIP1), amino terminus folds into a seven-bladed beta-propeller
SW:EF11_HUMAN	EEF1A1	35	11	0.78	0.11	SW:EF11_HUMAN P04720 homo sapiens (human), and oryctolagus cuniculus (rabbit). elongation factor 1-alpha 1 (ef-1-alpha-1) (elongation factor tu) (ef- tu). 12/1998 [MASS=50141]/Eukaryotic translation elongation factor 1 alpha 1, involved in cytoskeletal rearrangment, has putative roles in translational elongation and senescence and GTP binding; possibly involved in diabetes, Felty syndrome, and HIV life cycle
SW:PP1B_HUMAN	PPP1CB	34	1	0.78	0.00	SW:PP1B_HUMAN P37140 homo sapiens (human), rattus norvegicus (rat), mus musculus (mouse), oryctolagus cuniculus (rabbit), and gallus gallus (chicken). serine/threonine protein phosphatase pp1-beta catal [MASS=37187]/Protein phosphatase 1 catalytic subunit beta isoform, subunit of a serine-threonine phosphatase that regulates many metabolic processes
SW:PRSX_HUMAN	PSMC6	32	5	0.78	0.18	SW:PRSX_HUMAN Q92524 homo sapiens (human). 26s protease regulatory subunit s10b (proteasome subunit p42). 12/1998 [MASS=44161]/Proteasome (prosome, macropain) 26S subunit ATPase 6, part of both PA700 and PA700-dependent complexes, which regulate intracellular protease activity, may be involved in spermatogenesis
GP:AB011159_1	NCKAP1	16	7	0.78	0.08	GP:AB011159_1 Homo sapiens mRNA for KIAA0587 protein, complete cds. [MASS=129517]/NCK-associated protein 1, may play a role in regulating beta secretase activity in processing of beta APP, and may play a role in suppressing apoptosis; downregulated in patients with sporadic Alzheimer disease
SW:GBAK_HUMAN	GNAI3	41, 42, 43	4	0.77	0.10	SW:GBAK_HUMAN P08754 homo sapiens (human). guanine nucleotide-binding protein g(k), alpha subunit (g(i) alpha-3). 11/1997 [MASS=40401]/G protein alpha i3 subunit, a component of pertussis toxin sensitive heterotrimeric G protein complexes, transduces signals from G protein-coupled receptors to intracellular effectors, inhibits forskolin-stimulated cAMP production
SW:RAB2_HUMAN	RAB2	21, 43	5	0.77	0.05	SW:RAB2_HUMAN P08886 homo sapiens (human), and canis familiaris (dog). ras-related protein rab-2. 10/1994 [MASS=23546]/Ras-related GTP-binding protein 2, a GTPase which plays a role in vesicle transport from the ER to the Golgi complex; overexpression in nonmalignant peripheral blood lymphocytes is associated with Searzy syndrome
SW:SYD_HUMAN	DARS	2, 35, 37	4	0.77	0.15	SW:SYD_HUMAN P14868 homo sapiens (human). aspartyl-trna synthetase (ec 6.1.1.12) (aspartate--trna ligase) (asprs). 11/1997 [MASS=57192]/Aspartyl-tRNA synthetase, a class II aminoacyl tRNA synthetase that aminoacylates its cognate tRNA with aspartate for protein biosynthesis, associates with a multisynthetase complex, N-terminus may aid interaction with elongation factor 1 alpha
SW:IQGA_HUMAN	IQGAP1	11, 41	4	0.77	0.09	SW:IQGA_HUMAN P46940 homo sapiens (human). ras gtpase-activating-like protein iqgap1 (p195) (kiaa0051). 7/1999 [MASS=189252]/IQ motif-containing GTPase activating protein 1, an actin-associated calmodulin (CALM1)-regulated protein that serves as an effector for CDC42 and RAC1, modulates E-cadherin (CDH1)-mediation cellular adhesion, upregulated in colon carcinomas
SW:DAG1_HUMAN	DAG1	11, 16, 31	1	0.77	0.00	SW:DAG1_HUMAN Q14118 homo sapiens (human). dystroglycan precursor (dystrophin-associated glycoprotein 1) [contains: alpha-dystroglycan (alpha-dg); beta-dystroglycan (beta- dg)]. 5/2000 [MASS=97581]/Dystroglycan 1, component of a dystrophin-associated glycoprotein complex that binds laminin, may link the extracellular matrix and cytoskeleton, may play a role in synaptic function; deficiency is involved in the pathogenesis of muscular dystrophies
PIR2:T13152	WDR1	45	5	0.77	0.06	SW:WDR1_HUMAN O75083 homo sapiens (human). wd-repeat protein 1 (actin interacting protein 1) (nori-1). 10/2001 [MASS=66194]/WD repeat domain 1, contains WD40 repeats which are believed to be involved in protein-protein interactions, may bind actin, and may be involved in hearing
SWN:DB83_HUMAN	DB83	45	1	0.77	0.00	SWN:DB83_HUMAN P57088 homo sapiens (human). db83 protein. 8/2001 [MASS=27951]/Member of the UPF0121 uncharacterized protein family, has very strong similarity to uncharacterized rat LOC59303

SW:TCPZ_HUMAN	CCT6A	33	3	0.77	0.08	SW:TCPZ_HUMAN P40227 homo sapiens (human). t-complex protein 1, zeta subunit (tcp-1-zeta) (cct-zeta) (cct-zeta-1) (tcp20) (htr3). 7/1999 [MASS=58024]/Chaperonin containing T-complex 1 subunit 6A (zeta), part of a cytosolic hexadecamer structure involved in ATP-dependent folding of actin, tubulin and other proteins, decreased activity may result in misfolded tubulin aggregates in Alzheimers disease
SW:TDX2_HUMAN	PRDX2	10	8	0.77	0.16	SW:TDX2_HUMAN Q06830 homo sapiens (human). thioredoxin peroxidase 2 (thioredoxin-dependent peroxide reductase 2) (proliferation-associated protein pag) (natural killer cell enhancing factor a) (nkef-a). [MASS=22110]/Peroxiredoxin 2, a thioredoxin peroxidase member of the AhpC-TSA family, acts as an antioxidant, enhances natural killer activity, may be involved in erythrocyte differentiation, exists as a membrane-associated form in erythrocytes
SW:IMB1_HUMAN	KPNB1	24, 36	1	0.76	0.00	SW:IMB1_HUMAN Q14974 homo sapiens (human). importin beta-1 subunit (karyopherin beta-1 subunit) (nuclear factor p97) (importin 90). 12/1998 [MASS=97234]/Importin beta (karyopherin beta 1), a subunit of the NLS (nuclear localization signal) receptor complex, binds to the nuclear pore complex and mediates translocation of the importin alpha-NLS complex into the nucleus
SW:CAPB_HUMAN	CAPZB	11, 31	8	0.76	0.13	SW:CAPB_HUMAN P47756 homo sapiens (human). f-actin capping protein beta subunit (capz). 5/2000 [MASS=30629]/Capping protein Z-line beta 1, a subunit of an actin-binding protein that caps the barbed end of actin filaments and regulates actin polymerization dynamics, may have a role in cell motility
GP:AB046798_1	KIAA1578	45	1	0.76	0.00	GP:AB046798_1 Homo sapiens mRNA for KIAA1578 protein, partial cds; Start codon is not identified.. [MASS=132841]
GP:AF151840_1	ARSDR1	45	26	0.76	0.45	GP:AF167438_1 Homo sapiens androgen-regulated short-chain dehydrogenase/reductase 1 (ARSDR1) mRNA, complete cds; short-chain dehydrogenase/reductase family member./Member of the short-chain dehydrogenase-reductase family, has moderate similarity to a region of WW domain-containing oxidoreductase (mouse Wwox), which is an apoptosis activator
GP:AF155652_1	PCMF	45	1	0.76	0.00	GP:AF155652_1 Human potassium channel modulatory factor mRNA; PCMF. [MASS=41973]/Protein containing a ZZ zinc finger and a C2H2 type zinc finger domain, which bind nucleic acids, has high similarity to uncharacterized mouse 1700094M07Rik
SW:CLI1_HUMAN	CLIC1	42	1	0.76	0.00	SW:CLI1_HUMAN O00299 homo sapiens (human). chloride intracellular channel protein 1 (nuclear chloride ion channel 27) (ncc27) (p64 clcp). 5/2000 [MASS=26924]/Chloride intracellular channel 1 (nuclear chloride channel-27), an intracellular chloride channel that localizes predominantly to the nucleus, member of the glutathione transferase structural family
SW:MLEN_HUMAN	MYL6	11	11	0.76	0.10	SW:MLEN_HUMAN P16475 homo sapiens (human), bos taurus (bovine), and sus scrofa (pig). myosin light chain alkali, non-muscle isoform (mlc3nm) (lc17a) (lc17-nm). 5/2000 [MASS=16799]/Myosin alkali light chain smooth muscle and non-muscle, a member of the family of alkali myosin light chains, which play a role in the interaction between myosin and actin, intracellular vesicle movement, cytokinesis and cell location
SWN:LAD1_HUMAN	LAD1	11	1	0.76	0.00	SWN:LAD1_HUMAN O00515 homo sapiens (human). ladinin 1 (lad-1) (120 kda linear iga bullous dermatosis antigen) (97 kda linear iga bullous dermatosis antigen) (linear iga disease antigen homolog) (lada). 8 [MASS=57157]/Ladinin 1, an anchoring filament protein that is a component of basement membranes, recognized by circulating IgA autoantibodies in linear IgA disease, which is a blistering skin disease, may maintain dermal epidermal cohesion
SW:ITAV_HUMAN	ITGAV	6, 16, 41	1	0.75	0.00	SW:ITAV_HUMAN P06756 homo sapiens (human). vitronectin receptor alpha subunit precursor (integrin alpha-v) (cd51). 12/1998 [MASS=116052]/Alpha V subunit integrin, a subunit of the vitronectin receptor that is involved in cell-matrix interactions, chemotaxis, phagocytosis and angiogenesis, may contribute to the tumorigenicity of cutaneous malignant melanoma and invasive breast cancer
SW:PRS7_HUMAN	PSMC2	32, 44	7	0.75	0.17	SW:PRS7_HUMAN P35998 homo sapiens (human). 26s protease regulatory subunit 7 (mss1 protein). 11/1997 [MASS=48634]/26S protease regulatory subunit 7, ATPase subunit of the 26S proteasome, interacts with Tat protein, may be involved in cell cycle control and has a role in the activation of human immunodeficiency virus-1 (HIV-1) gene transcription
PIR2:T46299	TREX1	45	1	0.75	0.00	PIR2:T46299 hypothetical protein DKFZp434J0310.1 - human [MASS=38923]/Three prime repair exonuclease 1, member of the exonuclease family, displays 3'-5' exodeoxyribonuclease activity and may be involved in DNA repair
SW:WFS1_HUMAN	WFS1	18	1	0.75	0.00	SW:WFS1_HUMAN O76024 homo sapiens (human). wolframin. 5/2000 [MASS=100306]/Wolfram syndrome 1 (wolframin), may play a role in islet beta cell and neuron survival, may influence normal hearing and vision; gene mutation is detected in Wolfram syndrome and some types of hearing loss and may influence type 2 diabetes susceptibility
SW:AR21_HUMAN	ARPC3	8, 11	1	0.74	0.00	SW:AR21_HUMAN O15145 homo sapiens (human). arp2/3 complex 21 kda subunit (p21-arc). 12/1998 [MASS=20547]/Actin related protein 2/3 complex subunit 3 (21 kDa), a component of the Arp2/3 complex, may participate in the regulation of actin polymerization, may have a role in the protrusion of lamellipodia, has an essential function in at least HeLa cells
SW:KCCB_HUMAN	CAMK2B	34, 41	2	0.74	0.09	SW:KCCB_HUMAN Q13554 homo sapiens (human). calcium/calmodulin-dependent protein kinase type ii beta chain (cam-kinase ii beta chain) (ec 2.7.1.123) (camk-ii, beta subunit) (fragment). 5/2000 [MASS=15141]/Calcium calmodulin-dependent protein kinase II beta subunit, putative roles in signal transduction and cell growth, increased expression may play a role in schizophrenia; variant forms of the corresponding gene are expressed in tumor cells
SW:SN23_HUMAN	SNAP23	21, 43	2	0.74	0.06	SW:SN23_HUMAN O00161 homo sapiens (human). synaptosomal associated protein 23 (snap-23) (vesicle-membrane fusion protein snap-23). 5/2000 [MASS=23354]/Synaptosomal-associated protein 23, a member of the SNARE family of proteins that regulate membrane fusion during exocytosis, a t-SNARE that binds to syntaxins and is involved in docking and fusion of transport vesicles during exocytosis
SW:RB3D_HUMAN	RAB3D	16, 21, 43	1	0.74	0.00	SW:RB3D_HUMAN O95716 homo sapiens (human). ras-related protein rab-3d. 5/2000 [MASS=24267]/Ras-related GTP-binding protein 3d, putative small monomeric GTP-binding protein and GTPase that plays a role in regulated secretion

GP:AB008515_1	RanBPM	11, 31	1	0.74	0.00	GP:AB008515_1 Homo sapiens mRNA for RanBPM, complete cds. [MASS=55082]/Ran-binding protein 9, plays a role in microtubule nucleation, interacts specifically with RAN guanosine triphosphatase and mediates Ran-dependent centrosomal function
GP:AB040887_1	ZNF291	45	1	0.74	0.00	GP:AB040887_1 Homo sapiens mRNA for KIAA1454 protein, partial cds; Start codon is not identified.. [MASS=142702]/Protein of unknown function
GPN:AB047846_1	LOC51137	43	7	0.74	0.24	SW:COPG_HUMAN Q9y678 homo sapiens (human). coatomer gamma subunit (gamma-coat protein) (gamma-cop). 10/2001 [MASS=97718]/Coatomer protein complex subunit gamma 1, a subunit of the coat of COP I-coated vesicles, predicted to be involved in retrograde Golgi to endoplasmic reticulum transport, contains two clathrin-associated adaptin N-terminal domains
SW:CLD7_HUMAN	CLDN7	6	1	0.74	0.00	SW:CLD7_HUMAN O95471 homo sapiens (human). claudin-7. 5/2000 [MASS=22390]/Claudin 7, a putative integral membrane protein which may be involved in tight junction formation
SW:RS4_HUMAN	RPS4X	7, 35	3	0.73	0.14	SW:RS4_HUMAN P12750 homo sapiens (human), rattus norvegicus (rat), mus musculus (mouse), mesocricetus auratus (golden hamster), and felis silvestris catus (cat). 40s ribosomal protein s4, x isoform (sin [MASS=29467]/Ribosomal protein S4 X-linked, a component of the small 40S ribosomal subunit with roles in translation, cell cycle, and cell proliferation; gene is X-linked but escapes X inactivation, and may therefore contribute to haploinsufficency in Turner syndrome
SW:PLAK_HUMAN	DP3	6, 11, 29	12	0.73	0.19	SW:PLAK_HUMAN P14923 homo sapiens (human). junction plakoglobin (desmoplakin iii). 11/1997 [MASS=81498]/Junction plakoglobin (gamma catenin), links cell-cell adhesion molecules with the cytoskeleton, involved in desmosome organization, cell adhesion, cell prolifiration, apoptosis; loss of heterozygosity is associated with breast and ovarian tumors
SW:UGS1_HUMAN	GYS1	5, 18	5	0.73	0.15	SW:UGS1_HUMAN P13807 homo sapiens (human). glycogen [starch] synthase, muscle (ec 2.4.1.11). 5/2000 [MASS=83786]/Glycogen synthase 1 (muscle), catalyzes transfer of a glucosyl residue from UDP-glucose to glycogen, stimulated by insulin, Acipimox and Flouxetine; mutations in the corresponding gene may be associated with non-insulin-dependent diabetes mellitus
SW:RB35_HUMAN	RAB35	21, 43	1	0.73	0.00	SW:RB35_HUMAN Q15286 homo sapiens (human). ras-related protein rab-35 (rab-1c) (gtp-binding protein ray). 5/2000 [MASS=23025]/Ras-related GTP-binding protein 35, member of the Rab family of GTP-binding proteins, may function in vesicular transport
GP:AB020637_1	KIAA0830	45	1	0.73	0.00	GP:AB020637_1 Homo sapiens mRNA for KIAA0830 protein, partial cds. [MASS=57202]/Protein of unknown function
SW:KINH_HUMAN	KIF5B	43	2	0.73	0.05	SW:KINH_HUMAN P33176 homo sapiens (human). kinesin heavy chain (ubiquitous kinesin heavy chain) (ukhc). 7/1999 [MASS=109685]/Kinesin family member 5B (kinesin heavy chain), a microtubule-associated motor protein that may function in intracellular organelle transport and may play a role in susceptibility and resistance
SW:GFA1_HUMAN	GFPT1	5, 18	5	0.72	0.06	SW:GFA1_HUMAN Q06210 homo sapiens (human). glucosamine--fructose-6-phosphate aminotransferase [isomerizing] 1 (ec 2.6.1.16) (hexosephosphate aminotransferase 1) (d-fructose-6- phosphate amidotransferase [MASS=76616]/Glutamine-fructose-6-phosphate transaminase 1, catalyzes the first step in glucosamine formation, modulates glucose flux and functions in development of insulin resistance, upregulation in kidney associated with diabetic nephropathy
GP:AF144748_1	ENTPD2	45	1	0.72	0.00	SW:ENP2_HUMAN Q9y5l3 homo sapiens (human). ectonucleoside triphosphate diphosphohydrolase 2 (ec 3.6.1.3) (ntpdase2) (ecto-atpase) (cd39 antigen-like 1). 10/2001 [MASS=53665]/Ectonucleoside triphosphate diphosphohydrolase 2, a member of the CD39-like family that functions as a ecto-ATPase
GP:AK023914_1	FLJ13852	45	2	0.72	0.00	GP:AK023914_1 Homo sapiens cDNA FLJ13852 fis, clone THYRO1000934, weakly similar to PYRROLINE-5-CARBOXYLATE REDUCTASE (EC 1.5.1.2); unnamed protein product. [MASS=28663]/Protein with high similarity to pyrroline-5-carboxylate reductase 1 (human PYCR1), which catalyzes the NAD(P)H dependent reduction of pyrroline-5-carboxylate to proline, member of the delta 1-pyrroline-5-carboxylate reductase (P5CR) family
SW:AMP1_HUMAN	KIAA0094	45	1	0.72	0.00	SW:AMP1_HUMAN P53582 homo sapiens (human). putative methionine aminopeptidase 1 (ec 3.4.11.18) (metap 1) (peptidase m 1) (kiaa0094) (fragment). 11/1997 [MASS=44046]/Methionine aminopeptidase 1, metallopeptidase that cleaves N-terminal methionine when the adjacent residue is small and uncharged, enzymatic activity may not be inhibited by the angiogenesis inhibitor fungal fumagillin
GP:AB018358_1	KIAA0905	41	3	0.72	0.10	GP:AB018358_1 Homo sapiens mRNA for ABP125, complete cds; This sequence is a product of alternative splicing of human ABP130. [MASS=129053]/Secretion 31 homolog, a putative component of the COPII coat of secretory pathway vesicles involved in endoplasmic reticulum to Golgi transport, plays a role in intracellular protein trafficking
SW:RGP1_HUMAN	RANGAP1	41	1	0.72	0.00	SW:RGP1_HUMAN P46060 homo sapiens (human). ran-gtpase activating protein 1. 7/1999 [MASS=63542]/Ran GTPase activating protein 1, a GTPase activator for ras family GTP binding protein RAN, ubiquitin-like SUMO-1 modification results in localization to the nuclear pore complex, required for nuclear protein import when bound to RANBP2
SW:IF32_HUMAN	TRIP1	35	3	0.72	0.09	SW:IF32_HUMAN Q13347 homo sapiens (human). eukaryotic translation initiation factor 3 subunit 2 (eif-3 beta) (eif3 p36) (tgf-beta receptor interacting protein 1) (trip-1). 5/2000 [MASS=36502]/Eukaryotic translation initiation factor 3 subunit 2, an eIF3 subunit with a predicted role in translation initiation, binds transforming growth factor beta receptor II (TGFBR2) and acts as a modulator of TGFBR2 signaling pathways
GP:AF177171_1	TMOD3	11	2	0.72	0.00	GP:AF177171_1 Homo sapiens tropomodulin 3 (TMOD3) mRNA, complete cds. [MASS=39581]/Tropomodulin 3, putative actin-capping protein for the slow-growing end of filamentous actin, expressed ubiquitously
SW:CTN1_HUMAN	CTNNA1	6, 11, 41	27	0.71	0.19	SW:CTN1_HUMAN P35221 homo sapiens (human). alpha-1 catenin (cadherin-associated protein) (alpha e-catenin). 11/1997 [MASS=100071]/Catenin alpha 1 (cadherin-associated protein); binds cadherins and links them with the actin cytoskeleton

GP:AB032997_1	KIAA1171	45	3	0.71	0.13	GP:AB032997_1 Homo sapiens mRNA for KIAA1171 protein, partial cds; Start codon is not identified.; hh05501 cDNA clone for KIAA1171 has 960-bp and 414-bp insertions (may be introns) after the positions 1275 and 1339 of the sequence of KIAA1171, respectively.. [MASS=66540]/Protein of unknown function
GP:D87438_1	KIAA0251	45	1	0.71	0.00	GP:D87438_1 Human mRNA for KIAA0251 gene, partial cds; Similar to a C.elegans protein in cosmid C14H10. [MASS=90027]/Protein containing two pyridoxal-dependent group II decarboxylase conserved domains, which bind pyridoxal-phosphate groups, has strong similarity to uncharacterized mouse Kiaa0251-hp
GP:AF091035_1	RAB21	41	2	0.71	0.00	GP:AF091035_1 Homo sapiens GTP-binding protein RAB21 (RAB21) mRNA, complete cds. [MASS=24348]/Ras related GTP binding protein, member of the Rab subfamily of the Ras superfamily of small GTP binding proteins, may be involved in apically directed vesicle-mediated transport in polarized intestinal epithelium
SW:NEP_HUMAN	MME	32	34	0.71	0.19	SW:NEP_HUMAN P08473 homo sapiens (human). neprilysin (ec 3.4.24.11) (neutral endopeptidase) (nep) (enkephalinase) (common acute lymphocytic leukemia antigen) (calla) (neutral endopeptidase 24.11) (cd10) [MASS=85383]/Enkephalinase; membrane zinc metalloendopeptidase, may inactivate peptide hormones
SW:CP51_HUMAN	CYP51	19	3	0.71	0.04	SW:CP51_HUMAN Q16850 homo sapiens (human). cytochrome p450 51 (ec 1.14.14.1) (cypl1) (p450l1) (sterol 14-alpha demethylase) (lanosterol 14-alpha demethylase) (ldm) (p450-14dm). 5/2000 [MASS=56806]/Lanosterol 14-alpha-demethylase (sterol 14alpha-demethylase); cytochrome P450 enzyme involved in sterol biosynthesis
SW:MYSN_HUMAN	MYH9	11	26	0.71	0.26	SW:MYSN_HUMAN P35579 homo sapiens (human). myosin heavy chain, nonmuscle type a (cellular myosin heavy chain, type a) (nmmhc-a). 12/1998 [MASS=226532]/Non-muscle myosin heavy chain 9; motor protein that provides force for muscle contraction, cytokinesis and phagocytosis; contains an ATPase head domain and a rod-like tail domain
SW:ALFA_HUMAN	ALDOA	5	4	0.71	0.25	SW:ALFA_HUMAN P04075 homo sapiens (human). fructose-bisphosphate aldolase a (ec 4.1.2.13) (muscle-type aldolase). 5/2000 [MASS=39289]/Aldolase A (fructose-bisphosphate aldolase); reversibly cleaves FBP into DHAP and GAP in glycolysis
GP:AF227905_1	UGCGL1	33, 34	1	0.70	0.00	GP:AF227905_1 Homo sapiens UDP-glucose:glycoprotein glucosyltransferase 1 precursor, mRNA, complete cds; HUGT1. [MASS=177190]/UDP-glucose:glycoprotein glucosyltransferase; transfers glucose from UDP-glucose to improperly folded glycoproteins
SW:RHOB_HUMAN	ARHB	11, 41	6	0.70	0.04	SW:RHOB_HUMAN P01121 homo sapiens (human), mus musculus (mouse), and rattus norvegicus (rat). transforming protein rhob (h6). 12/1998 [MASS=22123]/Ras-related GTP binding protein of the rho subfamily, member B; may regulate assembly of actin stress fibers and focal adhesions; very strongly similar to murine Arhb
GP:AB040884_1	OSBPL8	45	1	0.70	0.00	GP:AB040884_1 Homo sapiens mRNA for KIAA1451 protein, partial cds; Start codon is not identified.. [MASS=56449]/Member of the oxysterol-binding protein (OSBP) family, which are involved in sterol biosynthesis and possibly regulation, contains a pleckstrin homology (PH) domain, has a region of moderate similarity to S. cerevisiae Osh7p
GP:U21252_1	anti-colorectal carcinoma heavy chain	45	1	0.70	0.00	GP:U21252_1 Human rearranged Ig gamma heavy chain V region (VH3-JH4b) mRNA, partial cds, clone JGpFv3-06 VH; from VH3 family gene and JH4b. [MASS=13752]
GP:AF038535_1	SYT7	43	1	0.70	0.00	GP:AF038535_1 Homo sapiens synaptotagmin VII mRNA, partial cds; similar to rat synaptotagmin VII. [MASS=47195]/Very strongly similar to synaptotagmin 7 (Rn.10193); may be a phospholipid-binding calcium sensor protein
SW:SYG_HUMAN	GARS	2, 35, 37	1	0.69	0.00	SW:SYG_HUMAN P41250 homo sapiens (human). glycyl-trna synthetase (ec 6.1.1.14) (glycine--trna ligase) (glyrs). 10/1996 [MASS=77531]/Glycyl-tRNA synthetase; functions in protein biosynthesis, aminoacylates its cognate tRNAs with phenylalanine/Glycyl-tRNA synthetase, a class II aminoacyl-tRNA synthetase that catalyzes aminoacylation of its cognate tRNA with glycine for protein biosynthesis; an autoantigen in dermatomyositis
GP:AB012191_1	NEDD8	16, 32, 34	2	0.69	0.04	GP:AB012191_1 Homo sapiens mRNA for Nedd8-conjugating enzyme hUbc12, complete cds. [MASS=20900]/Neurally expressed developmentally down-regulated 8, an ubiquitin-like protein that conjugates to CUL proteins to activate ubiquitin ligase complex dependent ubiquitination, possibly involved in cell cycle regulation
PIR2:T46394	DKFZP434H0820	45	5	0.69	0.17	PIR2:T46394 hypothetical protein DKFZp434H0820.1 - human (fragment) [MASS=78344]/Protein of unknown function, has moderate similarity to uncharacterized human C1ORF24
SW:9123_HUMAN	TCTE1L	45	3	0.69	0.07	SW:9123_HUMAN P51808 homo sapiens (human). protein 91/23. 11/1997 [MASS=13062]/T-complex-associated-testis-expressed 1-like, protein with similarity to murine Tctex1, which is a dynein light chain expressed in retina and in germ cells of the testis
SW:S23B_HUMAN	SEC23B	43	1	0.69	0.00	SW:S23B_HUMAN Q15437 homo sapiens (human). protein transport protein sec23 homolog isoform b. 11/1997 [MASS=86470]/Member of the SEC23 family of vesicle trafficking proteins
SW:RAC3_HUMAN	RAC3	41	2	0.69	0.00	SW:RAC3_HUMAN O14658 homo sapiens (human). ras-related c3 botulinum toxin substrate 3 (p21-rac3). 12/1998 [MASS=21379]/Ras-related C3 botulinum toxin substrate 3, a Rho family GTPase involved in integrin signaling via alphaIIb-beta3 (ITGA2B, ITGB3), binds CIB1, regulates cell-matrix adhesion and may activate the JNK pathway and stimulate tumor cell growth
SW:RIB1_HUMAN	RPN1	34	1	0.69	0.00	SW:RIB1_HUMAN P04843 homo sapiens (human). dolichyl-diphosphooligosaccharide--protein glycosyltransferase 67 kda subunit precursor (ec 2.4.1.119) (ribophorin i). 7/1999 [MASS=68569]/Ribophorin I, a putative subunit of oligosaccharyltransferase involved in transcription initiation and possibly protein retention in the endoplasmic reticulum
PIR2:T17218	DKFZP434P1750	45	1	0.68	0.00	PIR2:T17218 hypothetical protein DKFZp434P1750.1 - human [MASS=26577]/Protein of unknown function, has moderate similarity to a region of EBP50-PDZ interactor of 64 kD (human EPI64), which is a putative RAB GTPase activator that binds the PDZ domains of ERM-binding phosphoprotein 50 (SLC9A3R1) and E3KARP (SLC9A3R2)

SW:DYJ2_HUMAN	DNCLI2	45	4	0.68	0.10	SW:DYJ2_HUMAN O43237 homo sapiens (human). dynein light intermediate chain 2, cytosolic (lic53/55) (lic-2). 7/1998 [MASS=54099]/Cytoplasmic dynein light intermediate chain 2, a putative subunit of cytoplasmic dynein that may have ATPase activity
SW:TCPE_HUMAN	CCT5	33	4	0.68	0.14	SW:TCPE_HUMAN P48643 homo sapiens (human). t-complex protein 1, epsilon subunit (tcp-1-epsilon) (cct-epsilon) (kiaa0098). 11/1997 [MASS=59671]/Chaperonin containing T-complex 1 subunit 5 (epsilon), part of a cytosolic hexadecamer structure involved in ATP-dependent folding of actin, tubulin and other proteins, binds Epstein-Barr Virus-encoded EBNA3 and may mediate its initial folding
GP:AB002366_1	KIAA0368	45	1	0.67	0.00	GP:AB002366_1 Human mRNA for KIAA0368 gene, partial cds. [MASS=159478]/Protein of unknown function, has low similarity to a region of S. cerevisiae Ecm29p, which is involved in cell wall structure or biosynthesis
SW:ZO1_HUMAN	TJP1	45	1	0.67	0.00	SW:ZO1_HUMAN Q07157 homo sapiens (human). tight junction protein zo-1 (zona occludens 1 protein) (tight junction protein 1). 5/2000 [MASS=194723]/Tight junction protein 1, component of the blood brain barrier that may play roles in the organization and attachment of tight junction components, cellular differentiation, placental development, breast cancer progression, and pancreatic cancer
SW:RL7A_HUMAN	RPL7A	35	1	0.67	0.00	SW:RL7A_HUMAN P11518 homo sapiens (human), and rattus norvegicus (rat). 60s ribosomal protein l7a (surfeit locus protein 3) (pla-x polypeptide). 7/1999 [MASS=29864]/Ribosomal protein L7a (surfeit-3), a putative component of the 60S ribosomal subunit, likely to be involved in protein biosynthesis and in colorectal carcinogenesis; trk-2h fusion oncogene in breast cancer cells comprises a fragment of RPL7A fused to TRK
SW:HD_HUMAN	HD	16	1	0.67	0.00	SW:HD_HUMAN P42858 homo sapiens (human). huntingtin (huntington's disease protein) (hd protein). 12/1998 [MASS=347860]/Huntingtin, antiapoptotic protein, may be involved in intracellular transport; mutations in the gene cause Huntingtin disease and result in the production of a protein that interferes with transcription and proteasome-mediated protein degradation
SW:TDXN_HUMAN	PRDX4	34, 41	5	0.66	0.19	SW:TDXN_HUMAN Q13162 homo sapiens (human). thioredoxin peroxidase ao372 (thioredoxin-dependent peroxide reductase a0372) (antioxidant enzyme aoe372) (aoe37-2). 7/1999 [MASS=30540]/Peroxiredoxin 4, a thioredoxin dependent peroxidase that is regulated by interactions with other thiol peroxidases, may mediate hydrogen peroxide activation of NF-kappaB by modulating phosphorylation of cytoplasmic IkappaB-alpha (NFKBIA)
SW:PRS8_HUMAN	SUG1}	29, 32	9	0.66	0.15	SW:PRS8_HUMAN P47210 homo sapiens (human). 26s protease regulatory subunit 8 (proteasome subunit p45) (thyroid hormone receptor interacting protein 1) (trip1). 11/1997 [MASS=45653]/ATPase subunit 5 of the 26S proteasome, which is a multicatalytic proteinase complex involved in cellular protein degradation; may also function as a transcriptional modulator
SW:STB3_HUMAN	STXBP3	21, 43	6	0.66	0.15	SW:STB3_HUMAN O00186 homo sapiens (human). syntaxin binding protein 3 (unc-18 homolog 3) (unc-18c) (unc-18-3). 5/2000 [MASS=67574]/Syntaxin binding protein 3, binds syntaxin 4 (STX4), predicted to be involved in vesicle transport and docking and in neurotransmitter release
SW:CLH2_HUMAN	CLTCL1	16, 43	10	0.66	0.15	SW:CLH2_HUMAN P53675 homo sapiens (human). clathrin heavy chain 2 (clh-22). 5/2000 [MASS=187030]/Clathrin heavy polypeptide-like 1, may play roles in vesicle budding and in cytoskeleton-dependent trans-Golgi network membrane sorting; gene is among those deleted in velocardiofacial and DiGeorge syndromes, and is a fusion partner with ALK in lymphoma
GP:D38549_1	CYFIP1	45	2	0.66	0.11	GP:D38549_1 Human mRNA for KIAA0068 gene, partial cds; ha1025 is new. [MASS=147136]/Cytoplasmic FMRP interacting protein 1, a member of the CYFIP protein family, binds F-actin and active, GTP-bound RAC1, predicted to play a role in membrane ruffling formation and may be necessary for neuronal structure development or maintenance
GP:U86782_1	POH1	32	3	0.66	0.19	GP:U86782_1 Human 26S proteasome-associated pad1 homolog (POH1) mRNA, complete cds; human homolog of fission yeast pad1. [MASS=34577]/26S proteasome-associated pad1 homolog, a subunit of the 26S proteasome, confers multidrug resistance and resistance to ultraviolet light when overexpressed
SW:AR41_HUMAN	ARPC1B	8, 11	4	0.65	0.18	SW:AR41_HUMAN O15143 homo sapiens (human). arp2/3 complex 41 kda subunit (p41-arc). 12/1998 [MASS=40950]/Actin related protein 2/3 complex 1A, component of the Arp2/3 complex, interacts directly with an ARPC4 and ARPC5 heterodimer, may have a role in Arp2/3 complex assembly or maintenance, may regulate complex activity or intracellular distribution
PIR2:T08684	KIAA1265	45	1	0.65	0.00	PIR2:T08684 hypothetical protein DKFZp564L2123.1 - human (fragment) [MASS=60751]/Member of the ZIP zinc transporter family, which may be metal transporters, has moderate similarity to uncharacterized human LIV-1
SW:2AAA_HUMAN	PPP2R1A	45	1	0.65	0.00	SW:2AAA_HUMAN P30153 homo sapiens (human). serine/threonine protein phosphatase 2a, 65 kda regulatory subunit a, alpha isoform (pp2a, subunit a, pr65-alpha isoform) (pp2a, subunit a, r1-alpha isoform) ([MASS=65092]/Protein phosphatase 2 regulatory subunit A alpha isoform, a regulatory subunit of the PP2 enzyme complex, binds CTLA-4 (Cd152), CD28 and RelA (RELA); mutations in the gene are occasionally detected in cancer cells
SW:DYI2_HUMAN	DNCI2	45	3	0.65	0.01	SW:DYI2_HUMAN Q13409 homo sapiens (human). dynein intermediate chain 2, cytosolic (dh ic-2) (cytoplasmic dynein intermediate chain 2) (fragment). 5/2000 [MASS=39236]/Protein with strong similarity to cytoplasmic dynein intermediate polypeptide 2 (rat Dnci2), which may interact with p150Glued (rat Dctn1) subunit of dynactin
SW:IF2P_HUMAN	IF2	35	2	0.65	0.02	SW:IF2P_HUMAN O60841 homo sapiens (human). translation initiation factor if-2. 5/2000 [MASS=138755]/Translation initiation factor, member of the Tu elongation factor family, has moderate similarity to yeast YAL035W translation initiation factor 2 (eIF2)
GP:AF003521_1	JAG2	16	1	0.65	0.00	GP:AF003521_1 Homo sapiens Jagged 2 mRNA, complete cds; ligand for Notch receptor; Contains EGF repeats and DSL domain. [MASS=133394]/Jagged 2, a Notch receptor ligand that may coordinate differentiation among progenitors adopting identical cell fates, plays a role in hair cell development in the cochlea
SW:DIA1_HUMAN	DIAPH1	11	2	0.65	0.08	SW:DIA1_HUMAN O60610 homo sapiens (human). diaphanous protein homolog 1. 5/2000 [MASS=138979]/Diaphanous, contains profilin and rho binding domains and possibly regulates actin polymerization in inner ear hair cells; mutation of the gene is associated with nonsyndromal-postlingual deafness

GP:AK026010_1	FLJ22357	45	3	0.64	0.02	GP:AK026010_1 Homo sapiens cDNA: FLJ22357 fis, clone HRC06404; unnamed protein product. [MASS=97371]/Member of the rhomboid family of integral membrane proteins, has high similarity to uncharacterized human FLJ22341
GP:AB014718_1	TNFRSF10B	41	2	0.64	0.10	GP:AB014718_1 Homo sapiens DR5 gene, exon 9 and complete cds. [MASS=47894]/Tumor necrosis factor receptor superfamily member 10b, receptor that binds the ligand TRAIL (TNFSF10), induces apoptosis through interaction with FADD and activation of caspase 8 (CASP8), loss of apoptotic function is associated with cancer
SW:EGFR_HUMAN	EGFR	7, 11, 34, 41, 43	2	0.62	0.00	SW:EGFR_HUMAN P00533 homo sapiens (human). epidermal growth factor receptor precursor (ec 2.7.1.112). 12/1998 [MASS=134277]/Epidermal growth factor receptor, a receptor protein tyrosine kinase that binds epidermal growth factor (EGF) and transforming growth factor alpha (TGFA), involved in cell proliferation and differentiation, implicated in tumor invasion and metastasis
SW:HS71_HUMAN	HSPA1A	10, 25, 39	6	0.62	0.14	SW:HS71_HUMAN P08107 homo sapiens (human). heat shock 70 kda protein 1 (hsp70.1) (hsp70-1/hsp70-2). 5/2000 [MASS=70052]/Heat shock 70 kDa protein 1A, a member of the HSP70 chaperone family involved in protein folding, translocation, and complex assembly, blocks AU-rich mRNA decay by nuclear sequestering of AU-rich binding protein, may contribute to celiac disease
PIR2:T46901	PTD004	45	4	0.62	0.09	PIR2:T46901 hypothetical protein DKFZp761C10121.1 - human [MASS=44684]/Protein with high similarity to GTP-binding proteins
SW:CYSR_HUMAN	CSRP1	45	5	0.62	0.05	SW:CYSR_HUMAN P21291 homo sapiens (human). cysteine-rich protein 1 (crp1) (crp). 7/1999 [MASS=20436]/Cysteine and glycine-rich protein, a two zinc finger/LIM domain protein which interacts with alpha actinin (ACTN1); capable of homodimerization, may also be a DNA-binding protein
SW:XIP_HUMAN	HBXIP	45	1	0.62	0.00	SW:XIP_HUMAN O43504 homo sapiens (human). hepatitis b virus x interacting protein (hbx-interacting protein) (hbv x interacting protein). 5/2000 [MASS=9614]/Hepatitis B virus x-interacting protein, an antiviral response protein that interacts with hepatitis B virus protein x (HBx), inhibits hepatitis B viral replication and disrupts the viral life cycle by negatively regulating HBx transactivation activity
GP:AF001628_1	AblBP4	41	2	0.62	0.01	GP:AF001628_1 Homo sapiens interactor protein AblBP4 (AblBP4) mRNA, complete cds; member of the Abl interactor protein family; contains an SH3 domain and an SH3 binding domain. [MASS=49305]/Spectrin SH3 domain binding protein 1, has an SH3 domain, binds SH3 domains of EPS8, ABL1, and spectrin (SPTA1), acts in pinocytosis, inhibits cell proliferation; fusion of the corresponding gene with the MLL gene is linked to acute myelogenous leukemia
SW:MRP4_HUMAN	MRP4	10, 42	2	0.61	0.03	SW:MRP4_HUMAN O15439 homo sapiens (human). multidrug resistance-associated protein 4 (fragment). 5/2000 [MASS=18448]/Multidrug resistance protein 4, a member of the ATP-binding cassette transporter superfamily, transports cAMP, cGMP, and estradiol 17-beta-D-glucuronide, acts as a multidrug efflux pump, may be involved in cellular detoxification and xenobiotic resistance/Multidrug resistance protein 4, a member of the ATP-binding cassette transporter superfamily, transports cAMP, cGMP, and estradiol 17-beta-D-glucuronide, acts as a multidrug efflux pump, may be involved in cellular detoxification and xenobiotic resistance
GP:AC004839_2	BAP29	45	3	0.61	0.01	GP:AC004839_2 [MASS=28320/B-cell antigen receptor-associated protein 29, protein with strong similarity to murine Bcap29p, a B-cell receptor-associated protein that associates preferentially with IgD and weakly with IgM]
GP:AF126181_1	MAGED2	45	1	0.61	0.00	SW:MGD2_HUMAN Q9unf1 homo sapiens (human). melanoma-associated antigen d2 (mage-d2 antigen) (breast cancer associated gene 1 protein) (bcg-1) (11b6). 10/2001 [MASS=64954]/Member of the MAGE (melanoma antigen-encoding gene) family, which are expressed in a variety of tumors, has moderate similarity to neurotrophin-receptor interacting MAGE homolog (rat Maged1), which positively regulates LNGFR -mediated apoptosis
SW:AOP2_HUMAN	AOP2	10	3	0.61	0.03	SW:AOP2_HUMAN P30041 homo sapiens (human). antioxidant protein 2 (ec 1.11.1.7) (24 kda protein) (liver 2d page spot 40) (red blood cells page spot 12). 12/1998 [MASS=24904]/Protein with strong similarity to anti-oxidant proteins, member of the AhpC/TSA family
SW:CAP1_HUMAN	CAP	9, 41	1	0.60	0.00	SW:CAP1_HUMAN Q01518 homo sapiens (human). adenylyl cyclase-associated protein 1 (cap 1). 10/1996 [MASS=51673]/Adenylyl cyclase-associated protein 1, putative homolog of bifunctional S. cerevisiae Srv2p, C-terminus mediates actin binding and may play a role in regulating cell growth and morphogenesis, the N-terminal domain may bind and-or regulate adenylyl cyclase
SW:NC5R_HUMAN	DIA1	18, 42	2	0.60	0.02	SW:NC5R_HUMAN P00387 homo sapiens (human). nadh-cytochrome b5 reductase (ec 1.6.2.2) (b5r). 11/1997 [MASS=34104]/NADH-dependent cytochrome b5 reductase (diaphorase), soluble erythrocyte-specific form functions in methemoglobin reduction, ubiquitous membrane-bound form functions in lipid metabolism; mutations in the gene cause methemoglobinemia types I and II
PIR2:JC1365	FKBP2	33	3	0.60	0.14	PIR2:JC1365 FK506/rapamycin-binding protein FKBP13 precursor - human [MASS=15649]/FK506-binding protein 2 (FKBP13), an ER membrane-associated member of a family of peptidyl-prolyl cis-trans isomerases that bind the macrolide immunosuppressant drugs FK506 and rapamycin, does not play a role in the immunosuppressant action of FK506
SW:PRCZ_HUMAN	PSMA5	32	4	0.60	0.04	SW:PRCZ_HUMAN P28066 homo sapiens (human). proteasome zeta chain (ec 3.4.99.46) (macropain zeta chain) (multicatalytic endopeptidase complex zeta chain). 7/1999 [MASS=26469]/Proteasome subunit alpha type 5 (ZETA), component of the 20S catalytic core proteasome that is involved in cellular protein degradation, has ribonuclease activity
SW:RAPB_HUMAN	RAP1B	7, 41	2	0.59	0.04	SW:RAPB_HUMAN P09526 homo sapiens (human), and bos taurus (bovine). ras-related protein rap-1b (gtp-binding protein smg p21b). 7/1993 [MASS=20825]/Ras related protein 1b, member of the Ras superfamily of low molecular weight GTP-binding proteins, regulates cell cycle progression and cellular proliferation, may play a role in cAMP-responsive tumorigenesis

SW:MOES_HUMAN	MSN	6, 11, 41	1	0.59	0.00	SW:MOES_HUMAN P26038 homo sapiens (human). moesin (membrane-organizing extension spike protein). 6/1994 [MASS=67689]/Moesin, putative receptor that may link the cytoskeleton and plasma membrane and play roles in microvillus assembly and cell morphogenesis, may be an autoantigen in rheumatoid arthritis and may play a role in impaired brain development in Down syndrome
GP:AF024636_1	STK24	34, 41	1	0.59	0.00	GP:AF024636_1 Homo sapiens STE20-like kinase 3 (mst-3) mRNA, complete cds; protein serine/threonine kinase; similiar to yeast STE20. [MASS=47941]/Serine-threonine kinase 24 (Ste20 yeast homolog), member of the SPS1 subgroup of the STE20-like protein family, a serine-threonine kinase that prefers manganese as a cofactor and uses either GTP or ATP as a phosphate donor
GP:AB011173_1	KIAA0601	25	1	0.59	0.00	GP:AB011173_1 Homo sapiens mRNA for KIAA0601 protein, partial cds. [MASS=96760]/KIAA0601 protein, a riboflavin-binding protein, member of a FAD dependent enzyme superfamily, component of the HDAC1 histone deacetylase complex, may be involved in gene silencing via covalent chromatin modification
SW:HS74_HUMAN	HSPA4	10	3	0.59	0.16	heat shock 70 kda protein 4 (heat shock 70-related protein apg-2/Heat shock 70kD protein 4, putative ATP-binding molecular chaperone and member of the HSP110 family, binds RNA, may play a role in stress response and RNA stability
SW:ARP3_HUMAN	ACTR3	8, 11	6	0.58	0.13	SW:ARP3_HUMAN P32391 homo sapiens (human), and bos taurus (bovine). actin-like protein 3 (actin-2). 7/1999 [MASS=47371]/Actin-related protein 3 homolog, a component of the Arp2/3 protein complex, which is involved in actin cytoskeleton organization and biogenesis and may have a role in cell motility
PIR2:T13151	CD2AP	11, 31, 41	3	0.58	0.01	PIR2:T13151 adapter protein CMS - human [MASS=71451]/CMS: an adapter molecule involved in cytoskeletal rearrangements/CD2-associated protein, an adaptor that may play a role in kidney function and mediate cytoskeletal rearrangement; mouse Cd2ap is associated with congenital nephrotic syndrome and possibly Nail-Patella syndrome nephropathy and polycystic kidney disease
PIR2:A53016	MYO5A	11, 16, 43	1	0.58	0.00	PIR2:A53016 myosin heavy chain VA - human (fragment) [MASS=96052]/Class V myosin (Myoxin), a member of the myosin family of proteins, a motor protein that may be involved in vesicle transport and epidermal differentiation; mutation of the corresponding genge is associated with Griscelli syndrome
SW:MRP1_HUMAN	ABCC1	10, 26, 42	4	0.58	0.08	SW:MRP1_HUMAN P33527 homo sapiens (human). multidrug resistance-associated protein 1. 5/2000 [MASS=171561]/ATP-binding cassette subfamily C member 1 (multiple drug resistance protein 1), an ATP-binding cassette transporter that acts as a multidrug efflux pump conferring resistance to lipophilic drugs and chemotherapeutic agents
GP:AK024639_1	FLJ20986	45	1	0.58	0.00	GP:AK024639_1 Homo sapiens cDNA: FLJ20986 fis, clone CAE01156; unnamed protein product. [MASS=69591]/ contains a domain similar to a hydrolase/ PROBABLE CATION-TRANSPORTING ATPASE/Member of the haloacid dehalogenase or epoxide hydrolase family, has weak similarity to a region of sodium- and potassium-transporting ATPase alpha 4 (rat Atp1a4), which is an ATPase that is sensitive to inhibition by ouabain and vanadate
PIR2:JE0350	AGR2	45	1	0.58	0.00	PIR2:JE0350 Anterior gradient-2 - human [MASS=19979]/hAG-2, the human homologue of the Xenopus laevis cement gland gene XAG-2, is coexpressed with estrogen receptor in breast cancer cell lines/Anterior gradient 2 (Xenopus laevis) homolog, putative protein coexpressed with estrogen receptor in some breast cancer cell lines, expression in a colon carcinoma cell line may be regulated by the peroxisome proliferator-activated receptor gamma (PPARG)
SW:ARGR_HUMAN	ARMET	45	7	0.58	0.09	SW:ARGR_HUMAN P55145 homo sapiens (human). arginine-rich protein. 10/1996 [MASS=26906]/A gene from human chromosomal band 3p21.1 encodes a highly conserved arginine-rich protein and is mutated in renal cell carcinomas/Arginine-rich mutated in early stage tumors, may be involved in cell growth or maintenance; point mutations of the gene are seen in renal cell carcinoma, pancreatic cancer, squamous cell carcinoma and other cancers of the lung, breast, and prostate
SW:NSDL_HUMAN	NSDHL	19	6	0.58	0.16	SW:NSDL_HUMAN Q15738 homo sapiens (human). nad(p)-dependent steroid dehydrogenase-like protein (h105e3 protein). 5/2000 [MASS=41900]/NAD(P)H steroid dehydrogenase-like protein, a 3 beta-hydroxysteroid dehydrogenase that functions in cholesterol biosynthesis; mutations in the corresponding gene cause CHILD syndrome
GP:AB029025_1	KIAA1102	45	3	0.57	0.05	GP:AB029025_1 Homo sapiens mRNA for KIAA1102 protein, partial cds. [MASS=95613]/ contains a LIM domain/ EST/Protein containing a LIM domain, which may mediate protein-protein interactions
GP:AB033001_1	FLJ10209	45	2	0.57	0.10	GP:AB033001_1 Homo sapiens mRNA for KIAA1175 protein, partial cds; Start codon is not identified.. [MASS=70419]/ humun homologue of cytosolic sorting protein PACS-1a /Cytosolic sorting protein 1, may control the subcellular localization of proteins between the Golgi and endosomal compartments; may play a role in the pathogenesis of HIV-1
GP:AF112227_1	TDE1	45	1	0.57	0.00	The human TDE gene homologue: localization to 20q13.1-13.3 and variable expression in human tumor cell lines and tissue/ membrane protein/Tumor differentially expressed 1, a putative membrane protein that is overexpressed in lung tumors and colorectal tumor cells
SW:ATND_HUMAN	ATP1B3	42	3	0.57	0.07	SW:ATND_HUMAN P54709 homo sapiens (human). sodium/potassium-transporting atpase beta-3 chain (sodium/potassium-dependent atpase beta-3 subunit) (atpb-3). 7/1999 [MASS=31513]/ATPase (Na+/K+ transporting beta 3 subunit), proposed to actively transport sodium and potassium across the cell membrane to produce electrochemical gradients
SW:RB4A_HUMAN	RAB4A	21, 43	1	0.56	0.00	SW:RB4A_HUMAN P20338 homo sapiens (human). ras-related protein rab-4a. 10/1996 [MASS=23902]/GTP-binding protein, a member of the rab family of proteins, involved in early endosome trafficking and receptor recycling
GPN:AF217190_1	DDX36	45	2	0.56	0.00	contains a DEXDc, DEAD-like helicases superfamily domains/Member of the DEAD or DEAH box ATP-dependent RNA helicase family, contains two helicase conserved C-terminal domains, has low similarity to C. elegans MOG-4, which is involved in oogenesis and development/

SW:PLSL_HUMAN	LCP1	45	2	0.56	0.05	SW:PLSL_HUMAN P13796 homo sapiens (human). l-plastin (lymphocyte cytosolic protein 1) (lcp-1) (lc64p). 11/1997 [MASS=70289]/Lymphocyte cytosolic protein 1, member of the fibrin family, binds calcium and bundles actin, binds to the Ca2+ binding protein grancalcin (GCA), binds to the HLA-DR53 molecule, which is linked to autoimmune diseases; may contribute to tumorigenesis
GP:AF100757_1	COPS4	41	2	0.56	0.00	GP:AF100757_1 Homo sapiens COP9 complex subunit 4 mRNA, complete cds. [MASS=46198]/COP9 (constitutive photomorphogenic Arabidopsis homolog) subunit 4, a subunit of a complex related to the 26S proteasome regulatory complex, and possibly involved in regulating protein degradation
SW:SNAA_HUMAN	NAPA	32	3	0.56	0.01	SW:SNAA_HUMAN P54920 homo sapiens (human). alpha-soluble nsf attachment protein (snap-alpha). 5/2000 [MASS=33247]/N-ethylmaleimide-sensitive factor (NSF) attachment protein alpha, binds SNARE complexes and recruits NSF to form the 20s fusion particle, stimulates NSF ATPase activity promoting SNARE complex disassembly and exocytosis, functions in intra-Golgi transport
SW:DEST_HUMAN	DSTN	11	14	0.56	0.22	SW:DEST_HUMAN P18282 homo sapiens (human), and sus scrofa (pig). destrin (actin depolymerizing factor) (adf). 11/1997 [MASS=18506]/Actin depolymerizing factor, a member of the ADF/cofilin family that binds to actin and is predicted to depolymerize F-actin by altering filament tilt and twist; present in rod-like inclusions within neurons in the brains of Alzheimer's patients
SW:MYSA_HUMAN	MYH6	11	1	0.56	0.00	SW:MYSA_HUMAN P13533 homo sapiens (human). myosin heavy chain, cardiac muscle alpha isoform. 7/1998 [MASS=223690]/Cardiac myosin heavy chain 6, a putative structural component of muscle, may be required for heart development and function; mutation of corresponding gene is associated with familial hypertrophic cardiomyopathy
SW:LDLR_HUMAN	LDLR	19, 36, 43	3	0.55	0.04	SW:LDLR_HUMAN P01130 homo sapiens (human). low-density lipoprotein receptor precursor (ldl receptor). 5/2000 [MASS=95376]/Low density lipoprotein receptor, mediates uptake of low density lipoproteins, involved in lipid metabolism; gene variations are associated with familial hypercholesterolemia, hypertension, atherosclerosis, and coronary artery disease
SW:COF1_HUMAN	CFL1	11, 24, 41	14	0.55	0.21	SW:COF1_HUMAN P23528 homo sapiens (human). cofilin, non-muscle isoform. 11/1997 [MASS=18502]/Non-muscle cofilin, an actin-binding protein that assists translocation of actin from the cytoplasm to the nucleus; inactivation through phosphorylation by LIM-kinase leads to actin depolymerization
GPN:AF060225_1	KIAA1607	45	2	0.54	0.04	LYST-interacting protein LIP5;"Interactions of the Chediak-Higashi lysosomal-trafficking regulator protein with SNARE complex and signal transduction proteins"; dopamine responsive protein DRG-1/Protein containing a beige or BEACH domain and five WD domains (WD-40 repeats), has a region of moderate similarity to a region of lysosomal trafficking regulator protein (mouse Lyst), which is required for vesicular transport to and from lysosomes
GP:AK022489_1	MYO1B	11	1	0.54	0.00	GP:AK022489_1 Homo sapiens cDNA FLJ12427 fis, clone MAMMA1003127, highly similar to MYOSIN I ALPHA; unnamed protein product. [MASS=31145]/Myosin IB, a member of the unconventional myosin family of motor ATPases
SW:UBCC_HUMAN	UBE2N	7, 32, 34	1	0.53	0.00	SW:UBCC_HUMAN Q16781 homo sapiens (human). ubiquitin-conjugating enzyme e2-17 kda (ec 6.3.2.19) (ubiquitin- protein ligase) (ubiquitin carrier protein) (ubc13). 7/1999 [MASS=17138]/Ubiquitin-conjugating enzyme E2N (yeast UBC13 homolog), forms heterodimers with ubiquitin-conjugating enzyme E2 variants 1 or 2 (UBE2V1, UBE2V2), and catalyzes formation of unique lysine 63-linked polyubiquitin chains involved in IkappaB kinase activation
SW:VINC_HUMAN	VCL	6, 11	2	0.53	0.02	SW:VINC_HUMAN P18206 homo sapiens (human). vinculin. 12/1998 [MASS=116591]/Vinculin, a cytoskeletal protein that localizes to focal adhesions of cell-cell and cell-matrix junctions, also functions as a tumor suppressor; deficiency of alternate cardiac form, metavinculin, is associated with idiopathic dilated cardiomyopathy
SW:GLNA_HUMAN	GLUL	2, 26	1	0.53	0.00	SW:GLNA_HUMAN P15104 homo sapiens (human). glutamine synthetase (ec 6.3.1.2) (glutamate--ammonia ligase). 12/1998 [MASS=42064]/Glutamine synthase, catalyzes the condensation of glutamate and ammonia to form glutamine, may clear L-glutamate from synapses, reduced expression in the brain and abnormal presence in cerebral spinal fluid is associated with Alzheimer disease
SW:ESTD_HUMAN	ESD	26	1	0.53	0.00	SW:ESTD_HUMAN P10768 homo sapiens (human). esterase d (ec 3.1.1.1). 5/2000 [MASS=31463]/Esterase D (formylglutathione hydrolase), a carboxylesterase that may be involved in detoxification
PIR2:A59253	MYO1C	11	4	0.53	0.05	myosin I beta/Myosin IC, member of a family of ATPase motor proteins, predicted to participate in actin filament organization at the plasma membrane, may show ATP-independent actin filament binding, interacts with CBL
SW:AAAT_HUMAN	SLC1A5	42	4	0.52	0.12	SW:AAAT_HUMAN Q15758 homo sapiens (human). neutral amino acid transporter b(0) (atb(0)). 12/1998 [MASS=56621]/Solute carrier family 1 member 5, a sodium-dependent neutral amino acid transporter that comprises the amino acid transport system B(0), acts as a cell-surface receptor for RD114/simian type D
SW:GLYG_HUMAN	GYG	5, 18	6	0.51	0.11	SW:GLYG_HUMAN P46976 homo sapiens (human). glycogenin-1 (ec 2.4.1.186). 7/1999 [MASS=37347]Glycogenin (glycogenin glucosyltransferase), autocatalytic and self-glucosylating enzyme that primes de novo glycogen synthesis
SW:SYTC_HUMAN	TARS	2, 35, 37	4	0.51	0.06	SW:SYTC_HUMAN P26639 homo sapiens (human). threonyl-trna synthetase, cytoplasmic (ec 6.1.1.3) (threonine--trna ligase) (thrrs). 6/1994 [MASS=82124]/Threonyl-tRNA synthetase, a class II aminoacyl tRNA synthetase which aminoacylates its cognate tRNAs with threonine for protein synthesis, autoantigen in several autoimmune disorders
PIR2:JC4775	DNAJC3	10, 35, 41	2	0.51	0.27	PIR2:JC4775 p58k protein - human [MASS=57580]/The 58,000-dalton cellular inhibitor of the interferon-induced double-stranded RNA-activated protein kinase (PKR) is a member of the tetratricopeptide repeat family of proteins/DnaJ (Hsp40) homolog subfamily C member 3 (protein kinase inhibitor p58), a member of the tetratricopeptide repeat family of proteins that may act as a cochaperone that inhibits the activity of double-stranded RNA-dependent protein kinase (PRKR)
SW:ANX4_HUMAN	ANXA4	45	7	0.51	0.06	SW:ANX4_HUMAN P09525 homo sapiens (human). annexin iv (lipocortin iv) (endonexin i) (chromobindin 4) (protein ii) (p32.5) (placental anticoagulant protein ii) (pap-ii) (pp4-x) (35-beta calcimedin) (carb [MASS=35752]/ membrane aggregation/Annexin IV, a calcium-dependent phospholipid-binding protein involved in regulation of transmembrane conductance and endocytosis, inhibits phospholipase A2, and has in vitro anticoagulation activity, may confer paclitaxel resistance to cancer cell lines

SW:ADG_HUMAN	ADTG	43	4	0.51	0.13	SW:ADG_HUMAN O43747 homo sapiens (human). gamma-adaptin (golgi adaptor ha1/ap1 adaptin gamma subunit) (clathrin assembly protein complex 1 gamma large chain). 7/1999 [MASS=91592]/Adaptor-related protein complex 1 gamma 1 subunit, promotes the formation of clathrin coated vesicles and pits for intracellular transport; deletion of the corresponding gene occurs in Wilm's tumor, prostate adenocarcinomas, and hepatocellular carcinomas
GP:AB007851_1	PRPSAP2	25	4	0.51	0.10	GP:AB007851_1 Homo sapiens mRNA for 41-kDa phosphoribosylpyrophosphate synthetase-associated protein, complete cds. [MASS=40926]/Phosphoribosyl pyrophosphate synthetase-associated protein 2, a component of phosphoribosylpyrophosphate (PRPP) synthetase that is related to the other components of PRPP synthetase (PRPS1, PRPS2 and PRPSAP1)
SW:RB3B_HUMAN	RAB3B	21, 43	2	0.50	0.00	SW:RB3B_HUMAN P20337 homo sapiens (human). ras-related protein rab-3b. 10/1994 [MASS=24760]/Ras-related GTP-binding protein 3b, a GTP-binding protein and GTPase that is involved in exocytosis
GP:AF061258_1	LIM	41	1	0.50	0.00	GP:AF061258_1 Homo sapiens LIM protein mRNA, complete cds. [MASS=64028]/ similar to rat protein kinase C-binding enigma/Enigma homolog, contains LIM domains, binds oncoprotein Ret and may bind protein kinase C, may mediate Ret mitogenic signaling
GPN:U48734_1	ACTN4	11	8	0.50	0.03	alpha-actinin 4 (non-muscle alpha-actinin 4) (f-actin cross linking protein)/Alpha-actinin, a non-muscle cell actin-binding protein that has a role in endocytosis; a tumor suppressor, prognostic marker for breast cancer and mutations in the gene cause familial focal segmental glomerulosclerosis
SW:PROC_HUMAN	PYCR1	2	1	0.50	0.00	SW:PROC_HUMAN P32322 homo sapiens (human). pyrroline-5-carboxylate reductase (ec 1.5.1.2) (p5cr) (p5c reductase). 7/1999 [MASS=33375]/Pyrroline-5-carboxylate reductase 1, catalyzes the NAD(P)H dependent reduction of pyrroline-5-carboxylate to proline in the final step of proline synthesis, may also function NADP+ production in erythrocytes
SW:PHS3_HUMAN	PYGB	5, 18	10	0.48	0.06	SW:PHS3_HUMAN P11216 homo sapiens (human). glycogen phosphorylase, brain form (ec 2.4.1.1). 10/1996 [MASS=96683]/Brain glycogen phosphorylase, catalyzes the rate-limiting step in glycogen catabolism, activated by AMP and phosphorylation, may play a role in intestinal development; associated with gastric carcinomas displaying a differentiated intestinal phenotype
PIR2:T00261	KIAA0603	45	2	0.48	0.01	PIR2:T00261 hypothetical protein KIAA0603 - human [MASS=146606]/ contains a Phosphotyrosine-binding domain, phosphotyrosine-interaction (PI) domain; PTB/PI domain structure similar to those of pleckstrin homology (PH) and IRS-1-like PTB domains. / contains a TBC, TBC domain. Identification of a TBC domain in GYP6_YEAST and GYP7_YEAST, which are GTPase activator proteins of yeast Ypt6 and Ypt7, imply that these domains are GTPase activator proteins of Rab-like small GTPases/KIAA0603 gene product, contains a TBC domain similar to that found in the deubiquitinating enzyme USP6 oncogene
SW:B2MG_HUMAN	B2M	45	6	0.48	0.08	SW:B2MG_HUMAN P01884 homo sapiens (human), pan troglodytes (chimpanzee), and gorilla gorilla gorilla (lowland gorilla). beta-2-microglobulin precursor. 5/2000 [MASS=13715]/Beta 2-microglobulin, component of class I major histocompatibility antigen that bind and present antigenic peptides to cytotoxic T lymphocytes (CTLs), major component of hemodialysis-associated amyloid fibrils, associated with cancer progression
SW:CRP2_HUMAN	CRIP2	45	1	0.48	0.00	SW:CRP2_HUMAN P52943 homo sapiens (human). cysteine-rich protein 2 (crp2) (esp1 protein). 11/1997 [MASS=22493]/: CONTAINS 2 LIM DOMAINS. THE LIM DOMAIN BINDS 2 ZINC IONS
GP:AB029020_1	VDU1	32	1	0.48	0.00	GP:AB029020_1 Homo sapiens mRNA for KIAA1097 protein, partial cds. [MASS=110942]/ Similar to ubiquitin specific protease 20/Member of the ubiquitin carboxyl-terminal hydrolase family 2, contains a ubiquitin carboxyl-terminal hydrolases family 2 domain and a Zn-finger in ubiquitin-hydrolases and other proteins domain, has a region of low similarity to a region of human USP4
SW:AAK1_HUMAN	PRKAA1	34, 41	2	0.47	0.00	SW:AAK1_HUMAN Q13131 homo sapiens (human). 5'-amp-activated protein kinase, catalytic alpha-1 chain (ec 2.7.1.-) (ampk alpha-1 chain) (fragment). 7/1999 [MASS=19837]/AMP-activated protein kinase (alpha 1 catalytic subunit), a metabolic sensor of AMP levels, may have roles in signal transduction, may regulate the cystic fibrosis transmembrane conductance regulator (CFTR)
GP:AF015926_1	SLC9A3R1	31, 36, 42	1	0.47	0.00	Solute carrier family 9 isoform 3 regulatory factor 1 (sodium-hydrogen exchanger-regulatory factor), a cytoskeleton-linking protein that forms multiprotein complexes with members of the Ezrin-Radixin-Moesin family via two PDZ domains
PIR2:A49674	FLII	45	2	0.47	0.04	PIR2:A49674 flightless-I homolog - human (fragment) [MASS=144620]/Flightless I homolog (Drosophila), actin binding protein of the gelsolin family, interacts with other proteins including the repressor LRRFIP1, may function in signal transduction; gene maps within Smith Magenis syndrome microdeletion critical region
GP:AB018298_1	SEC24D	43	1	0.47	0.00	sec24-related protein D (human)/Protein with high similarity to SEC24 (S. cerevisiae) related gene family member C (human SEC24C), which is a putative COPII vesicle coat protein that forms a complex with Sec23Ap (human SEC23) and functions in ER-Golgi transport
SW:ATS1_HUMAN	ADAMTS1	41	5	0.47	0.18	SW:ATS1_HUMAN Q9uhi8 homo sapiens (human). adam-ts 1 precursor (ec 3.4.24.-) (a disintegrin and metalloproteinase with thrombospondin motifs 1) (adamts-1) (adam-ts1) (meth-1). 5/2000 [MASS=103498]/A disintegrin metalloprotease with a thrombospondin type 1 motif 1, a putative heparin-binding metalloprotease that inhibits endothelial cell proliferation, involved in angiogenesis; mouse Adamts1 may play a role in the pathogenesis of cancer cachexia
PIR2:JC6523	PSMD12	32	1	0.47	0.00	PIR2:JC6523 26S proteasome regulatory complex chain p55 - human [MASS=52904]/Proteasome (prosome, macropain) 26S subunit (non-ATPase, 12), a regulatory subunit of the 26S proteasome
GP:U83668_1	TUBB4Q	11	1	0.47	0.00	GP:U83668_1 Human beta-tubulin (TUB4q) gene, complete cds. [MASS=48377]/Protein of beta-tubulin subfamily, has similarity to beta2-tubulin (TUBB2), may have a role in the pathogenesis of facioscapulohumeral muscular dystrophy (FSHD1)

PIR2:T17320	unknown	45	2	0.46	0.04	PIR2:T17320 hypothetical protein DKFZp564J0863.1 - human (fragment) [MASS=61969]/ similar to Mus musculus ARL-6 interacting protein-2 (Aip-2)/ similar to GBP, Guanylate-binding protein, N-terminal domain. Transcription of the anti-viral guanylate-binding protein (GBP) is induced by interferon-gamma during macrophage induction. This family contains GBP1 and GPB2, both GTPases capable of binding GTP, GDP and GMP.
SW:HS7C_HUMAN	HSPA8	33	6	0.46	0.06	SW:HS7C_HUMAN P11142 homo sapiens (human). heat shock cognate 71 kda protein. 12/1998 [MASS=70898]/Heat shock 70kD protein 8, a constitutively expressed member of the heat shock HSP70 family of molecular chaperones; expression is elevated in the hearts of patients with hypertrophic cardiomyopathy
SW:LDHM_HUMAN	LDHA	5	5	0.46	0.14	SW:LDHM_HUMAN P00338 homo sapiens (human). l-lactate dehydrogenase m chain (ec 1.1.1.27) (ldh-a). 2/1996 [MASS=36558]/Lactate dehydrogenase muscle subunit, catalyzes the reversible NAD-dependent interconversion of pyruvate to L-lactate in glycolysis; mutations in the corresponding gene cause LDH-A deficiency
GP:U85992_1	unknown	45	1	0.45	0.00	GP:U85992_1 Human clone IMAGE:35527 unknown protein mRNA, partial cds. [MASS=19006]/ similar to ryanodine receptor, calcium release channel
SW:Y274_HUMAN	SAC3	42	1	0.45	0.00	SW:Y274_HUMAN Q92562 homo sapiens (human). hypothetical protein kiaa0274. 7/1998 [MASS=103635]/Protein containing two SacI homology domains, has a region of low similarity to suppressor of actin 1 (rat Sacm1l), which is an integral membrane lipid phosphatase that acts on PI 3 phosphate, PI 4 phosphate, and PI 3,5 bisphosphate
GP:AB015019_1	BAIAP2	16	1	0.45	0.00	GP:AB015019_1 Homo sapiens mRNA for BAP2-alpha protein, complete cds; BAI-associated protein 2(BAP2) -alpha; alternative splicing: see also AB015020. [MASS=57359]/Brain-specific angiogenesis inhibitor 1-associated protein 2, interacts with cytoplasmic portion of BAI1, may be a substrate for INSR, involved in cytoskeletal organization and lamellipodia and filopodia formation
SW:ACLY_HUMAN	ACLY	5, 19, 25	6	0.44	0.09	SW:ACLY_HUMAN P53396 homo sapiens (human). atp-citrate (pro-s-)-lyase (ec 4.1.3.8) (citrate cleavage enzyme). 10/1996 [MASS=121420]/ATP citrate lyase, catalyzes the formation of acetyl-CoA and oxaloacetate from citrate and CoA with the concomitant hydrolysis of ATP to ADP and phosphate, involved in cholesterol and fatty acid synthesis, nutritionally regulated
SW:COMT_HUMAN	COMT	26	4	0.44	0.19	SW:COMT_HUMAN P21964 homo sapiens (human). catechol o-methyltransferase, membrane-bound form (ec 2.1.1.6) (mb-comt) [contains: catechol o-methyltransferase, soluble form (s-comt)]. 5/2000 [MASS=30037]/Catechol-O-methyltransferase, a methyltransferase involved in the degradation of catecholamine neurotransmitters and catechol drugs, variant forms are associated with increased risks for obsessive-compulsive disorder and schizophrenia
SW:SNAG_HUMAN	NAPG	21, 43	2	0.43	0.31	SW:SNAG_HUMAN Q99747 homo sapiens (human). gamma-soluble nsf attachment protein (snap-gamma). 7/1999 [MASS=34746]/N-ethylmaleimide-sensitive factor (NSF) attachment protein gamma, member of a family of proteins involved in membrane fusion during exocytosis, may have roles in platelet exocytosis and in the attachment of mitochondria to the cytoskeleton
GP:AB040955_1	KIAA1522	45	1	0.43	0.00	GP:AB040955_1 Homo sapiens mRNA for KIAA1522 protein, partial cds; Start codon is not identified. fh14706 cDNA clone for KIAA1522 has a 241-bp deletion at the position between 1701 and 1943 of the sequence of KIAA1522.. [MASS=107934]/Protein of unknown function, has a region of weak similarity to a region of heavy polypeptide of neurofilament (mouse Nfh), which is a cytoskeleton structural protein that may regulate axon caliber, synaptic transmission and intermediate filament assembly
PIR2:S71949	ADAM12	45	4	0.43	0.01	PIR2:S71949 metalloproteinase 12 (EC 3.4.24.-) precursor - human [MASS=72759]/Meltrin alpha, member of the metalloproteinase-disintegrin family, metalloproteinase involved in cell adhesion and muscle cell differentiation and fusion
SW:SAH2_HUMAN	AHCYL1	26	2	0.43	0.04	SW:SAH2_HUMAN O43865 homo sapiens (human). putative adenosylhomocysteinase (ec 3.3.1.1) (s-adenosyl-l-homocysteine hydrolase) (adohcyase). 12/1998 [MASS=55628]/Protein with high similarity to s-adenosylhomocysteine hydrolase (mouse Ahcy), which reversably converts S-adenosylhomocysteine to adenosine and homocysteine and may be associated with epilepsy, member of the S-adenosylhomocysteine hydrolase family
GP:AC011001_19	unknown	45	1	0.41	0.00	GP:AC011001_19 Arabidopsis thaliana chromosome I BAC F4H5 genomic sequence, complete sequence; Putative membrane protein; Similar to predicted proteins in yeast, human and Drosophila. Predicted to be a membrane protein. [MASS=130186]/similar to GASTRIN/CHOLECYSTOKININ TYPE B RECEPTOR (CCK-B RECEPTOR) (CCK-BR)
SW:FLOH_HUMAN	SLC19A2	42	3	0.41	0.05	SW:FLOH_HUMAN O60779 homo sapiens (human). folate-like transporter dj206d15.1 on chromosome 1 (fragment). 7/1999 [MASS=52323]/Solute carrier family 19 member 2, functions as a thiamine transporter; mutations in the gene are associated with thiamine responsive megaloblastic anemia (TRMA) often combined with diabetes mellitus and deafness
SW:COA1_HUMAN	ACACA	19	2	0.41	0.05	SW:COA1_HUMAN Q13085 homo sapiens (human). acetyl-coa carboxylase 1 (ec 6.4.1.2) (acc-alpha) [includes: biotin carboxylase (ec 6.3.4.14)]. 7/1999 [MASS=265040]/Acetyl-Coenzyme A carboxylase alpha, catalyzes the rate-limiting step in long-chain fatty acid biogenesis; deficiency leads to defects in fatty acid synthesis
SW:RS12_HUMAN	RPS12	35	2	0.40	0.09	SW:RS12_HUMAN P25398 homo sapiens (human). 40s ribosomal protein s12. 5/2000 [MASS=14395]/Ribosomal protein S12, a component of the small 40S ribosomal subunit; overexpressed in colorectal cancer
GP:AB020706_1	AP2A2	45	1	0.38	0.00	GP:AB020706_1 Homo sapiens mRNA for KIAA0899 protein, partial cds. [MASS=102986]/ADAPTER-RELATED PROTEIN COMPLEX 2 ALPHA 2 SUBUNIT"/Alpha-adaptin-C, a protein that interacts with the polyglutamine-containing protein called huntingtin (HD) which is associated with Huntington's disease
GP:AJ239387_1	IGHV	45	1	0.37	0.00	GP:AJ239387_1 Homo sapiens mRNA for immunoglobulin heavy chain variable region, ID 81; ID 81. [MASS=13150]
SW:ERG7_HUMAN	LSS	19	1	0.37	0.00	SW:ERG7_HUMAN P48449 homo sapiens (human). lanosterol synthase (ec 5.4.99.7) (oxidosqualene--lanosterol cyclase) (2,3-epoxysqualene--lanosterol cyclase) (osc). 5/2000 [MASS=83309]/Lanosterol synthase, catalyzes the cyclization of (S)-2,3-oxidosqualene forming lanosterol in sterol biosynthesis
SW:PHS2_HUMAN	PYGM	5, 18	1	0.36	0.00	SW:PHS2_HUMAN P11217 homo sapiens (human). glycogen phosphorylase, muscle form (ec 2.4.1.1) (myophosphorylase). 5/2000 [MASS=97092]/Muscle glycogen phosphorylase, participates in glycogen catabolism; mutation of corresponding gene is associated with McArdle disease

SW:HPS1_HUMAN	ABHD2	16	1	0.36	0.00	SW:HPS1_HUMAN P08910 homo sapiens (human). protein phps1-2. 11/1997 [MASS=48315]/Member of the alpha/beta hydrolase fold family, has a region with weak similarity to a region of S. cerevisiae Eht1p (alcohol acyl transferase)
SW:DHSO_HUMAN	SORD	5	11	0.36	0.09	SW:DHSO_HUMAN Q00796 homo sapiens (human). sorbitol dehydrogenase (ec 1.1.1.14) (l-iditol 2-dehydrogenase). 7/1999 [MASS=38165]/Sorbitol dehydrogenase, an enzyme of the polyol pathway which catalyzes the conversion of sorbitol to fructose; may be involved in the development of diabetic complications; deficiency may be associated with some forms of congenital cataracts
GP:AK026904_1	FLJ23251	45	2	0.35	0.01	contains a repeated domain in ubiquitin activating enzyme E1 and members of the bacterial ThiF/MoeB/HesA family/Member of the UBA-THIF-type NAD-FAD binding fold family, has a region of low similarity to a region of S. pombe Uba2p, which is required for the activation of the ubiquitin-like S. pombe Ubl2p for conjugation to other enzymes
SW:RRAS_HUMAN	RRAS	41	3	0.35	0.01	SW:RRAS_HUMAN P10301 homo sapiens (human). ras-related protein r-ras (p23). 11/1997 [MASS=23480]/Related RAS viral oncogene homolog, inhibits apoptosis through BCL2 or Bcl-xl (BCL2L1), mediates myoblast differentiation, acts as a downstream effector of GRF2 in the activation of JNK, enhances cell-matrix adhesion by modulating integrins
GP:AJ245222_1	IGHV3-7	45	1	0.34	0.00	GP:AJ245222_1 Homo sapiens mRNA for immunoglobulin gamma heavy chain variable region, partial, clone 2A-3G17. [MASS=13498]
SW:FAS_HUMAN	FASN	19	90	0.34	0.15	SW:FAS_HUMAN P49327 homo sapiens (human). fatty acid synthase (ec 2.3.1.85) [includes: ec 2.3.1.38; ec 2.3.1.39; ec 2.3.1.41; ec 1.1.1.100; ec 4.2.1.61; ec 1.3.1.10; ec 3.1.2.14]. 7/1999 [MASS=273102]/Fatty acid synthase, multifunctional enzyme that synthesizes fatty acids from dietary proteins and carbohydrates; increased expression is associated with tumor growth and development, expression may serve as a prognostic maker for breast cancer
SWN:AKT3_HUMAN	AKT3	34, 41	1	0.33	0.00	SWN:AKT3_HUMAN Q9y243 homo sapiens (human). rac-gamma serine/threonine protein kinase (ec 2.7.1.-) (rac-pk-gamma) (protein kinase akt-3) (protein kinase b, gamma) (pkb gamma). 8/2001 [MASS=55775]/Protein kinase B gamma, a serine/threonine protein kinase that is activated by growth factors and 3-phosphoinositide; insulin-induced activity is upregulated in estrogen receptor negative breast cancer and androgen insensitive prostrate carcinoma
SW:IMA1_HUMAN	KPNA1	24, 25, 36, 40	1	0.33	0.00	SW:IMA1_HUMAN P52294 homo sapiens (human). importin alpha-1 subunit (karyopherin alpha-1 subunit) (srp1-beta) (rag cohort protein 2) (nucleoprotein interactor 1) (npi-1). 12/1998 [MASS=60307]/Karyopherin alpha (importin alpha), a subunit of the nuclear localization sequence (NLS) receptor complex that binds to and mediates the nuclear import of RAG1 and STAT1
GP:AK025588_1	EPS8R2	45	3	0.33	0.04	GP:AK025588_1 Homo sapiens cDNA: FLJ21935 fis, clone HEP04373; unnamed protein product. [MASS=83792]/ contains a SH3 domain/ similar to epidermal growth factor receptor pathway substrate 8 /Protein containing an Src homology 3 (SH3) domain, which bind proline-rich peptides, has moderate similarity to human EPS8, which is tyrosine-phosphorylated by epidermal growth factor receptor (human EGFR) and enhances EGF -dependent mitogenic signals
SW:ACDV_HUMAN	ACADVL	18, 19	1	0.32	0.00	SW:ACDV_HUMAN P49748 homo sapiens (human). acyl-coa dehydrogenase, very-long-chain specific, mitochondrial precursor (ec 1.3.99.-) (vlcad). 5/2000 [MASS=70390]/Very long chain acyl-coenzyme A dehydrogenase, oxidizes straight chain acyl-CoAs in the initial step of fatty acid beta-oxidation, severe deficiency results in infant cardiomyopathy with high mortality, mild deficiency results in hypoketotic hypoglycemia
SW:TNRC_HUMAN	LTBR	41	1	0.32	0.00	SW:TNRC_HUMAN P36941 homo sapiens (human). lymphotoxin-beta receptor precursor (tumor necrosis factor receptor 2 related protein) (tumor necrosis factor c receptor). 11/1997 [MASS=46709]/Lymphotoxin beta receptor, member of the tumor necrosis factor receptor family that specifically binds lymphotoxin-alpha/beta heterotrimers and mediates cytotoxic responses, may be involved in lymph gland development or organization
SW:143E_HUMAN	YWHAE	41	1	0.31	0.00	SW:143E_HUMAN P42655 homo sapiens (human), mus musculus (mouse), rattus norvegicus (rat), bos taurus (bovine), and ovis aries 14-3-3 protein epsilon (mitochondrial import stimulation factor l subunit) ([MASS=29174]/14-3-3 epsilon, may regulate the cell cycle by binding cdc25 phosphatases and linking cell cycle machinery with mitogenic signaling, binds DNA topoisomerase II alpha (TOP2A), prevents TOP2A binding of DNA and renders cells resistant to anticancer drugs
SW:RIN1_HUMAN	RIN1	41	1	0.31	0.00	SW:RIN1_HUMAN Q13671 homo sapiens (human). ras interaction/interference protein 1 (ras inhibitor jc99) (fragment). 11/1997 [MASS=52857]/Ras inhibitor 1, inhibits Ras (HRAS) - mediated transformation and may be regulated by serine phosphorylation and 14-3-3 protein binding; augments BCR-ABL oncogenic activity and is amplified in some oral squamous cell carcinomas
GP:AK022527_1	FLJ12465	45	2	0.30	0.05	GP:AK022527_1 Homo sapiens cDNA FLJ12465 fis, clone NT2RM1000802; unnamed protein product. [MASS=103079] similar to Peptidase_C2, Calpain family cysteine protease/A Novel Gene ' Niban ' Upregulated in Renal Carcinogenesis/Protein of unknown function, has high similarity to uncharacterized rat Niban
GP:D89053_1	FACL3	19	13	0.29	0.13	fatty-acid-Coenzyme A ligase, long-chain 3 /Fatty acid Coenzyme A ligase long chain 3, a putative long-chain fatty-acyl-CoA synthetase that may function in lipid synthesis and fatty acid degradation
SW:FKB5_HUMAN	FKBP5	33, 41	1	0.28	0.00	SW:FKB5_HUMAN Q13451 homo sapiens 51 kda fk506-binding protein (fkbp51) (peptidyl-prolyl cis-trans isomerase) (ec 5.2.1.8) (ppiase) (rotamase) (54 kda progesterone receptor-associated immunophilin) (fkb [MASS=51212]/FK506-binding protein 5, a peptidylprolyl cis-trans isomerase and member of the immunophilin family of FK506-binding proteins, forms a progesterone receptor complex with Hsp90 and p23, serves as a chaperone and mediates inhibition of calcineurin
SW:TRFL_HUMAN	LTF	26, 42	2	0.28	0.03	SW:TRFL_HUMAN P02788 homo sapiens (human). lactotransferrin precursor (lactoferrin). 7/1999 [MASS=78338]/Lactotransferrin, a member of the transferrin family, transports iron in extracellular fluid and may have serine protease activity, has antimicrobial, antifugual, and antiviral activity, potential theraputic or diagnostic target for autoimmune diseases

SW:TRAL_HUMAN	HSP75	10, 33	1	0.28	0.00	SW:TRAL_HUMAN Q12931 homo sapiens (human). tumor necrosis factor type 1 receptor associated protein (trap-1) (fragment). 5/2000 [MASS=75342]/Heat shock protein 75, member of the HSP90 family of molecular chaperones, binds and refolds denatured retinoblastoma (RB1) protein during M phase and after heat shock, binds the intracellular domain of tumor necrosis factor receptor type 1
GP:AB037745_1	KIAA1324	45	1	0.28	0.00	GP:AB037745_1 Homo sapiens mRNA for KIAA1324 protein, partial cds; Start codon is not identified.. [MASS=63365]
GPN:AL136939_1	ELOVL2	45	1	0.28	0.00	[FUNCTION] AFFECTS PLASMA MEMBRANE H+-ATPASE ACTIVITY. MAY ACT ON A GLUCOSE-SIGNALING PATHWAY THAT CONTROLS THE EXPRESSION OF SEVERAL GENES THAT ARE TRANSCRIPTIONALLY REGULATED BY GLUCOSE SUCH AS PMA1,HXT3 AND SNF3.[SUBCELLULAR LOCATION] INTEGRAL MEMBRANE PROTEIN (PROBABLE).[SIMILARITY] BELONGS TO GNS1/SUR4/YJL196C/C40H1.4 FAMILY./Elongation of very long chain fatty acids-like 2, protein with strong similarity to murine Ssc2, which is a member of a family of enzymes involved in tissue specific biosynthesis of very long chain fatty acids and sphingolipids
SW:DIMH_HUMAN	DHCR24	45	2	0.28	0.00	diminuto-like protein /24-dehydrocholesterol reductase, catalyzes the reduction of the delta (24) double bond of sterols in cholesterol biosynthesis, blocks apoptosis after oxidative stress and APP -induced toxicity; gene mutation is detected in desmosterolosis
GPN:Y14436_1	PPAP2A	16, 19	2	0.27	0.02	type-2 phosphatidic acid phosphatase alpha-1 /Phosphatidic acid phosphatase type 2a, catalyzes the dephosphorylation of various lipid phosphates, regulates the level of lipid phosphates which are involved in signal transduction
PIR2:T34532	MICAL	45	1	0.27	0.00	PIR2:T34532 hypothetical protein DKFZp434B1517.1 - human (fragment) [MASS=71502]CH, Calponin homology domain; Actin binding domains present in duplicate at the N-termini of spectrin-like proteins (including dystrophin, alpha-actinin/LIM, Zinc binding domain present in Lin-11, Isl-1, Mec-3.; Zinc-binding domain family. Some LIM domains bind protein partners via tyrosine-containing motifs. LIM domains are found in many key regulators of developmental pathways/Protein containing a calponin homology (CH) domain and LIM domains, has a region of moderate similarity to a region of beta spectrin (beta-fodrin, human SPTB), which is a component of the erythrocyte membrane-associated cytoskeleton
SW:41_HUMAN	EPB41	11	2	0.27	0.00	SW:41_HUMAN P11171 homo sapiens (human). protein 4.1 (band 4.1) (p4.1). 5/2000 [MASS=93239]/Erythrocyte membrane protein band 4.1, maintains cell shape by linking glycophorin C (GYPC) and band 3 proteins with the spectrin (SPTA1)-based cytoskeletal network; mutations in the corresponding gene are associated with hereditary elliptocytosis
SW:IMB3_HUMAN	KPNB3	24, 36	1	0.26	0.00	SW:IMB3_HUMAN O00410 homo sapiens (human). importin beta-3 subunit (karyopherin beta-3 subunit) (ran-binding protein 5). 12/1998 [MASS=123630]/Karyopherin beta 3, a subunit of the nuclear localization signal receptor complex and plays a role in nuclear import of ribosomal proteins; inhibited by interaction with hepatitis C virus nonstructural protein 5A
GP:U35146_1	KKIAMRE	16, 41	2	0.26	0.06	GP:U35146_1 Human p56 protein kinase (KKIAMRE), complete cds; similar to human p42 KKIALRE gene, GenBank Accession Number X66358; these protein kinases have mutually exclusive expression in testis (p56 KKIAMRE) and ovary (p42 KKIALRE). [MASS=56019]/Cyclin-dependent kinase-like 2, putative protein kinase whose activity is stimulated by epidermal growth factor (EGF), may play a role in sex differentiation
SW:NDR1_HUMAN	NDRG1	10	4	0.26	0.05	SW:NDR1_HUMAN Q92597 homo sapiens (human). ndrg1 protein (differentiation-related gene 1 protein) (drg1) (reducing agents and tunicamycin-responsive protein) (rtp) (nickel- specific induction protein ca [MASS=42835]/N-myc downstream regulated gene 1, induced by nickel, homocysteine, 2-mercaptoethanol, and tunicamycin, involved in cellular differentiation and negative control of cell proliferation, downregulated in a variety of cancers
SW:PRCE_HUMAN	**PSMB5**	32, 34	2	0.25	0.00	SW:PRCE_HUMAN P28074 homo sapiens (human). proteasome epsilon chain precursor (ec 3.4.99.46) (macropain epsilon chain) (multicatalytic endopeptidase complex epsilon chain) (proteasome subunit x) (protea [MASS=22897]/Proteasome (prosome, macropain) subunit beta type 5, which is a multicatalytic proteinase complex involved in cellular protein degradation and antigen processing; may be competitively inhibited by the HIV1 protease inhibitor Ritonavir
SW:PROS_HUMAN	**KLK3**	45	17	0.25	0.13	SW:PROS_HUMAN P07288 homo sapiens (human). prostate specific antigen precursor (ec 3.4.21.77) (psa) (gamma-seminoprotein) (semenogelase) (seminin) (p-30 antigen). 7/1999 [MASS=28741]/Kallikrein 3, (prostate specific antigen), serine protease, dissolves seminal coagulum, may play a role in regulation of cell growth, may be involved in prostate cancer invasion and metastasis, used as marker to test for and monitor prostate cancer
SW:FDFT_HUMAN	**FDFT1**	19	1	0.22	0.00	SW:FDFT_HUMAN P37268 homo sapiens (human). farnesyl-diphosphate farnesyltransferase (ec 2.5.1.21) (squalene synthetase) (sqs) (ss) (fpp:fpp farnesyltransferase). 10/1996 [MASS=48115]/Squalene synthase (farnesyl-diphosphate farnesyltransferase 1), catalyzes the conversion of farnesyl diphosphate to squalene in cholesterol biosynthesis, may be a potential target for cholesterol lowering therapy
GP:AK000542_1	**FLJ20535**	45	1	0.20	0.00	GP:AK000542_1 Homo sapiens cDNA FLJ20535 fis, clone KAT11013; unnamed protein product. [MASS=75854] contains a Tetratricopeptide repeats Domain/Protein containing three TPR (tetratrico peptide repeat) domains, which may mediate protein-protein interactions
SW:CD9_HUMAN	**CD9**	45	2	0.20	0.00	SW:CD9_HUMAN P21926 homo sapiens (human). cd9 antigen (p24) (leukocyte antigen mic3) (motility-related protein) (mrp-1). 7/1999 [MASS=25285]/ CD9
GP:AF029684_1	**IKKB**	34, 41	1	0.19	0.00	inhibitor of nuclear factor kappa b kinase beta subunit/Serine kinase that is a subunit of the IkappaB kinase (IKK) complex, phosphorylates IkappaB and activates NF-kappaB (RELA), activated by kinases NIK (MAP3K14) and MEKK1 (MAP3K1)
PIR2:I38346	**TTN**	11	1	0.18	0.00	PIR2:I38346 elastic titin - human (fragment) [MASS=883024]/Titin, a large sarcomeric protein that extends from the I band to the Z disk of sarcomeres, maintains resting tension in muscle
GP:AC005278_12	**F15K9.12**	45	1	0.17	0.00	GP:AC005278_12 Arabidopsis thaliana chromosome 1 BAC F15K9 sequence, complete sequence; Contains similarity to transcription initiation factor IIE, alpha subunit gb|X63468 from Homo sapiens.. [MASS=57306]

GPN:AF099989_1	**STK39**	34	2	0.13	0.00	STE20/SPS1-RELATED PROLINE-ALANINE RICH PROTEIN KINASE (STE-20RELATED KINASE) (DCHT) /Ste-20-related protein kinase, member of the STE20/SPS1 family, a serine/threonine kinase, activates p38 kinase, may respond to stress activated signals
SW:TMS2_HUMAN	**TMPRSS2**	45	10	0.12	0.05	SW:TMS2_HUMAN O15393 homo sapiens (human). transmembrane protease, serine 2 (ec 3.4.21.-). 7/1998 [MASS=53847]/Transmembrane protease serine 2 (epitheliasin), a putative serine endopeptidase with transmembrane, LDLRA (LDL receptor class A) and SRCR (scavenger receptor cysteine-rich) domains; highly expressed in androgen-dependent prostate cancer
SW:KLK2_HUMAN	**KLK2**	32	1	0.12	0.00	SW:KLK2_HUMAN P20151 homo sapiens (human). glandular kallikrein 2 precursor (ec 3.4.21.35) (tissue kallikrein) (prostate) (hgk-1). 10/1996 [MASS=28671]/Kallikrein 2, arginine selective serine protease, involved in activation of PSA (KLK3), may activate urokinase type plasminogen activator (PLAU), used as a marker with PSA (KLK3) to help discriminate between prostate cancer and benign prostate hyperplasia
Bold Italics represents ICAT^{TM} reagent labeled proteins that have ICAT^{TM} reagent ratios = or > 4-fold.						

AccessID	Gene	Functional Group	XPRESS Count	d0:d8 ratio	d0:d8 StdDev	Description
SW:PROS_HUMAN	**KLK3**	45	17	0.25	0.13	SW:PROS_HUMAN P07288 homo sapiens (human). prostate specific antigen precursor (ec 3.4.21.77) (psa) (gamma-seminoprotein) (semenogelase) (seminin) (p-30 antigen). 7/1999 [MASS=28741]/Kallikrein 3, (prostate specific antigen), serine protease, dissolves seminal coagulum, may play a role in regulation of cell growth, may be involved in prostate cancer invasion and metastasis, used as marker to test for and monitor prostate cancer
SW:TMS2_HUMAN	TMPRSS2	45	10	0.12	0.05	SW:TMS2_HUMAN O15393 homo sapiens (human). transmembrane protease, serine 2 (ec 3.4.21.-). 7/1998 [MASS=53847]/Transmembrane protease serine 2 (epitheliasin), a putative serine endopeptidase with transmembrane, LDLRA (LDL receptor class A) and SRCR (scavenger receptor cysteine-rich) domains; highly expressed in androgen-dependent prostate cancer
SW:FAS_HUMAN	FASN	19	90	0.34	0.15	SW:FAS_HUMAN P49327 homo sapiens (human). fatty acid synthase (ec 2.3.1.85) [includes: ec 2.3.1.38; ec 2.3.1.39; ec 2.3.1.41; ec 1.1.1.100; ec 4.2.1.61; ec 1.3.1.10; ec 3.1.2.14]. 7/1999 [MASS=273102]/Fatty acid synthase, multifunctional enzyme that synthesizes fatty acids from dietary proteins and carbohydrates; increased expression is associated with tumor growth and development, expression may serve as a prognostic maker for breast cancer
SW:LDLR_HUMAN	LDLR	19, 36, 43	3	0.55	0.04	SW:LDLR_HUMAN P01130 homo sapiens (human). low-density lipoprotein receptor precursor (ldl receptor). 5/2000 [MASS=95376]/Low density lipoprotein receptor, mediates uptake of low density lipoproteins, involved in lipid metabolism; gene variations are associated with familial hypercholesterolemia, hypertension, atherosclerosis, and coronary artery disease
SW:CTNB_HUMAN	CTNNB1	6, 11, 29, 41	19	0.79	0.26	SW:CTNB_HUMAN P35222 homo sapiens (human). beta-catenin. 2/1996 [MASS=85497]/Beta catenin, links cadherins to the cytoskeleton, may act as a component of the Wnt signal transduction pathway transmitting nuclear signals via a complex with LEF1 and TCF transcription factors; mutations in the gene are associated with various cancers
SW:P60_HUMAN	HSPD1	33	22	1.69	0.31	SW:P60_HUMAN P10809 homo sapiens (human). mitochondrial matrix protein p1 precursor (p60 lymphocyte protein) (60 kda chaperonin) (heat shock protein 60) (hsp-60) (protein cpn60) (groel protein) (hucha60 [MASS=61055]/Chaperonin 60, mitochondrial matrix protein induced by stress, component of the chaperonin complex that is implicated in mitochondrial protein folding and function, induced by inflammatory and immune responses, and implicated in coronary disease

Panel 3, pg 60

AccessID	Gene	Peptide	XPRESS	Description
GP:AF024636_1	STK24	K.MKDIPKRPFSQC*LSTIISPLFAELKEK.S	0.59	GP:AF024636_1 Homo sapiens STE20-like kinase 3 (mst-3) mRNA, complete cds; protein serine/threonine kinase; similiar to yeast STE20. [MASS=47941]/Serine-threonine kinase 24 (Ste20 yeast homolog), member of the SPS1 subgroup of the STE20-like protein family, a serine-threonine kinase that prefers manganese as a cofactor and uses either GTP or ATP as a phosphate donor
SW:FASA_HUMAN	TNFSF6	N.LEGLHHDGQFC*HKPC*PPGER.K	1.06	SW:FASA_HUMAN P25445 homo sapiens (human). fasl receptor precursor (apoptosis-mediating surface antigen fas) (apo-1 antigen) (cd95 antigen). 11/1997 [MASS=37732]/Apoptosis antigen ligand 1, a tumor necrosis factor alpha related cytokine that binds Fas and induces apoptosis, plays important roles in immune system development, immune response and tumorigenesis, may be a prognostic tumor marker

Panel 4, pgs. 61-238

Cellular Process	Gene	Functional Group	XPRESS Count	d0:d8 ratio	d0:d8 StdDev
Aging					
SW:SYV_HUMAN	VARS2	1	4	0.95	0.14
Amino Acid Metabolism					
SW:PROC_HUMAN	PYCR1	2	1	0.50	0.00
SW:SYTC_HUMAN	TARS	2	4	0.51	0.06
SW:GLNA_HUMAN	GLUL	2	1	0.53	0.00
SW:SYG_HUMAN	GARS	2	1	0.69	0.00
SW:SYD_HUMAN	DARS	2	4	0.77	0.15
SW:SYA_HUMAN	AARS	2	1	0.83	0.00
SW:SYR_HUMAN	RARS	2	7	0.84	0.08
SW:SYM_HUMAN	MARS	2	9	0.87	0.18
SW:SERC_HUMAN	PSA	2	2	0.87	0.15
PIR2:B55053	SCYE1	2	9	0.88	0.07
GP:U66669_1	HIBCH	2	1	0.91	0.00
SW:SYEP_HUMAN	EPRS	2	23	0.92	0.84
SW:SYQ_HUMAN	QARS	2	2	0.94	0.20
SW:SYK_HUMAN	KARS	2	7	1.01	0.18
SW:SYI_HUMAN	IARS	2	9	1.10	0.16

SW:CBS_HUMAN	CBS	2	1	1.13	0.00
SW:AATM_HUMAN	GOT2	2	4	1.21	0.02
SW:ODB2_HUMAN	DBT	2	1	1.23	0.00
SWN:SYFB_HUMAN	FRSB	2	4	1.25	0.44
SW:DHE3_HUMAN	GLUD1	2	8	1.31	0.24
SW:SERA_HUMAN	PHGDH	2	44	1.36	0.41
SW:IVD_HUMAN	IVD	2	1	1.37	0.00
SW:SYN_HUMAN	NARS	2	4	1.42	0.19
SW:G6PE_HUMAN	GDH	2	1	1.48	0.00
SW:AOFB_HUMAN	MAOB	2	1	1.59	0.00
SW:AOFA_HUMAN	MAOA	2	15	1.68	0.50
SW:ASNS_HUMAN	ASNS	2	1	1.85	0.00
SW:GLYM_HUMAN	SHMT2	2	8	1.98	0.70
Axonal Transport					
SW:DYNA_HUMAN	DCTN1	4	1	0.98	0.00
Carbohydrate Metabolism					
SW:PHS2_HUMAN	PYGM	5	1	0.36	0.00

SW:DHSO_HUMAN	SORD	5	11	0.36	0.09
SW:ACLY_HUMAN	ACLY	5	6	0.44	0.09
SW:LDHM_HUMAN	LDHA	5	5	0.46	0.14
SW:PHS3_HUMAN	PYGB	5	10	0.48	0.06
SW:GLYG_HUMAN	GYG	5	6	0.51	0.11
SW:ALFA_HUMAN	ALDOA	5	4	0.71	0.25
SW:GFA1_HUMAN	GFPT1	5	5	0.72	0.06
SW:UGS1_HUMAN	GYS1	5	5	0.73	0.15
SW:G3P2_HUMAN	GAPD	5	2	0.85	0.01
SW:G6PI_HUMAN	GPI	5	2	0.85	0.01
SW:ENOB_HUMAN	ENO3	5	4	0.86	0.13
GP:AF144074_1	G2AN	5	3	0.86	0.05
SW:GDE_HUMAN	AGL	5	18	0.92	0.22
SW:PGK1_HUMAN	PGK1	5	16	0.93	0.18
SW:DHAG_HUMAN	ALDH9A1	5	1	0.94	0.00
SW:ODO1_HUMAN	OGDH	5	9	0.94	0.18

SW:K6PL_HUMAN	PFKL	5	8	0.97	0.17
SW:DIAC_HUMAN	CTBS	5	1	1.00	0.00
SW:KPB1_HUMAN	PHKA1	5	3	1.00	0.09
SW:TPIS_HUMAN	TPI1	5	9	1.00	0.18
SW:ENOA_HUMAN	ENO1	5	3	1.01	0.08
SW:G19P_HUMAN	PRKCSH	5	3	1.01	0.47
GP:AJ131612_1	Slc25a10	5	1	1.02	0.00
SW:ODPB_HUMAN	PDHB	5	1	1.05	0.00
SW:HXK1_HUMAN	HK1	5	5	1.07	0.11
GP:AF113123_1	DCXR	5	2	1.09	0.01
SW:KPY1_HUMAN	PKM2	5	19	1.09	0.24
SW:GNT2_HUMAN	MGAT2	5	1	1.16	0.00
SW:ODPA_HUMAN	PDHA1	5	3	1.17	0.41
SW:GAL1_HUMAN	GALK1	5	1	1.19	0.00
SW:GLCM_HUMAN	GBA	5	2	1.21	0.09
SW:INSR_HUMAN	INSR	5	2	1.22	0.02

SW:ODPX_HUMAN	PDX1	5	3	1.24	0.16
GP:AB028128_1	DPM3	5	2	1.25	0.51
SW:ACON_HUMAN	ACO2	5	1	1.27	0.00
SW:GL6S_HUMAN	GNS	5	5	1.36	0.20
SW:KG3B_HUMAN	GSK3B	5	1	1.36	0.00
SW:DLDH_HUMAN	DLD	5	10	1.59	0.59
SW:CISY_HUMAN	CS	5	1	1.62	0.00
SW:BDH_HUMAN	BDH	5	4	1.76	0.25
SW:AGAL_HUMAN	GLA	5	1	1.80	0.00
SW:LYAG_HUMAN	GAA	5	2	1.94	0.01
SW:MAOM_HUMAN	ME2	5	2	1.96	0.04
SW:SPHM_HUMAN	SGSH	5	1	2.03	0.00
SW:IDHP_HUMAN	IDH2	5	7	2.04	0.65
SW:KC2B_HUMAN	CSNK2B	5	2	2.11	0.18
SW:MA2B_HUMAN	MAN2B1	5	1	2.14	0.00
SW:DHSB_HUMAN	SDHB	5	1	2.24	0.00

SW:PPCM_HUMAN	PCK2	5	6	2.45	1.09
SW:DHSA_HUMAN	SDHA	5	5	2.48	0.32
SW:K6PP_HUMAN	PFKP	5	1	2.96	0.00
SW:GPDM_HUMAN	GPD2	5	1	3.30	0.00
GP:AJ002744_1	GALNT7	5	1	4.00	0.00
Cell Adhesion					
SW:VINC_HUMAN	VCL	6	2	0.53	0.02
SW:MOES_HUMAN	MSN	6	1	0.59	0.00
SW:CTN1_HUMAN	CTNNA1	6	27	0.71	0.19
SW:PLAK_HUMAN	DP3	6	12	0.73	0.19
SW:CLD7_HUMAN	CLDN7	6	1	0.74	0.00
SW:ITAV_HUMAN	ITGAV	6	1	0.75	0.00
GP:AF306723_1	JUP	6	1	0.78	0.00
SW:CTNB_HUMAN	CTNNB1	6	19	0.79	0.26
SW:EZRI_HUMAN	VIL2	6	1	0.80	0.00
SW:ITA6_HUMAN	ITGA6	6	3	0.83	0.04
GP:AB002382_1	CTNND1	6	18	0.88	0.31
SW:ITA5_HUMAN	ITGA5	6	2	0.91	0.03

SW:EFA5_HUMAN	EFNA5	6	1	0.99	0.00
PIR2:G02390	MDC15	6	6	1.03	0.12
SW:DESP_HUMAN	DSP	6	7	1.15	0.13
SW:LMB2_HUMAN	LAMB2	6	2	1.22	0.15
SW:CD81_HUMAN	CD81	6	2	1.27	0.06
SW:ATC2_HUMAN	ATP2B2	6	9	1.28	0.35
SWN:ARVC_HUMAN	ARVCF	6	4	1.40	0.33
SW:RSP4_HUMAN	LAMR1	6	7	1.44	0.05
SW:RB13_HUMAN	RAB13	6	1	1.49	0.00
SW:PTPF_HUMAN	LAR	6	5	1.50	0.35
SW:MIC2_HUMAN	MIC2	6	11	1.55	0.30
SW:C166_HUMAN	ALCAM	6	8	1.58	0.27
GP:U17032_1	ARHGAP5	6	1	1.66	0.00
SWN:JAM1_HUMAN	JAM1	6	9	1.85	0.84
SW:ITB1_HUMAN	ITGB1	6	5	1.94	0.58
GP:U64791_1	GLG1	6	1	1.95	0.00
GP:U28811_1	CFR-1	6	14	1.97	0.53

SW:NB8M_HUMAN	NDUFB7	6	2	2.27	0.65
GP:AC005609_7	PCDHA4	6	1	2.70	0.00
SW:LU_HUMAN	LU	6	3	2.88	0.14
SW:LMG1_HUMAN	LAMC1	6	1	3.60	0.00
Cell Cycle Control					
SW:UBCC_HUMAN	UBE2N	7	1	0.53	0.00
SW:RAPB_HUMAN	RAP1B	7	2	0.59	0.04
SW:EGFR_HUMAN	EGFR	7	2	0.62	0.00
SW:RS4_HUMAN	RPS4X	7	3	0.73	0.14
SW:FKB1_HUMAN	FKBP1A	7	2	0.78	0.00
SW:P2AA_HUMAN	PPP2CA	7	7	0.78	0.11
SW:DYN2_HUMAN	DNM2	7	1	0.81	0.00
GP:AB002323_1	DNCH1	7	8	0.83	0.29
PIR2:T03842	SKB1	7	5	0.83	0.18
GP:U59435_1	PA2G4	7	7	0.84	0.18
SW:GPS1_HUMAN	GPS1	7	4	0.86	0.12
SW:RHOG_HUMAN	ARHG	7	5	0.90	0.29
SW:TCPB_HUMAN	CCT2	7	5	0.90	0.26

SW:G25B_HUMAN	CDC42	7	13	0.90	0.13
GP:AB006534_1	SPINT2	7	1	0.91	0.00
SW:143T_HUMAN	YWHAQ	7	3	0.91	0.05
PIR2:S69890	MIG2	7	2	0.93	0.03
SW:APP2_HUMAN	APLP2	7	2	0.95	0.08
SW:RHOA_HUMAN	ARHA	7	37	0.95	0.25
SW:TCPH_HUMAN	CCT7	7	2	0.95	0.10
SW:DYNA_HUMAN	DCTN1	7	1	0.98	0.00
SW:RAN_HUMAN	RAN	7	3	0.98	0.04
SW:RAPA_HUMAN	RAP1A	7	1	0.98	0.00
SW:TERA_HUMAN	VCP	7	41	0.99	0.20
SW:TCPD_HUMAN	CCT4	7	4	1.01	0.17
GP:D88435_1	GAK	7	2	1.05	0.04
SW:ERB2_HUMAN	ERBB2	7	5	1.07	0.09
SW:PP1A_HUMAN	PPP1CA	7	2	1.09	0.03
SW:FRAP_HUMAN	FRAP1	7	1	1.13	0.00
GP:U97276_1	Q6	7	1	1.17	0.00

PIR2:T00387	CLASP1	7	1	1.18	0.00
GP:AB020723_1	KIAA0916	7	1	1.23	0.00
SW:NPL1_HUMAN	NAP1L1	7	1	1.24	0.00
SW:RCC_HUMAN	CHC1	7	2	1.30	0.00
SW:P2BA_HUMAN	PPP3CA	7	3	1.30	0.16
GP:AF013591_1	SUDD	7	2	1.53	0.02
SW:RFA3_HUMAN	RPA3	7	2	1.61	0.19
SW:CUL2_HUMAN	CUL2	7	1	1.64	0.00
SW:MCM4_HUMAN	MCM4	7	3	1.65	0.14
SW:BUB3_HUMAN	BUB3	7	2	1.73	0.02
SW:ITB1_HUMAN	ITGB1	7	5	1.94	0.58
SW:NHPX_HUMAN	NHP2L1	7	2	2.21	0.20
Cell Elongation					
SW:ARP3_HUMAN	ACTR3	8	6	0.58	0.13
SW:AR41_HUMAN	ARPC1B	8	4	0.65	0.18
SW:AR21_HUMAN	ARPC3	8	1	0.74	0.00
SW:ARP2_HUMAN	ACTR2	8	5	0.99	0.15

SW:AR34_HUMAN	ARPC2	8	2	1.29	0.38
Cell Polarity					
SW:CAP1_HUMAN	CAP	9	1	0.60	0.00
GP:U40572_1	SNTB2	9	3	1.11	0.12
SW:VAB2_HUMAN	ATP6B2	9	7	1.47	0.34
Cell Stress					
SW:NDR1_HUMAN	NDRG1	10	4	0.26	0.05
SW:TRAL_HUMAN	HSP75	10	1	0.28	0.00
PIR2:JC4775	DNAJC3	10	2	0.51	0.27
SW:MRP1_HUMAN	ABCC1	10	4	0.58	0.08
SW:HS74_HUMAN	HSPA4	10	3	0.59	0.16
SW:AOP2_HUMAN	AOP2	10	3	0.61	0.03
SW:MRP4_HUMAN	MRP4	10	2	0.61	0.03
SW:HS71_HUMAN	HSPA1A	10	6	0.62	0.14
SW:TDX2_HUMAN	PRDX2	10	8	0.77	0.16
SW:ENPL_HUMAN	TRA1	10	5	0.84	0.11
SW:DNJ2_HUMAN	DNAJA1	10	1	0.86	0.00

GP:AB015798_1	HSJ2	10	1	0.91	0.00
SW:MK01_HUMAN	MAPK1	10	1	0.97	0.00
SW:TDX1_HUMAN	PRDX1	10	2	1.02	0.01
SW:RAC1_HUMAN	RAC1	10	18	1.08	0.53
SW:A4_HUMAN	APP	10	5	1.09	0.19
PIR2:T00361	KIAA0678	10	3	1.18	0.16
SW:MYSO_HUMAN	MYH10	10	4	1.18	0.49
SW:HS9B_HUMAN	HSPCB	10	10	1.22	0.52
SW:BCR_HUMAN	BCR	10	1	1.29	0.00
SW:SODC_HUMAN	SOD1	10	5	1.29	0.18
GP:D87116_1	MAP2K3	10	3	1.38	0.17
SW:PPOL_HUMAN	ADPRT	10	2	1.43	0.42
SW:AOPP_HUMAN	PRDX5	10	4	1.43	0.25
SW:GST1_HUMAN	MGST1	10	13	1.45	0.34
SW:H105_HUMAN	HSP105B	10	1	1.53	0.00
GP:AB032903_1	LOC51292	10	1	1.81	0.00
SW:TDXM_HUMAN	PRDX3	10	4	1.96	0.16
SW:CATA_HUMAN	CAT	10	3	2.24	0.12
Cell Structure					

PIR2:I38346	TTN	11	1	0.18	0.00
SW:41_HUMAN	EPB41	11	2	0.27	0.00
GP:U83668_1	TUBB4Q	11	1	0.47	0.00
GPN:U48734_1	ACTN4	11	8	0.50	0.03
PIR2:A59253	MYO1C	11	4	0.53	0.05
SW:VINC_HUMAN	VCL	11	2	0.53	0.02
GP:AK022489_1	MYO1B	11	1	0.54	0.00
SW:COF1_HUMAN	CFL1	11	14	0.55	0.21
SW:DEST_HUMAN	DSTN	11	14	0.56	0.22
SW:MYSA_HUMAN	MYH6	11	1	0.56	0.00
SW:ARP3_HUMAN	ACTR3	11	6	0.58	0.13
PIR2:T13151	CD2AP	11	3	0.58	0.01
PIR2:A53016	MYO5A	11	1	0.58	0.00
SW:MOES_HUMAN	MSN	11	1	0.59	0.00
SW:EGFR_HUMAN	EGFR	11	2	0.62	0.00
SW:AR41_HUMAN	ARPC1B	11	4	0.65	0.18
SW:DIA1_HUMAN	DIAPH1	11	2	0.65	0.08
SW:RHOB_HUMAN	ARHB	11	6	0.70	0.04
SW:CTN1_HUMAN	CTNNA1	11	27	0.71	0.19
SW:MYSN_HUMAN	MYH9	11	26	0.71	0.26
GP:AF177171_1	TMOD3	11	2	0.72	0.00

SW:PLAK_HUMAN	DP3	11	12	0.73	0.19
SW:AR21_HUMAN	ARPC3	11	1	0.74	0.00
GP:AB008515_1	RanBPM	11	1	0.74	0.00
SW:CAPB_HUMAN	CAPZB	11	8	0.76	0.13
SWN:LAD1_HUMAN	LAD1	11	1	0.76	0.00
SW:MLEN_HUMAN	MYL6	11	11	0.76	0.10
SW:DAG1_HUMAN	DAG1	11	1	0.77	0.00
SW:IQGA_HUMAN	IQGAP1	11	4	0.77	0.09
GP:AF306723_1	JUP	11	1	0.78	0.00
SW:CTNB_HUMAN	CTNNB1	11	19	0.79	0.26
GP:AB008567_1	SPTBN2	11	4	0.79	0.03
SW:EZRI_HUMAN	VIL2	11	1	0.80	0.00
SW:ABP2_HUMAN	FLNA	11	11	0.85	0.11
GP:AB002382_1	CTNND1	11	18	0.88	0.31
GP:AF128536_1	PACSIN2	11	4	0.89	0.45
SW:TBB2_HUMAN	TUBB2	11	30	0.91	0.31
GP:AF151793_1	AIP1	11	8	0.92	0.09

SW:UTRO_HUMAN	UTRN	11	7	0.92	0.24
SW:ACTB_HUMAN	ACTB	11	32	0.94	0.59
SW:RHOA_HUMAN	ARHA	11	37	0.95	0.25
PIR2:T46270	FLNB	11	12	0.95	0.39
SW:PRO1_HUMAN	PFN1	11	4	0.97	0.39
SW:CAZ2_HUMAN	CAPZA2	11	1	0.98	0.00
SW:DREB_HUMAN	DBN1	11	1	0.98	0.00
SW:ARP2_HUMAN	ACTR2	11	5	0.99	0.15
SW:SPCN_HUMAN	SPTAN1	11	2	1.02	0.35
GP:AB002387_1	MYO6	11	34	1.04	0.35
SW:ARF6_HUMAN	ARF6	11	2	1.07	0.05
SW:RAC1_HUMAN	RAC1	11	18	1.08	0.53
SW:TBA1_HUMAN	TUBA1	11	36	1.11	0.28
PIR2:G02520	PLEC1	11	7	1.12	0.19
SW:DESP_HUMAN	DSP	11	7	1.15	0.13
SW:PEBP_HUMAN	PBP	11	2	1.17	0.15
SW:RS29_HUMAN	RPS29	11	1	1.17	0.00
SW:DYL1_HUMAN	PIN	11	10	1.24	0.34
GP:AF022728_1	DTNB	11	1	1.27	0.00

SW:AR34_HUMAN	ARPC2	11	2	1.29	0.38
GP:AJ001714_1	MYO9A	11	1	1.34	0.00
GP:AB032179_1	EHM2	11	1	1.35	0.00
SW:AAC1_HUMAN	ACTN1	11	12	1.44	1.22
SW:MAPB_HUMAN	MAP1B	11	4	1.47	0.30
SW:TPMN_HUMAN	TPM4	11	6	1.47	0.30
SW:MAP4_HUMAN	MAP4	11	1	1.54	0.00
PIR2:A55575	ANK3	11	9	1.85	0.18
SW:ANK1_HUMAN	ANK1	11	4	1.94	0.82
GP:AB018266_1	MATR3	11	4	2.37	0.25
SW:ADDA_HUMAN	ADD1	11	1	2.64	0.00
SW:PNL1_HUMAN	PNUTL1	11	2	2.64	0.07
SW:LAMA_HUMAN	LMNA	11	1	2.95	0.00
SW:LAM1_HUMAN	LMNB1	11	1	3.22	0.00
Chromatin/Chromosome Structure					
SW:NPL1_HUMAN	NAP1L1	12	1	1.24	0.00
SW:RCC_HUMAN	CHC1	12	2	1.30	0.00
SW:HMG1_HUMAN	HMG1	12	3	1.33	0.21
SW:PPOL_HUMAN	ADPRT	12	2	1.43	0.42

SW:KU86_HUMAN	XRCC5	12	6	1.46	0.36
GP:AF041483_1	H2AFY	12	1	1.80	0.00
SW:RB48_HUMAN	RBBP4	12	1	1.80	0.00
SW:TOP1_HUMAN	TOP1	12	1	2.45	0.00
SW:H33_HUMAN	H3F3A	12	1	3.08	0.00
Cytokinesis					
SW:PNL1_HUMAN	PNUTL1	13	2	2.64	0.07
DNA Repair					
SW:G3P2_HUMAN	GAPD	14	2	0.85	0.01
PIR1:I38908	DDB1	14	2	0.86	0.03
SW:FRAP_HUMAN	FRAP1	14	1	1.13	0.00
SW:PPOL_HUMAN	ADPRT	14	2	1.43	0.42
SW:KU86_HUMAN	XRCC5	14	6	1.46	0.36
SW:APE1_HUMAN	APEX	14	13	1.57	0.38
SW:RFA3_HUMAN	RPA3	14	2	1.61	0.19
PIR2:A57099	PRKDC	14	13	1.74	0.27
SW:MSH3_HUMAN	MSH3	14	1	2.18	0.00

SW:RFA1_HUMAN	RPA1	14	1	2.30	0.00
DNA Synthesis					
SW:RAN_HUMAN	RAN	15	3	0.98	0.04
SW:MCM3_HUMAN	MCM3	15	1	1.16	0.00
SW:NPL1_HUMAN	NAP1L1	15	1	1.24	0.00
SW:RFA3_HUMAN	RPA3	15	2	1.61	0.19
SW:MCM4_HUMAN	MCM4	15	3	1.65	0.14
SW:RFA1_HUMAN	RPA1	15	1	2.30	0.00
SW:PUR_HUMAN	PURA	15	2	2.62	0.17
Differentiation					
GP:U35146_1	KKIAMRE	16	2	0.26	0.06
GPN:Y14436_1	PPAP2A	16	2	0.27	0.02
SW:HPS1_HUMAN	ABHD2	16	1	0.36	0.00
GP:AB015019_1	BAIAP2	16	1	0.45	0.00
PIR2:A53016	MYO5A	16	1	0.58	0.00
GP:AF003521_1	JAG2	16	1	0.65	0.00
SW:CLH2_HUMAN	CLTCL1	16	10	0.66	0.15
SW:HD_HUMAN	HD	16	1	0.67	0.00
GP:AB012191_1	NEDD8	16	2	0.69	0.04

SW:RB3D_HUMAN	RAB3D	16	1	0.74	0.00
SW:ITAV_HUMAN	ITGAV	16	1	0.75	0.00
SW:DAG1_HUMAN	DAG1	16	1	0.77	0.00
GP:AB011159_1	NCKAP1	16	7	0.78	0.08
SW:ITMA_HUMAN	ITM2A	16	1	0.83	0.00
SW:UTRO_HUMAN	UTRN	16	7	0.92	0.24
SW:APP2_HUMAN	APLP2	16	2	0.95	0.08
SW:ASAH_HUMAN	ASAH	16	1	0.99	0.00
SW:TPIS_HUMAN	TPI1	16	9	1.00	0.18
SW:TDX1_HUMAN	PRDX1	16	2	1.02	0.01
GP:AB037819_1	RRBP1	16	7	1.02	0.13
SW:KAP2_HUMAN	PRKAR2A	16	2	1.04	0.57
SW:ERB2_HUMAN	ERBB2	16	5	1.07	0.09
SW:RAC1_HUMAN	RAC1	16	18	1.08	0.53
SW:DESP_HUMAN	DSP	16	7	1.15	0.13
GP:AF308601_1	NOTCH2	16	2	1.16	0.06
PIR2:JE0334	RUVBL1	16	3	1.16	0.14
SW:PEBP_HUMAN	PBP	16	2	1.17	0.15

SW:GBI2_HUMAN	GNAI2	16	1	1.18	0.00
SW:A2HS_HUMAN	AHSG	16	4	1.21	0.13
GP:AF084523_1	CREG	16	1	1.22	0.00
SW:DYL1_HUMAN	PIN	16	10	1.24	0.34
SW:KAPA_HUMAN	PRKACA	16	2	1.28	0.55
SW:ATC2_HUMAN	ATP2B2	16	9	1.28	0.35
SW:DDXY_HUMAN	DBY	16	2	1.32	0.05
SW:SERA_HUMAN	PHGDH	16	44	1.36	0.41
SW:R10A_HUMAN	RPL10A	16	1	1.38	0.00
SW:OCRL_HUMAN	OCRL	16	2	1.42	1.00
SW:VAB2_HUMAN	ATP6B2	16	7	1.47	0.34
SW:DHA4_HUMAN	ALDH3A2	16	2	1.62	0.67
SW:DDX1_HUMAN	DDX1	16	6	1.67	0.10
PIR2:T09073	SFRS2IP	16	1	1.89	0.00
SW:MRP_HUMAN	CSRP3	16	21	2.13	0.55
SW:NRP_HUMAN	NRP1	16	8	2.20	1.33

SW:DDX5_HUMAN	DDX5	16	1	2.27	0.00
SW:GRBA_HUMAN	GRB10	16	3	2.55	2.22
SW:ATCK_HUMAN	ATP2C1	16	2	2.59	0.30
SW:FXR1_HUMAN	FXR1	16	1	2.74	0.00
SW:SORC_HUMAN	SRI	16	2	2.86	2.11
SW:LAMA_HUMAN	LMNA	16	1	2.95	0.00
GP:AF002668_1	DEGS	16	1	3.29	0.00
SW:LMG1_HUMAN	LAMC1	16	1	3.60	0.00
Dosage Compensation					
SW:UTX_HUMAN	UTX	17	1	1.39	0.00
Energy Generation					
SW:ACDV_HUMAN	ACADVL	18	1	0.32	0.00
SW:PHS2_HUMAN	PYGM	18	1	0.36	0.00
SW:PHS3_HUMAN	PYGB	18	10	0.48	0.06
SW:GLYG_HUMAN	GYG	18	6	0.51	0.11
SW:NC5R_HUMAN	DIA1	18	2	0.60	0.02
SW:GFA1_HUMAN	GFPT1	18	5	0.72	0.06
SW:UGS1_HUMAN	GYS1	18	5	0.73	0.15

SW:WFS1_HUMAN	WFS1	18	1	0.75	0.00
SW:G3P2_HUMAN	GAPD	18	2	0.85	0.01
SW:ENOB_HUMAN	ENO3	18	4	0.86	0.13
SW:KCRB_HUMAN	CKB	18	3	0.88	0.26
SW:GDE_HUMAN	AGL	18	18	0.92	0.22
SW:PGK1_HUMAN	PGK1	18	16	0.93	0.18
SW:ODO1_HUMAN	OGDH	18	9	0.94	0.18
SW:K6PL_HUMAN	PFKL	18	8	0.97	0.17
SW:KPB1_HUMAN	PHKA1	18	3	1.00	0.09
SW:TPIS_HUMAN	TPI1	18	9	1.00	0.18
SW:ENOA_HUMAN	ENO1	18	3	1.01	0.08
GP:AJ131612_1	Slc25a10	18	1	1.02	0.00
SW:ODPB_HUMAN	PDHB	18	1	1.05	0.00
SW:HEMZ_HUMAN	FECH	18	8	1.06	0.19
SW:HXK1_HUMAN	HK1	18	5	1.07	0.11
SW:CPT2_HUMAN	CPT2	18	1	1.08	0.00

SW:KPY1_HUMAN	PKM2	18	19	1.09	0.24
SW:FLRE_HUMAN	BLVRB	18	3	1.12	0.12
SW:COXS_HUMAN	COX17	18	1	1.18	0.00
SW:INSR_HUMAN	INSR	18	2	1.22	0.02
SW:THIK_HUMAN	ACAA1	18	15	1.26	0.25
SW:MDHC_HUMAN	MDH1	18	4	1.27	0.10
SW:ACON_HUMAN	ACO2	18	1	1.27	0.00
SW:CPT1_HUMAN	CPT1A	18	1	1.30	0.00
SW:D3D2_HUMAN	DCI	18	3	1.31	0.20
PIR2:JC5938	Txnl	18	2	1.31	0.01
SW:ECH1_HUMAN	ECH1	18	28	1.36	0.24
SW:KG3B_HUMAN	GSK3B	18	1	1.36	0.00
SW:KCRU_HUMAN	CKMT1	18	6	1.45	0.16
SW:ACPM_HUMAN	NDUFAB1	18	3	1.46	0.23
SW:OBRG_HUMAN	LEPR	18	1	1.46	0.00
SW:CAOP_HUMAN	ACOX1 or ACOX	18	1	1.53	0.00
SW:APE1_HUMAN	APEX	18	13	1.57	0.38

SW:DLDH_HUMAN	DLD	18	10	1.59	0.59
SW:CISY_HUMAN	CS	18	1	1.62	0.00
SW:ADRO_HUMAN	FDXR	18	1	1.82	0.00
SW:ADT1_HUMAN	SLC25A4	18	2	1.84	0.94
SW:NUAM_HUMAN	NDUFS1	18	1	1.87	0.00
SW:ECHB_HUMAN	HADHB	18	4	1.87	0.07
SW:LYAG_HUMAN	GAA	18	2	1.94	0.01
SW:COX1_HUMAN	MTCO1	18	1	1.97	0.00
SW:ECHA_HUMAN	HADHA	18	13	1.97	0.65
SW:ETFB_HUMAN	ETFB	18	2	1.99	0.48
PIR2:B53737	SLC25A3	18	21	2.02	0.42
SW:IDHP_HUMAN	IDH2	18	7	2.04	0.65
SW:CY1_HUMAN	CYC1	18	2	2.10	0.00
SW:NUPM_HUMAN	NDUFA8	18	5	2.10	0.44
SW:KC2B_HUMAN	CSNK2B	18	2	2.11	0.18
SW:ATPG_HUMAN	ATP5C1	18	3	2.15	0.32

SW:NUBM_HUMAN	NDUFV1	18	7	2.18	0.99
SW:UCR1_HUMAN	UQCRC1	18	8	2.24	0.43
SW:DHSB_HUMAN	SDHB	18	1	2.24	0.00
SW:NB8M_HUMAN	NDUFB7	18	2	2.27	0.65
SW:MDHM_HUMAN	MDH2	18	27	2.29	1.04
SW:UCRH_HUMAN	UQCRH	18	3	2.36	0.26
SW:ETFA_HUMAN	ETFA	18	1	2.36	0.00
SW:ATPA_HUMAN	ATP5A1	18	8	2.38	0.42
SW:UCR2_HUMAN	UQCRC2	18	1	2.42	0.00
SW:THIL_HUMAN	ACAT1	18	2	2.44	0.44
SW:UCRI_HUMAN	UQCRFS1	18	4	2.45	0.39
SW:PPCM_HUMAN	PCK2	18	6	2.45	1.09
SW:DHSA_HUMAN	SDHA	18	5	2.48	0.32
SW:ADT2_HUMAN	SLC25A5	18	8	2.53	1.17
SW:ADT3_HUMAN	SLC25A6	18	1	2.57	0.00
SW:ATPQ_HUMAN	ATP5H	18	3	2.67	0.53

SW:NIPM_HUMAN	NDUFS5	18	2	2.69	0.02
SW:COXG_HUMAN	COX6B	18	6	2.77	1.08
Lipid, Fat, and Sterol Metabolism					
SW:FDFT_HUMAN	FDFT1	19	1	0.22	0.00
GPN:Y14436_1	PPAP2A	19	2	0.27	0.02
GP:D89053_1	FACL3	19	13	0.29	0.13
SW:ACDV_HUMAN	ACADVL	19	1	0.32	0.00
SW:FAS_HUMAN	FASN	19	90	0.34	0.15
SW:ERG7_HUMAN	LSS	19	1	0.37	0.00
SW:COA1_HUMAN	ACACA	19	2	0.41	0.05
SW:ACLY_HUMAN	ACLY	19	6	0.44	0.09
SW:LDLR_HUMAN	LDLR	19	3	0.55	0.04
SW:NSDL_HUMAN	NSDHL	19	6	0.58	0.16
SW:CP51_HUMAN	CYP51	19	3	0.71	0.04
SW:LCFA_HUMAN	FACL1	19	14	0.81	0.13
SW:LCB2_HUMAN	SPTLC2	19	1	0.82	0.00
SW:DRS1_HUMAN	PECI	19	9	0.83	0.22
SWN:P23_HUMAN	p23	19	2	0.85	0.01

SW:KIME_HUMAN	MVK	19	1	0.91	0.00
GP:U66669_1	HIBCH	19	1	0.91	0.00
SW:ASAH_HUMAN	ASAH	19	1	0.99	0.00
GP:AF126782_1	RETSDR1	19	8	1.06	0.21
SW:OXYB_HUMAN	OSBP	19	3	1.08	0.26
SW:CPT2_HUMAN	CPT2	19	1	1.08	0.00
SW:FAAH_HUMAN	FAAH	19	3	1.10	0.22
SW:HBP_HUMAN	HDLBP	19	3	1.11	0.27
SW:NPC1_HUMAN	NPC1	19	1	1.16	0.00
SW:PEBP_HUMAN	PBP	19	2	1.17	0.15
SW:GLCM_HUMAN	GBA	19	2	1.21	0.09
SW:PI52_HUMAN	PIP5K2A	19	1	1.24	0.00
GP:AF034544_1	DHCR7	19	6	1.25	0.30
SW:THIK_HUMAN	ACAA1	19	15	1.26	0.25
SW:CPT1_HUMAN	CPT1A	19	1	1.30	0.00
SW:D3D2_HUMAN	DCI	19	3	1.31	0.20

SW:SAP_HUMAN	PSAP	19	14	1.31	0.91
GP:AB037108_1	TPRA40	19	2	1.36	0.09
SW:ECH1_HUMAN	ECH1	19	28	1.36	0.24
SW:SAP3_HUMAN	GM2A	19	3	1.39	0.14
GP:AF035959_1	PPAP2C	19	1	1.42	0.00
SW:OCRL_HUMAN	OCRL	19	2	1.42	1.00
GP:AB033078_1	SGPL1	19	2	1.44	0.06
SWN:CNE3_HUMAN	CPN3	19	28	1.47	0.27
SW:NLTP_HUMAN	SCP2	19	2	1.50	0.06
SW:CAOP_HUMAN	ACOX1 or ACOX	19	1	1.53	0.00
SW:PKBS_HUMAN	BZRP	19	2	1.57	0.04
SW:PXF_HUMAN	PXF	19	1	1.61	0.00
SW:DHA4_HUMAN	ALDH3A2	19	2	1.62	0.67
SW:HCD2_HUMAN	HADH2	19	4	1.67	0.12
SW:DHB4_HUMAN	HSD17B4	19	12	1.74	0.52
SW:AGAL_HUMAN	GLA	19	1	1.80	0.00
SW:ADRO_HUMAN	FDXR	19	1	1.82	0.00

SW:ECHB_HUMAN	HADHB	19	4	1.87	0.07
SW:CNBP_HUMAN	ZNF9	19	2	1.87	0.27
SW:MAOM_HUMAN	ME2	19	2	1.96	0.04
SW:ECHA_HUMAN	HADHA	19	13	1.97	0.65
SW:ETFB_HUMAN	ETFB	19	2	1.99	0.48
GP:AL023805_1	PLCB4	19	6	2.00	0.24
SW:GST3_HUMAN	MGST3	19	2	2.31	0.83
SW:ETFA_HUMAN	ETFA	19	1	2.36	0.00
SW:MAZ_HUMAN	MAZ	19	1	2.37	0.00
SW:THIL_HUMAN	ACAT1	19	2	2.44	0.44
GP:AF161397_1	HPCL2	19	2	2.53	0.16
SW:TPP1_HUMAN	CLN2	19	1	2.62	0.00
GP:AF002668_1	DEGS	19	1	3.29	0.00
SW:PA2M_HUMAN	PLA2G2A	19	3	3.94	1.93
GP:AJ002744_1	GALNT7	19	1	4.00	0.00
Meiosis					

PIR2:JE0334	RUVBL1	20	3	1.16	0.14
SW:CTOG_HUMAN	KIAA0097	20	4	1.43	0.10
Membrane Fusion					
SW:SNAG_HUMAN	NAPG	21	2	0.43	0.31
SW:RB3B_HUMAN	RAB3B	21	2	0.50	0.00
SW:RB4A_HUMAN	RAB4A	21	1	0.56	0.00
SW:STB3_HUMAN	STXBP3	21	6	0.66	0.15
SW:RB35_HUMAN	RAB35	21	1	0.73	0.00
SW:SN23_HUMAN	SNAP23	21	2	0.74	0.06
SW:RB3D_HUMAN	RAB3D	21	1	0.74	0.00
SW:RAB2_HUMAN	RAB2	21	5	0.77	0.05
SW:ANX7_HUMAN	ANXA7	21	4	0.87	0.02
GP:AF044670_1	VAP33	21	2	0.88	0.24
GP:AF004563_1	STXBP1	21	4	0.89	0.26
SWN:STX8_HUMAN	STX8	21	1	0.93	0.00
GP:AF032922_1	UNC-18C	21	2	1.09	0.03
SW:STB2_HUMAN	STXBP2	21	4	1.09	0.34
SW:NSF_HUMAN	NSF	21	6	1.12	0.16
SW:RAB7_HUMAN	RAB7	21	1	1.16	0.00
SW:RB13_HUMAN	RAB13	21	1	1.49	0.00
Mitosis					
SW:DYN2_HUMAN	DNM2	23	1	0.81	0.00
GP:AB002323_1	DNCH1	23	8	0.83	0.29

PIR2:T03842	SKB1	23	5	0.83	0.18
SW:G25B_HUMAN	CDC42	23	13	0.90	0.13
SWN:STX8_HUMAN	STX8	23	1	0.93	0.00
SW:DYNA_HUMAN	DCTN1	23	1	0.98	0.00
SW:RAN_HUMAN	RAN	23	3	0.98	0.04
PIR2:T47172	CORO1C or CRN	23	5	1.08	0.38
SW:PP1A_HUMAN	PPP1CA	23	2	1.09	0.03
PIR2:T00387	CLASP1	23	1	1.18	0.00
SW:CTOG_HUMAN	KIAA0097	23	4	1.43	0.10
SW:CUL2_HUMAN	CUL2	23	1	1.64	0.00
SW:BUB3_HUMAN	BUB3	23	2	1.73	0.02
Nuclear-Cytoplasmic Transport					
SW:IMB3_HUMAN	KPNB3	24	1	0.26	0.00
SW:IMA1_HUMAN	KPNA1	24	1	0.33	0.00
SW:COF1_HUMAN	CFL1	24	14	0.55	0.21
SW:IMB1_HUMAN	KPNB1	24	1	0.76	0.00
SW:ARS1_HUMAN	ASNA1	24	1	0.82	0.00
SW:C211_HUMAN	PTTG1IP	24	2	0.98	0.03

SW:RAN_HUMAN	RAN	24	3	0.98	0.04
SW:IMB2_HUMAN	KPNB2	24	1	1.06	0.00
SW:CRTC_HUMAN	CALR	24	21	1.09	0.26
SW:ER60_HUMAN	ERP60	24	17	1.21	0.54
SW:PAB1_HUMAN	PABPC1	24	13	1.22	0.44
SW:RCC_HUMAN	CHC1	24	2	1.30	0.00
PIR2:T13159	E1B-AP5	24	3	1.38	0.41
GP:AF037448_1	NSAP1	24	4	1.45	0.22
SW:CAS_HUMAN	CSE1L	24	3	1.46	0.18
SW:FXR2_HUMAN	FXR2	24	3	1.56	0.30
GP:D89729_1	XPO1	24	1	1.60	0.00
SW:NTF2_HUMAN	NTF2	24	2	2.12	0.23
SW:ROA1_HUMAN	HNRPA1	24	11	2.48	0.85
SW:FXR1_HUMAN	FXR1	24	1	2.74	0.00
Nucleotide Metabolism					
SW:IMA1_HUMAN	KPNA1	25	1	0.33	0.00
SW:ACLY_HUMAN	ACLY	25	6	0.44	0.09

GP:AB007851_1	PRPSAP2	25	4	0.51	0.10
GP:AB011173_1	KIAA0601	25	1	0.59	0.00
SW:HS71_HUMAN	HSPA1A	25	6	0.62	0.14
SW:PUR8_HUMAN	ADSL	25	2	0.80	0.00
SW:AMD2_HUMAN	AMPD2	25	1	0.81	0.00
PIR2:S71460	PRPS1	25	2	0.82	0.12
SW:SYA_HUMAN	AARS	25	1	0.83	0.00
SWN:ENT1_HUMAN	ENT1	25	1	0.83	0.00
SW:CST1_HUMAN	CSTF1	25	1	0.93	0.00
SW:SYQ_HUMAN	QARS	25	2	0.94	0.20
SW:IMD2_HUMAN	IMPDH2	25	8	0.95	0.32
SW:PUR6_HUMAN	PAICS	25	7	0.99	0.09
SW:RINI_HUMAN	RNH	25	1	1.01	0.00
GP:AF132941_1	LOC51068	25	1	1.02	0.00
PIR2:A57017	ABCE1	25	5	1.03	0.03
SW:NPM_HUMAN	NPM1	25	3	1.11	0.14
SW:NDK6_HUMAN	NME2	25	1	1.22	0.00

SW:PAB1_HUMAN	PABPC1	25	13	1.22	0.44
SWN:SYFB_HUMAN	FRSB	25	4	1.25	0.44
SW:ROF_HUMAN	HNRPF	25	3	1.37	0.10
PIR2:T13159	E1B-AP5	25	3	1.38	0.41
PIR2:T02673	HNRPR	25	3	1.43	0.18
GP:U85625_1	RNASE6PL	25	3	1.44	0.04
GP:AF037448_1	NSAP1	25	4	1.45	0.22
SW:PYR1_HUMAN	CAD	25	6	1.47	0.46
SW:ROK_HUMAN	HNRPK	25	6	1.51	0.30
SW:SMD3_HUMAN	SNRPD3	25	1	1.55	0.00
SW:PSS1_HUMAN	PAPSS1	25	1	1.56	0.00
SW:ROA0_HUMAN	HNRPA0	25	2	1.64	0.40
SW:ROH1_HUMAN	HNRPH1	25	4	1.66	0.22
SW:DDX1_HUMAN	DDX1	25	6	1.67	0.10
PIR2:JW0079	HNRPDL	25	1	1.72	0.00
GP:AC003972_1	RENT1	25	1	1.74	0.00
SW:RUXF_HUMAN	SNRPF	25	1	1.76	0.00
GP:AF177344_1	FLJ10581	25	1	1.89	0.00

PIR2:T09073	SFRS2IP	25	1	1.89	0.00
PIR2:I55595	RNPC2	25	1	1.92	0.00
PIR2:S78046	RNASE6	25	3	1.94	0.00
SW:DRN2_HUMAN	DNASE2	25	3	2.01	0.42
SW:SMD2_HUMAN	SNRPD2	25	2	2.02	0.82
SW:U2AF_HUMAN	U2AF65	25	1	2.05	0.00
GP:D21163_1	U5-116KD	25	1	2.11	0.00
SW:RU17_HUMAN	SNRP70	25	3	2.11	0.26
PIR2:A54601	HNRPD	25	9	2.17	0.65
SW:NHPX_HUMAN	NHP2L1	25	2	2.21	0.20
SW:DDX5_HUMAN	DDX5	25	1	2.27	0.00
SW:U2AG_HUMAN	U2AF35	25	2	2.34	0.02
SW:ROU_HUMAN	HNRPU	25	29	2.48	0.62
SW:ROA1_HUMAN	HNRPA1	25	11	2.48	0.85
SW:DD17_HUMAN	DDX17	25	1	2.58	0.00
SW:Y017_HUMAN	SF3B3	25	7	2.63	0.59
SW:NR54_HUMAN	NONO	25	2	3.38	1.09
SW:SFR7_HUMAN	SFRS7	25	2	3.66	0.49

Other Metabolism					
SW:TRFL_HUMAN	LTF	26	2	0.28	0.03
SW:SAH2_HUMAN	AHCYL1	26	2	0.43	0.04
SW:COMT_HUMAN	COMT	26	4	0.44	0.19
SW:ESTD_HUMAN	ESD	26	1	0.53	0.00
SW:GLNA_HUMAN	GLUL	26	1	0.53	0.00
SW:MRP1_HUMAN	ABCC1	26	4	0.58	0.08
PIR2:T46412	NEDD4	26	1	0.88	0.00
GP:AC005545_2	AP3D1	26	2	0.93	0.18
SW:PUR6_HUMAN	PAICS	26	7	0.99	0.09
SW:PON2_HUMAN	PON2	26	1	1.01	0.00
SW:DOPD_HUMAN	DDT	26	1	1.02	0.00
SW:HEMZ_HUMAN	FECH	26	8	1.06	0.19
GP:AF126782_1	RETSDR1	26	8	1.06	0.21
SW:A4_HUMAN	APP	26	5	1.09	0.19
SW:FLRE_HUMAN	BLVRB	26	3	1.12	0.12
SW:HYEP_HUMAN	EPHX1	26	6	1.13	0.03

SW:PEBP_HUMAN	PBP	26	2	1.17	0.15
SW:IPYR_HUMAN	PP	26	1	1.20	0.00
SW:TRSR_HUMAN	TFRC	26	2	1.20	0.12
SW:DYL1_HUMAN	PIN	26	10	1.24	0.34
PIR2:I37405	GALNT1	26	4	1.29	0.30
SW:OGT1_HUMAN	OGT	26	1	1.34	0.00
SW:MMSA_HUMAN	MMSDH	26	2	1.48	0.10
SW:AOFB_HUMAN	MAOB	26	1	1.59	0.00
SW:C1TC_HUMAN	MTHFD1	26	6	1.65	0.45
SW:FRIH_HUMAN	FTH1	26	7	1.67	0.26
SW:AOFA_HUMAN	MAOA	26	15	1.68	0.50
GP:AF277719_1	C(27)-3BETA-HS	26	1	2.02	0.00
SW:SPHM_HUMAN	SGSH	26	1	2.03	0.00
GP:X92689_1	GALNAC-T3	26	3	2.26	0.17
SW:ATCK_HUMAN	ATP2C1	26	2	2.59	0.30
GP:AL023881_1	DECR1	26	1	2.78	0.00
SW:SORC_HUMAN	SRI	26	2	2.86	2.11

Phosphate Metabolism					
SW:IPYR_HUMAN	PP	27	1	1.20	0.00
Pol III Transcription					
SW:RO60_HUMAN	SSA2	28	2	1.53	0.01
Pol II Transcription					
SW:PRS8_HUMAN	SUG1	29	9	0.66	0.15
SW:PLAK_HUMAN	DP3	29	12	0.73	0.19
GP:AF306723_1	JUP	29	1	0.78	0.00
SW:CTNB_HUMAN	CTNNB1	29	19	0.79	0.26
SW:HIP_HUMAN	ST13	29	5	0.86	0.10
PIR2:T46412	NEDD4	29	1	0.88	0.00
SW:BTF3_HUMAN	BTF3	29	1	0.91	0.00
SW:ENOA_HUMAN	ENO1	29	3	1.01	0.08
SW:TCPD_HUMAN	CCT4	29	4	1.01	0.17
GP:AF203687_1	PREB	29	2	1.09	0.06
SW:CRTC_HUMAN	CALR	29	21	1.09	0.26
SW:TF1B_HUMAN	TIF1B	29	4	1.10	0.26
PIR2:JE0334	RUVBL1	29	3	1.16	0.14
GP:AB006572_1	RMP	29	1	1.17	0.00

GP:AF000560_1	TIP20	29	2	1.21	0.57
GP:AF084523_1	CREG	29	1	1.22	0.00
SW:P2BA_HUMAN	PPP3CA	29	3	1.30	0.16
PIR2:I59405	TCEB2	29	2	1.32	0.00
SW:PPOL_HUMAN	ADPRT	29	2	1.43	0.42
SW:APE1_HUMAN	APEX	29	13	1.57	0.38
SW:CNBP_HUMAN	ZNF9	29	2	1.87	0.27
GP:AF007833_1	ZFP67	29	1	2.03	0.00
SW:RFA1_HUMAN	RPA1	29	1	2.30	0.00
SW:MAZ_HUMAN	MAZ	29	1	2.37	0.00
SW:PUR_HUMAN	PURA	29	2	2.62	0.17
Protein Complex Assembly					
GP:AF015926_1	SLC9A3R1	31	1	0.47	0.00
PIR2:T13151	CD2AP	31	3	0.58	0.01
GP:AB008515_1	RanBPM	31	1	0.74	0.00
SW:CAPB_HUMAN	CAPZB	31	8	0.76	0.13
SW:DAG1_HUMAN	DAG1	31	1	0.77	0.00
GP:U45976_1	PICALM	31	1	0.85	0.00

GP:AF044670_1	VAP33	31	2	0.88	0.24
SW:CAZ2_HUMAN	CAPZA2	31	1	0.98	0.00
SW:HS9A_HUMAN	HSPCA	31	7	0.99	0.41
SW:CYP4_HUMAN	PPID	31	1	1.19	0.00
PIR2:I59405	TCEB2	31	2	1.32	0.00
PIR2:T09073	SFRS2IP	31	1	1.89	0.00
SW:Y017_HUMAN	SF3B3	31	7	2.63	0.59
GP:AB006537_1	IL1RAP	31	1	3.20	0.00
SW:LMG1_HUMAN	LAMC1	31	1	3.60	0.00
Protein Degradation					
SW:KLK2_HUMAN	KLK2	32	1	0.12	0.00
SW:PRCE_HUMAN	PSMB5	32	2	0.25	0.00
PIR2:JC6523	PSMD12	32	1	0.47	0.00
GP:AB029020_1	VDU1	32	1	0.48	0.00
SW:UBCC_HUMAN	UBE2N	32	1	0.53	0.00
SW:SNAA_HUMAN	NAPA	32	3	0.56	0.01
SW:PRCZ_HUMAN	PSMA5	32	4	0.60	0.04
GP:U86782_1	POH1	32	3	0.66	0.19

SW:PRS8_HUMAN	SUG1	32	9	0.66	0.15
GP:AB012191_1	NEDD8	32	2	0.69	0.04
SW:NEP_HUMAN	MME	32	34	0.71	0.19
SW:PRS7_HUMAN	PSMC2	32	7	0.75	0.17
SW:PRSX_HUMAN	PSMC6	32	5	0.78	0.18
SW:PRCD_HUMAN	PSMB6	32	1	0.79	0.00
SW:PSD2_HUMAN	PSMD2	32	1	0.80	0.00
SW:PRSC_HUMAN	PSMD7	32	2	0.81	0.00
SW:PSD1_HUMAN	PSMD1	32	11	0.81	0.20
SW:Y253_HUMAN	NCSTN	32	2	0.81	0.05
SW:PRC5_HUMAN	PSC5	32	2	0.82	0.03
PIR2:JC6524	PSMD11	32	3	0.84	0.08
SW:PRC2_HUMAN	PSMA1	32	4	0.85	0.05
GP:D38048_1	PSMB7	32	1	0.88	0.00
SW:PRC8_HUMAN	PSMA3	32	2	0.88	0.06
GP:AB009398_1	PSMD13	32	5	0.88	0.24
PIR2:T46412	NEDD4	32	1	0.88	0.00
SW:UB5A_HUMAN	UBE2D1	32	2	0.90	0.01

SW:PRCI_HUMAN	PSMA6	32	12	0.97	0.27
SW:PRS4_HUMAN	PSMC1	32	12	0.99	0.17
SW:TPP2_HUMAN	TPP2	32	5	1.00	0.14
SW:DIAC_HUMAN	CTBS	32	1	1.00	0.00
GP:U41806_1	SQSTM1	32	4	1.01	0.21
GP:AB002310_1	UREB1	32	3	1.04	0.06
SW:PSD4_HUMAN	PSMD4	32	5	1.06	0.29
SWN:PSA7_HUMAN	PSMA7	32	4	1.06	0.22
PIR2:T14762	ACE2	32	1	1.10	0.00
SW:UBPA_HUMAN	USP10	32	1	1.10	0.00
SWN:UBPF_HUMAN	USP15	32	3	1.10	0.11
GP:AF039689_1	STUB1	32	4	1.16	0.13
SW:CATD_HUMAN	CTSD	32	17	1.18	0.28
GP:D87684_1	UBXD2	32	6	1.22	0.16
SW:UBCI_HUMAN	UBE2I	32	2	1.28	0.02
PIR2:I59405	TCEB2	32	2	1.32	0.00
SW:LONM_HUMAN	PRSS15	32	4	1.40	0.68
SW:PRTP_HUMAN	PPGB	32	2	1.45	0.04

SW:PPT_HUMAN	PPT1	32	7	1.57	0.39
SW:CATB_HUMAN	CTSB	32	5	1.62	0.25
SW:CUL2_HUMAN	CUL2	32	1	1.64	0.00
SW:CATH_HUMAN	CTSH	32	1	2.00	0.00
SW:RL40_HUMAN	UBA52	32	3	2.00	0.50
SW:TPP1_HUMAN	CLN2	32	1	2.62	0.00
GP:AF057145_1	ST14	32	1	3.98	0.00
GP:AB028980_1	USP24	32	1	9.55	0.00
Protein Folding					
SW:TRAL_HUMAN	HSP75	33	1	0.28	0.00
SW:FKB5_HUMAN	FKBP5	33	1	0.28	0.00
SW:HS7C_HUMAN	HSPA8	33	6	0.46	0.06
PIR2:JC1365	FKBP2	33	3	0.60	0.14
SW:TCPE_HUMAN	CCT5	33	4	0.68	0.14
GP:AF227905_1	UGCGL1	33	1	0.70	0.00
SW:TCPZ_HUMAN	CCT6A	33	3	0.77	0.08
SW:FKB1_HUMAN	FKBP1A	33	2	0.78	0.00

SW:CALX_HUMAN	CANX	33	4	0.84	0.04
SW:ER53_HUMAN	LMAN1	33	2	0.84	0.00
SW:DNJ2_HUMAN	DNAJA1	33	1	0.86	0.00
SW:HIP_HUMAN	ST13	33	5	0.86	0.10
SW:TCPB_HUMAN	CCT2	33	5	0.90	0.26
GP:AB015798_1	HSJ2	33	1	0.91	0.00
SW:TCPG_HUMAN	CCT3	33	7	0.92	0.12
SW:CYPB_HUMAN	PPIB	33	15	0.94	0.20
SW:TCPH_HUMAN	CCT7	33	2	0.95	0.10
SW:TCPA_HUMAN	CCT1	33	8	0.99	0.36
SW:TCPD_HUMAN	CCT4	33	4	1.01	0.17
SW:CYPH_HUMAN	PPIA	33	15	1.04	0.29
PIR2:T00363	KIAA0674	33	2	1.08	0.12
GP:AF039689_1	STUB1	33	4	1.16	0.13
SW:CYP4_HUMAN	PPID	33	1	1.19	0.00
SW:HS9B_HUMAN	HSPCB	33	10	1.22	0.52
SW:TCPQ_HUMAN	CCT8	33	3	1.29	0.06
GP:AF188611_1	HSPA5	33	1	1.60	0.00

SW:P60_HUMAN	HSPD1	33	22	1.69	0.31
SW:CYPM_HUMAN	PPIF	33	1	2.24	0.00
Protein Modification					
GPN:AF099989_1	STK39	34	2	0.13	0.00
GP:AF029684_1	IKKB	34	1	0.19	0.00
SW:PRCE_HUMAN	PSMB5	34	2	0.25	0.00
SWN:AKT3_HUMAN	AKT3	34	1	0.33	0.00
SW:AAK1_HUMAN	PRKAA1	34	2	0.47	0.00
SW:UBCC_HUMAN	UBE2N	34	1	0.53	0.00
GP:AF024636_1	STK24	34	1	0.59	0.00
SW:EGFR_HUMAN	EGFR	34	2	0.62	0.00
SW:TDXN_HUMAN	PRDX4	34	5	0.66	0.19
SW:RIB1_HUMAN	RPN1	34	1	0.69	0.00
GP:AB012191_1	NEDD8	34	2	0.69	0.04
GP:AF227905_1	UGCGL1	34	1	0.70	0.00
SW:KCCB_HUMAN	CAMK2B	34	2	0.74	0.09
SW:PP1B_HUMAN	PPP1CB	34	1	0.78	0.00

SW:P2AA_HUMAN	PPP2CA	34	7	0.78	0.11
SW:SRC_HUMAN	SRC	34	1	0.83	0.00
SW:KPC1_HUMAN	PRKCB1	34	1	0.85	0.00
SW:GPS1_HUMAN	GPS1	34	4	0.86	0.12
GP:AB009398_1	PSMD13	34	5	0.88	0.24
PIR2:T46412	NEDD4	34	1	0.88	0.00
SW:UB5A_HUMAN	UBE2D1	34	2	0.90	0.01
SW:G25B_HUMAN	CDC42	34	13	0.90	0.13
SW:KIME_HUMAN	MVK	34	1	0.91	0.00
GPN:AB025194_1	HD-PTP	34	1	0.93	0.00
SW:MK01_HUMAN	MAPK1	34	1	0.97	0.00
SW:LYN_HUMAN	LYN	34	2	0.98	0.02
SW:ARP2_HUMAN	ACTR2	34	5	0.99	0.15
PIR2:S52920	ADAM10	34	9	1.04	0.18
SW:KCCD_HUMAN	CAMK2D	34	3	1.04	0.01
SW:KRCB_HUMAN	AKT2	34	1	1.04	0.00
GP:AB002310_1	UREB1	34	3	1.04	0.06

SW:PTN1_HUMAN	PTPN1	34	3	1.05	0.15
SW:ERB2_HUMAN	ERBB2	34	5	1.07	0.09
SW:RAC1_HUMAN	RAC1	34	18	1.08	0.53
PIR2:T00363	KIAA0674	34	2	1.08	0.12
SW:P4HA_HUMAN	P4HA1	34	3	1.09	0.11
SW:PP1A_HUMAN	PPP1CA	34	2	1.09	0.03
PIR2:T14762	ACE2	34	1	1.10	0.00
SW:UBPA_HUMAN	USP10	34	1	1.10	0.00
SWN:UBPF_HUMAN	USP15	34	3	1.10	0.11
SW:PDI_HUMAN	P4HB	34	3	1.13	0.01
SW:GNT2_HUMAN	MGAT2	34	1	1.16	0.00
SW:EPA7_HUMAN	EPHA7	34	2	1.19	0.14
SW:INSR_HUMAN	INSR	34	2	1.22	0.02
GP:AB028128_1	DPM3	34	2	1.25	0.51
SW:UBCI_HUMAN	UBE2I	34	2	1.28	0.02
SW:KAPA_HUMAN	PRKACA	34	2	1.28	0.55
SW:BCR_HUMAN	BCR	34	1	1.29	0.00

PIR2:I37405	GALNT1	34	4	1.29	0.30
SWN:DUSC_HUMAN	DUSP12	34	3	1.30	0.17
SW:P2BA_HUMAN	PPP3CA	34	3	1.30	0.16
PIR2:JC5938	Txnl	34	2	1.31	0.01
SW:OGT1_HUMAN	OGT	34	1	1.34	0.00
GP:D87116_1	MAP2K3	34	3	1.38	0.17
SW:PPOL_HUMAN	ADPRT	34	2	1.43	0.42
SW:PTPF_HUMAN	LAR	34	5	1.50	0.35
SW:PSS1_HUMAN	PAPSS1	34	1	1.56	0.00
SW:PPT_HUMAN	PPT1	34	7	1.57	0.39
SW:PTK7_HUMAN	PTK7	34	9	1.66	0.30
PIR2:A57099	PRKDC	34	13	1.74	0.27
SW:RB48_HUMAN	RBBP4	34	1	1.80	0.00
SW:RL40_HUMAN	UBA52	34	3	2.00	0.50
SW:KC2B_HUMAN	CSNK2B	34	2	2.11	0.18
SW:MA2B_HUMAN	MAN2B1	34	1	2.14	0.00
GP:X92689_1	GALNAC-T3	34	3	2.26	0.17

GP:AB000449_1	VRK1	34	2	2.94	1.64
SW:CAG4_HUMAN	SIAT4A	34	1	2.99	0.00
Protein Synthesis					
SW:RS12_HUMAN	RPS12	35	2	0.40	0.09
PIR2:JC4775	DNAJC3	35	2	0.51	0.27
SW:SYTC_HUMAN	TARS	35	4	0.51	0.06
SW:IF2P_HUMAN	IF2	35	2	0.65	0.02
SW:RL7A_HUMAN	RPL7A	35	1	0.67	0.00
SW:SYG_HUMAN	GARS	35	1	0.69	0.00
SW:IF32_HUMAN	TRIP1	35	3	0.72	0.09
SW:RS4_HUMAN	RPS4X	35	3	0.73	0.14
SW:SYD_HUMAN	DARS	35	4	0.77	0.15
SW:EF11_HUMAN	EEF1A1	35	11	0.78	0.11
SW:SYA_HUMAN	AARS	35	1	0.83	0.00
SW:SYR_HUMAN	RARS	35	7	0.84	0.08
SW:SYM_HUMAN	MARS	35	9	0.87	0.18
SW:RL8_HUMAN	RPL8	35	4	0.88	0.57
PIR2:B55053	SCYE1	35	9	0.88	0.07
SW:SYEP_HUMAN	EPRS	35	23	0.92	0.84

SWN:E2BD_HUMAN	DKFZP586J0119	35	2	0.94	0.19
SW:SYQ_HUMAN	QARS	35	2	0.94	0.20
SW:SYV_HUMAN	VARS2	35	4	0.95	0.14
SW:IF5A_HUMAN	EIF5A	35	4	0.96	0.06
SW:RM03_HUMAN	MRPL3	35	1	0.96	0.00
SWN:SU12_HUMAN	GC20	35	4	0.98	0.06
SW:RL32_HUMAN	RPL32	35	7	1.00	0.12
GP:AF112214_1	RPL13	35	1	1.01	0.00
SW:SYK_HUMAN	KARS	35	7	1.01	0.18
GP:AB037819_1	RRBP1	35	7	1.02	0.13
GP:AF132941_1	LOC51068	35	1	1.02	0.00
SW:EF1G_HUMAN	EEF1G	35	7	1.05	0.15
SW:RS8_HUMAN	RPS8	35	9	1.07	0.56
SW:IF4G_HUMAN	EIF4G1	35	2	1.08	0.39
SW:EF2_HUMAN	EEF2	35	39	1.09	0.20
SW:SYI_HUMAN	IARS	35	9	1.10	0.16
GP:AF132939_1	LOC51067	35	1	1.11	0.00
SW:IF38_HUMAN	EIF3S8	35	5	1.11	0.32
SW:RL3_HUMAN	RPL3	35	2	1.11	0.01

SW:E2BE_HUMAN	EIF2B5	35	1	1.12	0.00
SW:RL9_HUMAN	RPL9	35	8	1.12	0.30
SW:RS5_HUMAN	RPS5	35	19	1.12	0.89
SW:RS25_HUMAN	RPS25	35	4	1.13	0.24
SW:IF2A_HUMAN	EIF2S1	35	1	1.16	0.00
SW:RS29_HUMAN	RPS29	35	1	1.17	0.00
SW:RS14_HUMAN	RPS14	35	3	1.20	0.12
SW:EF12_HUMAN	EEF1A2	35	6	1.22	0.11
SW:PAB1_HUMAN	PABPC1	35	13	1.22	0.44
SW:IF2G_HUMAN	EIF2S3	35	22	1.23	0.22
SW:IF37_HUMAN	EIF3S7	35	6	1.23	0.32
SW:RL4_HUMAN	RPL4	35	17	1.23	0.33
SW:RS17_HUMAN	RPS17	35	6	1.23	0.24
SW:RS3A_HUMAN	RPS3A	35	13	1.23	0.20
GP:AF257077_1	EIF2B3	35	2	1.24	0.11
SWN:SYFB_HUMAN	FRSB	35	4	1.25	0.44
SW:SR09_HUMAN	SRP9	35	7	1.25	0.29
SW:RL23_HUMAN	RPL23	35	10	1.30	0.27
SW:RS21_HUMAN	RPS21	35	3	1.30	0.29
SW:ERF1_HUMAN	ETF1	35	1	1.32	0.00

SW:RL5_HUMAN	RPL5	35	7	1.32	0.51
GPN:AF293383_1	ABCF1	35	1	1.33	0.00
SW:RS11_HUMAN	RPS11	35	8	1.33	0.07
SW:RLA0_HUMAN	RPLP0	35	14	1.35	0.20
SW:R27A_HUMAN	RPS27A	35	3	1.38	0.38
SW:R10A_HUMAN	RPL10A	35	1	1.38	0.00
SW:EFTU_HUMAN	TUFM	35	8	1.41	0.11
SW:SYN_HUMAN	NARS	35	4	1.42	0.19
SW:IF39_HUMAN	EIF3S9	35	5	1.44	0.20
SW:RL2A_HUMAN	RPL27A	35	7	1.44	0.56
SW:RSP4_HUMAN	LAMR1	35	7	1.44	0.05
SW:RL18_HUMAN	RPL18	35	5	1.49	0.46
SW:RL3L_HUMAN	RPL3L	35	11	1.51	0.24
SW:RS6_HUMAN	RPS6	35	5	1.52	0.13
SW:IF34_HUMAN	EIF3S4	35	1	1.53	0.00
SW:RL10_HUMAN	RPL10	35	14	1.53	1.04
SW:RL12_HUMAN	RPL12	35	35	1.62	0.58
SW:RL14_HUMAN	RPL14	35	23	1.63	0.47
SW:RL17_HUMAN	RPL17	35	4	1.63	0.06
SW:DDX1_HUMAN	DDX1	35	6	1.67	0.10
SW:R37A_HUMAN	RPL37A	35	2	1.69	0.23

SW:IF2B_HUMAN	EIF2S2	35	2	1.70	0.48
SW:RL44_HUMAN	RPL44	35	4	1.80	0.47
SW:RL40_HUMAN	UBA52	35	3	2.00	0.50
SW:RL24_HUMAN	RPL24	35	6	2.02	0.10
SW:DDX6_HUMAN	DDX6	35	3	2.06	0.72
SW:RS16_HUMAN	RPS16	35	8	2.18	0.76
SW:RS20_HUMAN	RPS20	35	1	2.42	0.00
SW:RS2_HUMAN	RPS2	35	7	2.46	1.54
SW:IF4E_HUMAN	EIF4E	35	1	2.94	0.00
Protein Translocation					
SW:IMB3_HUMAN	KPNB3	36	1	0.26	0.00
SW:IMA1_HUMAN	KPNA1	36	1	0.33	0.00
GP:AF015926_1	SLC9A3R1	36	1	0.47	0.00
SW:LDLR_HUMAN	LDLR	36	3	0.55	0.04
SW:IMB1_HUMAN	KPNB1	36	1	0.76	0.00
SW:EZRI_HUMAN	VIL2	36	1	0.80	0.00
SW:CALX_HUMAN	CANX	36	4	0.84	0.04
SW:ER53_HUMAN	LMAN1	36	2	0.84	0.00
SW:MPRI_HUMAN	IGF2R	36	76	0.86	0.21

SW:VPP1_HUMAN	ATP6N1	36	3	0.90	0.19
GP:Y18206_1	PPP1R6	36	1	0.92	0.00
GP:AB037819_1	RRBP1	36	7	1.02	0.13
GP:AF020797_1	HSMU1B	36	1	1.03	0.00
SW:MPRD_HUMAN	M6PR	36	1	1.03	0.00
GP:AF077032_1	FLJ10578	36	5	1.04	0.27
SW:IMB2_HUMAN	KPNB2	36	1	1.06	0.00
SW:SR19_HUMAN	SRP19	36	1	1.14	0.00
GP:AF195951_1	SRP68	36	2	1.17	0.00
SW:SR09_HUMAN	SRP9	36	7	1.25	0.29
GP:AF144700_1	TIMM13A	36	5	1.31	0.20
SW:ROM_HUMAN	HNRPM	36	2	1.41	0.23
SW:CAS_HUMAN	CSE1L	36	3	1.46	0.18
SW:PKBS_HUMAN	BZRP	36	2	1.57	0.04
SW:PXF_HUMAN	PXF	36	1	1.61	0.00
GP:U64791_1	GLG1	36	1	1.95	0.00
GP:U28811_1	CFR-1	36	14	1.97	0.53
GP:AF150087_1	TIMM8A	36	1	2.22	0.00

SW:SR14_HUMAN	SRP14	36	2	3.24	0.14
RNA Processing/Modifications					
SW:SYTC_HUMAN	TARS	37	4	0.51	0.06
SW:SYG_HUMAN	GARS	37	1	0.69	0.00
SW:SYD_HUMAN	DARS	37	4	0.77	0.15
SW:SYA_HUMAN	AARS	37	1	0.83	0.00
SW:SYR_HUMAN	RARS	37	7	0.84	0.08
SW:SYM_HUMAN	MARS	37	9	0.87	0.18
SW:SYEP_HUMAN	EPRS	37	23	0.92	0.84
SW:CST1_HUMAN	CSTF1	37	1	0.93	0.00
SW:SYQ_HUMAN	QARS	37	2	0.94	0.20
SW:SYV_HUMAN	VARS2	37	4	0.95	0.14
SW:SYK_HUMAN	KARS	37	7	1.01	0.18
SW:SYI_HUMAN	IARS	37	9	1.10	0.16
SW:NPM_HUMAN	NPM1	37	3	1.11	0.14
SW:PCB1_HUMAN	PCBP1	37	20	1.23	0.19
SWN:SYFB_HUMAN	FRSB	37	4	1.25	0.44
GP:AB020880_1	SART3	37	5	1.37	0.17

SW:ROF_HUMAN	HNRPF	37	3	1.37	0.10
PIR2:T13159	E1B-AP5	37	3	1.38	0.41
SW:SYN_HUMAN	NARS	37	4	1.42	0.19
PIR2:T02673	HNRPR	37	3	1.43	0.18
GP:AF037448_1	NSAP1	37	4	1.45	0.22
SW:ROK_HUMAN	HNRPK	37	6	1.51	0.30
SW:FBRL_HUMAN	FBL	37	1	1.53	0.00
SW:SMD3_HUMAN	SNRPD3	37	1	1.55	0.00
SW:ROA0_HUMAN	HNRPA0	37	2	1.64	0.40
SW:ROH1_HUMAN	HNRPH1	37	4	1.66	0.22
SW:DDX1_HUMAN	DDX1	37	6	1.67	0.10
PIR2:JW0079	HNRPDL	37	1	1.72	0.00
SW:PCB2_HUMAN	PCBP2	37	10	1.73	0.20
GP:AC003972_1	RENT1	37	1	1.74	0.00
SW:RUXF_HUMAN	SNRPF	37	1	1.76	0.00
GP:AF177344_1	FLJ10581	37	1	1.89	0.00
PIR2:I55595	RNPC2	37	1	1.92	0.00
SW:ROA3_HUMAN	FBRNP	37	2	1.93	0.06
SW:SMD2_HUMAN	SNRPD2	37	2	2.02	0.82

SW:U2AF_HUMAN	U2AF65	37	1	2.05	0.00
GP:D21163_1	U5-116KD	37	1	2.11	0.00
SW:RU17_HUMAN	SNRP70	37	3	2.11	0.26
PIR2:A54601	HNRPD	37	9	2.17	0.65
SW:NHPX_HUMAN	NHP2L1	37	2	2.21	0.20
SW:DDX5_HUMAN	DDX5	37	1	2.27	0.00
SW:U2AG_HUMAN	U2AF35	37	2	2.34	0.02
SW:ROU_HUMAN	HNRPU	37	29	2.48	0.62
SW:ROA1_HUMAN	HNRPA1	37	11	2.48	0.85
SW:DD17_HUMAN	DDX17	37	1	2.58	0.00
SW:Y017_HUMAN	SF3B3	37	7	2.63	0.59
SW:NR54_HUMAN	NONO	37	2	3.38	1.09
SW:SFR7_HUMAN	SFRS7	37	2	3.66	0.49
RNA Splicing					
GP:AF037448_1	NSAP1	38	4	1.45	0.22
SW:SMD3_HUMAN	SNRPD3	38	1	1.55	0.00
SW:RUXF_HUMAN	SNRPF	38	1	1.76	0.00

PIR2:T09073	SFRS2IP	38	1	1.89	0.00
PIR2:I55595	RNPC2	38	1	1.92	0.00
SW:SMD2_HUMAN	SNRPD2	38	2	2.02	0.82
SW:U2AF_HUMAN	U2AF65	38	1	2.05	0.00
GP:D21163_1	U5-116KD	38	1	2.11	0.00
SW:RU17_HUMAN	SNRP70	38	3	2.11	0.26
SW:U2AG_HUMAN	U2AF35	38	2	2.34	0.02
SW:ROA1_HUMAN	HNRPA1	38	11	2.48	0.85
SW:Y017_HUMAN	SF3B3	38	7	2.63	0.59
SW:NR54_HUMAN	NONO	38	2	3.38	1.09
SW:SFR7_HUMAN	SFRS7	38	2	3.66	0.49
RNA Turnover					
SW:HS71_HUMAN	HSPA1A	39	6	0.62	0.14
SW:RINI_HUMAN	RNH	39	1	1.01	0.00
GP:AF132941_1	LOC51068	39	1	1.02	0.00
PIR2:A57017	ABCE1	39	5	1.03	0.03
SW:PAB1_HUMAN	PABPC1	39	13	1.22	0.44
GP:U85625_1	RNASE6PL	39	3	1.44	0.04

GP:AC003972_1	RENT1	39	1	1.74	0.00
PIR2:S78046	RNASE6	39	3	1.94	0.00
PIR2:A54601	HNRPD	39	9	2.17	0.65
Recombination					
SW:IMA1_HUMAN	KPNA1	40	1	0.33	0.00
SW:FRAP_HUMAN	FRAP1	40	1	1.13	0.00
PIR2:JE0334	RUVBL1	40	3	1.16	0.14
SW:HMG1_HUMAN	HMG1	40	3	1.33	0.21
SW:KU86_HUMAN	XRCC5	40	6	1.46	0.36
SW:RFA3_HUMAN	RPA3	40	2	1.61	0.19
PIR2:A57099	PRKDC	40	13	1.74	0.27
SW:RFA1_HUMAN	RPA1	40	1	2.30	0.00
Signal Transduction					
GP:AF029684_1	IKKB	41	1	0.19	0.00
GP:U35146_1	KKIAMRE	41	2	0.26	0.06
SW:FKB5_HUMAN	FKBP5	41	1	0.28	0.00
SW:143E_HUMAN	YWHAE	41	1	0.31	0.00

SW:RIN1_HUMAN	RIN1	41	1	0.31	0.00
SW:TNRC_HUMAN	LTBR	41	1	0.32	0.00
SWN:AKT3_HUMAN	AKT3	41	1	0.33	0.00
SW:RRAS_HUMAN	RRAS	41	3	0.35	0.01
SW:ATS1_HUMAN	ADAMTS1	41	5	0.47	0.18
SW:AAK1_HUMAN	PRKAA1	41	2	0.47	0.00
GP:AF061258_1	LIM	41	1	0.50	0.00
PIR2:JC4775	DNAJC3	41	2	0.51	0.27
SW:COF1_HUMAN	CFL1	41	14	0.55	0.21
GP:AF100757_1	COPS4	41	2	0.56	0.00
PIR2:T13151	CD2AP	41	3	0.58	0.01
GP:AF024636_1	STK24	41	1	0.59	0.00
SW:RAPB_HUMAN	RAP1B	41	2	0.59	0.04
SW:MOES_HUMAN	MSN	41	1	0.59	0.00
SW:CAP1_HUMAN	CAP	41	1	0.60	0.00
GP:AF001628_1	AblBP4	41	2	0.62	0.01

SW:EGFR_HUMAN	EGFR	41	2	0.62	0.00
GP:AB014718_1	TNFRSF10B	41	2	0.64	0.10
SW:TDXN_HUMAN	PRDX4	41	5	0.66	0.19
SW:RAC3_HUMAN	RAC3	41	2	0.69	0.00
SW:RHOB_HUMAN	ARHB	41	6	0.70	0.04
GP:AF091035_1	RAB21	41	2	0.71	0.00
SW:CTN1_HUMAN	CTNNA1	41	27	0.71	0.19
GP:AB018358_1	KIAA0905	41	3	0.72	0.10
SW:RGP1_HUMAN	RANGAP1	41	1	0.72	0.00
SW:KCCB_HUMAN	CAMK2B	41	2	0.74	0.09
SW:ITAV_HUMAN	ITGAV	41	1	0.75	0.00
SW:IQGA_HUMAN	IQGAP1	41	4	0.77	0.09
SW:GBAK_HUMAN	GNAI3	41	4	0.77	0.10
SW:P2AA_HUMAN	PPP2CA	41	7	0.78	0.11
SW:FKB1_HUMAN	FKBP1A	41	2	0.78	0.00
SW:CTNB_HUMAN	CTNNB1	41	19	0.79	0.26
SW:Y253_HUMAN	NCSTN	41	2	0.81	0.05

GP:U70735_1	MOV34-34KD	41	1	0.82	0.00
SW:BASI_HUMAN	BSG	41	2	0.82	0.00
SW:SRC_HUMAN	SRC	41	1	0.83	0.00
SW:ITA6_HUMAN	ITGA6	41	3	0.83	0.04
SW:ABP2_HUMAN	FLNA	41	11	0.85	0.11
SWN:P23_HUMAN	p23	41	2	0.85	0.01
SW:KPC1_HUMAN	PRKCB1	41	1	0.85	0.00
SW:GPS1_HUMAN	GPS1	41	4	0.86	0.12
SW:MPRI_HUMAN	IGF2R	41	76	0.86	0.21
GP:AF124145_1	AMFR	41	1	0.87	0.00
GP:AF087020_1	PZR	41	12	0.88	0.08
GP:AB002382_1	CTNND1	41	18	0.88	0.31
PIR2:B55053	SCYE1	41	9	0.88	0.07
SW:RHOG_HUMAN	ARHG	41	5	0.90	0.29
SW:G25B_HUMAN	CDC42	41	13	0.90	0.13
SW:ITA5_HUMAN	ITGA5	41	2	0.91	0.03

GP:AB006534_1	SPINT2	41	1	0.91	0.00
SW:143T_HUMAN	YWHAQ	41	3	0.91	0.05
GP:AC002306_1	EDG4	41	1	0.92	0.00
SW:GBB2_HUMAN	GNB2	41	23	0.92	0.22
GP:AF151793_1	AIP1	41	8	0.92	0.09
GPN:AB025194_1	HD-PTP	41	1	0.93	0.00
GP:D87930_1	PPP1R12A	41	3	0.95	0.13
PIR2:T46270	FLNB	41	12	0.95	0.39
SW:RHOA_HUMAN	ARHA	41	37	0.95	0.25
SW:APP2_HUMAN	APLP2	41	2	0.95	0.08
PIR2:I38176	RAGA	41	1	0.96	0.00
GP:AF092130_1	MADHIP	41	1	0.97	0.00
PIR2:S29815	P2RY4	41	1	0.97	0.00
SW:MK01_HUMAN	MAPK1	41	1	0.97	0.00
SW:PRO1_HUMAN	PFN1	41	4	0.97	0.39
SW:LYN_HUMAN	LYN	41	2	0.98	0.02
SW:RAPA_HUMAN	RAP1A	41	1	0.98	0.00

SW:RAN_HUMAN	RAN	41	3	0.98	0.04
SW:EFA5_HUMAN	EFNA5	41	1	0.99	0.00
SW:CD59_HUMAN	CD59	41	8	1.00	0.26
SW:SRD6_HUMAN	PGRMC2	41	1	1.01	0.00
GP:U41806_1	SQSTM1	41	4	1.01	0.21
SW:KAP2_HUMAN	PRKAR2A	41	2	1.04	0.57
SW:KCCD_HUMAN	CAMK2D	41	3	1.04	0.01
SW:KRCB_HUMAN	AKT2	41	1	1.04	0.00
SW:PTN1_HUMAN	PTPN1	41	3	1.05	0.15
SW:FASA_HUMAN	TNFSF6	41	1	1.06	0.00
SW:FK38_HUMAN	FKBP8	41	3	1.06	0.31
GP:AF260566_1	HGS	41	1	1.06	0.00
SW:ERB2_HUMAN	ERBB2	41	5	1.07	0.09
SW:RAC1_HUMAN	RAC1	41	18	1.08	0.53
PIR2:T47172	CORO1C or CRN	41	5	1.08	0.38
GP:AK022871_1	TOLLIP	41	4	1.09	0.03

SW:A4_HUMAN	APP	41	5	1.09	0.19
PIR1:JC5394	DJ-1	41	7	1.10	0.32
GP:AB011126_1	FBP17	41	1	1.11	0.00
SW:143Z_HUMAN	YWHAZ	41	4	1.12	0.63
GP:AL096767_2	SBF1	41	1	1.15	0.00
SW:NTC1_HUMAN	NOTCH1	41	1	1.15	0.00
SW:GBI2_HUMAN	GNAI2	41	1	1.18	0.00
SW:EPA7_HUMAN	EPHA7	41	2	1.19	0.14
GP:AB002313_1	PLXNB	41	12	1.20	0.40
SW:ER60_HUMAN	ERP60	41	17	1.21	0.54
SW:INSR_HUMAN	INSR	41	2	1.22	0.02
SW:PI52_HUMAN	PIP5K2A	41	1	1.24	0.00
GPN:AF279372_1	ITPK1	41	3	1.25	0.11
SW:TRA2_HUMAN	TRAF2	41	2	1.25	0.26
SW:GBB1_HUMAN	GNB1	41	27	1.27	0.26
SW:KAPA_HUMAN	PRKACA	41	2	1.28	0.55
GP:AF020202_1	UNC13	41	3	1.29	0.09

SW:BCR_HUMAN	BCR	41	1	1.29	0.00
GP:AB037857_1	PTGFRN	41	10	1.30	0.21
SW:P2BA_HUMAN	PPP3CA	41	3	1.30	0.16
PIR2:JC5938	Txnl	41	2	1.31	0.01
SW:OGT1_HUMAN	OGT	41	1	1.34	0.00
GP:AK001521_1	DIP13B	41	4	1.35	0.12
SW:KG3B_HUMAN	GSK3B	41	1	1.36	0.00
GP:D87116_1	MAP2K3	41	3	1.38	0.17
SW:EBI2_HUMAN	EBI2	41	1	1.40	0.00
SW:THIO_HUMAN	TXN	41	1	1.41	0.00
SW:OCRL_HUMAN	OCRL	41	2	1.42	1.00
PIR2:I38026	TRAF4	41	2	1.43	0.18
SW:GBLP_HUMAN	GNB2L1	41	13	1.44	0.51
GP:AB033078_1	SGPL1	41	2	1.44	0.06
SW:RSP4_HUMAN	LAMR1	41	7	1.44	0.05
SW:OBRG_HUMAN	LEPR	41	1	1.46	0.00
SW:PTPF_HUMAN	LAR	41	5	1.50	0.35
SW:GBI1_HUMAN	GNAI1	41	4	1.56	0.16

SW:C166_HUMAN	ALCAM	41	8	1.58	0.27
SW:PTK7_HUMAN	PTK7	41	9	1.66	0.30
GP:U17032_1	ARHGAP5	41	1	1.66	0.00
SW:CAN1_HUMAN	CAPN1	41	1	1.73	0.00
SW:ITB1_HUMAN	ITGB1	41	5	1.94	0.58
GP:AB007867_1	PLXNB1	41	1	1.97	0.00
GP:AL023805_1	PLCB4	41	6	2.00	0.24
GP:AF043250_1	PLRG1	41	1	2.05	0.00
SW:KC2B_HUMAN	CSNK2B	41	2	2.11	0.18
SW:NRP_HUMAN	NRP1	41	8	2.20	1.33
GP:X92689_1	GALNAC-T3	41	3	2.26	0.17
SW:GST3_HUMAN	MGST3	41	2	2.31	0.83
SW:POR1_HUMAN	VDAC1	41	28	2.36	0.34
SW:MAZ_HUMAN	MAZ	41	1	2.37	0.00
SW:IBP2_HUMAN	IGFBP2	41	6	2.43	0.38
SW:GRBA_HUMAN	GRB10	41	3	2.55	2.22

SW:SORC_HUMAN	SRI	41	2	2.86	2.11
SW:LU_HUMAN	LU	41	3	2.88	0.14
GP:D63481_1	SCRIB	41	1	3.09	0.00
GP:AB006537_1	IL1RAP	41	1	3.20	0.00
GP:AF002668_1	DEGS	41	1	3.29	0.00
SW:RDC1_HUMAN	RDC1	41	4	3.86	1.24
SW:PA2M_HUMAN	PLA2G2A	41	3	3.94	1.93
SW:KDGG_HUMAN	DGKG	41	1	10.54	0.00
Small Molecule Transport					
SW:TRFL_HUMAN	LTF	42	2	0.28	0.03
SW:FLOH_HUMAN	SLC19A2	42	3	0.41	0.05
SW:Y274_HUMAN	SAC3	42	1	0.45	0.00
GP:AF015926_1	SLC9A3R1	42	1	0.47	0.00
SW:AAAT_HUMAN	SLC1A5	42	4	0.52	0.12
SW:ATND_HUMAN	ATP1B3	42	3	0.57	0.07
SW:MRP1_HUMAN	ABCC1	42	4	0.58	0.08
SW:NC5R_HUMAN	DIA1	42	2	0.60	0.02
SW:MRP4_HUMAN	MRP4	42	2	0.61	0.03

SW:CLI1_HUMAN	CLIC1	42	1	0.76	0.00
SW:GBAK_HUMAN	GNAI3	42	4	0.77	0.10
SW:ATHA_HUMAN	ATP4A	42	2	0.79	0.08
SWN:ENT1_HUMAN	ENT1	42	1	0.83	0.00
SW:ANX7_HUMAN	ANXA7	42	4	0.87	0.02
PIR2:T46412	NEDD4	42	1	0.88	0.00
SW:VATX_HUMAN	ATP6D	42	2	0.89	0.03
SW:VPP1_HUMAN	ATP6N1	42	3	0.90	0.19
GP:AF284422_1	LOC56996	42	1	0.92	0.00
SW:MOT4_HUMAN	SLC16A3	42	1	0.92	0.00
SWN:STX8_HUMAN	STX8	42	1	0.93	0.00
GP:AK022853_1	NTT73	42	1	0.94	0.00
SW:ICLN_HUMAN	CLNS1A	42	1	0.96	0.00
SW:MK01_HUMAN	MAPK1	42	1	0.97	0.00
SW:IEFS_HUMAN	STIP1	42	5	1.01	0.17
GP:AJ131612_1	Slc25a10	42	1	1.02	0.00
GP:AF288687_1	CGI-152	42	3	1.03	0.07

SW:CLC3_HUMAN	CLCN3	42	1	1.03	0.00
SW:ATN1_HUMAN	ATP1A1	42	54	1.04	0.22
GP:U81006_1	TM9SF2	42	3	1.05	0.06
SW:CPT2_HUMAN	CPT2	42	1	1.08	0.00
SW:ATCS_HUMAN	ATP2B4	42	6	1.10	0.21
SW:HBP_HUMAN	HDLBP	42	3	1.11	0.27
SW:ATHL_HUMAN	ATP12A	42	7	1.12	0.11
SW:NPC1_HUMAN	NPC1	42	1	1.16	0.00
SW:COXS_HUMAN	COX17	42	1	1.18	0.00
SW:VAB1_HUMAN	ATP6B1	42	2	1.20	0.08
SW:TRSR_HUMAN	TFRC	42	2	1.20	0.12
SW:ATC2_HUMAN	ATP2B2	42	9	1.28	0.35
SW:SAP_HUMAN	PSAP	42	14	1.31	0.91
GP:AF149418_1	SLC4A4	42	1	1.45	0.00
SW:TXTP_HUMAN	SLC25A1	42	2	1.45	0.00
SW:ATNB_HUMAN	ATP1B1	42	23	1.46	0.36

SW:VAB2_HUMAN	ATP6B2	42	7	1.47	0.34
SW:NLTP_HUMAN	SCP2	42	2	1.50	0.06
SW:ATCP_HUMAN	ATP2B1	42	21	1.73	0.61
SW:ADT1_HUMAN	SLC25A4	42	2	1.84	0.94
SW:ECHB_HUMAN	HADHB	42	4	1.87	0.07
SW:ECHA_HUMAN	HADHA	42	13	1.97	0.65
SW:POR2_HUMAN	VDAC2	42	34	1.99	0.32
PIR2:B53737	SLC25A3	42	21	2.02	0.42
SW:ATPG_HUMAN	ATP5C1	42	3	2.15	0.32
GP:AC002540_1	SLC25A13	42	1	2.16	0.00
SW:POR1_HUMAN	VDAC1	42	28	2.36	0.34
SW:ATPA_HUMAN	ATP5A1	42	8	2.38	0.42
SWN:POR3_HUMAN	VDAC3	42	6	2.48	0.55
SW:ADT2_HUMAN	SLC25A5	42	8	2.53	1.17
SW:ADT3_HUMAN	SLC25A6	42	1	2.57	0.00
SW:ATCK_HUMAN	ATP2C1	42	2	2.59	0.30
SW:SORC_HUMAN	SRI	42	2	2.86	2.11

SW:B3A2_HUMAN	SLC4A2	42	1	3.57	0.00
SW:AT2A_HUMAN	ATP9A	42	2	5.29	2.51
Vesicular Transport					
SW:SNAG_HUMAN	NAPG	43	2	0.43	0.31
GP:AB018298_1	SEC24D	43	1	0.47	0.00
SW:RB3B_HUMAN	RAB3B	43	2	0.50	0.00
SW:ADG_HUMAN	ADTG	43	4	0.51	0.13
SW:LDLR_HUMAN	LDLR	43	3	0.55	0.04
SW:RB4A_HUMAN	RAB4A	43	1	0.56	0.00
PIR2:A53016	MYO5A	43	1	0.58	0.00
SW:EGFR_HUMAN	EGFR	43	2	0.62	0.00
SW:STB3_HUMAN	STXBP3	43	6	0.66	0.15
SW:CLH2_HUMAN	CLTCL1	43	10	0.66	0.15
SW:S23B_HUMAN	SEC23B	43	1	0.69	0.00
GP:AF038535_1	SYT7	43	1	0.70	0.00
SW:KINH_HUMAN	KIF5B	43	2	0.73	0.05
SW:RB35_HUMAN	RAB35	43	1	0.73	0.00
GPN:AB047846_1	LOC51137	43	7	0.74	0.24
SW:SN23_HUMAN	SNAP23	43	2	0.74	0.06
SW:RB3D_HUMAN	RAB3D	43	1	0.74	0.00

SW:RAB2_HUMAN	RAB2	43	5	0.77	0.05
SW:GBAK_HUMAN	GNAI3	43	4	0.77	0.10
GP:AF091079_1	YKT6	43	1	0.78	0.00
SW:CLH1_HUMAN	CLTC	43	49	0.78	0.44
GP:AJ131245_1	SEC24B	43	1	0.81	0.00
SW:DYN2_HUMAN	DNM2	43	1	0.81	0.00
GP:D31886_1	RAB3GAP	43	3	0.83	0.11
SW:CALX_HUMAN	CANX	43	4	0.84	0.04
SW:ER53_HUMAN	LMAN1	43	2	0.84	0.00
GP:U45976_1	PICALM	43	1	0.85	0.00
SW:ADB_HUMAN	AP2B1	43	5	0.86	0.14
SW:MPRI_HUMAN	IGF2R	43	76	0.86	0.21
GP:AF044670_1	VAP33	43	2	0.88	0.24
GP:AF128536_1	PACSIN2	43	4	0.89	0.45
GP:AF004563_1	STXBP1	43	4	0.89	0.26
SW:G25B_HUMAN	CDC42	43	13	0.90	0.13
SW:143T_HUMAN	YWHAQ	43	3	0.91	0.05

SW:ACTZ_HUMAN	ACTR1A	43	7	0.92	0.04
SWN:STX8_HUMAN	STX8	43	1	0.93	0.00
GP:AC005545_2	AP3D1	43	2	0.93	0.18
SW:S23A_HUMAN	SEC23A	43	5	0.94	0.18
SW:ADB1_HUMAN	AP1B1	43	20	0.99	0.27
SW:TERA_HUMAN	VCP	43	41	0.99	0.20
GP:AC006942_1	ADTAA	43	5	1.00	0.28
GP:AF020797_1	HSMU1B	43	1	1.03	0.00
SW:MPRD_HUMAN	M6PR	43	1	1.03	0.00
GP:AC006378_1	BET1	43	1	1.04	0.00
PIR2:I53171	H-SP1	43	1	1.06	0.00
GP:AF260566_1	HGS	43	1	1.06	0.00
SW:COPB_HUMAN	COPB	43	1	1.07	0.00
SWN:SNX3_HUMAN	SNX3	43	1	1.07	0.00
SW:ARF6_HUMAN	ARF6	43	2	1.07	0.05
GP:AF151858_1	LOC50999	43	2	1.09	0.01
GP:AF032922_1	UNC-18C	43	2	1.09	0.03
SW:STB2_HUMAN	STXBP2	43	4	1.09	0.34
SW:AP50_HUMAN	AP2M1	43	3	1.10	0.08
SW:NSF_HUMAN	NSF	43	6	1.12	0.16

GPN:AB047847_1	COPG2	43	5	1.14	0.06
SW:COPP_HUMAN	COPB2	43	5	1.15	0.22
SW:RAB7_HUMAN	RAB7	43	1	1.16	0.00
GP:AB019435_1	P125	43	3	1.17	0.10
GP:U85946_1	SEC10L1	43	5	1.33	0.11
GPN:AF191298_1	VPS35	43	7	1.35	0.49
PIR2:S33377	CKAP4	43	5	1.35	0.22
SW:TM21_HUMAN	TMP21	43	3	1.37	0.60
SWN:CNE3_HUMAN	CPN3	43	28	1.47	0.27
SW:RB13_HUMAN	RAB13	43	1	1.49	0.00
SW:GDIB_HUMAN	GDI2	43	2	1.70	0.01
PIR2:I53799	KTN1	43	2	1.73	0.08
PIR2:A55575	ANK3	43	9	1.85	0.18
SW:COPA_HUMAN	COPA	43	15	1.95	3.01
Virulence					
SW:PRS7_HUMAN	PSMC2	44	7	0.75	0.17
SW:VE1_HPV14	E1	44	1	0.98	0.00
SW:EBI2_HUMAN	EBI2	44	1	1.40	0.00
SW:MCP_HUMAN	MCP	44	3	1.42	0.95
Unknown Function					

SW:TMS2_HUMAN	TMPRSS2	45	10	0.12	0.05
GP:AC005278_12	F15K9.12	45	1	0.17	0.00
GP:AK000542_1	FLJ20535	45	1	0.20	0.00
SW:CD9_HUMAN	CD9	45	2	0.20	0.00
SW:PROS_HUMAN	KLK3	45	17	0.25	0.13
PIR2:T34532	MICAL	45	1	0.27	0.00
GP:AB037745_1	KIAA1324	45	1	0.28	0.00
GPN:AL136939_1	ELOVL2	45	1	0.28	0.00
SW:DIMH_HUMAN	DHCR24	45	2	0.28	0.00
GP:AK022527_1	FLJ12465	45	2	0.30	0.05
GP:AK025588_1	EPS8R2	45	3	0.33	0.04
GP:AJ245222_1	IGHV3-7	45	1	0.34	0.00
GP:AK026904_1	FLJ23251	45	2	0.35	0.01
GP:AJ239387_1	IGHV	45	1	0.37	0.00
GP:AB020706_1	AP2A2	45	1	0.38	0.00
GP:AC011001_19	unknown	45	1	0.41	0.00
GP:AB040955_1	KIAA1522	45	1	0.43	0.00
PIR2:S71949	ADAM12	45	4	0.43	0.01
GP:U85992_1	unknown	45	1	0.45	0.00

PIR2:T17320	unknown	45	2	0.46	0.04
PIR2:A49674	FLII	45	2	0.47	0.04
SW:CRP2_HUMAN	CRIP2	45	1	0.48	0.00
PIR2:T00261	KIAA0603	45	2	0.48	0.01
SW:B2MG_HUMAN	B2M	45	6	0.48	0.08
SW:ANX4_HUMAN	ANXA4	45	7	0.51	0.06
GPN:AF060225_1	KIAA1607	45	2	0.54	0.04
GPN:AF217190_1	DDX36	45	2	0.56	0.00
SW:PLSL_HUMAN	LCP1	45	2	0.56	0.05
GP:AF112227_1	TDE1	45	1	0.57	0.00
GP:AB029025_1	KIAA1102	45	3	0.57	0.05
GP:AB033001_1	FLJ10209	45	2	0.57	0.10
GP:AK024639_1	FLJ20986	45	1	0.58	0.00
PIR2:JE0350	AGR2	45	1	0.58	0.00
SW:ARGR_HUMAN	ARMET	45	7	0.58	0.09
GP:AF126181_1	MAGED2	45	1	0.61	0.00
GP:AC004839_2	BAP29	45	3	0.61	0.01

SW:XIP_HUMAN	HBXIP	45	1	0.62	0.00
SW:CYSR_HUMAN	CSRP1	45	5	0.62	0.05
PIR2:T46901	PTD004	45	4	0.62	0.09
GP:AK026010_1	FLJ22357	45	3	0.64	0.02
PIR2:T08684	KIAA1265	45	1	0.65	0.00
SW:2AAA_HUMAN	PPP2R1A	45	1	0.65	0.00
SW:DYI2_HUMAN	DNCI2	45	3	0.65	0.01
GP:D38549_1	CYFIP1	45	2	0.66	0.11
GP:AB002366_1	KIAA0368	45	1	0.67	0.00
SW:ZO1_HUMAN	TJP1	45	1	0.67	0.00
PIR2:T17218	DKFZP434P1750	45	1	0.68	0.00
SW:DYJ2_HUMAN	DNCLI2	45	4	0.68	0.10
SW:9123_HUMAN	TCTE1L	45	3	0.69	0.07
PIR2:T46394	DKFZP434H0820	45	5	0.69	0.17
GP:AB040884_1	OSBPL8	45	1	0.70	0.00
GP:U21252_1	anti-colorectal car	45	1	0.70	0.00
GP:D87438_1	KIAA0251	45	1	0.71	0.00
GP:AB032997_1	KIAA1171	45	3	0.71	0.13
GP:AF144748_1	ENTPD2	45	1	0.72	0.00
GP:AK023914_1	FLJ13852	45	2	0.72	0.00
SW:AMP1_HUMAN	KIAA0094	45	1	0.72	0.00

GP:AB020637_1	KIAA0830	45	1	0.73	0.00
GP:AB040887_1	ZNF291	45	1	0.74	0.00
PIR2:T46299	TREX1	45	1	0.75	0.00
GP:AB046798_1	KIAA1578	45	1	0.76	0.00
GP:AF155652_1	PCMF	45	1	0.76	0.00
GP:AF151840_1	ARSDR1	45	26	0.76	0.45
SWN:DB83_HUMAN	DB83	45	1	0.77	0.00
PIR2:T13152	WDR1	45	5	0.77	0.06
SW:GC5L_HUMAN	GCN5L1	45	1	0.78	0.00
GP:AB011145_1	ERp44	45	9	0.78	0.13
SW:CC4H_HUMAN	LRBA	45	1	0.79	0.00
SW:LMO6_HUMAN	LMO6	45	1	0.79	0.00
GPN:AF239156_1	PDF1A	45	1	0.79	0.00
SW:G100_HUMAN	ADRM1	45	4	0.79	0.06
GPN:AB041832_1	WBP11	45	1	0.80	0.00
GP:AF151867_1	INTEGRAL TYPE	45	2	0.80	0.07
SW:ME18_HUMAN	ZNF144	45	1	0.81	0.00
GP:U06631_1	H326	45	2	0.81	0.07
GP:AC003956_1	Acetolactate synth	45	5	0.81	0.28
SW:SC13_HUMAN	SEC13L1	45	3	0.82	0.02
PIR2:T46292	BAG3	45	1	0.83	0.00
GP:AF293335_1	KIAA1967	45	2	0.83	0.01
GP:AK000303_1	FLJ20296	45	3	0.83	0.03
GPN:AF193795_1	VPS29	45	2	0.83	0.04
GP:AF068297_1	HDCMD45P	45	2	0.84	0.14
GP:AB037807_1	KIAA1386	45	1	0.85	0.00
PIR2:T08753	E46L	45	2	0.87	0.13

GP:AK022499_1	FLJ00365	45	1	0.88	0.00
SW:EF1D_HUMAN	EEF1D	45	2	0.88	0.01
GP:AB037856_1	FENS-1	45	3	0.88	0.16
GP:AF284574_1	NIT2	45	1	0.89	0.00
GP:AK022868_1	FLJ12806	45	1	0.89	0.00
PIR2:T46298	FLJ14362	45	1	0.89	0.00
SW:FA5_HUMAN	F5	45	1	0.89	0.00
SW:SR72_HUMAN	SRP72	45	1	0.89	0.00
GP:AF236056_1	GP73	45	3	0.89	0.04
GP:AF250859_1	MGAT1.2	45	1	0.90	0.00
SW:ROH2_HUMAN	HNRPH2	45	1	0.90	0.00
GPN:AF130092_1	KIAA1049	45	4	0.92	0.08
SW:CN37_HUMAN	CNP	45	14	0.92	0.15
GP:AK021647_1	MPPE1	45	1	0.93	0.00
SW:PPAL_HUMAN	ACP2	45	1	0.93	0.00
SW:EF1B_HUMAN	EEF1B1	45	3	0.93	0.05
GP:AF226054_1	GK001	45	2	0.94	0.01
GP:AC005067_2	NPD007	45	2	0.94	0.17
PIR2:T47174	CORO1B	45	3	0.94	0.18
GP:AB032993_1	GRIPAP1	45	1	0.95	0.00
GP:AJ245820_1	psk-1	45	1	0.95	0.00
GPN:AL512750_1	FLJ11127	45	1	0.95	0.00
GP:AK023834_1	FLJ13772	45	1	0.97	0.00

SW:LYII_HUMAN	CD36L2	45	2	0.97	0.07
PIR2:T47160	RAB14	45	6	0.97	0.25
GP:AJ293573_1	CEZANNE	45	1	0.98	0.00
GP:AK025999_1	E2-230K	45	1	0.98	0.00
SW:SP02_HUMAN	DLG3	45	1	0.98	0.00
GP:AB037728_1	KIAA1307	45	2	0.98	0.03
SW:SPC1_HUMAN	KIAA0102	45	3	0.98	0.03
PIR2:G01447	C5ORF8	45	3	0.98	0.04
SW:TGT_HUMAN	TGT	45	6	0.98	0.19
GP:AB014555_1	HIP12	45	1	0.99	0.00
PIR2:T46375	DKFZp434D1319	45	1	0.99	0.00
PIR2:I52882	RCD-8	45	2	0.99	0.02
GP:AB037773_1	KIAA1352	45	8	0.99	0.20
GP:AB020697_1	DDX30	45	1	1.00	0.00
GP:AK022827_1	FLJ12765	45	1	1.00	0.00
GP:U25756_1	Ki nuclear autoant	45	1	1.00	0.00
SW:CYTC_HUMAN	CST3	45	2	1.00	0.03
GP:AK023618_1	NDRG3	45	2	1.01	0.10
SW:TBA4_HUMAN	TUBA4	45	25	1.01	0.25
GP:AF129332_1	MUM2	45	1	1.02	0.00
PIR2:T17237	DKFZP434P106	45	1	1.02	0.00
SW:ANX6_HUMAN	ANXA6	45	3	1.02	0.02

GP:AK022763_1	MRPL44	45	2	1.02	0.20
GPN:AL109804_12	KIAA1271	45	2	1.02	0.27
GP:AK002163_1	FLJ11301	45	1	1.03	0.00
PIR2:T00050	DDEF2	45	1	1.03	0.00
SW:ACTY_HUMAN	ACTR1B	45	1	1.03	0.00
PIR2:T46333	macrothioredoxin	45	1	1.04	0.00
SW:LEGU_HUMAN	LGMN	45	8	1.04	0.16
GP:AK025520_1	GOCAP1	45	3	1.04	0.22
GPN:AF060511_1	LOC112473	45	1	1.05	0.00
PIR2:PH0268	EPPK1	45	3	1.05	0.01
GP:Z74021_1	RPS17L4	45	7	1.05	0.21
GP:AJ245621_1	CTL2	45	17	1.05	0.27
GP:AC005154_1	MGC3077	45	2	1.06	0.00
GP:X87832_1	PLXNA1	45	1	1.06	0.00
SW:YCE7_HUMAN	Hypothetical prote	45	1	1.06	0.00
GP:AF137372_1	RAB18	45	2	1.06	0.01
SW:ANXA_HUMAN	ANXA10	45	8	1.06	0.12
GP:AK001243_1	FLJ10381	45	1	1.07	0.00
GPN:AB040462_1	RTN4	45	1	1.07	0.00
PIR2:T46272	DKFZP564L0864	45	1	1.07	0.00
PIR2:T46254	RAGD	45	2	1.08	0.07
SW:DSR3_HUMAN	DSCR3	45	4	1.08	0.12
SW:SKP1_HUMAN	SKP1	45	3	1.08	0.12
SW:TBB1_HUMAN	TUBB1	45	22	1.08	0.36

PIR2:T12544	TBL2	45	1	1.09	0.00
GP:AL049795_2	LOC200081	45	2	1.09	0.06
GP:AB011163_1	KIF1B	45	1	1.10	0.00
SW:KNLC_HUMAN	KLC	45	1	1.10	0.00
GP:AF272357_1	NPDC1	45	2	1.10	0.01
GP:AB040882_1	KIAA1449	45	1	1.11	0.00
GP:AF226045_1	MRPS22	45	1	1.11	0.00
GP:D42085_1	KIAA0095	45	1	1.11	0.00
GP:AF151069_1	RPML2	45	4	1.11	0.04
PIR2:T50639	GPSN2	45	5	1.12	0.09
SW:PHB_HUMAN	PHB	45	1	1.13	0.00
PIR2:T00345	KIAA0590	45	1	1.14	0.00
GP:AK001718_1	FLJ10856	45	2	1.14	0.09
GP:AB018270_1	MYO1D	45	4	1.14	0.11
GP:AB015631_1	TMEM4	45	10	1.14	0.17
GP:AF155658_1	HSPC117	45	5	1.14	0.27
GPN:AF196479_1	tRNA 2,2-dimethy	45	1	1.15	0.00
GP:AL451015_9	unknown	45	1	1.16	0.00
GP:AB033011_1	KIAA1185	45	7	1.17	0.22
SW:HEXB_HUMAN	HEXB	45	6	1.17	0.22
GP:AF151062_1	LIP5 LYST-interac	45	8	1.17	0.25
SW:VATG_HUMAN	ATP6G1	45	1	1.18	0.00

SW:RS3_HUMAN	RPS3	45	5	1.18	0.40
GP:AK022956_1	TBLR1	45	1	1.19	0.00
PIR2:S55474	LLGL2	45	1	1.19	0.00
SW:1A01_HUMAN	HLAA	45	4	1.19	0.02
GP:AB038995_1	LOC51762	45	1	1.20	0.00
GP:AK001050_1	FLJ10188	45	1	1.20	0.00
SW:2ABA_HUMAN	PPP2R2A	45	2	1.20	0.03
GP:AK024781_1	FLJ21128	45	2	1.20	0.05
GP:AB018790_1	LOC244373	45	1	1.21	0.00
GP:AK002135_1	FLJ11273	45	1	1.21	0.00
GP:AF271388_1	CMAS	45	3	1.21	0.16
GP:AB033767_1	C20orf3	45	1	1.23	0.00
SWN:TALI_HUMAN	TLN	45	1	1.23	0.00
SWN:PM5P_HUMAN	PM5	45	4	1.23	0.27
GPN:AL136131_4	MRPS18A	45	1	1.24	0.00
PIR2:T42646	KIAA0731	45	2	1.24	0.00
GPN:AB014729_1	SMAP1	45	2	1.24	0.01
SW:COPD_HUMAN	ARCN1	45	2	1.24	0.07
GP:AB046829_1	KIAA1609	45	1	1.25	0.00
SW:PTPA_HUMAN	PPP2R4	45	2	1.25	0.01
SWN:UNRI_HUMAN	UNRIP	45	4	1.25	0.20

GP:AC005788_1	XPTP	45	4	1.26	0.20
GP:AK000330_1	FLJ20323	45	1	1.27	0.00
GP:AB037855_1	KIAA1434	45	1	1.28	0.00
PIR2:T08729	DKFZp566H073	45	2	1.28	0.00
GPN:AL449244_1	Hypothetical prote	45	1	1.29	0.00
GP:AF005888_1	NOC4	45	3	1.29	0.16
GP:AF116347_1	SMBP	45	5	1.29	0.23
GP:AB020694_1	KIAA0887	45	2	1.30	0.00
GP:U47924_19	C3f	45	2	1.30	0.07
GP:AF161380_1	Mrpl38	45	1	1.31	0.00
SW:DDX3_HUMAN	DDX3	45	14	1.31	0.36
PIR2:T08769	KIAA0747	45	8	1.34	0.14
PIR2:T08787	TES	45	1	1.35	0.00
SW:Y041_HUMAN	CENTB2	45	1	1.35	0.00
GP:AF078860_1	MRPL42	45	2	1.35	0.14
GP:AB002377_1	KIAA0379	45	4	1.35	0.17
GP:AK000325_1	FLJ20318	45	2	1.35	0.22
GP:AB046774_1	KIAA1554	45	1	1.36	0.00
GP:AF239727_1	MRPL39	45	1	1.36	0.00
GP:U97519_1	PODXL	45	1	1.36	0.00
GP:AJ011129_1	LOC64148	45	2	1.36	0.16
GP:AC007055_5	unknown	45	1	1.37	0.00
GP:AJ131186_1	NMP200	45	1	1.37	0.00
GP:AF059524_1	RTN3	45	3	1.37	0.05
PIR2:T12456	LOC152502	45	4	1.37	0.08
GP:AF030291_1	MCG4	45	3	1.37	0.38

SW:RBP2_HUMAN	RANBP2	45	3	1.37	0.58
SW:HEPS_HUMAN	HPN	45	2	1.38	0.65
GP:AB000095_1	SPINT1	45	7	1.39	0.22
GP:AK000512_1	C1orf27	45	1	1.40	0.00
SW:RL30_HUMAN	RPL30	45	27	1.40	0.25
GPN:AF305686_1	NJMU-R1	45	2	1.41	0.03
GP:S82470_1	LENG4	45	4	1.41	0.09
GP:AF055016_1	CLLD6	45	2	1.41	0.64
GP:U52426_1	STIM1	45	5	1.42	0.34
GP:AF177377_1	EML4	45	1	1.43	0.00
GP:AK022722_1	FLJ12660	45	1	1.43	0.00
GP:AF157325_1	EPLIN	45	5	1.43	0.39
GP:AL096857_1	hypothetical prote	45	2	1.44	0.15
GP:AB018313_1	VPS39	45	1	1.47	0.00
SWN:Z272_HUMAN	ZNF272	45	1	1.47	0.00
GP:U16406_1	HIV	45	1	1.47	0.00
GP:D87453_1	MRPS27	45	2	1.47	0.17
PIR2:T17219	SDFR1	45	4	1.48	0.37
GP:AK025859_1	FLJ22206	45	1	1.49	0.00
SW:L130_HUMAN	LRPPRC	45	4	1.50	0.09
GP:AK001207_1	PP199	45	1	1.51	0.00
GPN:AF307137_1	EHD4	45	1	1.51	0.00
SW:SMN1_HUMAN	SMN2	45	4	1.53	0.19
GP:U52111_2	RPL18A	45	27	1.54	0.43

SW:PCP_HUMAN	PRCP	45	1	1.57	0.00
SW:EP1_HUMAN	NPC2	45	11	1.58	0.16
PIR2:T46250	sialic acid-specific	45	1	1.60	0.00
SW:HE47_HUMAN	BAT1	45	3	1.62	0.23
GP:AF161494_1	MRPL15	45	3	1.66	0.06
GP:AL035413_5	KIAA0090	45	1	1.67	0.00
GP:AF111168_3	C14orf3	45	2	1.68	0.01
PIR2:T42692	LOC221927	45	1	1.69	0.00
GP:AF214737_1	C9orf10	45	10	1.70	0.57
GP:AK024512_1	FLJ20859	45	1	1.71	0.00
GP:AF157317_1	LOC55829	45	1	1.76	0.00
GP:AF161507_1	MRPL22	45	1	1.76	0.00
SWN:ZH10_HUMAN	ZNF345	45	1	1.79	0.00
GP:AB039669_1	ALEX3	45	4	1.80	0.19
SW:DDX9_HUMAN	DDX9	45	2	1.82	0.00
GP:AB043007_1	SDF2L1	45	2	1.84	0.06
GP:AF154502_1	DPP7	45	2	1.90	0.01
GP:AK000501_1	P17.3	45	1	1.93	0.00
SW:G732_HUMAN	TACSTD1	45	22	1.96	0.30
PIR2:A49656	ZNF147	45	1	1.97	0.00
GP:AL035689_4	HINT3	45	1	1.98	0.00
GP:S69272_1	SERPINB6	45	5	1.99	0.08
GP:AB046803_1	KIAA1583	45	6	1.99	0.11
GP:AF242773_1	hypothetical unkn	45	1	2.03	0.00

SWN:U123_HUMAN	PHF5A	45	1	2.03	0.00
GP:AK025822_1	FLJ22169	45	2	2.04	0.00
GP:AJ245620_1	CTL1	45	1	2.08	0.00
SWN:NDR2_HUMAN	NDRG2	45	2	2.12	0.01
GP:AK022590_1	FLJ12528	45	1	2.13	0.00
GP:D26361_1	KIAA0042	45	1	2.15	0.00
SW:TISB_HUMAN	BRF1	45	2	2.19	0.60
GP:AF220049_1	MDS029	45	3	2.22	0.51
SW:MA32_HUMAN	C1QBP	45	9	2.23	0.22
GP:AF146192_1	MRPS30	45	1	2.24	0.00
GP:U96114_1	WWP2	45	1	2.25	0.00
SW:Z142_HUMAN	ZNF142	45	1	2.28	0.00
SW:ES1_HUMAN	C21orf33	45	4	2.28	0.84
GP:AF151817_1	LOC51631	45	1	2.31	0.00
GP:AK001714_1	FLJ10852	45	2	2.32	0.41
SW:MIF_HUMAN	MIF	45	7	2.34	1.65
GP:AF042284_1	SQRDL	45	3	2.36	0.51
SW:TFPI_HUMAN	TFPI	45	1	2.40	0.00
GP:AF151809_1	CGI-51	45	1	2.42	0.00

GP:AF085361_1	MTCH2	45	5	2.58	0.98
GP:AJ001258_1	NIPSNAP1	45	1	2.60	0.00
GP:AC004528_1	WDR18	45	1	2.62	0.00
GP:AC004957_1	LOC222217	45	3	2.64	0.14
GP:AK024450_1	LOC89941	45	1	2.73	0.00
SW:PSS8_HUMAN	PRSS8	45	1	2.73	0.00
SW:SBP1_HUMAN	SELENBP1	45	2	2.89	0.05
PIR2:T08789	CDYL	45	1	3.26	0.00
GP:AK022587_1	FLJ12525	45	1	3.46	0.00
GPN:AJ278775_1	VL1	45	1	7.61	0.00
PIR2:S12444	hypothetical unkn	45	1	7.89	0.00

Description
SW:SYV_HUMAN P26640 homo sapiens (human). valyl-trna synthetase (ec 6.1.1.9) (valine--trna ligase) (valrs). 2/1996 [MASS=140377]/Valyl-tRNA synthetase 2, a putative class I tRNA sythetase, predicted to function in aminoacylation of valyl tRNAs for protein biosynthesis
SW:PROC_HUMAN P32322 homo sapiens (human). pyrroline-5-carboxylate reductase (ec 1.5.1.2) (p5cr) (p5c reductase). 7/1999 [MASS=33375]/Pyrroline-5-carboxylate reductase 1, catalyzes the NAD(P)H dependent reduction of pyrroline-5-carboxylate to proline in the final step of proline synthesis, may also function NADP+ production in erythrocytes
SW:SYTC_HUMAN P26639 homo sapiens (human). threonyl-trna synthetase, cytoplasmic (ec 6.1.1.3) (threonine--trna ligase) (thrrs). 6/1994 [MASS=82124]/Threonyl-tRNA synthetase, a class II aminoacyl tRNA synthetase which aminoacylates its cognate tRNAs with threonine for protein synthesis, autoantigen in several autoimmune disorders
SW:GLNA_HUMAN P15104 homo sapiens (human). glutamine synthetase (ec 6.3.1.2) (glutamate--ammonia ligase). 12/1998 [MASS=42064]/Glutamine synthase, catalyzes the condensation of glutamate and ammonia to form glutamine, may clear L-glutamate from synapses, reduced expression in the brain and abnormal presence in cerebral spinal fluid is associated with Alzheimer disease
SW:SYG_HUMAN P41250 homo sapiens (human). glycyl-trna synthetase (ec 6.1.1.14) (glycine--trna ligase) (glyrs). 10/1996 [MASS=77531]/Glycyl-tRNA synthetase; functions in protein biosynthesis, aminoacylates its cognate tRNAs with phenylalanine/Glycyl-tRNA synthetase, a class II aminoacyl-tRNA synthetase that catalyzes aminoacylation of its cognate tRNA with glycine for protein biosynthesis; an autoantigen in dermatomyositis
SW:SYD_HUMAN P14868 homo sapiens (human). aspartyl-trna synthetase (ec 6.1.1.12) (aspartate--trna ligase) (asprs). 11/1997 [MASS=57192]/Aspartyl-tRNA synthetase, a class II aminoacyl tRNA synthetase that aminoacylates its cognate tRNA with aspartate for protein biosynthesis, associates with a multisynthetase complex, N-terminus may aid interaction with elongation factor 1 alpha
SW:SYA_HUMAN P49588 homo sapiens (human). alanyl-trna synthetase (ec 6.1.1.7) (alanine--trna ligase) (alars). 7/1998 [MASS=106801]/Alanyl-tRNA synthetase, aminoacylates its cognate tRNA with alanine for protein biosynthesis, acts as an autoantigen in patients with polymyositis
SW:SYR_HUMAN P54136 homo sapiens (human). arginyl-trna synthetase (ec 6.1.1.19) (arginine--trna ligase) (argrs). 5/2000 [MASS=74977]/Arginyl-tRNA synthetase, aminoacylates its cognate tRNAs with arginine for protein biosynthesis
SW:SYM_HUMAN P56192 homo sapiens (human). methionyl-trna synthetase (ec 6.1.1.10) (methionine--trna ligase) (metrs). 12/1998 [MASS=101129]/Methionine-tRNA synthetase, putative tRNA synthetase that is predicted to aminoacylate its cognate tRNAs with methionine for protein biosynthesis, required for rRNA synthesis in the nucleolus
SW:SERC_HUMAN Q9y617 homo sapiens (human). phosphoserine aminotransferase (ec 2.6.1.52) (psat). 5/2000 [MASS=35189]/Member of the aminotransferases class-V family of pyridoxal-phosphate-dependent enzymes, has moderate similarity to S. cerevisiae Ser1p, which is a 3-phosphoserine transaminase involved in synthesis of serine from 3-phosphoglycerate
PIR2:B55053 endothelial monocyte-activating protein II precursor - human [MASS=34254]/Endothelial monocyte activating polypeptide II, a proinflammatory cytokine that interacts with ATP synthase and inhibits endothelial cell growth, released during apoptosis, may sensitize tumors to killing by tumor necrosis factor alpha (TNF)
GP:U66669_1 Homo sapiens 3-hydroxyisobutyryl-coenzyme A hydrolase mRNA, complete cds. [MASS=42908]/Beta-hydroxyisobutyryl-coenzyme A hydrolase, enzyme that hydrolyzes 3-hydroxyisobutyryl CoA, an intermediate of valine catabolism
SW:SYEP_HUMAN P07814 homo sapiens (human). multifunctional aminoacyl-trna synthetase [includes: glutamyl-trna synthetase (ec 6.1.1.17) (glutamate--trna ligase); prolyl-trna synthetase (ec 6.1.1.15) (pro [MASS=163026]/Glutamyl-prolyl-tRNA synthetase, a bifunctional enzyme with two functionally separable domains, one that aminoacylates prolyl-tRNA with proline and another that is believed to aminoacylate glutamyl-tRNA with glutamate for protein biosynthesis
SW:SYQ_HUMAN P47897 homo sapiens (human). glutaminyl-trna synthetase (ec 6.1.1.18) (glutamine--trna ligase) (glnrs). 5/2000 [MASS=87799]/Glutaminyl-tRNA synthetase, aminoacylates cognate tRNAs with glutamine for protein biosynthesis, also suppresses FAS (TNFRSF6)-mediated apoptosis by inhibiting ASK1 (MAP3K5) kinase activity, contains N-terminal appended and C-terminal catalytic domains
SW:SYK_HUMAN Q15046 homo sapiens (human). lysyl-trna synthetase (ec 6.1.1.6) (lysine--trna ligase) (lysrs) (kiaa0070). 7/1998 [MASS=68034]/Lysyl-tRNA synthetase, a class II aminoacyl tRNA synthetase, aminoacylates its cognate tRNAs with lysine for protein biosynthesis, packaged into HIV virions, exists as cytoplasmic and mitochondrial alternative forms
SW:SYI_HUMAN P41252 homo sapiens (human). isoleucyl-trna synthetase, cytoplasmic (ec 6.1.1.5) (isoleucine--trna ligase) (ilers) (irs). 7/1999 [MASS=144959]/Isoleucine-tRNA synthetase, a class I aminoacyl tRNA synthetase, aminoacylates isoleucyl-tRNA with isoleucine for protein biosynthesis, acts as an autoantigen in some autoimmune diseases

SW:CBS_HUMAN P35520 homo sapiens (human). cystathionine beta-synthase (ec 4.2.1.22) (serine sulfhydrase) (beta-thionase). 10/2001 [MASS=60455]/Cystathionine beta-synthase, catalyzes condensation of serine and homocysteine to form cystathionine, thereby removing toxic homocysteine; deficiency causes homocystinuria with associated vascular disease
SW:AATM_HUMAN P00505 homo sapiens (human). aspartate aminotransferase, mitochondrial precursor (ec 2.6.1.1) (transaminase a) (glutamate oxaloacetate transaminase-2). 7/1999 [MASS=47476]/Mitochondrial aspartate aminotransferase (glutamic oxaloacetic transaminase), catalyzes the reversible transfer of the amino group from aspartate to 2-oxoglutarate to form oxaloacetate and glutamate
SW:ODB2_HUMAN P11182 homo sapiens (human). lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex, mitochondrial precursor (ec 2.3.1.-) (e2) (dihydrolipoamide branch [MASS=53487]/Dihydrolipoamide branched chain transacylase E2, a subunit of the branched-chain alpha-ketoacid dehydrogenase complex; mutation of the corresponding gene causes type II maple syrup urine disease (branched chain alpha ketoaciduria)
SWN:SYFB_HUMAN Q9nsd9 homo sapiens (human). phenylalanyl-trna synthetase beta chain (ec 6.1.1.20) (phenylalanine--trna ligase beta chain) (phers) (protein hspc173). 8/2001 [MASS=66130]/Phenylalanyl-tRNA synthetase beta-subunit, regulatory subunit that forms heterodimers with the catalytic alpha subunit (FARSL), involved in protein synthesis, may play a role in tumorigenic events
SW:DHE3_HUMAN P00367 homo sapiens (human). glutamate dehydrogenase 1 precursor (ec 1.4.1.3) (gdh). 5/2000 [MASS=61398]/Glutamate dehydrogenase, catalyzes the reversible deamination of L-glutamate into alpha-ketoglutarate, mitochondrial enzyme with role in neurotransmission; deficiency is associated with neurodegenerative disorders
SW:SERA_HUMAN O43175 homo sapiens (human). d-3-phosphoglycerate dehydrogenase (ec 1.1.1.95) (pgdh). 7/1999 [MASS=56665]/3-phosphoglycerate dehydrogenase, enzyme that catalyzes the first step of serine biosynthesis which is the oxidation of 3-phosphoglycerate to 3-phosphohydroxypyruvate; mutation of the corresponding gene causes microcephaly, retardation, and seizures
SW:IVD_HUMAN P26440 homo sapiens (human). isovaleryl-coa dehydrogenase precursor (ec 1.3.99.10) (ivd). 7/1998 [MASS=46319]/Mitochondrial isovaleryl-CoA dehydrogenase, catalyzes the conversion of isovaleryl-CoA to 3-methylcrotonyl-CoA in leucine metabolism; deficiency causes isovaleric acidemia
SW:SYN_HUMAN O43776 homo sapiens (human). asparaginyl-trna synthetase, cytoplasmic (ec 6.1.1.22) (asparagine-- trna ligase) (asnrs). 5/2000 [MASS=62943]/Asparaginyl-tRNA synthetase, a class II aminoacyl tRNA synthetase, aminoacylates its cognate tRNAs with asparagine for protein biosynthesis, acts as an autoantigen in patients with inflammatory myopathy in interstitial lung disease
SW:G6PE_HUMAN O95479 homo sapiens (human). gdh/6pgl endoplasmic bifunctional protein precursor [includes: glucose 1-dehydrogenase (ec 1.1.1.47) (hexose-6-phosphate dehydrogenase); 6- phosphogluconolacto [MASS=88879]/Glutamate dehydrogenase, catalyzes the reversible deamination of L-glutamate into alpha-ketoglutarate, mitochondrial enzyme with role in neurotransmission; deficiency is associated with neurodegenerative disorders
SW:AOFB_HUMAN P27338 homo sapiens (human). amine oxidase [flavin-containing] b (ec 1.4.3.4) (monoamine oxidase) (mao-b). 12/1998 [MASS=58763]/Monoamine oxidase B, an oxidase involved in the metabolism of various biologically important amines such as dopamine, requires covalently bound FAD as a cofactor, may play a role in aging and behavior
(human). amine oxidase [flavin-containing] a (ec 1.4.3.4) (monoamine oxidase) (mao-a). 12/1998 [MASS=59682]/Monoamine oxidase A, an enzyme involved in degradation of amine neurotransmitters, may be associated with neuropsychiatric disorders, including impulsive aggression and panic disorder, and Parkinson disease
SW:ASNS_HUMAN P08243 homo sapiens (human). asparagine synthetase [glutamine-hydrolyzing] (ec 6.3.5.4) (glutamine-dependent asparagine synthetase) (ts11 cell cycle control protein). 2/1996 [MASS=64299]/Asparagine synthase, catalyzes ATP-dependent conversion of aspartate to asparagine using an amine group from glutamine or ammonia, expression is induced upon amino acid and glucose deprivation and induction increases cancer cell resistance to chemotherapy
SW:GLYM_HUMAN P34897 homo sapiens (human). serine hydroxymethyltransferase, mitochondrial precursor (ec 2.1.2.1) (serine methylase) (glycine hydroxymethyltransferase) (shmt). 5/2000 [MASS=55993]/Serine hydroxymethyltransferase 2 (mitochondrial), a pyridoxal phosphate-dependent enzyme that catalyzes the conversion of serine and tetrahydrofolate to glycine and 5,10-methylenetetrahydrofolate, may play a role in glycine biosynthesis
SW:DYNA_HUMAN Q14203 homo sapiens (human). dynactin, 150 kda isoform (150 kda dynein-associated polypeptide) (dp-150) (dap-150) (p150-glued) (p135) (fragment). 5/2000 [MASS=140784]/Dynactin 1 ((p150, Glued (Drosophila) homolog), microtubule associated protein, interacts with HsEg5 (KNSL1), may play a role in cell division, level is reduced in apoptotic cells
SW:PHS2_HUMAN P11217 homo sapiens (human). glycogen phosphorylase, muscle form (ec 2.4.1.1) (myophosphorylase). 5/2000 [MASS=97092]/Muscle glycogen phosphorylase, participates in glycogen catabolism; mutation of corresponding gene is associated with McArdle disease

SW:DHSO_HUMAN Q00796 homo sapiens (human). sorbitol dehydrogenase (ec 1.1.1.14) (l-iditol 2-dehydrogenase). 7/1999 [MASS=38165]/Sorbitol dehydrogenase, an enzyme of the polyol pathway which catalyzes the conversion of sorbitol to fructose; may be involved in the development of diabetic complications; deficiency may be associated with some forms of congenital cataracts
SW:ACLY_HUMAN P53396 homo sapiens (human). atp-citrate (pro-s-)-lyase (ec 4.1.3.8) (citrate cleavage enzyme). 10/1996 [MASS=121420]/ATP citrate lyase, catalyzes the formation of acetyl-CoA and oxaloacetate from citrate and CoA with the concomitant hydrolysis of ATP to ADP and phosphate, involved in cholesterol and fatty acid synthesis, nutritionally regulated
SW:LDHM_HUMAN P00338 homo sapiens (human). l-lactate dehydrogenase m chain (ec 1.1.1.27) (ldh-a). 2/1996 [MASS=36558]/Lactate dehydrogenase muscle subunit, catalyzes the reversible NAD-dependent interconversion of pyruvate to L-lactate in glycolysis; mutations in the corresponding gene cause LDH-A deficiency
SW:PHS3_HUMAN P11216 homo sapiens (human). glycogen phosphorylase, brain form (ec 2.4.1.1). 10/1996 [MASS=96683]/Brain glycogen phosphorylase, catalyzes the rate-limiting step in glycogen catabolism, activated by AMP and phosphorylation, may play a role in intestinal development; associated with gastric carcinomas displaying a differentiated intestinal phenotype
SW:GLYG_HUMAN P46976 homo sapiens (human). glycogenin-1 (ec 2.4.1.186). 7/1999 [MASS=37347]Glycogenin (glycogenin glucosyltransferase), autocatalytic and self-glucosylating enzyme that primes de novo glycogen synthesis
SW:ALFA_HUMAN P04075 homo sapiens (human). fructose-bisphosphate aldolase a (ec 4.1.2.13) (muscle-type aldolase). 5/2000 [MASS=39289]/Aldolase A (fructose-bisphosphate aldolase); reversibly cleaves FBP into DHAP and GAP in glycolysis
SW:GFA1_HUMAN Q06210 homo sapiens (human). glucosamine--fructose-6-phosphate aminotransferase [isomerizing] 1 (ec 2.6.1.16) (hexosephosphate aminotransferase 1) (d-fructose-6- phosphate amidotransferase [MASS=76616]/Glutamine-fructose-6-phosphate transaminase 1, catalyzes the first step in glucosamine formation, modulates glucose flux and functions in development of insulin resistance, upregulation in kidney associated with diabetic nephropathy
SW:UGS1_HUMAN P13807 homo sapiens (human). glycogen [starch] synthase, muscle (ec 2.4.1.11). 5/2000 [MASS=83786]/Glycogen synthase 1 (muscle), catalyzes transfer of a glucosyl residue from UDP-glucose to glycogen, stimulated by insulin, Acipimox and Flouxetine; mutations in the corresponding gene may be associated with non-insulin-dependent diabetes mellitus
SW:G3P2_HUMAN P04406 homo sapiens (human). glyceraldehyde 3-phosphate dehydrogenase, liver (ec 1.2.1.12). 7/1999 [MASS=35922]/Glyceraldehyde-3-phosphate dehydrogenase, catalyzes reversible oxidation and phosphorylation of glyceraldehyde-3-phosphate to 1,3-diphosphoglycerate in glycolysis, involved in apoptosis, may play a role in neurodegeneration in diseases like Alzheimer's
SW:G6PI_HUMAN P06744 homo sapiens (human). glucose-6-phosphate isomerase (gpi) (ec 5.3.1.9) (phosphoglucose isomerase) (pgi) (phosphohexose isomerase) (phi) (neuroleukin) (nlk). 5/2000 [MASS=63189]/Glucose phosphate isomerase, plays a role in glycolysis and gluconeogenesis, tumor-secreted form (neuroleukin) acts as an autocrine factor to stimulate motility, invasion and metastasis of cancer cells; deficiency is associated with hemolytic anemia
SW:ENOB_HUMAN P13929 homo sapiens (human). beta enolase (ec 4.2.1.11) (2-phospho-d-glycerate hydro-lyase) (skeletal muscle enolase) (mse). 7/1998 [MASS=46856]/Enolase 3 (muscle-specific enolase, beta enolase), a putative enolase which catalyzes the conversion of 2-phospho-D-glycerate to phosphoenolpyruvate in muscle glycolysis, deficiency is associated with exercise intolerance and myalgias
GP:AF144074_1 Homo sapiens glucosidase II alpha subunit mRNA, complete cds; similar to sequences encoded by GenBank Accession Numbers D42041 and U92793. [MASS=109438]/Alpha glucosidase II (alpha neutral subunit), trims alpha(1,3)-linked glucose from Glc(3)Man(9)GlcNAc(2) structures, localizes to the endoplasmic
SW:GDE_HUMAN P35573 homo sapiens (human). glycogen debranching enzyme (glycogen debrancher) [includes: 4-alpha-glucanotransferase (ec 2.4.1.25) (oligo-1,4-1,4-glucantransferase); amylo-1,6-glucosidase [MASS=172497]/Glycogen debranching enzyme, (amylo-1,6-glucosidase 4-alpha-glucanotransferase), catalyzes glycantransferase and glucosidase activities required for glycogen degradation; mutations and dysregulation are associated with type III glycogen storage diseases
SW:PGK1_HUMAN P00558 homo sapiens (human). phosphoglycerate kinase 1 (ec 2.7.2.3) (primer recognition protein 2) (prp 2). 7/1999 [MASS=44597]/Phosphoglycerate kinase 1, catalyzes conversion of 1,3-diphosphoglycerate to 3-phosphoglycerate in glycolysis, forming one molecule of ATP; PGK1 gene transcription is induced by hypoxia and mutation is associated with non-spherocytic hemolytic anemia
SW:DHAG_HUMAN P49189 homo sapiens (human). aldehyde dehydrogenase, e3 isozyme (ec 1.2.1.3) (gamma-aminobutyraldehyde dehydrogenase) (ec 1.2.1.19) (r-aminobutyraldehyde dehydrogenase). 5/2000 [MASS=53533]/Gamma-aminobutyraldehyde dehydrogenase (aldehyde dehydrogenase 9, subfamily A1), member of NAD(P)(+)-dependent aldehyde dehydrogenase family, catalyzes the dehydrogenation of gamma-aminobutyraldehyde, may regulate carnitine biosynthesis
SW:ODO1_HUMAN Q02218 homo sapiens (human). 2-oxoglutarate dehydrogenase e1 component, mitochondrial precursor (ec 1.2.4.2) (alpha-ketoglutarate dehydrogenase). 7/1999 [MASS=113475]/2-Oxoglutarate dehydrogenase (alpha-ketoglutarate dehydrogenase), E1 component of the complex that converts alpha-ketoglutarate to succinyl coenzyme A in the Krebs cycle; deficiency has been observed in Alzheimer and Parkinson disease

SW:K6PL_HUMAN P17858 homo sapiens (human). 6-phosphofructokinase, liver type (ec 2.7.1.11) (phosphofructokinase 1) (phosphohexokinase) (phosphofructo-1-kinase isozyme b). 10/1996 [MASS=85148]/Liver phosphofructokinase, catalyses the phosphorylation of fructose-6-phosphate to fructose-1,6-bisphosphate in glycolysis, deficiency is linked to glycogenosis type VII while overexpression may lead to the cognitive diabilites of Down's syndrome
SW:DIAC_HUMAN Q01459 homo sapiens (human). di-n-acetylchitobiase precursor (ec 3.2.1.-). 7/1999 [MASS=43760]/Chitobiase (di-N-acetylchitobiase), a lysosomal glycosidase involved in the degradation of asparagine-linked glycoproteins
SW:KPB1_HUMAN P46020 homo sapiens (human). phosphorylase b kinase alpha regulatory chain, skeletal muscle isoform (phosphorylase kinase alpha m subunit). 2/1996 [MASS=137338]/Phosphorylase kinase regulatory subunit alpha-1 (muscle), which phosphorylates and thereby activates muscle-specific glycogen phosphorylase (PYGM); mutations in the corresponding gene are associated with muscle glycogenosis, a glycogen storage disease
SW:TPIS_HUMAN P00938 homo sapiens (human), and pan troglodytes (chimpanzee). triosephosphate isomerase (ec 5.3.1.1) (tim). 7/1998 [MASS=26538]/Triosephosphate isomerase 1, catalyzes the reversible interconversion of glyceraldehyde 3-phosphate and dihydroxyacetone phosphate in glycolysis; variant forms cause hemolytic anemia and neurodegeneration; variant form is an antigen on melanoma cells
SW:ENOA_HUMAN P06733 homo sapiens (human). alpha enolase (ec 4.2.1.11) (2-phospho-d-glycerate hydro-lyase) (non-neural enolase) (nne) (phosphopyruvate hydratase). 7/1998 [MASS=47038]/Enolase 1 (alpha enolase), converts 2-phospho-D-glycerate to phosphoenolpyruvate in glycolysis, an autoantigen in multiple autoimmune diseases, shorter alternative form c-myc promoter binding protein (MPB1) is a transcriptional repressor
SW:G19P_HUMAN P14314 homo sapiens (human). protein kinase c substrate, 80 kda protein, heavy chain (pkcsh) (80k-h protein). 7/1999 [MASS=59296]/Protein kinase C substrate 80K-H, acidic protein that is phosphorylated by type I and II protein kinase C, may play a role in fibroblast growth factor and Ras signal transduction, may be a receptor for advanced glycation end products
GP:AJ131612_1 Homo sapiens dic gene, exons 1-11. [MASS=31325]/Solute carrier family 25 member 10 (dicarboxylate carrier), a putative dicarboxylic acid transporter predicted to reside in the inner mitochondrial membrane, may be involved in gluconeogenesis
SW:ODPB_HUMAN P11177 homo sapiens (human). pyruvate dehydrogenase e1 component beta subunit, mitochondrial precursor (ec 1.2.4.1) (pdhe1-b). 7/1999 [MASS=39219]/E1 beta subunit of pyruvate dehydrogenase complex, oxidatively decarboxylates pyruvate to acetyl-CoA
SW:HXK1_HUMAN P19367 homo sapiens (human). hexokinase, type i (ec 2.7.1.1) (hk i) (brain form hexokinase). 12/1998 [MASS=102503]/Hexokinase Type I (ATP:D-hexose 6-phosphotransferase), catalyzes ATP-dependent conversion of glucose to glucose 6 phosphate in glycolysis, deficiency may lead to non-spherocytic hemolytic anemia
GP:AF113123_1 Homo sapiens carbonyl reductase mRNA, complete cds; CR. [MASS=25913]/Protein with high similarity to murine Cbr2, carbonyl reductase, which is involved in differentiation of adipocytes from adipoblasts, member of the glucose/ribitol dehydrogenase family
SW:KPY1_HUMAN P14618 homo sapiens (human). pyruvate kinase, m1 isozyme (ec 2.7.1.40) (pyruvate kinase muscle isozyme) (cytosolic thyroid hormone-binding protein) (cthbp) (thbp1). 12/1998 [MASS=57747]/Pyruvate kinase muscle (pyruvate kinase 3), glycolytic enzyme that converts phosphoenolpyruvate to pyruvate with phosphorylation of ADP to ATP, exists as M1 and M2 alternative forms, may have roles in viral transformation and cell differentiation
SW:GNT2_HUMAN Q10469 h alpha-1,6-mannosyl-glycoprotein beta-1,2-n- acetylglucosaminyltransferase (ec 2.4.1.143) (n-glycosyl- oligosaccharide-glycoprotein n-acetylglucosaminyltransferase ii) (beta-1,2-n- [MASS=51550]/UDP-N-acetylglucosamine: alpha-6-D-mannoside-beta-1,2- N-acetylglucosaminyltransferase II, catalyzes the conversion of oligomannose to complex N-glycans; activity is reduced or absent in type II congenital disorders of glycosylation
SW:ODPA_HUMAN P08559 homo sapiens (human). pyruvate dehydrogenase e1 component alpha subunit, somatic form, mitochondrial precursor (ec 1.2.4.1) (pdhe1-a type i). 7/1999 [MASS=43296]/E1 alpha subunit of pyruvate dehydrogenase complex, somatic form, oxidatively decarboxylates pyruvate to acetyl-CoA; mutation of the corresponding gene causes the majority of pyruvate dehydrogenase deficiencies
SW:GAL1_HUMAN P51570 homo sapiens (human). galactokinase 1 (ec 2.7.1.6). 5/2000 [MASS=42272]/Galactokinase 1, an essential enzyme for galactose metabolism, catalyzes the ATP-dependent phosphorylation of galactose to produce galactose-1-phosphate, deficiency leads to cataract formation
SW:GLCM_HUMAN P04062 homo sapiens (human). glucosylceramidase precursor (ec 3.2.1.45) (beta-glucocerebrosidase) (acid beta-glucosidase) (d-glucosyl-n-acylsphingosine glucohydrolase) (alglucerase) (imigl [MASS=59697]/Acid beta glucosidase (beta-glucocerebrosidase), a lysosomal membrane protein that hydrolyzes glucosylceramide and glucosylsphingosine, may play a role in epidermal differentiation; mutations in the corresponding gene cause Gaucher's disease
SW:INSR_HUMAN P06213 homo sapiens (human). insulin receptor precursor (ec 2.7.1.112) (ir). 5/2000 [MASS=156281]/Insulin receptor, a transmembrane receptor protein tyrosine kinase involved in carbohydrate metabolism, energy pathways, and cell growth; gene mutation is associated with insulin-resistant diabetes mellitus and leprechaunism

SW:ODPX_HUMAN O00330 homo sapiens (human). pyruvate dehydrogenase protein x component, mitochondrial precursor (dihydrolipoamide dehydrogenase-binding protein of pyruvate dehydrogenase complex) (e3-bind [MASS=54138]/Dihydrolipoamide dehydrogenase-binding protein (protein X), lipoyl-containing component of the pyruvate dehydrogenase complex, anchors the dihydrolipoamide dehydrogenase (E3) to the dihydrolipoamide transacetylase (E2) core, deficiency causes disease
GP:AB028128_1 Homo sapiens DPM3 mRNA for dolichol-phosphate-mannose synthase, complete cds. [MASS=10080]/Dolichyl-phosphate mannosyltransferase subunit 3 (prostin 1), part of a complex that produces mannosyl donors for glycoconjugate biosynthesis, stabilizes DPM1 and is stabilized by DPM2; expression is associated with a lack of invasive potential in tumors
SW:ACON_HUMAN Q99798 homo sapiens (human). aconitate hydratase, mitochondrial precursor (ec 4.2.1.3) (citrate hydro-lyase) (aconitase). 5/2000 [MASS=85425]/Aconitase 2 mitochondrial (aconitate hydratase), catalyzes the conversion of citrate to cis-aconitate in the tricarboxylic acid cycle, may be involved in iron homeostasis; deficiency may be associated with lifelong exercise intolerence
SW:GL6S_HUMAN P15586 homo sapiens (human). n-acetylglucosamine-6-sulfatase precursor (ec 3.1.6.14) (g6s) (glucosamine-6-sulfatase). 7/1998 [MASS=62082]/N-acetylglucosamine-6-sulfate sulfatase, an enzyme that hydrolyzes sulfate groups from glycosaminoglycans and is involved in the catabolism of heparan sulfate and keratan sulfate; deficiency causes Sanfilippo disease type D
SW:KG3B_HUMAN P49841 homo sapiens (human). glycogen synthase kinase-3 beta (ec 2.7.1.37) (gsk-3 beta). 7/1999 [MASS=46768]/Glycogen synthase kinase-3 beta, a serine threonine protein kinase that phosphorylates several cytoplasmic and nuclear proteins, involved in embryonic development, and may hyperphosporylate tau (MAPT) in
SW:DLDH_HUMAN P09622 homo sapiens (human). dihydrolipoamide dehydrogenase, mitochondrial precursor (ec 1.8.1.4). 5/2000 [MASS=54150]/Dihydrolipoamide dehydrogenase, E3 component of pyruvate dehydrogenase complex, also component of alpha-ketoglutarate dehydrogenase and branched-chain alpha-ketoacid dehydrogenase complexes and the glycine cleavage system
SW:CISY_HUMAN O75390 homo sapiens (human). citrate synthase, mitochondrial precursor (ec 4.1.3.7). 7/1999 [MASS=51706]/Citrate synthase, converts acetyl-CoA and oxaloacetate into citrate plus CoA in the tricarboxylic acid cycle
SW:BDH_HUMAN Q02338 homo sapiens (human). d-beta-hydroxybutyrate dehydrogenase precursor (ec 1.1.1.30) (bdh) (3-hydroxybutyrate dehydrogenase) (fragment). 12/1998 [MASS=38137]/D-beta-hydroxybutyrate dehydrogenase, a member of the short-chain alcohol dehydrogenase superfamily that requires phosphatidylcholine as an allosteric activator, involved carbohydrate and fatty acid metabolism
SW:BDH_HUMAN P06280 homo sapiens (human). alpha-galactosidase a precursor (ec 3.2.1.22) (melibiase) (alpha-d-galactoside galactohydrolase) (alpha-d-galactosidase a). 7/1998 [MASS=48767]/Alpha-galactosidase A (alpha-D-galactoside galactohydrolase), hydrolyzes glycosphingolipids to release alpha-D-galactosyl residues; mutation of the corresponding gene causes Fabry disease
SW:LYAG_HUMAN P10253 homo sapiens (human). lysosomal alpha-glucosidase precursor (ec 3.2.1.20) (acid maltase). 5/2000 [MASS=105338]/Acid alpha-glucosidase, lysosomal alpha-glucosidase that hydrolyzes alpha(1->4) and alpha(1->6) linkages in glycogen during glycogen catabolism; heritable deficiency causes glycogenosis type II or Pompe disease
SW:MAOM_HUMAN P23368 homo sapiens (human). nad-dependent malic enzyme, mitochondrial precursor (ec 1.1.1.38) (nad-me). 5/2000 [MASS=65444]/Malic enzyme 2, a NAD(+)-dependent mitochondrial form of malic enzyme, catalyzes the oxidative decarboxylation of malate to form pyruvate
SW:SPHM_HUMAN P51688 homo sapiens (human). n-sulphoglucosamine sulphohydrolase precursor (ec 3.10.1.1) (sulfoglucosamine sulfamidase) (sulphamidase). 5/2000 [MASS=56695]/N-sulfoglucosamine sulfohydrolase (sulfamidase), catalyzes the hydrolysis of the N-linked sulfate group from heparan sulfate; mutation of the corresponding gene causes the lysosomal storage disease Sanfilippo A syndrome (mucopolysaccharidosis type IIIA)
SW:IDHP_HUMAN P48735 homo sapiens (human). isocitrate dehydrogenase [nadp], mitochondrial precursor (ec 1.1.1.42) (oxalosuccinate decarboxylase) (idh) (nadp+-specific icdh) (idp) (icd-m). 2/1996 [MASS=50948]/Isocitrate dehydrogenase 2 (NADP+) mitochondrial, catalyzes the oxidative decarboxylation of isocitrate to form alpha-ketoglutarate
SW:KC2B_HUMAN P13862 homo sapiens (human), mus musculus (mouse), rattus norvegicus (rat), bos taurus (bovine), sus scrofa (pig), oryctolagus cuniculus (rabbit), and gallus gallus (chicken). casein kinase [MASS=24942]/Casein kinase II beta subunit, regulatory subunit of casein kinase II (CK2), confers stability and specificity to CK2 catalytic subunits, may mediate formation of the tetrameric CK2 complex, and may be involved in heat stress response
SW:MA2B_HUMAN O00754 homo sapiens (human). lysosomal alpha-mannosidase precursor (ec 3.2.1.24) (mannosidase, alpha b) (lysosomal acid alpha-mannosidase) (laman). 5/2000 [MASS=113673]/Mannosidase alpha class 2B member 1, catalyzes the hydrolysis of alpha-mannoside linkages in glycoprotein catabolism, enzyme activity is inhibited by azafuranose analogs of mannose, deficiency is associated with alpha-mannosidosis
SW:DHSB_HUMAN P21912 homo sapiens (human). succinate dehydrogenase [ubiquinone] iron-sulfur protein, mitochondrial precursor (ec 1.3.5.1) (ip) (ip subunit of complex ii). 5/2000 [MASS=31629]/Succinate dehydrogenase complex iron sulfur subunit B, part of an enzyme complex that transports electrons from succinate to ubiquinone in the TCA cycle and aerobic respiratory chain, may be involved in familial pheochromocytoma

SW:PPCM_HUMAN Q16822 homo sapiens (human). phosphoenolpyruvate carboxykinase, mitochondrial precursor [gtp] (ec 4.1.1.32) (phosphoenolpyruvate carboxylase) (pepck-m). 7/1999 [MASS=70637]/Phosphoenolpyruvate carboxykinase 2, catalyzes the formation of phosphoenolpyruvate by decarboxylation of oxaloacetate, rate-limiting step of gluconeogenesis
SW:DHSA_HUMAN P31040 homo sapiens (human). succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial precursor (ec 1.3.5.1) (fp) (flavoprotein subunit of complex ii). 5/2000 [MASS=72692]/Succinate dehydrogenase complex subunit A (flavoprotein), transports electrons from succinate to ubiquinone in the TCA cycle and respiratory chain; gene mutation is associated with Leigh syndrome, which is a complex II respiratory chain deficiency
SW:K6PP_HUMAN Q01813 homo sapiens (human). 6-phosphofructokinase, type c (ec 2.7.1.11) (phosphofructokinase 1) (phosphohexokinase) (phosphofructo-1-kinase isozyme c) (6-phosphofructokinase, platelet typ [MASS=85596]/Platelet-type phosphofructokinase, rate-limiting enzyme of glycolysis that catalyzes the formation of fructose 1,6-bisphosphate from fructose 6-phosphate and ATP; expression may be elevated upon malignant transformation
SW:GPDM_HUMAN P43304 homo sapiens (human). glycerol-3-phosphate dehydrogenase, mitochondrial precursor (ec 1.1.99.5) (gpd-m) (gpdh-m). 5/2000 [MASS=80815]/Mitochondrial glycerol-3-phosphate dehydrogenase, component of the glycerol phosphate shuttle; mutation of the calcium binding domain in the corresponding gene has been found in a patient with type A diabetes
GP:AJ002744_1 Homo sapiens mRNA for UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase 7. [MASS=75402]/UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 7, enzyme that functions in O-glycosylation and is specific for partially glycosylated substrates
SW:VINC_HUMAN P18206 homo sapiens (human). vinculin. 12/1998 [MASS=116591]/Vinculin, a cytoskeletal protein that localizes to focal adhesions of cell-cell and cell-matrix junctions, also functions as a tumor suppressor; deficiency of alternate cardiac form, metavinculin, is associated with idiopathic dilated cardiomyopathy
SW:MOES_HUMAN P26038 homo sapiens (human). moesin (membrane-organizing extension spike protein). 6/1994 [MASS=67689]/Moesin, putative receptor that may link the cytoskeleton and plasma membrane and play roles in microvillus assembly and cell morphogenesis, may be an autoantigen in rheumatoid arthritis and may play a role in impaired brain development in Down syndrome
SW:CTN1_HUMAN P35221 homo sapiens (human). alpha-1 catenin (cadherin-associated protein) (alpha e-catenin). 11/1997 [MASS=100071]/Catenin alpha 1 (cadherin-associated protein); binds cadherins and links them with the actin cytoskeleton
SW:PLAK_HUMAN P14923 homo sapiens (human). junction plakoglobin (desmoplakin iii). 11/1997 [MASS=81498]/Junction plakoglobin (gamma catenin), links cell-cell adhesion molecules with the cytoskeleton, involved in desmosome organization, cell adhesion, cell prolifiration, apoptosis; loss of heterozygosity is associated with breast and ovarian tumors
SW:CLD7_HUMAN O95471 homo sapiens (human). claudin-7. 5/2000 [MASS=22390]/Claudin 7, a putative integral membrane protein which may be involved in tight junction formation
SW:ITAV_HUMAN P06756 homo sapiens (human). vitronectin receptor alpha subunit precursor (integrin alpha-v) (cd51). 12/1998 [MASS=116052]/Alpha V subunit integrin, a subunit of the vitronectin receptor that is involved in cell-matrix interactions, chemotaxis, phagocytosis and angiogenesis, may contribute to the tumorigenicity of cutaneous malignant melanoma and invasive breast cancer
GP:BC000441_1 Homo sapiens, junction plakoglobin, clone MGC:8404 IMAGE:2820715, mRNA, complete cds. [MASS=81727]/Junction plakoglobin (gamma catenin), links cell-cell adhesion molecules with the cytoskeleton, involved in desmosome organization, cell adhesion, cell prolifiration, apoptosis; loss of heterozygosity is associated with breast and ovarian tumors
SW:CTNB_HUMAN P35222 homo sapiens (human). beta-catenin. 2/1996 [MASS=85497]/Beta catenin, links cadherins to the cytoskeleton, may act as a component of the Wnt signal transduction pathway transmitting nuclear signals via a complex with LEF1 and TCF transcription factors; mutations in the gene are associated with various cancers
SW:EZRI_HUMAN P15311 homo sapiens (human). ezrin (p81) (cytovillin) (villin-2). 12/1998 [MASS=69268]/Villin 2 (ezrin), a member of the band 4.1 superfamily, links the cytoskeleton to the plasma membrane and thereby regulates cell adhesion and cortical morphogenesis, may play a role in rheumatoid arthritis and retinal degeneration
SW:ITA6_HUMAN P23229 homo sapiens (human). integrin alpha-6 precursor (vla-6) (cd49f). 5/2000 [MASS=119462]/Integrin alpha 6, a laminin receptor and component of hemidesmosomes, participates in the maintenance of epidermal integrity; gene mutations are responsible for epidermolysis bullosa and overexpression is correlated with carcinoma invasiveness
GP:AB002382_1 Human mRNA for KIAA0384 gene, complete cds. [MASS=104952]/Catenin delta 1, a member of the catenin family of cadherin-binding proteins that link cadherins to the cytoskeleton, acts in cell signaling, plays a role in cell migration, loss of expession is correlated with bladder, colorectal and other cancer
SW:ITA5_HUMAN P08648 homo sapiens (human). integrin alpha-5 precursor (fibronectin receptor alpha subunit) (integrin alpha-f) (vla-5) (cd49e). 7/1999 [MASS=114508]/Integrin alpha 5, acts as a receptor for fibronectin, mediates binding of the cell to the extracellular matrix, involved in cell migration and trophoblast invasion; upregulation is associated with metastatic melanomas and carcinomas

SW:EFA5_HUMAN P52803 homo sapiens (human). ephrin-a5 precursor (eph-related receptor tyrosine kinase ligand 7) (lerk-7) (al-1). 5/2000 [MASS=26297]/Ephrin A5, a ligand of Eph-related receptor tyrosine kinases that is attached to the membrane via glycosylphosphatidylinositol linkage and is developmentally regulated in the brain, and may play a role during neurogenesis
PIR2:G02390 disintegrin-like metalloproteinase MDC15 (EC 3.4.24.-) - human [MASS=87719]/Metargidin, member of the ADAM family of disintegrin domain-containing zinc metalloproteases, interacts specifically with the alphavbeta3 integrin, upregulated in atherosclerotic lesions and increased expression occurs during atrial fibrillation
SW:DESP_HUMAN P15924 homo sapiens (human). desmoplakin i and ii (dpi and dpii) (fragment). 5/2000 [MASS=201359]/Desmoplakin, a desmosomal plaque protein involved in cell adhesion and tumor migration, cleaved by caspases during desmosomal disruption associated with keratinocyte apoptosis; gene mutation is associated with hereditary palmoplantar keratoderma
SW:LMB2_HUMAN P55268 homo sapiens (human). laminin beta-2 chain precursor (s-laminin). 7/1999 [MASS=196080]/Laminin beta 2 (s-laminin), a basement membrane protein that forms a heterotrimer with other laminin proteins, mediates cell-matrix adhesion, cell migration, and possibly wound healing; lower expression is associated with Walker Warburg Syndrome
SW:CD81_HUMAN P18582 homo sapiens (human), and pan troglodytes (chimpanzee). cd81 antigen (26 kda cell surface protein tapa-1). 5/2000 [MASS=25809]/CD81 antigen, member of the transmembrane 4 superfamily (TM4SF) that regulates lymphoma cell growth, may be involved in cell motility and the defense response, associates with integrins in the plasma membrane
SW:ATC2_HUMAN P16615 h sarcoplasmic/endoplasmic reticulum calcium atpase isoform 2 (ec 3.6.1.38) (calcium pump 2) (serca2) (sr ca(2+)-atpase 2) (calcium- transporting atpase sarcoplasmic reticulum type, [MASS=114757]/Sarcoplasmic reticulum Ca2+-ATPase 2 (slow twitch muscle, cardiac, and nonmuscle form), pumps calcium from the cytoplasm to the ER; reduced activity in the heart is implicated in dilated cardiomyopathy and gene mutations are associated with Darier disease
SWN:ARVC_HUMAN O00192 homo sapiens (human). armadillo repeat protein deleted in velo-cardio-facial syndrome. 8/2001 [MASS=104642]/Armadillo repeat gene deleted in velocardiofacial syndrome, binds cadherins and may play a role in cell adhesion at the adherens junction; hemizygosity of the corresponding gene is associated with velocardiofacial syndrome
SW:RSP4_HUMAN P08865 homo sapiens (human). 40s ribosomal protein sa (p40) (34/67 kda laminin receptor) (colon carcinoma laminin-binding protein) (nem/1chd4). 5/2000 [MASS=32854]/Laminin receptor 1, a ribosomal protein of the small 40S ribosomal subunit, plays a role in cancer cell and basement membrane glycoprotein laminin interactions during tumor invasion and metastasis, expression correlates with cancer cell aggressiveness
SW:RB13_HUMAN P51153 homo sapiens (human). ras-related protein rab-13. 12/1998 [MASS=22774]/Ras-related GTP-binding protein 13, a putative RAB small monomeric GTPase that is likely to play a role in intracellular protein trafficking and cell adhesion
SW:PTPF_HUMAN P10586 homo sapiens (human). lar protein precursor (leukocyte antigen related) (ec 3.1.3.48). 10/1994 [MASS=211845]/Protein tyrosine phosphatase receptor-type F (leukocyte common antigen related), regulates insulin receptor signaling and cell migration, inhibits tumor formation in nude mice
SW:MIC2_HUMAN P14209 homo sapiens (human). t-cell surface glycoprotein e2 precursor (e2 antigen) (cd99) (mic2 protein) (12e7). 5/2000 [MASS=18848]/T-cell surface glycoprotein E2, a cell surface glycoprotein involved in T cell adhesion and apoptosis, activates MAP kinases, may be involved in Golgi-membrane transport, downregulated in EBV-associated Hodgkins disease
SW:C166_HUMAN Q13740 homo sapiens (human). cd166 antigen precursor (activated leukocyte-cell adhesion molecule) (alcam). 7/1999 [MASS=65132]/Activated leukocyte cell adhesion molecule, an immunoglobulin superfamily member and ligand for CD6, involved in hematopoietic cell adhesion, may play a role in osteogenesis, marker for tumor progression in malignant melanoma
GP:U17032_1 Human p190-B (p190-B) mRNA, complete cds; member of the Rho GAP family. [MASS=171569]/Rho GTPase activating protein 5/Rho GTPase-activating protein (GAP) 5, has GAP activity for ARHA, RAC1 and CDC42, which are ras-related GTP binding proteins of the rho subfamily; may be involved in the integrin receptor signaling pathway and in cell adhesion
SWN:JAM1_HUMAN Q9y624 homo sapiens (human). junctional adhesion molecule precursor (jam) (platelet adhesion molecule 1) (pam-1) (platelet f11 receptor). 8/2001 [MASS=32583]/Junctional adhesion molecule 1, participates in platelet adhesion and aggregation and may play roles in intracellular signaling, the assembly of tight junctions, and the inflammatory response, may be involved in the pathogenesis of immune thrombocytopenia
SW:ITB1_HUMAN P05556 homo sapiens (human). fibronectin receptor beta subunit precursor (integrin beta-1) (cd29) (integrin vla-4 beta subunit). 7/1999 [MASS=88465]/Integrin beta 1, involved in extracellular matrix interactions and signal transduction, plays roles in cell adhesion, migration, proliferation and development, may be involved in tumor metastasis
GP:U64791_1 Human Golgi membrane sialoglycoprotein MG160 (GLG1) mRNA, complete cds; fibroblast growth factor. [MASS=134593]/Golgi apparatus protein 1, a cysteine-rich membrane sialoglycoprotein that may be a receptor for fibroblast growth factor (FGF), may be involved in cell adhesion
Human cysteine-rich fibroblast growth factor receptor (CFR-1) mRNA/Golgi apparatus protein 1, a cysteine-rich membrane sialoglycoprotein that may be a receptor for fibroblast growth factor (FGF), may be involved in cell adhesion

SW:NB8M_HUMAN P17568 homo sapiens (human). nadh-ubiquinone oxidoreductase b18 subunit (ec 1.6.5.3) (ec 1.6.99.3) (complex i-b18) (ci-b18) (cell adhesion protein sqm1). 7/1998 [MASS=15648]/Subunit of the NADH-ubiquinone oxidoreductase (complex I), a multiprotein complex that transports electrons from NADH to ubiquinone, functions as a cell adhesion molecule with a role in metastasis, may have a role in drug transport
GP:AC005609_7 Homo sapiens chromosome 5, BAC clone 203o13 (LBNL H155), complete sequence. [MASS=84896]/Protocadherin alpha 4, a member of a family of cadherin-like cell adhesion proteins that may have a role in forming neuronal connections in the brain
SW:LU_HUMAN P50895 homo sapiens (human). lutheran blood group glycoprotein precursor (b-cam cell surface glycoprotein) (auberger b antigen) (f8/g253 antigen). 11/1997 [MASS=67375]/Precursor of Lutheran blood group glycoprotein and B-CAM, laminin receptors and cell adhesion molecules, have a role in the blood-brain barrier, contribute to vasoocculsion in sickle cell disease and possibly tumorigenesis
SW:LMG1_HUMAN P11047 homo sapiens (human). laminin gamma-1 chain precursor (laminin b2 chain). 7/1998 [MASS=177607]/Laminin C1, an extracellular matrix glycoprotein that may be involved in cell-matrix adhesion and the regulation of cell shape
SW:UBCC_HUMAN Q16781 homo sapiens (human). ubiquitin-conjugating enzyme e2-17 kda (ec 6.3.2.19) (ubiquitin- protein ligase) (ubiquitin carrier protein) (ubc13). 7/1999 [MASS=17138]/Ubiquitin-conjugating enzyme E2N (yeast UBC13 homolog), forms heterodimers with ubiquitin-conjugating enzyme E2 variants 1 or 2 (UBE2V1, UBE2V2), and catalyzes formation of unique lysine 63-linked polyubiquitin chains involved in IkappaB kinase activation
SW:RAPB_HUMAN P09526 homo sapiens (human), and bos taurus (bovine). ras-related protein rap-1b (gtp-binding protein smg p21b). 7/1993 [MASS=20825]/Ras related protein 1b, member of the Ras superfamily of low molecular weight GTP-binding proteins, regulates cell cycle progression and cellular proliferation, may play a role in cAMP-responsive tumorigenesis
SW:EGFR_HUMAN P00533 homo sapiens (human). epidermal growth factor receptor precursor (ec 2.7.1.112). 12/1998 [MASS=134277]/Epidermal growth factor receptor, a receptor protein tyrosine kinase that binds epidermal growth factor (EGF) and transforming growth factor alpha (TGFA), involved in cell proliferation and differentiation, implicated in tumor invasion and metastasis
SW:RS4_HUMAN P12750 homo sapiens (human), rattus norvegicus (rat), mus musculus (mouse), mesocricetus auratus (golden hamster), and felis silvestris catus (cat). 40s ribosomal protein s4, x isoform (sin [MASS=29467]/Ribosomal protein S4 X-linked, a component of the small 40S ribosomal subunit with roles in translation, cell cycle, and cell proliferation; gene is X-linked but escapes X inactivation, and may therefore contribute to haploinsufficency in Turner syndrome
SW:FKB1_HUMAN P20071 homo sapiens (human), and oryctolagus cuniculus (rabbit). fk506-binding protein (fkbp-12) (peptidyl-prolyl cis-trans isomerase) (ec 5.2.1.8) (ppiase) (rotamase) (immunophilin fkbp12 [MASS=11820]/FK506-binding protein 1A, peptidyl prolyl cis-trans isomerase, modulates the Ca2+-release activity of ryanodine receptors, complex with FK506 inhibits calcineurin-dependent lymphokine gene transcription and mediates FK506 immunosuppressive activity
SW:P2AA_HUMAN P05323 homo sapiens (human), oryctolagus cuniculus (rabbit), sus scrofa (pig), and bos taurus (bovine). serine/threonine protein phosphatase 2a, catalytic subunit, alpha isoform (ec 3.1.3. [MASS=35594]/Protein phosphatase 2 catalytic subunit alpha, a catalytic subunit of protein phosphatase 2A involved in regulating diverse cellular processes via protein phosphorylation
SW:DYN2_HUMAN P50570 homo sapiens (human). dynamin 2. 10/1996 [MASS=98018]/Dynamin II, member of a family of 100-kD guanosine triphosphatases, regulates budding of endocytic vesicles at the plasma membrane and may function in the formation of transport vesicles at the trans-Golgi
GP:AB002323_1 Human mRNA for KIAA0325 gene, partial cds. [MASS=238445]/Dynein cytoplasmic heavy chain 1, a member of a family of dynein ATPases that function as motor proteins, plays a role in mitotic spindle formation
PIR2:T03842 fission yeast Skb1 protein homolog - human [MASS=72786]/Protein arginine methyltransferase 5, methylates target proteins on arginine residues, may inhibit mitosis
GP:U59435_1 Human cell cycle protein p38-2G4 homolog (hG4-1) mRNA, complete cds. [MASS=43813]/Proliferation associated 2G4, interacts with the juxtamembrane domain of ERBB3, dissociates from ERBB3 and translocates from the cytoplasm to the nucleus following treatment with heregulin
SW:GPS1_HUMAN Q13098 homo sapiens (human). g protein pathway suppressor 1 (gps1 protein) (mfh protein). 11/1997 [MASS=53372]/G protein pathway suppressor 1, suppressor of G protein and MAP kinase-mediated signaling pathways
SW:RHOG_HUMAN P35238 homo sapiens (human), and cricetus cricetus (black-bellied hamster). rho-related gtp-binding protein rhog. 11/1995 [MASS=21309]/Aplysia ras-related homolog G (RhoG), a Ras-related GTP-binding protein of the rho-subfamily which regulates reorganization of the actin cytoskeleton and may be involved in the regulation of cholesterol excretion in patients with Tangier disease
SW:TCPB_HUMAN P78371 homo sapiens (human). t-complex protein 1, beta subunit (tcp-1-beta) (cct-beta). 7/1999 [MASS=57488]/Chaperonin containing T-complex polypeptide-1 (TCP1) subunit 2, the beta subunit of the chaperonin containing complex (CCT), plays a role in the folding of cytosolic proteins, may be required for the proper folding of cyclin E

SW:G25B_HUMAN P21181 homo sapiens (human), mus musculus (mouse), and bos taurus (bovine). g25k gtp-binding protein, brain isoform (gp) (cdc42 homolog). 12/1998 [MASS=21311]/Cell division cycle 42 (GTP binding protein 25kD), Rho GTPase involved in actin cytoskeleton organization, cell migration, cell cycle progression and apoptosis, downregulated in fibroblasts and macrophages from patients with Tangiers disease
GP:AB006534_1 Homo sapiens mRNA for hepatocyte growth factor activator inhibitor type 2, complete cds. [MASS=28169]/Serine protease inhibitor Kunitz type 2 (bikunin), inhibits hepatocyte growth factor activator (HGFAC) and serine proteases involved in coagulation and fibrinolysis, overexpressed in pancreatic cancer, may play roles in urolithiasis and glioma progression
SW:143T_HUMAN P27348 homo sapiens (human). 14-3-3 protein tau (14-3-3 protein theta) (14-3-3 protein t-cell) (hs1 protein). 11/1997 [MASS=27764]/14-3-3 theta (14-3-3 tau in T-cells), may modulate T-cell signaling and cytokine expression through interaction with and inhibition of protein kinase C and phosphatidylinositol 3-kinase, may promote cell survival during amyotrophic lateral sclerosis (ALS)
PIR2:S69890 mitogen inducible gene mig-2 - human [MASS=81993]/Mitogen inducible 2, a mitogen-induced protein that may be involved in cell cycle control and cell proliferation
SW:APP2_HUMAN Q06481 homo sapiens (human). amyloid-like protein 2 precursor (amyloid protein homolog) (apph) (cdei-box binding protein) (cdebp). 5/2000 [MASS=86956]/Amyloid precursor-like protein 2, a nuclear protein whcih may contribute to neurogenesis and cell cycle control
SW:RHOA_HUMAN P06749 homo sapiens (human), and bos taurus (bovine). transforming protein rhoa (h12). 7/1998 [MASS=21768]/Ras homolog gene family member A, monomeric GTPase of the Rho family that mediates cell surface receptor and integrin signaling, induces actin stress fiber and focal adhesion formation, activity may contribute to cellular transformation and tumor invasion
SW:TCPH_HUMAN Q99832 homo sapiens (human). t-complex protein 1, eta subunit (tcp-1-eta) (cct-eta) (hiv-1 nef interacting protein). 7/1998 [MASS=59367]/Chaperonin containing T-complex polypeptide-1 (TCP1) subunit 7, the eta subunit of the chaperonin containing complex (CCT), plays a role in protein folding and in the response to chemical stress, may be required for proper folding of cyclin E
SW:DYNA_HUMAN Q14203 homo sapiens (human). dynactin, 150 kda isoform (150 kda dynein-associated polypeptide) (dp-150) (dap-150) (p150-glued) (p135) (fragment). 5/2000 [MASS=140784]/Dynactin 1 ((p150, Glued (Drosophila) homolog), microtubule associated protein, interacts with HsEg5 (KNSL1), may play a role in cell division, level is reduced in apoptotic cells
SW:RAN_HUMAN P17080 homo sapiens (human). gtp-binding nuclear protein ran (tc4). 12/1998 [MASS=24354]/RAN, member of the ras family of GTP binding proteins, couples completion of DNA synthesis to mitosis and induces mitotic spindle formation, involved in nuclear transport of RNA and proteins, interacts with polyglutamate repeats of the androgen receptor
SW:RAPA_HUMAN P10113 homo sapiens (human), rattus norvegicus (rat), and bos taurus (bovine). ras-related protein rap-1a (c21kg) (krev-1 protein) (gtp-binding protein smg-p21a) (g-22k). 12/1998 [MASS=20987]/RAP1A member of RAS oncogene family (Ras-related protein 1a), a member of the Ras superfamily of low molecular weight GTPases that is involved in cell cycle control and negative regulation of cellular proliferation, acts as a tumor suppressor
SW:TERA_HUMAN P55072 homo sapiens (human). transitional endoplasmic reticulum atpase (ter atpase) (15s mg(2+)-atpase p97 subunit) (valosin containing protein) (vcp) [contains: valosin]. 7/1999 [MASS=89322]/Valosin-containing protein, a putative clathrin-binding ATPase involved in cell cycle control, ubiquitin-dependent protein degradation, and JAK-STAT signaling, may be involved in DNA repair via BRCA1, may be involved in receptor-mediated endocytosis
SW:TCPD_HUMAN P50991 homo sapiens (human). t-complex protein 1, delta subunit (tcp-1-delta) (cct-delta) (stimulator of tar rna binding). 5/2000 [MASS=57839]/Chaperonin containing T-complex 1 subunit 4 (delta), part of a cytosolic hexadecamer structure involved in ATP-dependent folding of actin, tubulin and other proteins
GP:D88435_1 Homo sapiens mRNA for HsGAK, complete cds. [MASS=143165]/Cyclin G-associated kinase, a putative serine/threonine protein kinase that shares homology with tensin and auxilin, may play a role in cell cycle regulation
SW:ERB2_HUMAN P04626 homo sapiens (human). receptor protein-tyrosine kinase erbb-2 precursor (ec 2.7.1.112) (p185erbb2) (neu proto-oncogene) (c-erbb-2) (tyrosine kinase-type cell surface receptor her2) [MASS=137910]/Avian erythroblastosis oncogene B 2, a receptor tyrosine kinase and most oncopotent member of the EGF receptor family, heterodimerizes with other EGFRs; overexpression contributes to growth, metastasis and chemoresistance of epithelial-derived tumors
SW:PP1A_HUMAN P08129 homo sapiens (human), mus musculus (mouse), rattus norvegicus (rat), and oryctolagus cuniculus (rabbit). serine/threonine protein phosphatase pp1-alpha 1 catalytic subunit (ec 3.1.3 [MASS=37512]/Protein phosphatase 1 catalytic subunit alpha isoform, plays roles in diverse cellular signal transduction processes that involve protein dephosphorylation, regulates of cell growth and apoptosis and may be a tumor suppressor
SW:FRAP_HUMAN P42345 homo sapiens (human). fkbp-rapamycin associated protein (frap) (rapamycin target protein). 7/1999 [MASS=288892]/FK506 binding protein 12-rapamycin associated protein 1, serine/threonine and 1-phosphatidylinositol 4-kinase, regulates translation, cell cycle and p53 (TP53) -dependent apoptosis; altered expression is associated with recurrent prostate tumors
GP:U97276_1 Homo sapiens quiescin (Q6) mRNA, complete cds, alternatively spliced; alternatively spliced; probable sulfhydryl oxidase; thioredoxin superfamily member. [MASS=82578]/Quiescin Q6, a quiescence-inducible protein that contains 9 quiescin homology zones and has similarity to thioredoxins and S. cerevisiae Erv1p and sulfhydryl oxidases, may play a role in the induction of quiencence

PIR2:T00387 KIAA0622 protein - human (fragment) [MASS=141604]/CLIP-associating protein 1 (Mast), a microtubule-associated protein with a putative role in centrosome separation and organization of the bipolar mitotic spindle
GP:AB020723_1 Homo sapiens mRNA for KIAA0916 protein, partial cds; k06582 cDNA clone for KIAA0916 has a nucleotide substitution at the position 1955 (C- T; nonsense mutation) of the sequence of KIAA0916.. [MASS=134896]/Protein associated with Myc, a putative transcriptional regulator that binds the Myc oncoprotein (human Myc) and may regulate Myc activated transcription, binds and inhibits adenylyl cyclase types I (ADCY1) and V (ADCY6)
SW:NPL1_HUMAN P55209 homo sapiens (human). nucleosome assembly protein 1-like 1 (nap-1 related protein). 10/1996 [MASS=45374]/Nucleosome assembly protein 1-like 1, member of the NAP/SET protein family, binds histones H2A and H2B, a histone chaperone that mediates assembly of nucleosomes, complex with histone acetyltransferase coactivator p300 (EP300) may stimulate transcription
SW:RCC_HUMAN P18754 homo sapiens (human). regulator of chromosome condensation (cell cycle regulatory protein). 7/1999 [MASS=44969]/Regulator of chromosome condensation 1, a chromatin-binding protein that functions as a guanine nucleotide exchange factor for RAN, plays roles in nucleocytoplasmic transport, mitotic spindle formation, and nuclear envelope assembly
SW:P2BA_HUMAN Q08209 homo sapiens (human). serine/threonine protein phosphatase 2b catalytic subunit, alpha isoform (ec 3.1.3.16) (calmodulin-dependent calcineurin a subunit, alpha isoform) (cam-prp cat [MASS=58688]/Calcineurin A alpha, catalytic subunit of calcium/calmodulin regulated protein phosphatase, regulates activity of transcription factors involved in signal transduction and growth control
GP:AF013591_1 Homo sapiens homolog of the Aspergillus nidulans sudD gene product mRNA, complete cds. [MASS=59117]/SudD (suppressor of bimD6 Aspergillus nidulans) homolog, a member of the SUDD family of proteins, has similarity to Aspergillus nidulans SUDD, which is a suppressor of the bimD6 chromosome-spindle attachment defect
SW:RFA3_HUMAN P35244 homo sapiens (human). replication protein a 14 kda subunit (rp-a) (rf-a) (replication factor-a protein 3). 11/1997 [MASS=13569]/Replication protein A 3, a subunit of replication protein A, which is a single-stranded DNA-binding protein complex with roles in DNA replication, repair, and recombination
SW:CUL2_HUMAN Q13617 homo sapiens (human). cullin homolog 2 (cul-2). 12/1998 [MASS=86956]/Cullin 2, has E3 ubiquitin ligase activity when present in a complex containing von Hippel Lindau tumor suppressor (VHL)- elogin B (TCEB2)-elogin C (TCEB1); modification by ubiquitin-like protein NEDD8 may be important for VHL tumor suppressor function
SW:MCM4_HUMAN P33991 homo sapiens (human). dna replication licensing factor mcm4 (cdc21 homolog) (p1-cdc21). 5/2000 [MASS=96611]/Minichromosome maintenance deficient 4, forms a single stranded ATP-dependent DNA helicase with MCM6 and MCM7, may monitor sites of unreplicated DNA, displacement from replicated chromatin may ensure that DNA is only replicated once per cell cycle
SW:BUB3_HUMAN O43684 homo sapiens (human). mitotic checkpoint protein bub3. 5/2000 [MASS=37155]/Budding uninhibited by benzimidazoles 3 homolog, involved in the mitotic spindle checkpoint, localization to unattached kinetochores suggests a role in detecting microtubule attachment, required for the localization of BUB1 and BUB1B to kinetochores
SW:ITB1_HUMAN P05556 homo sapiens (human). fibronectin receptor beta subunit precursor (integrin beta-1) (cd29) (integrin vla-4 beta subunit). 7/1999 [MASS=88465]/Integrin beta 1, involved in extracellular matrix interactions and signal transduction, plays roles in cell adhesion, migration, proliferation and development, may be involved in tumor metastasis
SW:NHPX_HUMAN P55769 homo sapiens (human). nhp2/rs6 family protein yel026w homolog (high mobility group-like nuclear protein 2 homolog) (otk27). 5/2000 [MASS=14174]/Non-histone chromosome protein 2 (S. cerevisiae)-like 1, a member of a family of RNP-associated proteins, a component of the spliceosome and rRNA processing machinery, recognizes a shared stem-internal loop-stem structure in its RNA targets
SW:ARP3_HUMAN P32391 homo sapiens (human), and bos taurus (bovine). actin-like protein 3 (actin-2). 7/1999 [MASS=47371]/Actin-related protein 3 homolog, a component of the Arp2/3 protein complex, which is involved in actin cytoskeleton organization and biogenesis and may have a role in cell motility
SW:AR41_HUMAN O15143 homo sapiens (human). arp2/3 complex 41 kda subunit (p41-arc). 12/1998 [MASS=40950]/Actin related protein 2/3 complex 1A, component of the Arp2/3 complex, interacts directly with an ARPC4 and ARPC5 heterodimer, may have a role in Arp2/3 complex assembly or maintenance, may regulate complex activity or intracellular distribution
SW:AR21_HUMAN O15145 homo sapiens (human). arp2/3 complex 21 kda subunit (p21-arc). 12/1998 [MASS=20547]/Actin related protein 2/3 complex subunit 3 (21 kDa), a component of the Arp2/3 complex, may participate in the regulation of actin polymerization, may have a role in the protrusion of lamellipodia, has an essential function in at least HeLa cells
SW:ARP2_HUMAN O15142 homo sapiens (human). actin-like protein 2. 7/1999 [MASS=44761]/Actin-related protein 2 homolog, a component of the Arp2/3 protein complex, which is involved in actin filament nucleation and polymerization, may form the nucleation interface with the pointed end of the actin filament

SW:AR34_HUMAN O15144 homo sapiens (human). arp2/3 complex 34 kda subunit (p34-arc). 7/1998 [MASS=34333]/Actin related protein 2/3 complex subunit 2, component of the Arp2/3 complex, which is involved in assembly of the actin cytoskeleton, interacts directly with ARPC4, possibly as an early intermediate in Arp2/3 complex formation
SW:CAP1_HUMAN Q01518 homo sapiens (human). adenylyl cyclase-associated protein 1 (cap 1). 10/1996 [MASS=51673]/Adenylyl cyclase-associated protein 1, putative homolog of bifunctional S. cerevisiae Srv2p, C-terminus mediates actin binding and may play a role in regulating cell growth and morphogenesis, the N-terminal domain may bind and-or regulate adenylyl cyclase
GP:U40572_1 Human beta2-syntrophin (SNT B2) mRNA, complete cds; contains two pleckstrin homology domains and a domain related to both the tumor discs-large protein and the zonula occludens protein; dystrophin-binding intracellular membrane cytoskeletal protein. [MASS=57950]/Syntrophin beta 2, a membrane-associated protein that binds to dystrophin (DMD) and utrophin-dystrophin related protein (UTRN), may link proteins to the actin cytoskeleton
SW:VAB2_HUMAN P21281 homo sapiens (human). vacuolar atp synthase subunit b, brain isoform (ec 3.6.1.34) (endomembrane proton pump 58 kda subunit) (v-atpase b subunit) (ho57). 7/1999 [MASS=56517]/Vacuolar-type H(+)-ATPase (beta isoform 2), 56 kDa subunit of the ATPase catalytic domain which may assist in transepithelial H+ transport in the kidney, may effect vacuolar acidification, and may play a role in the polarization of osteoclasts
SW:NDR1_HUMAN Q92597 homo sapiens (human). ndrg1 protein (differentiation-related gene 1 protein) (drg1) (reducing agents and tunicamycin-responsive protein) (rtp) (nickel- specific induction protein ca [MASS=42835]/N-myc downstream regulated gene 1, induced by nickel, homocysteine, 2-mercaptoethanol, and tunicamycin, involved in cellular differentiation and negative control of cell proliferation, downregulated in a variety of cancers
SW:TRAL_HUMAN Q12931 homo sapiens (human). tumor necrosis factor type 1 receptor associated protein (trap-1) (fragment). 5/2000 [MASS=75342]/Heat shock protein 75, member of the HSP90 family of molecular chaperones, binds and refolds denatured retinoblastoma (RB1) protein during M phase and after heat shock, binds the intracellular domain of tumor necrosis factor receptor type 1
PIR2:JC4775 p58k protein - human [MASS=57580]/The 58,000-dalton cellular inhibitor of the interferon-induced double-stranded RNA-activated protein kinase (PKR) is a member of the tetratricopeptide repeat family of proteins/DnaJ (Hsp40) homolog subfamily C member 3 (protein kinase inhibitor p58), a member of the tetratricopeptide repeat family of proteins that may act as a cochaperone that inhibits the activity of double-stranded RNA-dependent protein kinase (PRKR)
SW:MRP1_HUMAN P33527 homo sapiens (human). multidrug resistance-associated protein 1. 5/2000 [MASS=171561]/ATP-binding cassette subfamily C member 1 (multiple drug resistance protein 1), an ATP-binding cassette transporter that acts as a multidrug efflux pump conferring resistance to lipophilic drugs and chemotherapeutic agents
heat shock 70 kda protein 4 (heat shock 70-related protein apg-2/Heat shock 70kD protein 4, putative ATP-binding molecular chaperone and member of the HSP110 family, binds RNA, may play a role in stress response and RNA stability
SW:AOP2_HUMAN P30041 homo sapiens (human). antioxidant protein 2 (ec 1.11.1.7) (24 kda protein) (liver 2d page spot 40) (red blood cells page spot 12). 12/1998 [MASS=24904]/Protein with strong similarity to anti-oxidant proteins, member of the AhpC/TSA family
SW:MRP4_HUMAN O15439 homo sapiens (human). multidrug resistance-associated protein 4 (fragment). 5/2000 [MASS=18448]/Multidrug resistance protein 4, a member of the ATP-binding cassette transporter superfamily, transports cAMP, cGMP, and estradiol 17-beta-D-glucuronide, acts as a multidrug efflux pump, may be involved in cellular detoxification and xenobiotic resistance/Multidrug resistance protein 4, a member of the ATP-binding cassette transporter superfamily, transports cAMP, cGMP, and estradiol 17-beta-D-glucuronide, acts as a multidrug efflux pump, may be involved in cellular detoxification and xenobiotic resistance
SW:HS71_HUMAN P08107 homo sapiens (human). heat shock 70 kda protein 1 (hsp70.1) (hsp70-1/hsp70-2). 5/2000 [MASS=70052]/Heat shock 70 kDa protein 1A, a member of the HSP70 chaperone family involved in protein folding, translocation, and complex assembly, blocks AU-rich mRNA decay by nuclear sequestering of AU-rich binding protein, may contribute to celiac disease
SW:TDX2_HUMAN Q06830 homo sapiens (human). thioredoxin peroxidase 2 (thioredoxin-dependent peroxide reductase 2) (proliferation-associated protein pag) (natural killer cell enhancing factor a) (nkef-a). [MASS=22110]/Peroxiredoxin 2, a thioredoxin peroxidase member of the AhpC-TSA family, acts as an antioxidant, enhances natural killer activity, may be involved in erythrocyte differentiation, exists as a membrane-associated form in erythrocytes
SW:ENPL_HUMAN P14625 homo sapiens (human). endoplasmin precursor (94 kda glucose-regulated protein) (grp94) (gp96 homolog) (tumor rejection antigen 1). 10/1996 [MASS=92469]/Tumor rejection antigen 1, a putative molecular chaperone that may play roles in protein folding, cytoprotection, the immune response, and the heat shock and stress responses; vaccination with TRA1 elicits immune responses to cancer
SW:DNJ2_HUMAN P31689 homo sapiens (human). dnaj protein homolog 2 (hsj-2). 7/1999 [MASS=44868]/DnaJ homolog subfamily A member 1, heat shock protein, expressed in many tissues

GP:AB015798_1 Homo sapiens HSJ2 mRNA for DnaJ homolog, complete cds; DnaJ homologue HSJ2a. [MASS=36087]/DnaJ homolog subfamily A member 1, heat shock protein, expressed in many tissues
SW:MK01_HUMAN P28482 homo sapiens (human). mitogen-activated protein kinase 1 (ec 2.7.1.-) (extracellular signal-regulated kinase 2) (erk2) (mitogen-activated protein kinase 2) (map kinase 2) (mapk 2) [MASS=41390]/Mitogen-activated protein kinase 1, a serine-threonine kinase effector of the RAS-MAP kinase pathway, translocates to the nucleus to mediate transcription when activated, involved in the regulation of cell growth, differentiation, migration and apoptosis
SW:TDX1_HUMAN P32119 homo sapiens (human). thioredoxin peroxidase 1 (thioredoxin-dependent peroxide reductase 1) (thiol-specific antioxidant protein) (tsa) (prp) (natural killer cell enhancing factor b) [MASS=21892]/Peroxiredoxin 1, oxidative stress-inducible antioxidant protein with peroxidase activity, may have anticytotoxic and antiapoptotic activity and may have a role in cell proliferation
SW:RAC1_HUMAN P15154 homo sapiens (human), mus musculus (mouse), and canis familiaris (dog). ras-related c3 botulinum toxin substrate 1 (p21-rac1) (ras-like protein tc25). 12/1998 [MASS=21450]/Ras-related C3 botulinum toxin substrate 1, a monomeric GTPase of the Rho family, involved in transducing signals that regulate proliferation, apoptosis, cytoskeletal organization, and response to oxidative stress, contributes to tumor cell invasiveness
SW:A4_HUMAN P05067 homo sapiens (human). alzheimer's disease amyloid a4 protein precursor (protease nexin-ii) (pn-ii) (appi) [contains: beta-amyloid protein (beta-app) (a-beta)]. 5/2000 [MASS=86943]/Amyloid beta (A4) precursor protein, cell surface protease inhibitor that reduces copper, deposits of proteolytic peptide products are found in Alzheimer's disease and Down syndrome brains, deficiency is associated with early-onset Alzheimer's disease
PIR2:T00361 hypothetical protein KIAA0678 - human (fragment) [MASS=114535]/Protein containing a DnaJ domain, which are part of chaperone (protein folding) system that mediates interaction with heat shock proteins, has moderate similarity to a region of C. elegans rme-8, which is required for some types of endocytosis
SW:MYSO_HUMAN P35580 homo sapiens (human). myosin heavy chain, nonmuscle type b (cellular myosin heavy chain, type b) (nmmhc-b). 12/1998 [MASS=228939]/Myosin heavy chain 10 (non-muscle), a putative ATP- and actin-binding motor protein; expression of an alternative splice form is coincident with neuronal cell differentiation
SW:HS9B_HUMAN P08238 homo sapiens (human). heat shock protein hsp 90-beta (hsp 84) (hsp 90). 5/2000 [MASS=83163]/Heat shock 90kD protein 1 beta, involved in regulation of both cytochrome c-dependent apoptosis and antiapoptosis via the Akt/PKB (AKT1) serine-threonine kinase, elevated expression is reported in patients with active systemic lupus erythematosus (SLE)
SW:BCR_HUMAN P11274 homo sapiens (human). breakpoint cluster region protein (ec 2.7.1.-). 7/1999 [MASS=142806]/Breakpoint cluster region, GTPase-activating protein for p21rac with serine/threonine kinase activity; translocation of the corresponding gene is associated with Philadelphia chromosome-positive chronic myeloid leukemia
SW:SODC_HUMAN P00441 homo sapiens (human). superoxide dismutase [cu-zn] (ec 1.15.1.1). 5/2000 [MASS=15805]/Copper zinc superoxide dismutase, an enzyme that catalyzes the dismutation of the superoxide radical to molecular oxygen and hydrogen peroxide; mutations are associated with some cases of familial amyotrophic lateral sclerosis
GP:D87116_1 Human mRNA for MAP kinase kinase 3b ,complete cds; MKK3b. [MASS=39318]/Mitogen activated protein kinase kinase 3, phosphorylates MAP kinase p38, involved in stress and inflammatory responses, senescence, and apoptosis, also has roles in ischemic kidney injury, and H. influenzae infection
SW:PPOL_HUMAN P09874 homo sapiens (human). poly [adp-ribose] polymerase (ec 2.4.2.30) (parp) (adprt) (nad(+) adp-ribosyltransferase) (poly[adp-ribose] synthetase). 11/1997 [MASS=112953]/ADP-ribosyltransferase, catalyzes formation of ADP ribose polymers attached to proteins using NAD(+) as substrate in response to DNA damage, modulates chromatin structure and plays a role in DNA repair and apoptosis
SW:AOPP_HUMAN P30044 homo sapiens (human). putative peroxisomal antioxidant enzyme (liver tissue 2d-page spot 71b). 12/1998 [MASS=16864]/Peroxiredoxin 5, catalyzes the reduction of hydrogen peroxide through Cys sulfhydryl group oxidation and reduction by thioredoxin, may be involved in oxidative stress and inflammatory responses, may contribute to tendon degeneration during aging
SW:GST1_HUMAN P10620 homo sapiens (human). microsomal glutathione s-transferase 1 (ec 2.5.1.18) (microsomal gst- 1). 5/2000 [MASS=17599]/Microsomal glutathione S-transferase 1, may play a role in protection against oxidative stress
SW:H105_HUMAN Q92598 homo sapiens (human). heat-shock protein 105 kda (heat shock 110 kda protein) (kiaa0201). 5/2000 [MASS=96865]/Heat shock protein (105 kDa), member of the high molecular weight family of heat shock proteins, expression is induced by heat shock and is increased in cancer cells
GP:AB032903_1 Homo sapiens GMPR2 mRNA for guanosine monophosphate reductase isolog, complete cds. [MASS=37874]/Guanosine monophosphate reductase, enzyme with a predicted role in purine interconversion
SW:TDXM_HUMAN P30048 homo sapiens (human). mitochondrial thioredoxin-dependent peroxide reductase precursor (antioxidant protein 1) (aop-1) (mer5 protein homolog) (hbc189). 5/2000 [MASS=27693]/Peroxiredoxin 3, a mitochondrial antioxidant protein involved in oxygen and radical metabolism, has an antiapoptotic function, and inactivated by the apoptosis-inducing lectin abrin A
SW:CATA_HUMAN P04040 homo sapiens (human). catalase (ec 1.11.1.6). 5/2000 [MASS=59756]/Catalase, a tetrameric hemoprotein that detoxifies H2O, part of the oxidative stress response, activity is altered in some forms of cancer and increased during septic shock; gene mutation causes acatalasemia

PIR2:I38346 elastic titin - human (fragment) [MASS=883024]/Titin, a large sarcomeric protein that extends from the I band to the Z disk of sarcomeres, maintains resting tension in muscle
SW:41_HUMAN P11171 homo sapiens (human). protein 4.1 (band 4.1) (p4.1). 5/2000 [MASS=93239]/Erythrocyte membrane protein band 4.1, maintains cell shape by linking glycophorin C (GYPC) and band 3 proteins with the spectrin (SPTA1)-based cytoskeletal network; mutations in the corresponding gene are associated with hereditary elliptocytosis
GP:U83668_1 Human beta-tubulin (TUB4q) gene, complete cds. [MASS=48377]/Protein of beta-tubulin subfamily, has similarity to beta2-tubulin (TUBB2), may have a role in the pathogenesis of facioscapulohumeral muscular dystrophy (FSHD1)
alpha-actinin 4 (non-muscle alpha-actinin 4) (f-actin cross linking protein)/Alpha-actinin, a non-muscle cell actin-binding protein that has a role in endocytosis; a tumor suppressor, prognostic marker for breast cancer and mutations in the gene cause familial focal segmental glomerulosclerosis
myosin I beta/Myosin IC, member of a family of ATPase motor proteins, predicted to participate in actin filament organization at the plasma membrane, may show ATP-independent actin filament binding, interacts with CBL
SW:VINC_HUMAN P18206 homo sapiens (human). vinculin. 12/1998 [MASS=116591]/Vinculin, a cytoskeletal protein that localizes to focal adhesions of cell-cell and cell-matrix junctions, also functions as a tumor suppressor; deficiency of alternate cardiac form, metavinculin, is associated with idiopathic dilated cardiomyopathy
GP:AK022489_1 Homo sapiens cDNA FLJ12427 fis, clone MAMMA1003127, highly similar to MYOSIN I ALPHA; unnamed protein product. [MASS=31145]/Myosin IB, a member of the unconventional myosin family of motor ATPases
SW:COF1_HUMAN P23528 homo sapiens (human). cofilin, non-muscle isoform. 11/1997 [MASS=18502]/Non-muscle cofilin, an actin-binding protein that assists translocation of actin from the cytoplasm to the nucleus; inactivation through phosphorylation by LIM-kinase leads to actin depolymerization
SW:DEST_HUMAN P18282 homo sapiens (human), and sus scrofa (pig). destrin (actin depolymerizing factor) (adf). 11/1997 [MASS=18506]/Actin depolymerizing factor, a member of the ADF/cofilin family that binds to actin and is predicted to depolymerize F-actin by altering filament tilt and twist; present in rod-like inclusions within neurons in the brains of Alzheimer's patients
SW:MYSA_HUMAN P13533 homo sapiens (human). myosin heavy chain, cardiac muscle alpha isoform. 7/1998 [MASS=223690]/Cardiac myosin heavy chain 6, a putative structural component of muscle, may be required for heart development and function; mutation of corresponding gene is associated with familial hypertrophic cardiomyopathy
SW:ARP3_HUMAN P32391 homo sapiens (human), and bos taurus (bovine). actin-like protein 3 (actin-2). 7/1999 [MASS=47371]/Actin-related protein 3 homolog, a component of the Arp2/3 protein complex, which is involved in actin cytoskeleton organization and biogenesis and may have a role in cell motility
PIR2:T13151 adapter protein CMS - human [MASS=71451]/CMS: an adapter molecule involved in cytoskeletal rearrangements/CD2-associated protein, an adaptor that may play a role in kidney function and mediate cytoskeletal rearrangement; mouse Cd2ap is associated with congenital nephrotic syndrome and possibly Nail-Patella syndrome nephropathy and polycystic kidney disease
PIR2:A53016 myosin heavy chain VA - human (fragment) [MASS=96052]/Class V myosin (Myoxin), a member of the myosin family of proteins, a motor protein that may be involved in vesicle transport and epidermal differentiation; mutation of the corresponding genge is associated with Griscelli syndrome
SW:MOES_HUMAN P26038 homo sapiens (human). moesin (membrane-organizing extension spike protein). 6/1994 [MASS=67689]/Moesin, putative receptor that may link the cytoskeleton and plasma membrane and play roles in microvillus assembly and cell morphogenesis, may be an autoantigen in rheumatoid arthritis and may play a role in impaired brain development in Down syndrome
SW:EGFR_HUMAN P00533 homo sapiens (human). epidermal growth factor receptor precursor (ec 2.7.1.112). 12/1998 [MASS=134277]/Epidermal growth factor receptor, a receptor protein tyrosine kinase that binds epidermal growth factor (EGF) and transforming growth factor alpha (TGFA), involved in cell proliferation and differentiation, implicated in tumor invasion and metastasis
SW:AR41_HUMAN O15143 homo sapiens (human). arp2/3 complex 41 kda subunit (p41-arc). 12/1998 [MASS=40950]/Actin related protein 2/3 complex 1A, component of the Arp2/3 complex, interacts directly with an ARPC4 and ARPC5 heterodimer, may have a role in Arp2/3 complex assembly or maintenance, may regulate complex activity or intracellular distribution
SW:DIA1_HUMAN O60610 homo sapiens (human). diaphanous protein homolog 1. 5/2000 [MASS=138979]/Diaphanous, contains profilin and rho binding domains and possibly regulates actin polymerization in inner ear hair cells; mutation of the gene is associated with nonsyndromal-postlingual deafness
SW:RHOB_HUMAN P01121 homo sapiens (human), mus musculus (mouse), and rattus norvegicus (rat). transforming protein rhob (h6). 12/1998 [MASS=22123]/Ras-related GTP binding protein of the rho subfamily, member B; may regulate assembly of actin stress fibers and focal adhesions; very strongly similar to murine Arhb
SW:CTN1_HUMAN P35221 homo sapiens (human). alpha-1 catenin (cadherin-associated protein) (alpha e-catenin). 11/1997 [MASS=100071]/Catenin alpha 1 (cadherin-associated protein); binds cadherins and links them with the actin cytoskeleton
SW:MYSN_HUMAN P35579 homo sapiens (human). myosin heavy chain, nonmuscle type a (cellular myosin heavy chain, type a) (nmmhc-a). 12/1998 [MASS=226532]/Non-muscle myosin heavy chain 9; motor protein that provides force for muscle contraction, cytokinesis and phagocytosis; contains an ATPase head domain and a rod-like tail domain
GP:AF177171_1 Homo sapiens tropomodulin 3 (TMOD3) mRNA, complete cds. [MASS=39581]/Tropomodulin 3, putative actin-capping protein for the slow-growing end of filamentous actin, expressed ubiquitously

SW:PLAK_HUMAN P14923 homo sapiens (human). junction plakoglobin (desmoplakin iii). 11/1997 [MASS=81498]/Junction plakoglobin (gamma catenin), links cell-cell adhesion molecules with the cytoskeleton, involved in desmosome organization, cell adhesion, cell prolifiration, apoptosis; loss of heterozygosity is associated with breast and ovarian tumors
SW:AR21_HUMAN O15145 homo sapiens (human). arp2/3 complex 21 kda subunit (p21-arc). 12/1998 [MASS=20547]/Actin related protein 2/3 complex subunit 3 (21 kDa), a component of the Arp2/3 complex, may participate in the regulation of actin polymerization, may have a role in the protrusion of lamellipodia, has an essential function in at least HeLa cells
GP:AB008515_1 Homo sapiens mRNA for RanBPM, complete cds. [MASS=55082]/Ran-binding protein 9, plays a role in microtubule nucleation, interacts specifically with RAN guanosine triphosphatase and mediates Ran-dependent centrosomal function
SW:CAPB_HUMAN P47756 homo sapiens (human). f-actin capping protein beta subunit (capz). 5/2000 [MASS=30629]/Capping protein Z-line beta 1, a subunit of an actin-binding protein that caps the barbed end of actin filaments and regulates actin polymerization dynamics, may have a role in cell motility
SWN:LAD1_HUMAN O00515 homo sapiens (human). ladinin 1 (lad-1) (120 kda linear iga bullous dermatosis antigen) (97 kda linear iga bullous dermatosis antigen) (linear iga disease antigen homolog) (lada). 8 [MASS=57157]/Ladinin 1, an anchoring filament protein that is a component of basement membranes, recognized by circulating IgA autoantibodies in linear IgA disease, which is a blistering skin disease, may maintain dermal epidermal cohesion
SW:MLEN_HUMAN P16475 homo sapiens (human), bos taurus (bovine), and sus scrofa (pig). myosin light chain alkali, non-muscle isoform (mlc3nm) (lc17a) (lc17-nm). 5/2000 [MASS=16799]/Myosin alkali light chain smooth muscle and non-muscle, a member of the family of alkali myosin light chains, which play a role in the interaction between myosin and actin, intracellular vesicle movement, cytokinesis and cell location
SW:DAG1_HUMAN Q14118 homo sapiens (human). dystroglycan precursor (dystrophin-associated glycoprotein 1) [contains: alpha-dystroglycan (alpha-dg); beta-dystroglycan (beta- dg)]. 5/2000 [MASS=97581]/Dystroglycan 1, component of a dystrophin-associated glycoprotein complex that binds laminin, may link the extracellular matrix and cytoskeleton, may play a role in synaptic function; deficiency is involved in the pathogenesis of muscular dystrophies
SW:IQGA_HUMAN P46940 homo sapiens (human). ras gtpase-activating-like protein iqgap1 (p195) (kiaa0051). 7/1999 [MASS=189252]/IQ motif-containing GTPase activating protein 1, an actin-associated calmodulin (CALM1)-regulated protein that serves as an effector for CDC42 and RAC1, modulates E-cadherin (CDH1)-mediation cellular adhesion, upregulated in colon carcinomas
GP:BC000441_1 Homo sapiens, junction plakoglobin, clone MGC:8404 IMAGE:2820715, mRNA, complete cds. [MASS=81727]/Junction plakoglobin (gamma catenin), links cell-cell adhesion molecules with the cytoskeleton, involved in desmosome organization, cell adhesion, cell prolifiration, apoptosis; loss of heterozygosity is associated with breast and ovarian tumors
SW:CTNB_HUMAN P35222 homo sapiens (human). beta-catenin. 2/1996 [MASS=85497]/Beta catenin, links cadherins to the cytoskeleton, may act as a component of the Wnt signal transduction pathway transmitting nuclear signals via a complex with LEF1 and TCF transcription factors; mutations in the gene are associated with various cancers
GP:AB008567_1 Homo sapiens mRNA for beta-spectrin III, complete cds. [MASS=271295]/Beta III spectrin, member of a family of actin-cross linking proteins of the membrane-associated cytoskeleton, associates with Golgi and cytoplasmic vesicles
SW:EZRI_HUMAN P15311 homo sapiens (human). ezrin (p81) (cytovillin) (villin-2). 12/1998 [MASS=69268]/Villin 2 (ezrin), a member of the band 4.1 superfamily, links the cytoskeleton to the plasma membrane and thereby regulates cell adhesion and cortical morphogenesis, may play a role in rheumatoid arthritis and retinal degeneration
SW:ABP2_HUMAN P21333 homo sapiens (human). endothelial actin-binding protein (abp-280) (nonmuscle filamin) (filamin 1). 11/1997 [MASS=280761]/Filamin A (alpha), an actin crosslinking phosphoprotein involved in actin cytoskeletal organization, signal transduction, and mechanical stimulus response, may contribute to cell adhesion; genetic mutations are associated with periventricular heterotopia
GP:AB002382_1 Human mRNA for KIAA0384 gene, complete cds. [MASS=104952]/Catenin delta 1, a member of the catenin family of cadherin-binding proteins that link cadherins to the cytoskeleton, acts in cell signaling, plays a role in cell migration, loss of expession is correlated with bladder, colorectal and other cancer
GP:AF128536_1 Homo sapiens cytoplasmic phosphoprotein PACSIN2 mRNA, complete cds; related to PACSIN1; contains CDC15 N-terminal domain, 3 EH domain-binding NPF motifs, and a C-terminal SH3 domain. [MASS=55905]/Protein kinase C and casein kinase substrate in neurons 2, member of the PACSIN family of cytoplasmic adapter proteins, may function to organize the actin cytoskeleton and regulate vesicular traffic
SW:TBB2_HUMAN P05217 homo sapiens (human). tubulin beta-2 chain. 7/1999 [MASS=49831]/Tubulin beta 2, a member of the tubulin family of structural proteins that polymerizes to form microtubules, soluble form binds nuclear envelope, may serve as a marker for prostate adenocarcinoma
GP:AF151793_1 Homo sapiens ALG-2 interacting protein 1 (AIP1) mRNA, complete cds. [MASS=96079]/Protein with very strong similarity to murine Mm.28049, which interacts with the activin type IIA receptor and signaling molecule Smad3, has very strong similarity to rat Rn.29998, which is a synaptic scaffolding protein, contains PDZ and WW domains

SW:UTRO_HUMAN P46939 homo sapiens (human). utrophin (dystrophin-related protein 1) (drp1) (drp). 7/1999 [MASS=394494]/Utrophin, a membrane-associated protein that interacts with cytoskeletal proteins, associated with muscle and neuromuscular junction development and cell adhesion, may partially compensate for dystrophin (DMD) deficiency in Duchenne's muscular dystrophy
SW:ACTB_HUMAN P02570 homo sapiens (human), mus musculus (mouse), rattus norvegicus (rat), bos taurus (bovine), ovis aries (sheep), equus caballus (horse), trichosurus vulpecula (brush-tailed possum), an [MASS=41737]/Beta actin, a non-muscle cell actin that is the site of action for cytochalasin B effects on cell motility and also inhibits phospholipase D activity; mutation of the gene is associated with neutrophil dysfunction and recurrent infections
SW:RHOA_HUMAN P06749 homo sapiens (human), and bos taurus (bovine). transforming protein rhoa (h12). 7/1998 [MASS=21768]/Ras homolog gene family member A, monomeric GTPase of the Rho family that mediates cell surface receptor and integrin signaling, induces actin stress fiber and focal adhesion formation, activity may contribute to cellular transformation and tumor invasion
PIR2:T46270 hypothetical protein DKFZp564N1563.1 - human (fragment) [MASS=77321]/Filamin B (beta, actin-binding protein-278), may be involved in actin cytoskeleton organization through interaction with the cytoplasmic domain of glycoprotein Ib alpha (GP1BA) and mediation of thyrotropin-induced actin microfilament disruption
SW:PRO1_HUMAN P07737 homo sapiens (human). profilin i. 12/1998 [MASS=14923]/Profilin I, a protein that regulates actin polymerization in response to extracellular signals and may suppress breast cancer cell tumorigenicity
SW:CAZ2_HUMAN P47755 homo sapiens (human). f-actin capping protein alpha-2 subunit (capz). 12/1998 [MASS=32949]/Capping protein Z-line (alpha 2), subunit of an actin-binding protein that may play a role in cell motility; corresponding gene is amplified in malignant gliomas and may be involved in tumorigenesis
SW:DREB_HUMAN Q16643 homo sapiens (human). drebrin e. 7/1998 [MASS=71425]/Drebrin 1, developmentally regulated actin-binding protein expressed in brain, levels are reduced in Altzheimer's patients
SW:ARP2_HUMAN O15142 homo sapiens (human). actin-like protein 2. 7/1999 [MASS=44761]/Actin-related protein 2 homolog, a component of the Arp2/3 protein complex, which is involved in actin filament nucleation and polymerization, may form the nucleation interface with the pointed end of the actin filament
SW:SPCN_HUMAN Q13813 homo sapiens (human). spectrin alpha chain, brain (spectrin, non-erythroid alpha chain) (fodrin alpha chain) (sptan1). 11/1997 [MASS=284282]/Non-erythroid alpha-spectrin 1 (alpha-fodrin), a member of a family of actin crosslinking proteins of the membrane-associated cytoskeleton, binds calcium, cleaved during apoptosis, acts as an autoantigen in the development of Sjogren syndrome
GP:AB002387_1 Human mRNA for KIAA0389 gene, complete cds. [MASS=148714]/Myosin VI, an unconventional myosin motor protein, may function in membrane trafficking in the secretory and endocytic pathways; mutations in the corresponding gene are associated with deafness
SW:ARF6_HUMAN P26438 homo sapiens (human), mus musculus (mouse), and rattus norvegicus (rat). adp-ribosylation factor 6. 12/1998 [MASS=19951]/ADP-ribosylation factor 6, GTP-binding protein that stimulates cholera toxin activity and is involved in endocytosis, exocytosis, membrane trafficking, and possibly regulation of glucose transport
SW:RAC1_HUMAN P15154 homo sapiens (human), mus musculus (mouse), and canis familiaris (dog). ras-related c3 botulinum toxin substrate 1 (p21-rac1) (ras-like protein tc25). 12/1998 [MASS=21450]/Ras-related C3 botulinum toxin substrate 1, a monomeric GTPase of the Rho family, involved in transducing signals that regulate proliferation, apoptosis, cytoskeletal organization, and response to oxidative stress, contributes to tumor cell invasiveness
SW:TBA1_HUMAN P04687 homo sapiens (human). tubulin alpha-1 chain, brain-specific. 7/1999 [MASS=50158]/Alpha-tubulin, a member of a family of structural proteins that polymerize to form microtubules
PIR2:G02520 plectin - human [MASS=518488]/Plectin 1, a member of the plakin family that crosslinks the cytoskeleton and the plasma membrane in hemidesmosomes and focal contacts; mutation of the corresponding gene causes muscular dystrophy with epidermolysis bullosa simplex (MDEBS)
SW:DESP_HUMAN P15924 homo sapiens (human). desmoplakin i and ii (dpi and dpii) (fragment). 5/2000 [MASS=201359]/Desmoplakin, a desmosomal plaque protein involved in cell adhesion and tumor migration, cleaved by caspases during desmosomal disruption associated with keratinocyte apoptosis; gene mutation is associated with hereditary palmoplantar keratoderma
SW:PEBP_HUMAN P30086 homo sapiens (human). phosphatidylethanolamine-binding protein (pebp) (neuropolypeptide h3). 7/1999 [MASS=20926]/Phosphatidylethanolamine-binding protein, binds GTP, may regulate cAMP accumulation, enhance acetylcholine synthesis, and play a role in organizing phospholipids in the myelin sheath
SW:RS29_HUMAN P30054 homo sapiens (human), mus musculus (mouse), rattus norvegicus (rat), and bos taurus (bovine). 40s ribosomal protein s29. 5/2000 [MASS=6546]Ribosomal protein S29, a component of the small 40S ribosomal subunit, contains a zinc finger-like motif, enhances activity of the tumor suppressor Krev-1 (RAP1A)
SW:DYL1_HUMAN Q15701 homo sapiens (human), mus musculus (mouse), rattus norvegicus (rat), and oryctolagus cuniculus (rabbit). dynein light chain 1, cytoplasmic (protein inhibitor of neuronal nitric oxid [MASS=10366]/Dynein cytoplasmic light polypeptide (protein inhibitor of nitric oxide synthase), a component of the cytoplasmic dynein motor complex, inhibits neuronal nitric oxide synthase (NOS1), regulates the proapoptotic activity of BCL2-interacting protein BCL2L11
GP:AF022728_1 Homo sapiens beta-dystrobrevin (BDTN) mRNA, complete cds; member of the dystrophin gene family. [MASS=71356]/Beta-dystrobrevin, a member of the dystrobrevin subfamily within the dystrophin family of proteins, part of the syntrophin-associated protein complex

SW:AR34_HUMAN O15144 homo sapiens (human). arp2/3 complex 34 kda subunit (p34-arc). 7/1998 [MASS=34333]/Actin related protein 2/3 complex subunit 2, component of the Arp2/3 complex, which is involved in assembly of the actin cytoskeleton, interacts directly with ARPC4, possibly as an early intermediate in Arp2/3 complex formation
GP:AJ001714_1 Homo sapiens mRNA for myosin-IXA. [MASS=90079]/Myosin IXA, a member of the unconventional myosin family that contains a GTPase activating protein (GAP) domain; the corresponding gene is a candidate for Bardet Biedl syndrome, characterized by mental retardation, obesity, and retinitis pigmentosa
GP:AB032179_1 Homo sapiens EHM2 mRNA, complete cds; similar to mouse Ehm2. [MASS=58628]/Protein containing two FERM (Band 4.1) family domains, which link cytoplasmic proteins to membranes, has low similarity to myosin regulatory light chain interacting protein (human MIR), which may be linked to mental retardation
SW:AAC1_HUMAN P12814 homo sapiens (human). alpha-actinin 1, cytoskeletal isoform (f-actin cross linking protein). 11/1997 [MASS=102974]/Alpha-actinin isoform 1, a non-muscle cell actin-binding protein that interacts with collagen (human COL17A1) and functions in actin filament stabilization, may play a role in cell shape control
SW:MAPB_HUMAN P46821 homo sapiens (human). microtubule-associated protein 1b [contains: map1 light chain lc1]. 7/1999 [MASS=270620]/MAP1B
SW:TPMN_HUMAN P12324 homo sapiens (human). tropomyosin, cytoskeletal type (tm30-nm). 7/1999 [MASS=29033]/Tropomyosin 4, a member of a family of actin filament binding proteins involved in a variety of cytoskeletal-related functions; fusion of the gene with ALK has been seen in inflammatory myofibroblastic tumors
SW:MAP4_HUMAN P27816 homo sapiens (human). microtubule-associated protein 4. 6/1994 [MASS=121180]/Microtubule-associated protein 4, a microtubule-associated protein that stabilizes microtubules and may regulate microtubule dynamics during mitosis; target of a Poliovirus protease
PIR2:A55575 ankyrin 3, long splice form - human [MASS=480403]/Ankyrin 3 (ankyrin G), may link integral membrane proteins to the cytoskeleton, may play a role in localizing sodium channels to the axonal initial segment and nodes of Ranvier, may play a role in vesicle transport
SW:ANK1_HUMAN P16157 homo sapiens (human). ankyrin 1 (erythrocyte ankyrin) (ankyrin r) (ankyrins 2.1 and 2.2). 5/2000 [MASS=206146]/Ankyrin 1, a cytoskeletal anchor protein that attaches cytoskeletal elements to the plasma membrane; alteration of the corresponding gene is associated with hereditary spherocytosis
GP:AB018266_1 Homo sapiens mRNA for KIAA0723 protein, complete cds. [MASS=94623]/Homo sapiens matrin 3 mRNA, complete cds/Matrin 3, an acidic protein that is a component of the nuclear matrix
SW:ADDA_HUMAN P35611 homo sapiens (human). erythrocyte adducin alpha subunit. 7/1998 [MASS=80971]/Adducin 1 alpha, a subunit of the membrane-skeletal adducin complex, may promote assembly of spectrin-actin complexes and regulate ion transport; mutations in the corresponding gene may be associated with hypertension
SW:PNL1_HUMAN Q99719 homo sapiens (human). peanut-like protein 1 (cell division control related protein 1) (cdcrel-1). 5/2000 [MASS=42777]/Peanut-like (CDCREL-1), member of the septin family of GTP-binding proteins, may be involved in vesicle targeting and fusion, may have a role in velo cardio facial or DiGeorge syndrome; PNUTL1 gene translocations are associated with acute myeloid leukemia
SW:LAMA_HUMAN P02545 homo sapiens (human). lamin a (70 kda lamin). 5/2000 [MASS=74139]/Lamin A, a structural protein of the nuclear lamina; mutations of the corresponding gene are associated with Emery-Dreifuss muscular dystrophy and partial lipodystrophies
SW:LAM1_HUMAN P20700 homo sapiens (human). lamin b1. 5/2000 [MASS=66277]/Lamin B1, present in the nuclear outer membrane, may be a structural member of the nuclear lamina, cleaved by proteases during apoptosis, targeted by autoantibodies in chronic fatigue syndrome
SW:NPL1_HUMAN P55209 homo sapiens (human). nucleosome assembly protein 1-like 1 (nap-1 related protein). 10/1996 [MASS=45374]/Nucleosome assembly protein 1-like 1, member of the NAP/SET protein family, binds histones H2A and H2B, a histone chaperone that mediates assembly of nucleosomes, complex with histone acetyltransferase coactivator p300 (EP300) may stimulate transcription
SW:RCC_HUMAN P18754 homo sapiens (human). regulator of chromosome condensation (cell cycle regulatory protein). 7/1999 [MASS=44969]/Regulator of chromosome condensation 1, a chromatin-binding protein that functions as a guanine nucleotide exchange factor for RAN, plays roles in nucleocytoplasmic transport, mitotic spindle formation, and nuclear envelope assembly
SW:HMG1_HUMAN P09429 homo sapiens (human). high mobility group protein hmg1 (hmg-1). 5/2000 [MASS=24763]/High-mobility group (nonhistone chromosomal) protein 1, induces DNA bending, binds damaged DNA, activates and represses transcription, involved in the DNA damage response and V(D)J recombination, may be a target for therapeutic intervention of sepsis
SW:PPOL_HUMAN P09874 homo sapiens (human). poly [adp-ribose] polymerase (ec 2.4.2.30) (parp) (adprt) (nad(+) adp-ribosyltransferase) (poly[adp-ribose] synthetase). 11/1997 [MASS=112953]/ADP-ribosyltransferase, catalyzes formation of ADP ribose polymers attached to proteins using NAD(+) as substrate in response to DNA damage, modulates chromatin structure and plays a role in DNA repair and apoptosis

SW:KU86_HUMAN P13010 h atp-dependent dna helicase ii, 80 kda subunit (lupus ku autoantigen protein p86) (ku86) (ku80) (86 kda subunit of ku antigen) (thyroid- lupus autoantigen) (tlaa) (ctc box binding [MASS=82573]/X-ray repair complementing defective repair in Chinese hamster cells 5, binds ds-DNA free ends, binds Ku70 (G22P1) to regulate DNA-PK, involved in DNA repair, V(D)J recombination, cell adhesion, and enzyme activation, may play a role in tumor progression
GP:AF041483_1 Homo sapiens histone macroH2A1.2 mRNA, complete cds. [MASS=39601]/H2A histone family member Y, a histone H2A subtype containing a unique non-histone domain, involved in compaction of DNA into nucleosomes and X chromosome inactivation
SW:RB48_HUMAN Q09028 homo sapiens (human). chromatin assembly factor 1 p48 subunit (caf-1 p48 subunit) (retinoblastoma binding protein p48) (retinoblastoma-binding protein 4) (msi1 protein homolog). 12/ [MASS=47656]/Retinoblastoma binding protein 4, a nuclear protein that forms complexes with a variety of proteins including RB1, HDAC1, BRCA1, E2F, which function in histone acetylation, regulation of cell proliferation, or transcriptional repression
SW:TOP1_HUMAN P11387 homo sapiens (human). dna topoisomerase i (ec 5.99.1.2). 12/1998 [MASS=90754]/DNA topoisomerase I, a monomeric enzyme that relaxes supercoiled DNA and is mutated in camptothecin (CPT)-resistant human leukemia cell lines, a major self-antigen found in patients with systemic sclerosis
SW:H33_HUMAN P06351 homo sapiens (human), mus musculus (mouse), rattus norvegicus (rat), oryctolagus cuniculus (rabbit), gallus gallus (chicken), spisula solidissima (atlantic surf-clam), drosophila mel [MASS=15197]/H3 histone family 3A, a member of the H3 histone family of proteins involved in compaction of DNA into nucleosomes, a replacement histone; expression does not depend on DNA replication
SW:PNL1_HUMAN Q99719 homo sapiens (human). peanut-like protein 1 (cell division control related protein 1) (cdcrel-1). 5/2000 [MASS=42777]/Peanut-like (CDCREL-1), member of the septin family of GTP-binding proteins, may be involved in vesicle targeting and fusion, may have a role in velo cardio facial or DiGeorge syndrome; PNUTL1 gene translocations are associated with acute myeloid leukemia
SW:G3P2_HUMAN P04406 homo sapiens (human). glyceraldehyde 3-phosphate dehydrogenase, liver (ec 1.2.1.12). 7/1999 [MASS=35922]/Glyceraldehyde-3-phosphate dehydrogenase, catalyzes reversible oxidation and phosphorylation of glyceraldehyde-3-phosphate to 1,3-diphosphoglycerate in glycolysis, involved in apoptosis, may play a role in neurodegeneration in diseases like Alzheimer's
SW:DDB1_HUMAN Q16531 h dna damage binding protein 1 (damage-specific dna binding protein 1) (ddb p127 subunit) (ddba) (uv-damaged dna-binding protein 1) (uv-ddb 1) (xeroderma pigmentosum group e complem [MASS=126968]/Damage-specific DNA-binding protein 1, larger subunit of a complex that recognizes and binds damaged DNA and stimulates repair, not essential for DNA repair; deficiencies are associated with xeroderma pigmentosum complementation group E
SW:FRAP_HUMAN P42345 homo sapiens (human). fkbp-rapamycin associated protein (frap) (rapamycin target protein). 7/1999 [MASS=288892]/FK506 binding protein 12-rapamycin associated protein 1, serine/threonine and 1-phosphatidylinositol 4-kinase, regulates translation, cell cycle and p53 (TP53) -dependent apoptosis; altered expression is associated with recurrent prostate tumors
SW:PPOL_HUMAN P09874 homo sapiens (human). poly [adp-ribose] polymerase (ec 2.4.2.30) (parp) (adprt) (nad(+) adp-ribosyltransferase) (poly[adp-ribose] synthetase). 11/1997 [MASS=112953]/ADP-ribosyltransferase, catalyzes formation of ADP ribose polymers attached to proteins using NAD(+) as substrate in response to DNA damage, modulates chromatin structure and plays a role in DNA repair and apoptosis
SW:KU86_HUMAN P13010 h atp-dependent dna helicase ii, 80 kda subunit (lupus ku autoantigen protein p86) (ku86) (ku80) (86 kda subunit of ku antigen) (thyroid- lupus autoantigen) (tlaa) (ctc box binding [MASS=82573]/X-ray repair complementing defective repair in Chinese hamster cells 5, binds ds-DNA free ends, binds Ku70 (G22P1) to regulate DNA-PK, involved in DNA repair, V(D)J recombination, cell adhesion, and enzyme activation, may play a role in tumor progression
SW:APE1_HUMAN P27695 homo sapiens (human). dna-(apurinic or apyrimidinic site) lyase (ec 4.2.99.18) (ap endonuclease 1) (apex nuclease) (apen) (ref-1 protein). 12/1998 [MASS=35423]/Apurinic/apyrimidinic endonuclease 1, multifunctional DNA repair enzyme that coordinates the repair of abasic sites and repair synthesis, acts as a transcription regulator; mutations may correlate with inclusion body myositis and colorectal tumorigenesis
SW:RFA3_HUMAN P35244 homo sapiens (human). replication protein a 14 kda subunit (rp-a) (rf-a) (replication factor-a protein 3). 11/1997 [MASS=13569]/Replication protein A 3, a subunit of replication protein A, which is a single-stranded DNA-binding protein complex with roles in DNA replication, repair, and recombination
PIR2:A57099 DNA-activated protein kinase, catalytic subunit - human [MASS=465428]/DNA-dependent protein kinase catalytic subunit, a DNA-binding protein kinase involved in DNA double-strand break repair and somatic recombination of antibody genes; absence of mouse Prkdc is associated with severe combined immunodeficiency
SW:MSH3_HUMAN P20585 homo sapien/Mismatch repair protein 3, dimerizes with MSH2 to form damaged-DNA recognition complex MutS beta, repairs short insertion-deletion loops (2-8 base pairs), may bind PCNA to effect repair, maintains stability of the genome and may suppress tumorss (human). dna mismatch repair protein msh3 (divergent upstream protein) (dup) (mismatch repair protein 1) (mrp1). 12/1998 [MASS=127384]

SW:RFA1_HUMAN P27694 homo sapiens (human). replication protein a 70 kda dna-binding subunit (rp-a) (rf-a) (replication factor-a protein 1) (single-stranded dna-binding protein). 11/1997 [MASS=68138]/Replication protein A1 (70 kDa), a DNA replication factor A subunit, has roles in DNA replication, recombination, repair, may contribute to latent virus reactivation, inactivated by anti-cancer drug adozelesin
SW:RAN_HUMAN P17080 homo sapiens (human). gtp-binding nuclear protein ran (tc4). 12/1998 [MASS=24354]/RAN, member of the ras family of GTP binding proteins, couples completion of DNA synthesis to mitosis and induces mitotic spindle formation, involved in nuclear transport of RNA and proteins, interacts with polyglutamate repeats of the androgen receptor
SW:MCM3_HUMAN P25205 homo sapiens (human). dna replication licensing factor mcm3 (dna polymerase alpha holoenzyme-associated protein p1) (rlf beta subunit) (p102 protein) (p1-mcm3). 5/2000 [MASS=90952]/Minichromosome maintenance deficient 3, associates with the DNA polymerase alpha-primase complex, involved in the initiation of DNA replication, selectively degraded during apoptosis
SW:NPL1_HUMAN P55209 homo sapiens (human). nucleosome assembly protein 1-like 1 (nap-1 related protein). 10/1996 [MASS=45374]/Nucleosome assembly protein 1-like 1, member of the NAP/SET protein family, binds histones H2A and H2B, a histone chaperone that mediates assembly of nucleosomes, complex with histone acetyltransferase coactivator p300 (EP300) may stimulate transcription
SW:RFA3_HUMAN P35244 homo sapiens (human). replication protein a 14 kda subunit (rp-a) (rf-a) (replication factor-a protein 3). 11/1997 [MASS=13569]/Replication protein A 3, a subunit of replication protein A, which is a single-stranded DNA-binding protein complex with roles in DNA replication, repair, and recombination
SW:MCM4_HUMAN P33991 homo sapiens (human). dna replication licensing factor mcm4 (cdc21 homolog) (p1-cdc21). 5/2000 [MASS=96611]/Minichromosome maintenance deficient 4, forms a single stranded ATP-dependent DNA helicase with MCM6 and MCM7, may monitor sites of unreplicated DNA, displacement from replicated chromatin may ensure that DNA is only replicated once per cell cycle
SW:RFA1_HUMAN P27694 homo sapiens (human). replication protein a 70 kda dna-binding subunit (rp-a) (rf-a) (replication factor-a protein 1) (single-stranded dna-binding protein). 11/1997 [MASS=68138]/Replication protein A1 (70 kDa), a DNA replication factor A subunit, has roles in DNA replication, recombination, repair, may contribute to latent virus reactivation, inactivated by anti-cancer drug adozelesin
SW:PUR_HUMAN Q00577 homo sapiens (human). transcriptional activator protein pur-alpha (purine-rich single- stranded dna-binding protein alpha). 7/1998 [MASS=34911]/Purine rich element binding protein A, a single-stranded DNA-RNA binding protein implicated in the control of transcription and DNA replication; interacts with HIV Tat protein and JC virus T antigen to modulate host and viral gene expression
GP:U35146_1 Human p56 protein kinase (KKIAMRE), complete cds; similar to human p42 KKIALRE gene, GenBank Accession Number X66358; these protein kinases have mutually exclusive expression in testis (p56 KKIAMRE) and ovary (p42 KKIALRE). [MASS=56019]/Cyclin-dependent kinase-like 2, putative protein kinase whose activity is stimulated by epidermal growth factor (EGF), may play a role in sex differentiation
type-2 phosphatidic acid phosphatase alpha-1 /Phosphatidic acid phosphatase type 2a, catalyzes the dephosphorylation of various lipid phosphates, regulates the level of lipid phosphates which are involved in signal transduction
SW:HPS1_HUMAN P08910 homo sapiens (human). protein phps1-2. 11/1997 [MASS=48315]/Member of the alpha/beta hydrolase fold family, has a region with weak similarity to a region of S. cerevisiae Eht1p (alcohol acyl transferase)
GP:AB015019_1 Homo sapiens mRNA for BAP2-alpha protein, complete cds; BAI-associated protein 2(BAP2) -alpha; alternative splicing: see also AB015020. [MASS=57359]/Brain-specific angiogenesis inhibitor 1-associated protein 2, interacts with cytoplasmic portion of BAI1, may be a substrate for INSR, involved in cytoskeletal organization and lamellipodia and filopodia formation
PIR2:A53016 myosin heavy chain VA - human (fragment) [MASS=96052]/Class V myosin (Myoxin), a member of the myosin family of proteins, a motor protein that may be involved in vesicle transport and epidermal differentiation; mutation of the corresponding genge is associated with Griscelli syndrome
GP:AF003521_1 Homo sapiens Jagged 2 mRNA, complete cds; ligand for Notch receptor; Contains EGF repeats and DSL domain. [MASS=133394]/Jagged 2, a Notch receptor ligand that may coordinate differentiation among progenitors adopting identical cell fates, plays a role in hair cell development in the cochlea
SW:CLH2_HUMAN P53675 homo sapiens (human). clathrin heavy chain 2 (clh-22). 5/2000 [MASS=187030]/Clathrin heavy polypeptide-like 1, may play roles in vesicle budding and in cytoskeleton-dependent trans-Golgi network membrane sorting; gene is among those deleted in velocardiofacial and DiGeorge syndromes, and is a fusion partner with ALK in lymphoma
SW:HD_HUMAN P42858 homo sapiens (human). huntingtin (huntington's disease protein) (hd protein). 12/1998 [MASS=347860]/Huntingtin, antiapoptotic protein, may be involved in intracellular transport; mutations in the gene cause Huntingtin disease and result in the production of a protein that interferes with transcription and proteasome-mediated protein degradation
GP:AB012191_1 Homo sapiens mRNA for Nedd8-conjugating enzyme hUbc12, complete cds. [MASS=20900]/Neurally expressed developmentally down-regulated 8, an ubiquitin-like protein that conjugates to CUL proteins to activate ubiquitin ligase complex dependent ubiquitination, possibly involved in cell cycle regulation

SW:RB3D_HUMAN O95716 homo sapiens (human). ras-related protein rab-3d. 5/2000 [MASS=24267]/Ras-related GTP-binding protein 3d, putative small monomeric GTP-binding protein and GTPase that plays a role in regulated secretion
SW:ITAV_HUMAN P06756 homo sapiens (human). vitronectin receptor alpha subunit precursor (integrin alpha-v) (cd51). 12/1998 [MASS=116052]/Alpha V subunit integrin, a subunit of the vitronectin receptor that is involved in cell-matrix interactions, chemotaxis, phagocytosis and angiogenesis, may contribute to the tumorigenicity of cutaneous malignant melanoma and invasive breast cancer
SW:DAG1_HUMAN Q14118 homo sapiens (human). dystroglycan precursor (dystrophin-associated glycoprotein 1) [contains: alpha-dystroglycan (alpha-dg); beta-dystroglycan (beta- dg)]. 5/2000 [MASS=97581]/Dystroglycan 1, component of a dystrophin-associated glycoprotein complex that binds laminin, may link the extracellular matrix and cytoskeleton, may play a role in synaptic function; deficiency is involved in the pathogenesis of muscular dystrophies
GP:AB011159_1 Homo sapiens mRNA for KIAA0587 protein, complete cds. [MASS=129517]/NCK-associated protein 1, may play a role in regulating beta secretase activity in processing of beta APP, and may play a role in suppressing apoptosis; downregulated in patients with sporadic Alzheimer disease
SW:ITMA_HUMAN O43736 homo sapiens (human). integral membrane protein 2a (e25 protein). 5/2000 [MASS=29741]/Integral membrane protein 2, a putative type II integral membrane protein with a leucine zipper motif
SW:UTRO_HUMAN P46939 homo sapiens (human). utrophin (dystrophin-related protein 1) (drp1) (drp). 7/1999 [MASS=394494]/Utrophin, a membrane-associated protein that interacts with cytoskeletal proteins, associated with muscle and neuromuscular junction development and cell adhesion, may partially compensate for dystrophin (DMD) deficiency in Duchenne's muscular dystrophy
SW:APP2_HUMAN Q06481 homo sapiens (human). amyloid-like protein 2 precursor (amyloid protein homolog) (apph) (cdei-box binding protein) (cdebp). 5/2000 [MASS=86956]/Amyloid precursor-like protein 2, a nuclear protein whcih may contribute to neurogenesis and cell cycle control
SW:ASAH_HUMAN Q13510 homo sapiens (human). acid ceramidase precursor (ec 3.5.1.23) (acylsphingosine deacylase) (n-acylsphingosine amidohydrolase) (ac) (putative 32 kda heart protein) (php32). 5/2000 [MASS=44650]/N-acylsphingosine amidohydrolase (acid ceramidase), catalyzes hydrolysis of ceramide to sphingosine and free fatty acid, inhibits apoptosis, upregulated in prostate cancer, deficiency is associated with Farber disease
SW:TPIS_HUMAN P00938 homo sapiens (human), and pan troglodytes (chimpanzee). triosephosphate isomerase (ec 5.3.1.1) (tim). 7/1998 [MASS=26538]/Triosephosphate isomerase 1, catalyzes the reversible interconversion of glyceraldehyde 3-phosphate and dihydroxyacetone phosphate in glycolysis; variant forms cause hemolytic anemia and neurodegeneration; variant form is an antigen on melanoma cells
SW:TDX1_HUMAN P32119 homo sapiens (human). thioredoxin peroxidase 1 (thioredoxin-dependent peroxide reductase 1) (thiol-specific antioxidant protein) (tsa) (prp) (natural killer cell enhancing factor b) [MASS=21892]/Peroxiredoxin 1, oxidative stress-inducible antioxidant protein with peroxidase activity, may have anticytotoxic and antiapoptotic activity and may have a role in cell proliferation
GP:AB037819_1 Homo sapiens mRNA for KIAA1398 protein, partial cds; Start codon is not identified.. [MASS=170212]/Ribosome binding protein 1, a putative ribosome receptor, may play a role in protein biosynthesis, appears to be involved in cardiac development, may play a role in cardiac remodeling in heart failure
SW:KAP2_HUMAN P13861 homo sapiens (human). camp-dependent protein kinase type ii-alpha regulatory chain. 5/2000 [MASS=45387]/cAMP-dependent Protein kinase A regulatory subunit alpha (type II), binds A-kinase anchoring proteins to mediate holoenzyme localization and plays important roles in sperm motility and in trophoblast cell differentiation
SW:ERB2_HUMAN P04626 homo sapiens (human). receptor protein-tyrosine kinase erbb-2 precursor (ec 2.7.1.112) (p185erbb2) (neu proto-oncogene) (c-erbb-2) (tyrosine kinase-type cell surface receptor her2) [MASS=137910]/Avian erythroblastosis oncogene B 2, a receptor tyrosine kinase and most oncopotent member of the EGF receptor family, heterodimerizes with other EGFRs; overexpression contributes to growth, metastasis and chemoresistance of epithelial-derived tumors
SW:RAC1_HUMAN P15154 homo sapiens (human), mus musculus (mouse), and canis familiaris (dog). ras-related c3 botulinum toxin substrate 1 (p21-rac1) (ras-like protein tc25). 12/1998 [MASS=21450]/Ras-related C3 botulinum toxin substrate 1, a monomeric GTPase of the Rho family, involved in transducing signals that regulate proliferation, apoptosis, cytoskeletal organization, and response to oxidative stress, contributes to tumor cell invasiveness
SW:DESP_HUMAN P15924 homo sapiens (human). desmoplakin i and ii (dpi and dpii) (fragment). 5/2000 [MASS=201359]/Desmoplakin, a desmosomal plaque protein involved in cell adhesion and tumor migration, cleaved by caspases during desmosomal disruption associated with keratinocyte apoptosis; gene mutation is associated with hereditary palmoplantar keratoderma
GP:AF308601_1 Homo sapiens NOTCH 2 (N2) mRNA, complete cds. [MASS=265404]/Notch (Drosophila) homolog 2, a transcriptional co-activator of the Notch family of receptors, interacts with MAML1, functions in apoptosis induction and possibly in skeletal development, constitutive activation may contribute to neoplastic transformation
PIR2:JE0334 nuclear matrix protein NMP 238 - human [MASS=50228]/RuvB like 1, a member of the TIP49 family of proteins, a nuclear protein which contains ATPase-helicase motifs, may interact with the transactivation domain of c-myc (MYC)
SW:PEBP_HUMAN P30086 homo sapiens (human). phosphatidylethanolamine-binding protein (pebp) (neuropolypeptide h3). 7/1999 [MASS=20926]/Phosphatidylethanolamine-binding protein, binds GTP, may regulate cAMP accumulation, enhance acetylcholine synthesis, and play a role in organizing phospholipids in the myelin sheath

SW:GBI2_HUMAN P04899 homo sapiens (human). guanine nucleotide-binding protein g(i), alpha-2 subunit (adenylate cyclase-inhibiting g alpha protein). 12/1998 [MASS=40320]/G protein alpha subunit i2, a component of pertussis toxin sensitive heterotrimeric G protein complexes that transduces signals to effectors and inhibits adenylyl cyclase; mutations in the gene are associated with tachycardia and endocrine tumors
SW:A2HS_HUMAN P02765 homo sapiens (human). alpha-2-hs-glycoprotein precursor (fetuin) (alpha-2-z-globulin). 5/2000 [MASS=39325]/Alpha 2-HS-glycoprotein, inhibits insulin receptor (INSR) tyrosine kinase activity and may play roles in bone metabolism, monocyte recruitment, cell death, cell adhesion, and the immune response; genotype may be associated with osteoporosis and stature
GP:AF084523_1 Homo sapiens cellular repressor of E1A-stimulated genes CREG mRNA, complete cds. [MASS=24075]/Repressor of transcriptional activation and transformation by the adenovirus E1A protein, binds the general transcription factor TBP and the tumor suppressor pRb (RB1), involved in transcriptional control of cell growth and differentiation
SW:DYL1_HUMAN Q15701 homo sapiens (human), mus musculus (mouse), rattus norvegicus (rat), and oryctolagus cuniculus (rabbit). dynein light chain 1, cytoplasmic (protein inhibitor of neuronal nitric oxid [MASS=10366]/Dynein cytoplasmic light polypeptide (protein inhibitor of nitric oxide synthase), a component of the cytoplasmic dynein motor complex, inhibits neuronal nitric oxide synthase (NOS1), regulates the proapoptotic activity of BCL2-interacting protein BCL2L11
SW:KAPA_HUMAN P17612 homo sapiens (human). camp-dependent protein kinase, alpha-catalytic subunit (ec 2.7.1.37) (pka c-alpha). 5/2000 [MASS=40458]/Catalytic subunit C alpha of cAMP-dependent protein kinase, plays a role in transcriptional regulation and may mediate suppression of apoptosis, may also serve as a tumor biomarker; alternative form C alpha 2 may play a role in sperm development
SW:ATC2_HUMAN P16615 h sarcoplasmic/endoplasmic reticulum calcium atpase isoform 2 (ec 3.6.1.38) (calcium pump 2) (serca2) (sr ca(2+)-atpase 2) (calcium- transporting atpase sarcoplasmic reticulum type, [MASS=114757]/Sarcoplasmic reticulum Ca2+-ATPase 2 (slow twitch muscle, cardiac, and nonmuscle form), pumps calcium from the cytoplasm to the ER; reduced activity in the heart is implicated in dilated cardiomyopathy and gene mutations are associated with Darier disease
SW:DDXY_HUMAN O15523 homo sapiens (human). dead box protein 3, y-chromosomal. 7/1999 [MASS=73095]/DEAD/H box polypeptide Y chromosome, a putative ATP-dependent RNA helicase, plays a role in spermatogenesis; deletion of the corresponding gene is associated with male infertility
SW:SERA_HUMAN O43175 homo sapiens (human). d-3-phosphoglycerate dehydrogenase (ec 1.1.1.95) (pgdh). 7/1999 [MASS=56665]/3-phosphoglycerate dehydrogenase, enzyme that catalyzes the first step of serine biosynthesis which is the oxidation of 3-phosphoglycerate to 3-phosphohydroxypyruvate; mutation of the corresponding gene causes microcephaly, retardation, and seizures
SW:R10A_HUMAN P53025 homo sapiens (human). 60s ribosomal protein l10a (csa-19). 10/1996 [MASS=24859]/Ribosomal protein L10a, a component of the large 60S ribosomal subunit; expression in the thymus is downregulated by cyclosporin-A
SW:OCRL_HUMAN Q01968 homo sapiens (human). lowe's oculocerebrorenal syndrome protein. 7/1998 [MASS=111485]/Oculocerebrorenal syndrome of Lowe, phosphatidylinositol-4,5-bisphosphate 5-phosphatase, may play a role in intracellular protein trafficking; mutation of the corresponding gene causes Lowe oculocerebrorenal syndrome
SW:VAB2_HUMAN P21281 homo sapiens (human). vacuolar atp synthase subunit b, brain isoform (ec 3.6.1.34) (endomembrane proton pump 58 kda subunit) (v-atpase b subunit) (ho57). 7/1999 [MASS=56517]/Vacuolar-type H(+)-ATPase (beta isoform 2), 56 kDa subunit of the ATPase catalytic domain which may assist in transepithelial H+ transport in the kidney, may effect vacuolar acidification, and may play a role in the polarization of osteoclasts
SW:DHA4_HUMAN P51648 homo sapiens (human). fatty aldehyde dehydrogenase (ec 1.2.1.3) (aldehyde dehydrogenase, microsomal) (aldh class 3). 7/1999 [MASS=54848]/Aldehyde dehyrogenase 3 family member A2, catalyzes the oxidation of long chain fatty aldehydes and leukotrienes; mutation of the corresponding gene causes Sjogren Larsson syndrome, a disorder marked by mental retardation, spasticity, and ichthyosis
SW:DDX1_HUMAN Q92499 homo sapiens (human). dead box protein 1 (dead box protein-retinoblastoma) (dbp-rb). 5/2000 [MASS=82432]/DEAD box protein 1, a member of the DEAD-H box ATP-dependent RNA helicase protein family, plays a role in the processing of pre-mRNAs, may interact with CSTF2; corresponding gene is coamplified with MYC in some neuroblastoma and retinoblastoma cell lines
PIR2:T09073 splicing factor Sip1 - human [MASS=128875]/Splicing factor arginine serine rich 2 interacting protein, a SR domain family protein that interacts with the RNA polymerase II C-terminal domain and several splicing factors, is essential in mRNA splicing and possibly spliceosome A-complex formation
SW:MRP_HUMAN P49006 homo sapiens (human). marcks-related protein (mac-marcks). 12/1998 [MASS=19398]/Cysteine-and glycine-rich protein 3, a zinc-finger LIM domain protein that is an essential regulator of cardiac muscle development, expression is decreased in chronic heart failure
SW:NRP_HUMAN O14786 homo sapiens (human). neuropilin precursor (vascular endothelial cell growth factor 165 receptor). 5/2000 [MASS=103121]/Neuropilin 1, a receptor for VEGF (165) and the axonal chemorepellent Semaphorin III, involved in organogenesis, axon guidance and angiogenesis, may regulate cell proliferation and response to wounding, upregulated in neuroblastoma vascular endothelium

SW:DDX5_HUMAN P17844 homo sapiens (human). probable rna-dependent helicase p68 (dead-box protein p68) (dead box protein 5). 7/1998 [MASS=69148]/DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 5 (RNA helicase 68kD), a ATP-dependent RNA helicase that has ATP-independent RNA renaturation activity and catalyses branch migration, binds estrogen receptor alpha and function as a transcriptional coactivator
SW:GRBA_HUMAN Q13322 homo sapiens (human). growth factor receptor-bound protein 10 (grb10 adaptor protein) (insulin receptor binding protein grb-ir) (kiaa0207). 5/2000 [MASS=67231]/Growth factor receptor bound protein 10, an adaptor protein with PH and SH2 domains that binds to various receptor and cytosolic kinases and may mediate growth factor and Src family kinase signaling; variants may be associated with Russell-Silver Syndrome
SW:ATCK_HUMAN P98194 homo sapiens (human). calcium-transporting atpase 2c1 (ec 3.6.1.38) (atp-dependent ca2+ pump pmr1). 5/2000 [MASS=100606]/ATPase (Ca2+ transporting) type 2c member I, a a Ca2+-transporting P-type ATPase involved in Ca2+ homeostasis that may also may play a role in epidermal differentiation; mutations in the gene cause Hailey-Hailey disease, a blistering skin disease
SW:FXR1_HUMAN P51114 homo sapiens (human). fragile x mental retardation syndrome related protein 1. 10/1996 [MASS=69692]/Fragile X mental retardation autosomal homolog 1, binds FMR1, associates with mRNPs and with 60S ribosomal subunits, may have a role in the ribosomal and RNA metabolism of neurons; identified as a scleroderma autoantigen processed during apoptosis
SW:SORC_HUMAN P30626 homo sapiens (human). sorcin (22 kda protein) (cp-22) (v19). 11/1997 [MASS=21676]/Sorcin, an EF-hand calcium-binding protein, may be involved in multidrug resistance, a potential modulator of intracellular calcium levels through interaction with the ryanodine receptor
SW:LAMA_HUMAN P02545 homo sapiens (human). lamin a (70 kda lamin). 5/2000 [MASS=74139]/Lamin A, a structural protein of the nuclear lamina; mutations of the corresponding gene are associated with Emery-Dreifuss muscular dystrophy and partial lipodystrophies
GP:AF002668_1 Homo sapiens putative fatty acid desaturase MLD mRNA, complete cds; putative fatty acid desaturase. [MASS=37866]/Degenerative spermatocyte homolog (Drosophila), member of the membrane fatty acid desaturase family, regulates the biosynthesis of the epidermal growth factor receptor (EGFR)
SW:LMG1_HUMAN P11047 homo sapiens (human). laminin gamma-1 chain precursor (laminin b2 chain). 7/1998 [MASS=177607]/Laminin C1, an extracellular matrix glycoprotein that may be involved in cell-matrix adhesion and the regulation of cell shape
SW:UTX_HUMAN O15550 homo sapiens (human). ubiquitously transcribed x chromosome tetratricopeptide repeat protein (ubiquitously transcribed tpr protein on the x chromosome). 7/1999 [MASS=154232]/Protein that has very strong similarity to murine Utx, which contains tetratricopeptide repeats and is widely transcribed; corresponding gene is found on X chromosomes and escapes X-inactivation
SW:ACDV_HUMAN P49748 homo sapiens (human). acyl-coa dehydrogenase, very-long-chain specific, mitochondrial precursor (ec 1.3.99.-) (vlcad). 5/2000 [MASS=70390]/Very long chain acyl-coenzyme A dehydrogenase, oxidizes straight chain acyl-CoAs in the initial step of fatty acid beta-oxidation, severe deficiency results in infant cardiomyopathy with high mortality, mild deficiency results in hypoketotic hypoglycemia
SW:PHS2_HUMAN P11217 homo sapiens (human). glycogen phosphorylase, muscle form (ec 2.4.1.1) (myophosphorylase). 5/2000 [MASS=97092]/Muscle glycogen phosphorylase, participates in glycogen catabolism; mutation of corresponding gene is associated with McArdle disease
SW:PHS3_HUMAN P11216 homo sapiens (human). glycogen phosphorylase, brain form (ec 2.4.1.1). 10/1996 [MASS=96683]/Brain glycogen phosphorylase, catalyzes the rate-limiting step in glycogen catabolism, activated by AMP and phosphorylation, may play a role in intestinal development; associated with gastric carcinomas displaying a differentiated intestinal phenotype
SW:GLYG_HUMAN P46976 homo sapiens (human). glycogenin-1 (ec 2.4.1.186). 7/1999 [MASS=37347]Glycogenin (glycogenin glucosyltransferase), autocatalytic and self-glucosylating enzyme that primes de novo glycogen synthesis
SW:NC5R_HUMAN P00387 homo sapiens (human). nadh-cytochrome b5 reductase (ec 1.6.2.2) (b5r). 11/1997 [MASS=34104]/NADH-dependent cytochrome b5 reductase (diaphorase), soluble erythrocyte-specific form functions in methemoglobin reduction, ubiquitous membrane-bound form functions in lipid metabolism; mutations in the gene cause methemoglobinemia types I and II
SW:GFA1_HUMAN Q06210 homo sapiens (human). glucosamine--fructose-6-phosphate aminotransferase [isomerizing] 1 (ec 2.6.1.16) (hexosephosphate aminotransferase 1) (d-fructose-6- phosphate amidotransferase [MASS=76616]/Glutamine-fructose-6-phosphate transaminase 1, catalyzes the first step in glucosamine formation, modulates glucose flux and functions in development of insulin resistance, upregulation in kidney associated with diabetic nephropathy
SW:UGS1_HUMAN P13807 homo sapiens (human). glycogen [starch] synthase, muscle (ec 2.4.1.11). 5/2000 [MASS=83786]/Glycogen synthase 1 (muscle), catalyzes transfer of a glucosyl residue from UDP-glucose to glycogen, stimulated by insulin, Acipimox and Flouxetine; mutations in the corresponding gene may be associated with non-insulin-dependent diabetes mellitus

SW:WFS1_HUMAN O76024 homo sapiens (human). wolframin. 5/2000 [MASS=100306]/Wolfram syndrome 1 (wolframin), may play a role in islet beta cell and neuron survival, may influence normal hearing and vision; gene mutation is detected in Wolfram syndrome and some types of hearing loss and may influence type 2 diabetes susceptibility
SW:G3P2_HUMAN P04406 homo sapiens (human). glyceraldehyde 3-phosphate dehydrogenase, liver (ec 1.2.1.12). 7/1999 [MASS=35922]/Glyceraldehyde-3-phosphate dehydrogenase, catalyzes reversible oxidation and phosphorylation of glyceraldehyde-3-phosphate to 1,3-diphosphoglycerate in glycolysis, involved in apoptosis, may play a role in neurodegeneration in diseases like Alzheimer's
SW:ENOB_HUMAN P13929 homo sapiens (human). beta enolase (ec 4.2.1.11) (2-phospho-d-glycerate hydro-lyase) (skeletal muscle enolase) (mse). 7/1998 [MASS=46856]/Enolase 3 (muscle-specific enolase, beta enolase), a putative enolase which catalyzes the conversion of 2-phospho-D-glycerate to phosphoenolpyruvate in muscle glycolysis, deficiency is associated with exercise intolerance and myalgias
SW:KCRB_HUMAN P12277 homo sapiens (human). creatine kinase, b chain (ec 2.7.3.2) (b-ck). 7/1999 [MASS=42644]/Brain creatine kinase, involved in energy homeostasis, expression is elevated in some forms of cancer; CK-MB is a dimer of subunits CKM and CKB, and is an important serum marker for acute myocardial infarction
SW:GDE_HUMAN P35573 homo sapiens (human). glycogen debranching enzyme (glycogen debrancher) [includes: 4-alpha-glucanotransferase (ec 2.4.1.25) (oligo-1,4-1,4-glucantransferase); amylo-1,6-glucosidase [MASS=172497]/Glycogen debranching enzyme, (amylo-1,6-glucosidase 4-alpha-glucanotransferase), catalyzes glycantransferase and glucosidase activities required for glycogen degradation; mutations and dysregulation are associated with type III glycogen storage diseases
SW:PGK1_HUMAN P00558 homo sapiens (human). phosphoglycerate kinase 1 (ec 2.7.2.3) (primer recognition protein 2) (prp 2). 7/1999 [MASS=44597]/Phosphoglycerate kinase 1, catalyzes conversion of 1,3-diphosphoglycerate to 3-phosphoglycerate in glycolysis, forming one molecule of ATP; PGK1 gene transcription is induced by hypoxia and mutation is associated with non-spherocytic hemolytic anemia
SW:ODO1_HUMAN Q02218 homo sapiens (human). 2-oxoglutarate dehydrogenase e1 component, mitochondrial precursor (ec 1.2.4.2) (alpha-ketoglutarate dehydrogenase). 7/1999 [MASS=113475]/2-Oxoglutarate dehydrogenase (alpha-ketoglutarate dehydrogenase), E1 component of the complex that converts alpha-ketoglutarate to succinyl coenzyme A in the Krebs cycle; deficiency has been observed in Alzheimer and Parkinson disease
SW:K6PL_HUMAN P17858 homo sapiens (human). 6-phosphofructokinase, liver type (ec 2.7.1.11) (phosphofructokinase 1) (phosphohexokinase) (phosphofructo-1-kinase isozyme b). 10/1996 [MASS=85148]/Liver phosphofructokinase, catalyses the phosphorylation of fructose-6-phosphate to fructose-1,6-bisphosphate in glycolysis, deficiency is linked to glycogenosis type VII while overexpression may lead to the cognitive diabilites of Down's syndrome
SW:KPB1_HUMAN P46020 homo sapiens (human). phosphorylase b kinase alpha regulatory chain, skeletal muscle isoform (phosphorylase kinase alpha m subunit). 2/1996 [MASS=137338]/Phosphorylase kinase regulatory subunit alpha-1 (muscle), which phosphorylates and thereby activates muscle-specific glycogen phosphorylase (PYGM); mutations in the corresponding gene are associated with muscle glycogenosis, a glycogen storage disease
SW:TPIS_HUMAN P00938 homo sapiens (human), and pan troglodytes (chimpanzee). triosephosphate isomerase (ec 5.3.1.1) (tim). 7/1998 [MASS=26538]/Triosephosphate isomerase 1, catalyzes the reversible interconversion of glyceraldehyde 3-phosphate and dihydroxyacetone phosphate in glycolysis; variant forms cause hemolytic anemia and neurodegeneration; variant form is an antigen on melanoma cells
SW:ENOA_HUMAN P06733 homo sapiens (human). alpha enolase (ec 4.2.1.11) (2-phospho-d-glycerate hydro-lyase) (non-neural enolase) (nne) (phosphopyruvate hydratase). 7/1998 [MASS=47038]/Enolase 1 (alpha enolase), converts 2-phospho-D-glycerate to phosphoenolpyruvate in glycolysis, an autoantigen in multiple autoimmune diseases, shorter alternative form c-myc promoter binding protein (MPB1) is a transcriptional repressor
GP:AJ131612_1 Homo sapiens dic gene, exons 1-11. [MASS=31325]/Solute carrier family 25 member 10 (dicarboxylate carrier), a putative dicarboxylic acid transporter predicted to reside in the inner mitochondrial membrane, may be involved in gluconeogenesis
SW:ODPB_HUMAN P11177 homo sapiens (human). pyruvate dehydrogenase e1 component beta subunit, mitochondrial precursor (ec 1.2.4.1) (pdhe1-b). 7/1999 [MASS=39219]/E1 beta subunit of pyruvate dehydrogenase complex, oxidatively decarboxylates pyruvate to acetyl-CoA
SW:HEMZ_HUMAN P22830 homo sapiens (human). ferrochelatase precursor (ec 4.99.1.1) (protoheme ferro-lyase) (heme synthetase). 12/1998 [MASS=47834]/Ferrochelatase (protoheme ferrochelatase), catalyzes the final step in the heme biosynthetic pathway by inserting ferrous iron into protoporphyrin IX to form heme; reduced activity and mutations in the corresponding gene are associated with protoporphyria
SW:HXK1_HUMAN P19367 homo sapiens (human). hexokinase, type i (ec 2.7.1.1) (hk i) (brain form hexokinase). 12/1998 [MASS=102503]/Hexokinase Type I (ATP:D-hexose 6-phosphotransferase), catalyzes ATP-dependent conversion of glucose to glucose 6 phosphate in glycolysis, deficiency may lead to non-spherocytic hemolytic anemia
SW:CPT2_HUMAN P23786 homo sapiens (human). carnitine o-palmitoyltransferase ii, mitochondrial precursor (ec 2.3.1.21) (cpt ii). 5/2000 [MASS=73777]/Carnitine palmitoyltransferase II, a mitochondrial long-chain fatty acid oxidation enzyme; mutations are associated with a lipid metabolism disorder that includes recurrent myopathy with progressive rhabdomyolysis, muscle weakness and myoglobinuria

SW:KPY1_HUMAN P14618 homo sapiens (human). pyruvate kinase, m1 isozyme (ec 2.7.1.40) (pyruvate kinase muscle isozyme) (cytosolic thyroid hormone-binding protein) (cthbp) (thbp1). 12/1998 [MASS=57747]/Pyruvate kinase muscle (pyruvate kinase 3), glycolytic enzyme that converts phosphoenolpyruvate to pyruvate with phosphorylation of ADP to ATP, exists as M1 and M2 alternative forms, may have roles in viral transformation and cell differentiation
SW:FLRE_HUMAN P30043 homo sapiens (human). flavin reductase (ec 1.6.99.1) (fr) (nadph-dependent diaphorase) (nadph-flavin reductase) (flr) (biliverdin reductase b) (ec 1.3.1.24) (bvr-b) (biliverdin-ix b [MASS=21988]/Biliverdin-IX beta reductase (NADPH-flavin reductase), catalyzes the conversion of biliverdin-IX beta to bilirubin-IX beta, the major heme catabolite produced during early fetal development; also has NAD(P)H-linked flavin reductase activity
SW:COXS_HUMAN Q14061 homo sapiens (human). cytochrome c oxidase copper chaperone. 7/1999 [MASS=6784]/Cytochrome c oxidase assembly protein 17, a putative copper binding protein, may function to transport copper to mitochondria for assembly into cytochrome oxidase complex; mutation does not appear to be a common cause of COX deficiency disorders
SW:INSR_HUMAN P06213 homo sapiens (human). insulin receptor precursor (ec 2.7.1.112) (ir). 5/2000 [MASS=156281]/Insulin receptor, a transmembrane receptor protein tyrosine kinase involved in carbohydrate metabolism, energy pathways, and cell growth; gene mutation is associated with insulin-resistant diabetes mellitus and leprechaunism
SW:THIK_HUMAN P09110 homo sapiens (human). 3-ketoacyl-coa thiolase, peroxisomal precursor (ec 2.3.1.16) (beta-ketothiolase) (acetyl-coa acyltransferase) (peroxisomal 3-oxoacyl- coa thiolase). 7/1999 [MASS=44292]/Peroxisomal 3-oxoacyl-coenzyme A thiolase (peroxisomal 3-ketoacyl-Coenzyme A thiolase), functions in peroxisomal beta-oxidation of fatty acids, deficiency is associated with rhizomelic chondrodysplasia punctata (RCDP)
SW:MDHC_HUMAN P40925 homo sapiens (human). malate dehydrogenase, cytoplasmic (ec 1.1.1.37). 5/2000 [MASS=36295]/Cytosolic malate dehydrogenase, part of the malate-aspartate shuttle where it putatively catalyzes the reduction of oxaloacetate to malate
SW:ACON_HUMAN Q99798 homo sapiens (human). aconitate hydratase, mitochondrial precursor (ec 4.2.1.3) (citrate hydro-lyase) (aconitase). 5/2000 [MASS=85425]/Aconitase 2 mitochondrial (aconitate hydratase), catalyzes the conversion of citrate to cis-aconitate in the tricarboxylic acid cycle, may be involved in iron homeostasis; deficiency may be associated with lifelong exercise intolerence
SW:CPT1_HUMAN P50416 homo sapiens (human). carnitine o-palmitoyltransferase i, mitochondrial liver isoform (ec 2.3.1.21) (cpt i) (cpti-l). 7/1999 [MASS=88429]/Liver carnitine palmitoyltransferase I, enzyme of long-chain fatty acid beta-oxidation pathway; mutations in the corresponding gene are associated with carnitine palmitoyltransferase I deficiency
SW:D3D2_HUMAN P42126 homo sapiens (human). 3,2-trans-enoyl-coa isomerase, mitochondrial precursor (ec 5.3.3.8) (dodecenoyl-coa delta-isomerase). 7/1999 [MASS=32816]/Dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenzyme A isomerase), catalyzes the isomerization of 3-cis and 3-trans enoyl CoA esters to 2-trans enoyl CoA esters, functions in mitochondrial beta-oxidation of unsaturated fatty acids
PIR2:JC5938 thioredoxin-like protein - human [MASS=32251]/Thioredoxin-like 32, a thioredoxin related protein that has thioredoxin-like reducing activity
SW:ECH1_HUMAN Q13011 homo sapiens (human). delta3,5-delta2,4-dienoyl-coa isomerase precursor (ec 5.3.3.-). 7/1999 [MASS=35994]/Enoyl Coenzyme A hydratase 1 (peroxisomal), putative enzyme that may play a role in peroxisomal beta-oxidation
SW:KG3B_HUMAN P49841 homo sapiens (human). glycogen synthase kinase-3 beta (ec 2.7.1.37) (gsk-3 beta). 7/1999 [MASS=46768]/Glycogen synthase kinase-3 beta, a serine threonine protein kinase that phosphorylates several cytoplasmic and nuclear proteins, involved in embryonic development, and may hyperphosporylate tau (MAPT) in
SW:KCRU_HUMAN P12532 homo sapiens (human). creatine kinase, ubiquitous mitochondrial precursor (ec 2.7.3.2) (u- mtck) (mia-ck) (acidic-type mitochondrial creatine kinase). 7/1999 [MASS=47037]/Mitochondrial creatine kinase 1 (ubiquitous), mitochondrial isoform that has a probable role in the phosphocreatine shuttle, plays a role in energy pathways; inactivation is involved in anthracycline cardiotoxicity
SW:ACPM_HUMAN O14561 homo sapiens (human). acyl carrier protein, mitochondrial precursor (acp) (nadh-ubiquinone oxidoreductase 9.6 kda subunit) (ec 1.6.5.3) (ec 1.6.99.3) (ci-sdap). 5/2000 [MASS=14806]/NADH-ubiquinone oxidoreductase subunit of alpha-beta subcomplex 1 (8 kD), a probable acyl carrier component of the multiprotein complex that transports electrons from NADH to ubiquinone, present within the hydrophobic fraction of complex I
SW:OBRG_HUMAN O15243 homo sapiens (human). leptin receptor gene-related protein (ob-r gene related protein) (ob- rgrp). 7/1999 [MASS=14254]/Leptin receptor, member of the gp130 (IL6ST) cytokine-receptor family, signals through the JAK/STAT cascade and functions in regulation of appetite, body fat, bone formation, and reproduction; mutations in the gene cause obesity and pituitary dysfunction
SW:CAOP_HUMAN Q15067 homo sapiens (human). acyl-coenzyme a oxidase, peroxisomal (ec 1.3.3.6) (palmitoyl-coa oxidase) (aox). 11/1997 [MASS=74502]/Peroxisomal acyl-coenzyme A oxidase, catalyzes the first step in very long chain fatty acid beta-oxidation, desaturates acyl-CoA to 2-trans-enoyl-CoA and produces hydrogen peroxide
SW:APE1_HUMAN P27695 homo sapiens (human). dna-(apurinic or apyrimidinic site) lyase (ec 4.2.99.18) (ap endonuclease 1) (apex nuclease) (apen) (ref-1 protein). 12/1998 [MASS=35423]/Apurinic/apyrimidinic endonuclease 1, multifunctional DNA repair enzyme that coordinates the repair of abasic sites and repair synthesis, acts as a transcription regulator; mutations may correlate with inclusion body myositis and colorectal tumorigenesis

SW:DLDH_HUMAN P09622 homo sapiens (human). dihydrolipoamide dehydrogenase, mitochondrial precursor (ec 1.8.1.4). 5/2000 [MASS=54150]/Dihydrolipoamide dehydrogenase, E3 component of pyruvate dehydrogenase complex, also component of alpha-ketoglutarate dehydrogenase and branched-chain alpha-ketoacid dehydrogenase complexes and the glycine cleavage system
SW:CISY_HUMAN O75390 homo sapiens (human). citrate synthase, mitochondrial precursor (ec 4.1.3.7). 7/1999 [MASS=51706]/Citrate synthase, converts acetyl-CoA and oxaloacetate into citrate plus CoA in the tricarboxylic acid cycle
SW:ADRO_HUMAN P22570 homo sapiens (human). nadph:adrenodoxin oxidoreductase precursor (ec 1.18.1.2) (adrenodoxin reductase) (ferredoxin-nadp(+) reductase). 7/1999 [MASS=53809]/Ferredoxin reductase, mitochondrial flavoprotein that mediates electron transport from NADPH to cytochrome P450scc
SW:ADT1_HUMAN P12235 homo sapiens (human). adp,atp carrier protein, heart/skeletal muscle isoform t1 (adp/atp translocase 1) (adenine nucleotide translocator 1) (ant 1). 10/1994 [MASS=33064]/Solute carrier family 25 member 4, an ADP:ATP transporter that may act in mitochondrial genome stability, altered transport capacity due to autoimmune response leads to myocarditis and cardiomyopathy; mutation causes progressive external ophthalmoplegia
SW:NUAM_HUMAN P28331 homo sapiens (human). nadh-ubiquinone oxidoreductase 75 kda subunit precursor (ec 1.6.5.3) (ec 1.6.99.3) (complex i-75kd) (ci-75kd). 7/1999 [MASS=79574]/NADH-dehydrogenase ubiquinone Fe-S protein 1 (75kD), a multiprotein complex that transports electrons from NADH to ubiquinone, present within the hydrophobic fraction of complex I; genetic variants are associated with mitochondrial complex I deficiency
SW:ECHB_HUMAN P55084 homo sapiens (human). trifunctonal enzyme beta subunit, mitochondrial precursor (tp-beta) [includes: 3-ketoacyl-coa thiolase (ec 2.3.1.16) (acetyl-coa acyltransferase) (beta-ketothi [MASS=51294]/3-hydroxyacyl-CoA dehydrogenase, 3-ketoacyl-CoA thiolase trifunctional protein beta subunit, involved in fatty acid beta-oxidation; variants are associated with trifunctional protein deficiency, sudden infant death syndrome and liver failure
SW:LYAG_HUMAN P10253 homo sapiens (human). lysosomal alpha-glucosidase precursor (ec 3.2.1.20) (acid maltase). 5/2000 [MASS=105338]/Acid alpha-glucosidase, lysosomal alpha-glucosidase that hydrolyzes alpha(1->4) and alpha(1->6) linkages in glycogen during glycogen catabolism; heritable deficiency causes glycogenosis type II or Pompe disease
SW:COX1_HUMAN P00395 homo sapiens (human). cytochrome c oxidase polypeptide i (ec 1.9.3.1). 5/2000 [MASS=57041]/Mitochondrial cytochrome c oxidase subunit I, a subunit of complex IV of the mitochondrial respiratory chain; mutations in the corresponding gene may be associated with mitochondrial diseases and acquired idiopathic sideroblastic anemia
SW:ECHA_HUMAN P40939 homo sapiens (human). mitochondrial trifunctional enzyme alpha subunit precursor (tp-alpha) [includes: long-chain enoyl-coa hydratase (ec 4.2.1.17); long chain 3-hydroxyacyl-coa deh [MASS=82960]/Mitochondrial long-chain enoyl-CoA hydratase/3-hydroxyacyl-CoA dehydrogenase/3-ketoacyl-CoA thiolase alpha subunit, involved in fatty acid beta-oxidation, mutations are associated with trifuctional protein deficiency and Reye-like syndrome
SW:ETFB_HUMAN P38117 homo sapiens (human). electron transfer flavoprotein beta-subunit (beta-etf). 5/2000 [MASS=27844]/Electron transfer flavoprotein beta subunit, shuttles electrons between primary flavoprotein dehydrogenases involved in mitochondrial fatty acid metabolism and ubiquinone oxidoreductase; genetic variants are associated with type II glutaric acidemia
PIR2:B53737 phosphate carrier protein precursor, mitochodrial, splice form B - human [MASS=39959]/Mitochondrial phosphate carrier (solute carrier family 25 member 3), catalyzes the transport of phosphate from the cytoplasm to the mitochondrial matrix for ATP synthesis during oxidative phosphorylation
SW:IDHP_HUMAN P48735 homo sapiens (human). isocitrate dehydrogenase [nadp], mitochondrial precursor (ec 1.1.1.42) (oxalosuccinate decarboxylase) (idh) (nadp+-specific icdh) (idp) (icd-m). 2/1996 [MASS=50948]/Isocitrate dehydrogenase 2 (NADP+) mitochondrial, catalyzes the oxidative decarboxylation of isocitrate to form alpha-ketoglutarate
SW:CY1_HUMAN P08574 homo sapiens (human). cytochrome c1, heme protein precursor. 7/1999 [MASS=35390]/Cytochrome c1, a member of the cytochrome bc1 complex
SW:NUPM_HUMAN P51970 homo sapiens (human). nadh-ubiquinone oxidoreductase 19 kda subunit (ec 1.6.5.3) (ec 1.6.99.3) (complex i-19kd) (ci-19kd) (complex i-pgiv) (ci-pgiv). 5/2000 [MASS=19974]/NADH dehydrogenase ubiquinone 1 alpha subcomplex 8 (19 kDa), a subunit of NADH-ubiquinone oxidoreductase (complex I), a multiprotein complex that transports electrons from NADH to ubiquinone
SW:KC2B_HUMAN P13862 homo sapiens (human), mus musculus (mouse), rattus norvegicus (rat), bos taurus (bovine), sus scrofa (pig), oryctolagus cuniculus (rabbit), and gallus gallus (chicken). casein kinase [MASS=24942]/Casein kinase II beta subunit, regulatory subunit of casein kinase II (CK2), confers stability and specificity to CK2 catalytic subunits, may mediate formation of the tetrameric CK2 complex, and may be involved in heat stress response
SW:ATPG_HUMAN P36542 homo sapiens (human). atp synthase gamma chain, mitochondrial precursor (ec 3.6.1.34). 5/2000 [MASS=32996]/ATP synthase H+ transporting mitochondrial F1 complex gamma 1, putative component of multisubunit enzyme that synthesizes ATP during oxidative phosphorylation, exists in tissue-specific alternative forms that are spliced in response to acidic conditions

SW:NUBM_HUMAN P49821 homo sapiens (human). nadh-ubiquinone oxidoreductase 51 kda subunit precursor (ec 1.6.5.3) (ec 1.6.99.3) (complex i-51kd) (ci-51kd). 5/2000 [MASS=50956]/NADH dehydrogenase ubiquinone flavoprotein 1 (51 kDa), a subunit of NADH-ubiquinone oxidoreductase (Complex I); genetic variants are associated with mitochondrial complex I deficiency, leukodystrophy, and myoclonic epilepsy
SW:UCR1_HUMAN P31930 homo sapiens (human). ubiquinol-cytochrome c reductase complex core protein i precursor (ec 1.10.2.2). 7/1999 [MASS=52619]/Ubiquinol-cytochrome c reductase core protein I, a subunit of the ubiquinol-cytochrome c oxidoreductase component of the mitochondrial respiratory chain, may function as an electron transporter in aerobic respiration and oxidative phosphorylation
SW:DHSB_HUMAN P21912 homo sapiens (human). succinate dehydrogenase [ubiquinone] iron-sulfur protein, mitochondrial precursor (ec 1.3.5.1) (ip) (ip subunit of complex ii). 5/2000 [MASS=31629]/Succinate dehydrogenase complex iron sulfur subunit B, part of an enzyme complex that transports electrons from succinate to ubiquinone in the TCA cycle and aerobic respiratory chain, may be involved in familial pheochromocytoma
SW:NB8M_HUMAN P17568 homo sapiens (human). nadh-ubiquinone oxidoreductase b18 subunit (ec 1.6.5.3) (ec 1.6.99.3) (complex i-b18) (ci-b18) (cell adhesion protein sqm1). 7/1998 [MASS=15648]/Subunit of the NADH-ubiquinone oxidoreductase (complex I), a multiprotein complex that transports electrons from NADH to ubiquinone, functions as a cell adhesion molecule with a role in metastasis, may have a role in drug transport
SW:MDHM_HUMAN P40926 homo sapiens (human). malate dehydrogenase, mitochondrial precursor (ec 1.1.1.37). 5/2000 [MASS=35531]/Mitochondrial malate dehydrogenase, part of the malate-aspartate shuttle where it putatively catalyzes the oxidation of malate to oxaloacetate
SW:UCRH_HUMAN P07919 homo sapiens (human). ubiquinol-cytochrome c reductase complex 11 kda protein precursor (ec 1.10.2.2) (mitochondrial hinge protein) (cytochrome c1, nonheme 11 kda protein) (complex [MASS=10755]/Ubiquinol-cytochrome c reductase hinge protein, hinges cytochrome c with cytochrome c1 in the mitochondrial respiratory chain, may function to accelerate apoptosis by enhancing cytochrome c release from the mitochondria
SW:ETFA_HUMAN P13804 homo sapiens (human). electron transfer flavoprotein alpha-subunit precursor (alpha-etf). 5/2000 [MASS=35080]/Electron transfer flavoprotein alpha subunit, shuttles electrons between flavoprotein dehydrogenases of mitochondrial fatty acid metabolism and ubiquinone oxidoreductase, deficiency associated with Type II glutaricaciduria
SW:ATPA_HUMAN P25705 homo sapiens (human). atp synthase alpha chain, mitochondrial precursor (ec 3.6.1.34). 12/1998 [MASS=59751]/ATP synthase H+ transporting mitochondrial F1 complex alpha subunit isoform 1 cardiac muscle, part of the synthase enzymatic complex that catalyzes the synthesis of ATP during oxidative phosphorylation
SW:UCR2_HUMAN P22695 homo sapiens (human). ubiquinol-cytochrome c reductase complex core protein 2 precursor (ec 1.10.2.2) (complex iii subunit ii). 7/1999 [MASS=48470]/Ubiquinol-cytochrome c reductase core protein II, a putative ubiquinol-cytochrome c reductase subunit of the mitochondrial cytochrome bc1 complex, likely to play a role in oxidative phosphorylation, may be involved in aerobic respiration
SW:THIL_HUMAN P24752 homo sapiens (human). acetyl-coa acetyltransferase, mitochondrial precursor (ec 2.3.1.9) (acetoacetyl-coa thiolase) (t2). 7/1999 [MASS=45200]/Acetyl-Coenzyme A acetyltransferase 1 (mitochondrial acetoacetyl-coenzyme A thiolase); mutations in the corresponding gene are associated with 3-ketothiolase deficiency
SW:UCRI_HUMAN P47985 homo sapiens (human). ubiquinol-cytochrome c reductase iron-sulfur subunit, mitochondrial precursor (ec 1.10.2.2) (rieske iron-sulfur protein) (risp). 7/1999 [MASS=29652]/Ubiquinol-cytochrome c reductase Rieske iron-sulfur polypeptide 1, a subunit of cytochrome bc1 complex, which transfers electron from ubiquinol to cytochrome c, located in the mitochondrion; deficient mitochondrial uptake may cause mitochondrial myopathy
SW:PPCM_HUMAN Q16822 homo sapiens (human). phosphoenolpyruvate carboxykinase, mitochondrial precursor [gtp] (ec 4.1.1.32) (phosphoenolpyruvate carboxylase) (pepck-m). 7/1999 [MASS=70637]/Phosphoenolpyruvate carboxykinase 2, catalyzes the formation of phosphoenolpyruvate by decarboxylation of oxaloacetate, rate-limiting step of gluconeogenesis
SW:DHSA_HUMAN P31040 homo sapiens (human). succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial precursor (ec 1.3.5.1) (fp) (flavoprotein subunit of complex ii). 5/2000 [MASS=72692]/Succinate dehydrogenase complex subunit A (flavoprotein), transports electrons from succinate to ubiquinone in the TCA cycle and respiratory chain; gene mutation is associated with Leigh syndrome, which is a complex II respiratory chain deficiency
SW:ADT2_HUMAN P05141 homo sapiens (human). adp,atp carrier protein, fibroblast isoform (adp/atp translocase 2) (adenine nucleotide translocator 2) (ant 2). 7/1999 [MASS=32895]/Solute carrier family 25 member 5 (adenine nucleotide translocator 2), may mediate the exchange of ADP and ATP between the cytosol and mitochondria, expression is altered in dilated cardiomyopathy
SW:ADT3_HUMAN P12236 homo sapiens (human). adp,atp carrier protein, liver isoform t2 (adp/atp translocase 3) (adenine nucleotide translocator 3) (ant 3). 11/1995 [MASS=32866]/Solute carrier family 25 member 6 (adenine nucleotide translocator), member of the ADP/ATP translocase family
SW:ATPQ_HUMAN O75947 homo sapiens (human). atp synthase d chain, mitochondrial (ec 3.6.1.34). 5/2000 [MASS=18360]/Protein with high similarity to subunit d of the mitochondrial H(+)-ATP synthase (rat Atp5jd), which is part of a multisubunit enzyme that catalyzes the synthesis of ATP during oxidative phosphorylation

SW:NIPM_HUMAN O43920 homo sapiens (human). nadh-ubiquinone oxidoreductase 15 kda subunit (ec 1.6.5.3) (ec 1.6.99.3) (complex i-15 kda) (ci-15 kda). 7/1999 [MASS=12386]/NADH dehydrogenase Fe-S protein 5 (15kD) (NADH-coenzyme Q reductase), putative subunit of NADH-ubiquinone oxidoreductase (complex I), a multiprotein complex that transports electrons from NADH to ubiquinone in the mitochondrial respiratory chain
SW:COXG_HUMAN P14854 homo sapiens (human). cytochrome c oxidase polypeptide vib (ec 1.9.3.1) (aed). 11/1997 [MASS=10061]/Cytochrome c oxidase subunit VIb, a putative subunit of cytochrome C oxidase, which couples reduction of oxygen with proton translocation during oxidative phosphorylation
SW:FDFT_HUMAN P37268 homo sapiens (human). farnesyl-diphosphate farnesyltransferase (ec 2.5.1.21) (squalene synthetase) (sqs) (ss) (fpp:fpp farnesyltransferase). 10/1996 [MASS=48115]/Squalene synthase (farnesyl-diphosphate farnesyltransferase 1), catalyzes the conversion of farnesyl diphosphate to squalene in cholesterol biosynthesis, may be a potential target for cholesterol lowering therapy
type-2 phosphatidic acid phosphatase alpha-1 /Phosphatidic acid phosphatase type 2a, catalyzes the dephosphorylation of various lipid phosphates, regulates the level of lipid phosphates which are involved in signal transduction
fatty-acid-Coenzyme A ligase, long-chain 3 /Fatty acid Coenzyme A ligase long chain 3, a putative long-chain fatty-acyl-CoA synthetase that may function in lipid synthesis and fatty acid degradation
SW:ACDV_HUMAN P49748 homo sapiens (human). acyl-coa dehydrogenase, very-long-chain specific, mitochondrial precursor (ec 1.3.99.-) (vlcad). 5/2000 [MASS=70390]/Very long chain acyl-coenzyme A dehydrogenase, oxidizes straight chain acyl-CoAs in the initial step of fatty acid beta-oxidation, severe deficiency results in infant cardiomyopathy with high mortality, mild deficiency results in hypoketotic hypoglycemia
SW:FAS_HUMAN P49327 homo sapiens (human). fatty acid synthase (ec 2.3.1.85) [includes: ec 2.3.1.38; ec 2.3.1.39; ec 2.3.1.41; ec 1.1.1.100; ec 4.2.1.61; ec 1.3.1.10; ec 3.1.2.14]. 7/1999 [MASS=273102]/Fatty acid synthase, multifunctional enzyme that synthesizes fatty acids from dietary proteins and carbohydrates; increased expression is associated with tumor growth and development, expression may serve as a prognostic maker for breast cancer
SW:ERG7_HUMAN P48449 homo sapiens (human). lanosterol synthase (ec 5.4.99.7) (oxidosqualene--lanosterol cyclase) (2,3-epoxysqualene--lanosterol cyclase) (osc). 5/2000 [MASS=83309]/Lanosterol synthase, catalyzes the cyclization of (S)-2,3-oxidosqualene forming lanosterol in sterol biosynthesis
SW:COA1_HUMAN Q13085 homo sapiens (human). acetyl-coa carboxylase 1 (ec 6.4.1.2) (acc-alpha) [includes: biotin carboxylase (ec 6.3.4.14)]. 7/1999 [MASS=265040]/Acetyl-Coenzyme A carboxylase alpha, catalyzes the rate-limiting step in long-chain fatty acid biogenesis; deficiency leads to defects in fatty acid synthesis
SW:ACLY_HUMAN P53396 homo sapiens (human). atp-citrate (pro-s-)-lyase (ec 4.1.3.8) (citrate cleavage enzyme). 10/1996 [MASS=121420]/ATP citrate lyase, catalyzes the formation of acetyl-CoA and oxaloacetate from citrate and CoA with the concomitant hydrolysis of ATP to ADP and phosphate, involved in cholesterol and fatty acid synthesis, nutritionally regulated
SW:LDLR_HUMAN P01130 homo sapiens (human). low-density lipoprotein receptor precursor (ldl receptor). 5/2000 [MASS=95376]/Low density lipoprotein receptor, mediates uptake of low density lipoproteins, involved in lipid metabolism; gene variations are associated with familial hypercholesterolemia, hypertension, atherosclerosis, and coronary artery disease
SW:NSDL_HUMAN Q15738 homo sapiens (human). nad(p)-dependent steroid dehydrogenase-like protein (h105e3 protein). 5/2000 [MASS=41900]/NAD(P)H steroid dehydrogenase-like protein, a 3 beta-hydroxysteroid dehydrogenase that functions in cholesterol biosynthesis; mutations in the corresponding gene cause CHILD syndrome
SW:CP51_HUMAN Q16850 homo sapiens (human). cytochrome p450 51 (ec 1.14.14.1) (cypl1) (p450l1) (sterol 14-alpha demethylase) (lanosterol 14-alpha demethylase) (ldm) (p450-14dm). 5/2000 [MASS=56806]/Lanosterol 14-alpha-demethylase (sterol 14alpha-demethylase); cytochrome P450 enzyme involved in sterol biosynthesis
SW:LCFA_HUMAN P41215 homo sapiens (human). long-chain-fatty-acid--coa ligase 1 (ec 6.2.1.3) (long-chain acyl-coa synthetase 1) (lacs 1) (palmitoyl-coa ligase). 10/1996 [MASS=78348]/Long chain fatty acid-Coenzyme A ligase (palmitoyl-CoA ligase), a member of the long chain acyl-CoA synthetase family required for lipid synthesis and fatty acid degradation
SW:LCB2_HUMAN O15270 homo sapiens (human). serine palmitoyltransferase 2 (ec 2.3.1.50) (long chain base biosynthesis protein 2) (lcb 2) (serine-palmitoyl-coa transferase 2) (spt 2) (kiaa0526). 5/2000 [MASS=62924]/Serine palmitoyltransferase long chain base subunit 2, member of the aminolevulinate synthase superfamily, catalyzes the first step in ceramide formation, involved in epidermal cell response to UV exposure and in leukemia cell ectopside-induced apoptosis
SW:DRS1_HUMAN O75521 homo sapiens (human). dbi-related protein 1 (drs-1). 5/2000 [MASS=40151]/Peroxisomal D3,D2-enoyl-CoA isomerase, catalyzes the isomerization of 3-cis-octenoyl-CoA to 2-trans-octenoyl-CoAm, a step in the beta oxidation of fatty acids in peroxisomes
SWN:P23_HUMAN Q15185 homo sapiens (human). telomerase-binding protein p23 (hsp90 co-chaperone) (progesterone receptor complex p23). 8/2001 [MASS=18697]/Inactive progesterone receptor (23kD), cochaperone with prostaglandin E synthase activity that is a component of the unstimulated progesterone receptor complex and that enhances receptor complex formation through interactions with Hsp90 (HSPCA)

SW:KIME_HUMAN Q03426 homo sapiens (human). mevalonate kinase (ec 2.7.1.36) (mk). 7/1999 [MASS=42451]/Mevalonate kinase (mevalonic aciduria), a peroxisomal enzyme involved in isoprenoid and cholesterol biosynthesis; mutations in the corresponding gene cause mevalonic aciduria, hyperimmunoglobulinemia D and periodic fever syndrome
GP:U66669_1 Homo sapiens 3-hydroxyisobutyryl-coenzyme A hydrolase mRNA, complete cds. [MASS=42908]/Beta-hydroxyisobutyryl-coenzyme A hydrolase, enzyme that hydrolyzes 3-hydroxyisobutyryl CoA, an intermediate of valine catabolism
SW:ASAH_HUMAN Q13510 homo sapiens (human). acid ceramidase precursor (ec 3.5.1.23) (acylsphingosine deacylase) (n-acylsphingosine amidohydrolase) (ac) (putative 32 kda heart protein) (php32). 5/2000 [MASS=44650]/N-acylsphingosine amidohydrolase (acid ceramidase), catalyzes hydrolysis of ceramide to sphingosine and free fatty acid, inhibits apoptosis, upregulated in prostate cancer, deficiency is associated with Farber disease
GP:AF126782_1 Homo sapiens retinal short-chain dehydrogenase/reductase retSDR4 mRNA, complete cds. [MASS=32268]/Short-chain dehydrogenase-reductase 1, catalyzes the NADPH-dependent reduction of all-trans-retinal to retinol, may play a role in visual system phototransduction; the corresponding gene is deleted in many neuroblastoma cell lines with MYCN amplification
SW:OXYB_HUMAN P22059 homo sapiens (human). oxysterol-binding protein. 11/1995 [MASS=89421]/Oxysterol binding protein, member of a family of intracellular lipid receptors, contains a pleckstrin domain and an oxysterol binding domain, binds oxysterols, may play a role in the regulation of cholesterol metabolism and oxysterol-induced cell death
SW:CPT2_HUMAN P23786 homo sapiens (human). carnitine o-palmitoyltransferase ii, mitochondrial precursor (ec 2.3.1.21) (cpt ii). 5/2000 [MASS=73777]/Carnitine palmitoyltransferase II, a mitochondrial long-chain fatty acid oxidation enzyme; mutations are associated with a lipid metabolism disorder that includes recurrent myopathy with progressive rhabdomyolysis, muscle weakness and myoglobinuria
SW:FAAH_HUMAN O00519 homo sapiens (human). fatty-acid amide hydrolase (ec 3.1.-.-) (oleamide hydrolase). 5/2000 [MASS=63038]/Fatty acid amide hydrolase, degrades neuromodulatory fatty acid amides, including anandamide, predicted to have a role in a wide variety of physiologic efffects such as voluntary movement, pain, sleep, and fertility, may have a role in Parkinson disease
SW:HBP_HUMAN Q00341 homo sapiens (human). high density lipoprotein binding protein (hdl-binding protein). 12/1998 [MASS=141440]/High density lipoprotein binding protein, binds and inhibits cleavage of the 3' UTR of vitellogenin mRNA, binds and promotes nuclear export of tRNA, binds high density lipoproteins and may have roles in cholesterol metabolism and atherogenesis
SW:NPC1_HUMAN O15118 homo sapiens (human). niemann-pick c1 protein precursor. 5/2000 [MASS=142149]/Niemann-Pick disease type C1, a lysosomal sterol transporter involved in cholesterol metabolism; mutation of the corresponding gene causes Niemann-Pick type C1 disease and mutation of mouse Npc1 causes a disease like Niemann-Pick type C1 disease
SW:PEBP_HUMAN P30086 homo sapiens (human). phosphatidylethanolamine-binding protein (pebp) (neuropolypeptide h3). 7/1999 [MASS=20926]/Phosphatidylethanolamine-binding protein, binds GTP, may regulate cAMP accumulation, enhance acetylcholine synthesis, and play a role in organizing phospholipids in the myelin sheath
SW:GLCM_HUMAN P04062 homo sapiens (human). glucosylceramidase precursor (ec 3.2.1.45) (beta-glucocerebrosidase) (acid beta-glucosidase) (d-glucosyl-n-acylsphingosine glucohydrolase) (alglucerase) (imigl [MASS=59697]/Acid beta glucosidase (beta-glucocerebrosidase), a lysosomal membrane protein that hydrolyzes glucosylceramide and glucosylsphingosine, may play a role in epidermal differentiation; mutations in the corresponding gene cause Gaucher's disease
SW:PI52_HUMAN P48426 homo sapiens (human). phosphatidylinositol-4-phosphate 5-kinase type ii alpha (ec 2.7.1.68) (pip5kii-alpha) (1-phosphatidylinositol-4-phosphate kinase) (ptdins(4)p-5-kinase b isofor [MASS=46193]/Phosphatidylinositol-4-phosphate 5-kinase type II, alpha, a member of a family of kinases responsible for the synthesis of PtdIns(4,5)P2
GP:AF034544_1 Homo sapiens delta7-sterol reductase mRNA, complete cds; D7SR. [MASS=54516]/7-dehydrocholesterol reductase, catalyzes the reduction of the C7-C8 (delta 7) double bond of 7-dehydrocholesterol in the last step of cholesterol biosynthesis; mutations in the corresponding gene are associated with Smith-Lemli-Opitz
SW:THIK_HUMAN P09110 homo sapiens (human). 3-ketoacyl-coa thiolase, peroxisomal precursor (ec 2.3.1.16) (beta-ketothiolase) (acetyl-coa acyltransferase) (peroxisomal 3-oxoacyl- coa thiolase). 7/1999 [MASS=44292]/Peroxisomal 3-oxoacyl-coenzyme A thiolase (peroxisomal 3-ketoacyl-Coenzyme A thiolase), functions in peroxisomal beta-oxidation of fatty acids, deficiency is associated with rhizomelic chondrodysplasia punctata (RCDP)
SW:CPT1_HUMAN P50416 homo sapiens (human). carnitine o-palmitoyltransferase i, mitochondrial liver isoform (ec 2.3.1.21) (cpt i) (cpti-l). 7/1999 [MASS=88429]/Liver carnitine palmitoyltransferase I, enzyme of long-chain fatty acid beta-oxidation pathway; mutations in the corresponding gene are associated with carnitine palmitoyltransferase I deficiency
SW:D3D2_HUMAN P42126 homo sapiens (human). 3,2-trans-enoyl-coa isomerase, mitochondrial precursor (ec 5.3.3.8) (dodecenoyl-coa delta-isomerase). 7/1999 [MASS=32816]/Dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenzyme A isomerase), catalyzes the isomerization of 3-cis and 3-trans enoyl CoA esters to 2-trans enoyl CoA esters, functions in mitochondrial beta-oxidation of unsaturated fatty acids

SW:SAP_HUMAN P07602 h proactivator polypeptide precursor [contains: saposin a (protein a); saposin b (sphingolipid activator protein 1) (sap-1) (dispersin) (sulfatide/gm1 activator); saposin c (co-beta- [MASS=58113]/Prosaposin, precursor of saposins A, B, C, and D which transport gangliosides and activate sphingolipid hydrolysis, stimulates neurite growth and inhibits apoptosis; variants are associated with metachromatic leukodystrophy and Gaucher disease
GP:AB037108_1 Homo sapiens mRNA for seven transmembrane domain orphan receptor, complete cds; seven transmembrane domain containing protein. [MASS=41090]/Protein with strong similarity to murine Tpra40, which is a seven transmembrane domain protein expressed in 3T3 adipocytes, and that has elevated expression in epididymal fat of genetically diabetic and obese mice
SW:ECH1_HUMAN Q13011 homo sapiens (human). delta3,5-delta2,4-dienoyl-coa isomerase precursor (ec 5.3.3.-). 7/1999 [MASS=35994]/Enoyl Coenzyme A hydratase 1 (peroxisomal), putative enzyme that may play a role in peroxisomal beta-oxidation
SW:SAP3_HUMAN P17900 homo sapiens (human). ganglioside gm2 activator precursor (cerebroside sulfate activator protein) (shingolipid activator protein 3) (sap-3). 7/1999 [MASS=20822]/GM2 ganglioside activator protein, binds glycolipids and is a cofactor for GM2 ganglioside hydrolysis by beta hexosaminidase A, activates phospholipase D, and inhibits platelet activating factor; mutation of the gene causes GM2-gangliosidosis variant AB
GP:AF035959_1 Homo sapiens type-2 phosphatidic acid phosphatase-gamma (PAP2-g) mRNA, complete cds; phosphatidate phosphohydrolase; phospholipid phosphatase. [MASS=32574]/Phosphatidic acid phosphatase 2c, hydrolyzes phospholipids, may play a role in signal transduction
SW:OCRL_HUMAN Q01968 homo sapiens (human). lowe's oculocerebrorenal syndrome protein. 7/1998 [MASS=111485]/Oculocerebrorenal syndrome of Lowe, phosphatidylinositol-4,5-bisphosphate 5-phosphatase, may play a role in intracellular protein trafficking; mutation of the corresponding gene causes Lowe oculocerebrorenal syndrome
GP:AB033078_1 Homo sapiens mRNA for KIAA1252 protein, partial cds; Start codon is not identified.. [MASS=64962]/Protein with strong similarity to sphingosine phosphate lyase 1 (mouse Sgpl1), which is a member of the carbon-carbon lyase subclass of aldehyde-lyases that catalyzes cleavage of sphingosine phosphate and is involved in proliferative signal transduction
SWN:CNE3_HUMAN O75131 homo sapiens (human). copine iii. 8/2001 [MASS=60131]/Copine III, a member of the copine family of phospholipid binding proteins, contains C2 and integrin A domains, may play a role in membrane trafficking, displays protein kinase activity, however, it does not contain a traditional kinase catalytic domain
SW:NLTP_HUMAN P22307 homo sapiens (human). nonspecific lipid-transfer protein precursor (nsl-tp) (sterol carrier protein 2) (scp-2) (sterol carrier protein x) (scp-x) (scpx). 5/2000 [MASS=58994]/Sterol carrier protein 2, catalyzes the exchange of phospholipids between membranes, stimulates cholesterol metabolism and may regulate steroidogenesis; alternative form, SCPX, is a 3 oxoacyl CoA thiolase
SW:CAOP_HUMAN Q15067 homo sapiens (human). acyl-coenzyme a oxidase, peroxisomal (ec 1.3.3.6) (palmitoyl-coa oxidase) (aox). 11/1997 [MASS=74502]/Peroxisomal acyl-coenzyme A oxidase, catalyzes the first step in very long chain fatty acid beta-oxidation, desaturates acyl-CoA to 2-trans-enoyl-CoA and produces hydrogen peroxide
SW:PKBS_HUMAN P30536 homo sapiens (human). peripheral-type benzodiazepine receptor (pbr) (pkbs) (mitochondrial benzodiazepine receptor). 6/1994 [MASS=18779]/Benzodiazepine receptor (peripheral), involved in steroid biosynthesis, cell proliferation, and may contribute to mitochondrial biogenesis and inhibit oxygen radical induced apoptosis; expression, nuclear location may correlate to breast tumor progression
SW:PXF_HUMAN P40855 homo sapiens (human). peroxisomal farnesylated protein (33 kda housekeeping protein). 12/1998 [MASS=32807]/Peroxisomal farnesylated protein, peroxisomal protein that binds several peroxisomal membrane proteins (PMP), involved in early stages of PMP import and peroxisomal biogenesis; deficiency is associated with Zellweger syndrome complementation group J
SW:DHA4_HUMAN P51648 homo sapiens (human). fatty aldehyde dehydrogenase (ec 1.2.1.3) (aldehyde dehydrogenase, microsomal) (aldh class 3). 7/1999 [MASS=54848]/Aldehyde dehyrogenase 3 family member A2, catalyzes the oxidation of long chain fatty aldehydes and leukotrienes; mutation of the corresponding gene causes Sjogren Larsson syndrome, a disorder marked by mental retardation, spasticity, and ichthyosis
SW:HCD2_HUMAN Q99714 homo sapiens (human). 3-hydroxyacyl-coa dehydrogenase type ii (ec 1.1.1.35) (endoplasmic reticulum-associated amyloid beta-peptide binding protein) (short- chain type dehydrogenase/ [MASS=26923]/Hydroxyacyl-Coenzyme A dehydrogenase (type II), catalyzes the oxidation of steroids and alcohols, binds amyloid-beta protein; overexpressed and mediates neurotoxicity of Alzheimer's disease, mutation in the corresponding gene causes hyperinsulinism
SW:DHB4_HUMAN P51659 homo sapiens (human). estradiol 17 beta-dehydrogenase 4 (ec 1.1.1.62) (17-beta-hsd 4) (17-beta-hydroxysteroid dehydrogenase 4). 11/1997 [MASS=79686]/Type IV 17 beta-hydroxysteroid dehydrogenase, a peroxisomal multifunctional enzyme with estradiol 17 beta-dehydrogenase and D-3 hydroxyacyl CoA dehydratase activities, involved in steroid and bile acid metabolism
SW:BDH_HUMAN P06280 homo sapiens (human). alpha-galactosidase a precursor (ec 3.2.1.22) (melibiase) (alpha-d-galactoside galactohydrolase) (alpha-d-galactosidase a). 7/1998 [MASS=48767]/Alpha-galactosidase A (alpha-D-galactoside galactohydrolase), hydrolyzes glycosphingolipids to release alpha-D-galactosyl residues; mutation of the corresponding gene causes Fabry disease
SW:ADRO_HUMAN P22570 homo sapiens (human). nadph:adrenodoxin oxidoreductase precursor (ec 1.18.1.2) (adrenodoxin reductase) (ferredoxin-nadp(+) reductase). 7/1999 [MASS=53809]/Ferredoxin reductase, mitochondrial flavoprotein that mediates electron transport from NADPH to cytochrome P450scc

SW:ECHB_HUMAN P55084 homo sapiens (human). trifunctonal enzyme beta subunit, mitochondrial precursor (tp-beta) [includes: 3-ketoacyl-coa thiolase (ec 2.3.1.16) (acetyl-coa acyltransferase) (beta-ketothi [MASS=51294]/3-hydroxyacyl-CoA dehydrogenase, 3-ketoacyl-CoA thiolase trifunctional protein beta subunit, involved in fatty acid beta-oxidation; variants are associated with trifunctional protein deficiency, sudden infant death syndrome and liver failure
SW:CNBP_HUMAN P20694 homo sapiens (human), and rattus norvegicus (rat). cellular nucleic acid binding protein (cnbp). 11/1997 [MASS=19463]/Zinc-finger protein that binds to sterol regulatory element (SRE) and may function in sterol-mediated repression of genes encoding the low density lipoprotein receptor and enzymes of the cholesterol biosynthetic pathway
SW:MAOM_HUMAN P23368 homo sapiens (human). nad-dependent malic enzyme, mitochondrial precursor (ec 1.1.1.38) (nad-me). 5/2000 [MASS=65444]/Malic enzyme 2, a NAD(+)-dependent mitochondrial form of malic enzyme, catalyzes the oxidative decarboxylation of malate to form pyruvate
SW:ECHA_HUMAN P40939 homo sapiens (human). mitochondrial trifunctional enzyme alpha subunit precursor (tp-alpha) [includes: long-chain enoyl-coa hydratase (ec 4.2.1.17); long chain 3-hydroxyacyl-coa deh [MASS=82960]/Mitochondrial long-chain enoyl-CoA hydratase/3-hydroxyacyl-CoA dehydrogenase/3-ketoacyl-CoA thiolase alpha subunit, involved in fatty acid beta-oxidation, mutations are associated with trifuctional protein deficiency and Reye-like syndrome
SW:ETFB_HUMAN P38117 homo sapiens (human). electron transfer flavoprotein beta-subunit (beta-etf). 5/2000 [MASS=27844]/Electron transfer flavoprotein beta subunit, shuttles electrons between primary flavoprotein dehydrogenases involved in mitochondrial fatty acid metabolism and ubiquinone oxidoreductase; genetic variants are associated with type II glutaric acidemia
GP:AL023805_1 Human DNA sequence from clone RP4-811H13 on chromosome 20p12. Contains part of the PLCB4 gene for Phospholipase C beta 4, STSs, GSSs and a CpG island, complete sequence; combines with dJ1119D9.2.1 and .2 in Em:AL031652 to form isoforms 5 and 6; may a [MASS=61433]/1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase beta 4/Phospholipase C beta 4, member of a G protein-regulated family of phospholipases that hydrolyze phosphatidylinositol 4,5-bisphosphate to the second messengers inositol 1,4,5-trisphosphate and diacylglycerol
SW:GST3_HUMAN O14880 homo sapiens (human). microsomal glutathione s-transferase 3 (ec 2.5.1.18) (microsomal gst- 3) (microsomal gst-iii). 5/2000 [MASS=16516]/Microsomal glutathione S-transferase 3, a microsomal membrane protein that has glutathione-dependent transferase and peroxidase activities, member of a family that includes 5-lipoxygenase activating protein (ALOX5AP) and leukotriene-C4 synthase (LTC4S)
SW:ETFA_HUMAN P13804 homo sapiens (human). electron transfer flavoprotein alpha-subunit precursor (alpha-etf). 5/2000 [MASS=35080]/Electron transfer flavoprotein alpha subunit, shuttles electrons between flavoprotein dehydrogenases of mitochondrial fatty acid metabolism and ubiquinone oxidoreductase, deficiency associated with Type II glutaricaciduria
SW:MAZ_HUMAN P56270 homo sapiens (human). myc-associated zinc finger protein (mazi) (purine-binding transcription factor) (pur-1) (zf87) (zif87). 7/1999 [MASS=48608]/MYC-associated zinc finger protein (purine-binding transcription factor), functions both as a positive and a negative regulator of gene expression and may also have roles in initiating and terminating transcription
SW:THIL_HUMAN P24752 homo sapiens (human). acetyl-coa acetyltransferase, mitochondrial precursor (ec 2.3.1.9) (acetoacetyl-coa thiolase) (t2). 7/1999 [MASS=45200]/Acetyl-Coenzyme A acetyltransferase 1 (mitochondrial acetoacetyl-coenzyme A thiolase); mutations in the corresponding gene are associated with 3-ketothiolase deficiency
GP:AF161397_1 Homo sapiens HSPC279 mRNA, partial cds. [MASS=64199]/Homo sapiens mRNA for 2-hydroxyphytanoyl-CoA lyase; thiamine pyrophosphate dependent enzyme/2-Hydroxyphytanoyl-CoA lyase (peroxisomal 2-hydroxyphytanoyl-CoA lyase), catalyzes the thiamine pyrophosphate-dependent cleavage of C-C bonds during alpha-oxidation of 3-methyl-branched fatty acids to form formyl-CoA and 2-methyl-branched fatty aldehyde
SW:TPP1_HUMAN O14773 homo sapiens (human). tripeptidyl-peptidase i precursor (ec 3.4.14.9) (tpp-i) (tripeptidyl aminopeptidase) (lysosomal pepstatin insensitive protease) (lpic). 5/2000 [MASS=61229]/Tripeptidyl peptidase I (ceroid-lipofuscinosis neuronal 2), a lysosomal serine-type peptidase required for degradation of ATP synthase subunit c (ATP5G1 and ATP5G2); mutations in the corresponding gene cause late infantile neuronal ceroid lipofuscinosis
GP:AF002668_1 Homo sapiens putative fatty acid desaturase MLD mRNA, complete cds; putative fatty acid desaturase. [MASS=37866]/Degenerative spermatocyte homolog (Drosophila), member of the membrane fatty acid desaturase family, regulates the biosynthesis of the epidermal growth factor receptor (EGFR)
SW:PA2M_HUMAN P14555 homo sapiens (human). phospholipase a2, membrane associated precursor (ec 3.1.1.4) (phosphatidylcholine 2-acylhydrolase) (group ii phospholipase a2) (non-pancreatic secretory phosph [MASS=16083]/Group IIA phospholipase A2, a secreted member of the phospholipase A2 family that hydrolyzes the phospholipid sn-2 ester bond, plays roles in phospholipid metabolism, host defense, and inflammation; gene loss reported in a sporadic colorectal tumor
GP:AJ002744_1 Homo sapiens mRNA for UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase 7. [MASS=75402]/UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 7, enzyme that functions in O-glycosylation and is specific for partially glycosylated substrates

PIR2:JE0334 nuclear matrix protein NMP 238 - human [MASS=50228]/RuvB like 1, a member of the TIP49 family of proteins, a nuclear protein which contains ATPase-helicase motifs, may interact with the transactivation domain of c-myc (MYC)
SW:CTOG_HUMAN Q14008 homo sapiens (human). ch-tog protein (colonic and hepatic tumor over-expressed protein) (kiaa0097). 5/2000 [MASS=225509]/Microtubule-associated protein that promotes rapid plus end microtubule assembly necessary for mitotic spindle assembly
SW:SNAG_HUMAN Q99747 homo sapiens (human). gamma-soluble nsf attachment protein (snap-gamma). 7/1999 [MASS=34746]/N-ethylmaleimide-sensitive factor (NSF) attachment protein gamma, member of a family of proteins involved in membrane fusion during exocytosis, may have roles in platelet exocytosis and in the attachment of mitochondria to the cytoskeleton
SW:RB3B_HUMAN P20337 homo sapiens (human). ras-related protein rab-3b. 10/1994 [MASS=24760]/Ras-related GTP-binding protein 3b, a GTP-binding protein and GTPase that is involved in exocytosis
SW:RB4A_HUMAN P20338 homo sapiens (human). ras-related protein rab-4a. 10/1996 [MASS=23902]/GTP-binding protein, a member of the rab family of proteins, involved in early endosome trafficking and receptor recycling
SW:STB3_HUMAN O00186 homo sapiens (human). syntaxin binding protein 3 (unc-18 homolog 3) (unc-18c) (unc-18-3). 5/2000 [MASS=67574]/Syntaxin binding protein 3, binds syntaxin 4 (STX4), predicted to be involved in vesicle transport and docking and in neurotransmitter release
SW:RB35_HUMAN Q15286 homo sapiens (human). ras-related protein rab-35 (rab-1c) (gtp-binding protein ray). 5/2000 [MASS=23025]/Ras-related GTP-binding protein 35, member of the Rab family of GTP-binding proteins, may function in vesicular transport
SW:SN23_HUMAN O00161 homo sapiens (human). synaptosomal associated protein 23 (snap-23) (vesicle-membrane fusion protein snap-23). 5/2000 [MASS=23354]/Synaptosomal-associated protein 23, a member of the SNARE family of proteins that regulate membrane fusion during exocytosis, a t-SNARE that binds to syntaxins and is involved in docking and fusion of transport vesicles during exocytosis
SW:RB3D_HUMAN O95716 homo sapiens (human). ras-related protein rab-3d. 5/2000 [MASS=24267]/Ras-related GTP-binding protein 3d, putative small monomeric GTP-binding protein and GTPase that plays a role in regulated secretion
SW:RAB2_HUMAN P08886 homo sapiens (human), and canis familiaris (dog). ras-related protein rab-2. 10/1994 [MASS=23546]/Ras-related GTP-binding protein 2, a GTPase which plays a role in vesicle transport from the ER to the Golgi complex; overexpression in nonmalignant peripheral blood lymphocytes is associated with Searzy syndrome
SW:ANX7_HUMAN P20073 homo sapiens (human). annexin vii (synexin). 5/2000 [MASS=50316]/Annexin A7 (synexin), a calcium-dependent GTPase that acts as a voltage-dependent calcium channel, interaction with galectin 3 (LGALS3) suggests roles in apoptosis and exocytosis, may function as a tumor suppressor
GP:AF044670_1 Homo sapiens 33 kDa Vamp-associated protein (VAP33) mRNA, complete cds; VAP-33. [MASS=27318]/Vesicle-associated membrane protein (VAMP)-associated protein A, binds v-SNAREs, t-SNAREs, VAPB, and VAMP, predicted to be involved in vesicle transport and fusion
GP:AF004563_1 Homo sapiens hUNC18b alternatively-spliced mRNA, complete cds; alternatively-spliced; similar to rat n-Sec1. [MASS=68736]/Syntaxin-binding protein 1, binds syntaxins, may be involved in synaptic vesicle exocytosis
SWN:STX8_HUMAN Q9unk0 homo sapiens (human). syntaxin 8. 8/2001 [MASS=26907]/Syntaxin 8, member of the soluble NSF attachment protein receptor (SNARE) family, plays a role in endosome trafficking, may mediate vesicle docking and fusion, may regulate CFTR -mediated chloride currents
GP:AF032922_1 Homo sapiens syntaxin 4 binding protein UNC-18c (UNC-18c) mRNA, complete cds. [MASS=67764]/Syntaxin binding protein 3, binds syntaxin 4 (STX4), predicted to be involved in vesicle transport and docking and in neurotransmitter release
SW:STB2_HUMAN Q15833 homo sapiens (human). syntaxin binding protein 2 (unc-18 homolog 2) (unc-18b). 5/2000 [MASS=66439]/Syntaxin-binding protein 2, a member of the Sec1 family of proteins involved in synaptic transmission and secretion, may be involved in intracellular vesicular transport
SW:NSF_HUMAN P46459 homo sapiens (human). vesicular-fusion protein nsf (n-ethylmaleimide-sensitive fusion protein) (nem-sensitive fusion protein). 12/1998 [MASS=82654]/N-ethylmaleimide-sensitive factor, an ATPase involved in membrane fusion during exocytosis
SW:RAB7_HUMAN P51149 homo sapiens (human). ras-related protein rab-7. 7/1998 [MASS=23490]/Ras-related GTP-binding protein 7, a member of the rab family of proteins that is involved in vesicle transport, membrane fusion, and vacuole formation; implicated in Chediak Higashi Syndrome
SW:RB13_HUMAN P51153 homo sapiens (human). ras-related protein rab-13. 12/1998 [MASS=22774]/Ras-related GTP-binding protein 13, a putative RAB small monomeric GTPase that is likely to play a role in intracellular protein trafficking and cell adhesion
SW:DYN2_HUMAN P50570 homo sapiens (human). dynamin 2. 10/1996 [MASS=98018]/Dynamin II, member of a family of 100-kD guanosine triphosphatases, regulates budding of endocytic vesicles at the plasma membrane and may function in the formation of transport vesicles at the trans-Golgi
GP:AB002323_1 Human mRNA for KIAA0325 gene, partial cds. [MASS=238445]/Dynein cytoplasmic heavy chain 1, a member of a family of dynein ATPases that function as motor proteins, plays a role in mitotic spindle formation

PIR2:T03842 fission yeast Skb1 protein homolog - human [MASS=72786]/Protein arginine methyltransferase 5, methylates target proteins on arginine residues, may inhibit mitosis
SW:G25B_HUMAN P21181 homo sapiens (human), mus musculus (mouse), and bos taurus (bovine). g25k gtp-binding protein, brain isoform (gp) (cdc42 homolog). 12/1998 [MASS=21311]/Cell division cycle 42 (GTP binding protein 25kD), Rho GTPase involved in actin cytoskeleton organization, cell migration, cell cycle progression and apoptosis, downregulated in fibroblasts and macrophages from patients with Tangiers disease
SWN:STX8_HUMAN Q9unk0 homo sapiens (human). syntaxin 8. 8/2001 [MASS=26907]/Syntaxin 8, member of the soluble NSF attachment protein receptor (SNARE) family, plays a role in endosome trafficking, may mediate vesicle docking and fusion, may regulate CFTR -mediated chloride currents
SW:DYNA_HUMAN Q14203 homo sapiens (human). dynactin, 150 kda isoform (150 kda dynein-associated polypeptide) (dp-150) (dap-150) (p150-glued) (p135) (fragment). 5/2000 [MASS=140784]/Dynactin 1 ((p150, Glued (Drosophila) homolog), microtubule associated protein, interacts with HsEg5 (KNSL1), may play a role in cell division, level is reduced in apoptotic cells
SW:RAN_HUMAN P17080 homo sapiens (human). gtp-binding nuclear protein ran (tc4). 12/1998 [MASS=24354]/RAN, member of the ras family of GTP binding proteins, couples completion of DNA synthesis to mitosis and induces mitotic spindle formation, involved in nuclear transport of RNA and proteins, interacts with polyglutamate repeats of the androgen receptor
PIR2:T47172 hypothetical protein DKFZp762H186.1 - human (fragment) [MASS=55769]/Coronin actin-binding protein 1C, a member of the coronin-like protein family, has five WD repeats and a coiled-coil motif, a putative actin binding protein that may play a role in mitosis, cytokinesis, cell motility, signal transduction, and phagocytosis
SW:PP1A_HUMAN P08129 homo sapiens (human), mus musculus (mouse), rattus norvegicus (rat), and oryctolagus cuniculus (rabbit). serine/threonine protein phosphatase pp1-alpha 1 catalytic subunit (ec 3.1.3 [MASS=37512]/Protein phosphatase 1 catalytic subunit alpha isoform, plays roles in diverse cellular signal transduction processes that involve protein dephosphorylation, regulates of cell growth and apoptosis and may be a tumor suppressor
PIR2:T00387 KIAA0622 protein - human (fragment) [MASS=141604]/CLIP-associating protein 1 (Mast), a microtubule-associated protein with a putative role in centrosome separation and organization of the bipolar mitotic spindle
SW:CTOG_HUMAN Q14008 homo sapiens (human). ch-tog protein (colonic and hepatic tumor over-expressed protein) (kiaa0097). 5/2000 [MASS=225509]/Microtubule-associated protein that promotes rapid plus end microtubule assembly necessary for mitotic spindle assembly
SW:CUL2_HUMAN Q13617 homo sapiens (human). cullin homolog 2 (cul-2). 12/1998 [MASS=86956]/Cullin 2, has E3 ubiquitin ligase activity when present in a complex containing von Hippel Lindau tumor suppressor (VHL)- elogin B (TCEB2)-elogin C (TCEB1); modification by ubiquitin-like protein NEDD8 may be important for VHL tumor suppressor function
SW:BUB3_HUMAN O43684 homo sapiens (human). mitotic checkpoint protein bub3. 5/2000 [MASS=37155]/Budding uninhibited by benzimidazoles 3 homolog, involved in the mitotic spindle checkpoint, localization to unattached kinetochores suggests a role in detecting microtubule attachment, required for the localization of BUB1 and BUB1B to kinetochores
SW:IMB3_HUMAN O00410 homo sapiens (human). importin beta-3 subunit (karyopherin beta-3 subunit) (ran-binding protein 5). 12/1998 [MASS=123630]/Karyopherin beta 3, a subunit of the nuclear localization signal receptor complex and plays a role in nuclear import of ribosomal proteins; inhibited by interaction with hepatitis C virus nonstructural protein 5A
SW:IMA1_HUMAN P52294 homo sapiens (human). importin alpha-1 subunit (karyopherin alpha-1 subunit) (srp1-beta) (rag cohort protein 2) (nucleoprotein interactor 1) (npi-1). 12/1998 [MASS=60307]/Karyopherin alpha (importin alpha), a subunit of the nuclear localization sequence (NLS) receptor complex that binds to and mediates the nuclear import of RAG1 and STAT1
SW:COF1_HUMAN P23528 homo sapiens (human). cofilin, non-muscle isoform. 11/1997 [MASS=18502]/Non-muscle cofilin, an actin-binding protein that assists translocation of actin from the cytoplasm to the nucleus; inactivation through phosphorylation by LIM-kinase leads to actin depolymerization
SW:IMB1_HUMAN Q14974 homo sapiens (human). importin beta-1 subunit (karyopherin beta-1 subunit) (nuclear factor p97) (importin 90). 12/1998 [MASS=97234]/Importin beta (karyopherin beta 1), a subunit of the NLS (nuclear localization signal) receptor complex, binds to the nuclear pore complex and mediates translocation of the importin alpha-NLS complex into the nucleus
SW:ARS1_HUMAN O43681 homo sapiens (human). arsenical pump-driving atpase (ec 3.6.1.-) (arsenite-translocating atpase) (arsenical resistance atpase) (arsa) (asna-i). 5/2000 [MASS=38793]/Arsenite transporter ATP-binding homolog 1, a soluble putative arsenite transporter with similarity to bacterial arsA that has ATPase activity, may function in nucleocytoplasmic transport of a nucleolar component, and is stimulated by arsenite
SW:C211_HUMAN P53801 homo sapiens (human). putative surface glycoprotein c21orf1 precursor (c21orf3). 7/1999 [MASS=20324]/Pituitary tumor-transforming gene 1 interacting protein, binds to pituitary tumor-transforming gene (PTTG1) and may promote nuclear translocation of PPTG1 to the nucleus

SW:RAN_HUMAN P17080 homo sapiens (human). gtp-binding nuclear protein ran (tc4). 12/1998 [MASS=24354]/RAN, member of the ras family of GTP binding proteins, couples completion of DNA synthesis to mitosis and induces mitotic spindle formation, involved in nuclear transport of RNA and proteins, interacts with polyglutamate repeats of the androgen receptor
SW:IMB2_HUMAN Q92973 homo sapiens (human). importin beta-2 subunit (karyopherin beta-2 subunit) (transportin) (m9 region interaction protein) (mip). 5/2000 [MASS=101310]/Transportin (karyopherin beta 2), a component of the nuclear pore complex, mediates the import of HNRPA1 by binding the M9 nuclear localization sequence, also binds nuclear Ran GTP and nucleoporin Nup153; may mediate mRNA transport
SW:CRTC_HUMAN P27797 homo sapiens (human). calreticulin precursor (crp55) (calregulin) (hacbp) (erp60) (52 kda ribonucleoprotein autoantigen ro/ss-a). 7/1998 [MASS=48142]/Calreticulin, an ER-resident Ca2+-binding protein and lectin-binding chaperone involved in protein folding, Ca2+ homeostasis, cell adhesion, and integrin signaling; anti-angiogenic fragment, vasostatin, is a potential anti-cancer agent
SW:ER60_HUMAN P30101 homo sapiens (human). probable protein disulfide isomerase er-60 precursor (ec 5.3.4.1) (erp60) (58 kda microsomal protein) (p58) (grp58) (erp57). 7/1998 [MASS=56782]/Glucose regulated 58kDa protein, acts as a protein disulfide isomerase and possibly a protease, involved in folding and maturation of N-linked glycoproteins and MHC class I antigen processing; identified as a sperm antigen in immunological infertility
SW:PAB1_HUMAN P11940 homo sapiens (human). polyadenylate-binding protein 1 (poly(a) binding protein 1) (pabp 1). 7/1998 [MASS=70671]/Poly(A)-binding protein cytoplasmic 1, binds to poly(A) tails of mRNA and plays roles in regulating mRNA stability and translation, also implicated in mRNA transport from the nucleus to the cytoplasm
SW:RCC_HUMAN P18754 homo sapiens (human). regulator of chromosome condensation (cell cycle regulatory protein). 7/1999 [MASS=44969]/Regulator of chromosome condensation 1, a chromatin-binding protein that functions as a guanine nucleotide exchange factor for RAN, plays roles in nucleocytoplasmic transport, mitotic spindle formation, and nuclear envelope assembly
PIR2:T13159 E1B-55kDa-associated protein - human [MASS=95810]/E1B-55kDa-associated protein 5, a heterogeneous nuclear ribonucleoprotein involved in nucleocytoplasmic transport of adenovirus and cellular mRNAs, binds adenovirus early 1B (E1B-55 kD) protein and may regulate viral oncogenic transformation
GP:AF037448_1 Homo sapiens RRM RNA binding protein Gry-rbp (GRY-RBP) mRNA, complete cds; RRM RNA binding protein; Glycine, arginine and tyrosine-rich at C-terminus. [MASS=69633]/NS1 associated protein 1, component of the ApoB mRNA editosome involved in apolipoprotein B (APOB) mRNA editing, may bind RNA, may play a role in the regulation of mRNA splicing or transport from the nucleus
SW:CAS_HUMAN P55060 homo sapiens (human). cellular apoptosis susceptibility protein. 11/1997 [MASS=110314]/CSE1 chromosome segregation 1-like (yeast), importin-alpha nuclear export receptor, functions in toxin and TNF resistance and apoptosis, may regulate cell proliferation; corresponding gene is amplified in breast and colon carcinoma cell lines
SW:FXR2_HUMAN P51116 homo sapiens (human). fragile x mental retardation syndrome related protein 2. 10/1996 [MASS=74128]/Fragile X mental retardation gene autosomal homolog 2, binds mRNA, forms homomers or heteromers with FMR1 and FXR1, associates with the 60S ribosomal subunit and with actively translating polyribosomes, shuttles between the cytoplasm and nucleolus
GP:D89729_1 Homo sapiens mRNA for CRM1 protein, complete cds. [MASS=123386]/Exportin 1, a cell cycle-regulated nuclear export receptor, mediates NES containing protein export from the nucleus, also involved in nuclear export of HIV1 RNA, may be required for autophagy
SW:NTF2_HUMAN P13662 homo sapiens (human), and rattus norvegicus (rat). nuclear transport factor 2 (ntf-2) (placental protein 15) (pp15). 7/1999 [MASS=14478]/Nuclear transport factor 2, cytosolic protein involved in nuclear import of proteins containing nuclear localization signals mediated by GDP-RAN and nucleoporins
SW:ROA1_HUMAN P09651 homo sapiens (human). heterogeneous nuclear ribonucleoprotein a1 (helix-destabilizing protein) (single-strand binding protein) (hnrnp core protein a1). 11/1997 [MASS=38715]/Heterogeneous nuclear ribonucleoprotein A1, an RNA-binding protein involved in mRNA splicing and translational control, undergoes nucleocytoplasmic shuttling possibly for mRNA export and telomerase recruitment; an autoantigen in autoimmune disorders
SW:FXR1_HUMAN P51114 homo sapiens (human). fragile x mental retardation syndrome related protein 1. 10/1996 [MASS=69692]/Fragile X mental retardation autosomal homolog 1, binds FMR1, associates with mRNPs and with 60S ribosomal subunits, may have a role in the ribosomal and RNA metabolism of neurons; identified as a scleroderma autoantigen processed during apoptosis
SW:IMA1_HUMAN P52294 homo sapiens (human). importin alpha-1 subunit (karyopherin alpha-1 subunit) (srp1-beta) (rag cohort protein 2) (nucleoprotein interactor 1) (npi-1). 12/1998 [MASS=60307]/Karyopherin alpha (importin alpha), a subunit of the nuclear localization sequence (NLS) receptor complex that binds to and mediates the nuclear import of RAG1 and STAT1
SW:ACLY_HUMAN P53396 homo sapiens (human). atp-citrate (pro-s-)-lyase (ec 4.1.3.8) (citrate cleavage enzyme). 10/1996 [MASS=121420]/ATP citrate lyase, catalyzes the formation of acetyl-CoA and oxaloacetate from citrate and CoA with the concomitant hydrolysis of ATP to ADP and phosphate, involved in cholesterol and fatty acid synthesis, nutritionally regulated

GP:AB007851_1 Homo sapiens mRNA for 41-kDa phosphoribosylpyrophosphate synthetase-associated protein, complete cds. [MASS=40926]/Phosphoribosyl pyrophosphate synthetase-associated protein 2, a component of phosphoribosylpyrophosphate (PRPP) synthetase that is related to the other components of PRPP synthetase (PRPS1, PRPS2 and PRPSAP1)
GP:AB011173_1 Homo sapiens mRNA for KIAA0601 protein, partial cds. [MASS=96760]/KIAA0601 protein, a riboflavin-binding protein, member of a FAD dependent enzyme superfamily, component of the HDAC1 histone deacetylase complex, may be involved in gene silencing via covalent chromatin modification
SW:HS71_HUMAN P08107 homo sapiens (human). heat shock 70 kda protein 1 (hsp70.1) (hsp70-1/hsp70-2). 5/2000 [MASS=70052]/Heat shock 70 kDa protein 1A, a member of the HSP70 chaperone family involved in protein folding, translocation, and complex assembly, blocks AU-rich mRNA decay by nuclear sequestering of AU-rich binding protein, may contribute to celiac disease
SW:PUR8_HUMAN P30566 homo sapiens (human). adenylosuccinate lyase (ec 4.3.2.2) (adenylosuccinase) (asl) (asase). 5/2000 [MASS=54889]/Adenylosuccinate lyase, catalyzes two steps in adenosine monophosphate biosynthesis; deficiency is associated with psychomotor retardation, epilepsy, and autism
SW:AMD2_HUMAN Q01433 homo sapiens (human). amp deaminase 2 (ec 3.5.4.6) (amp deaminase isoform l). 11/1997 [MASS=88198]/Adenosine monophosphate deaminase 2 (isoform L), catalyzes the deamination of adenosine monophosphate to form inosine monophosphate in purine nucleotide metabolism
PIR2:S71460 ribose-phosphate pyrophosphokinase (EC 2.7.6.1) 39K regulatory chain - human [MASS=39480]/Phosphoribosyl pyrophosphate (PRPP) synthetase 1, generates PRPP, which is required for de novo purine and pyrimdine biosynthesis; mutations causing superactivity are associated with gout and neurological impairment
SW:SYA_HUMAN P49588 homo sapiens (human). alanyl-trna synthetase (ec 6.1.1.7) (alanine--trna ligase) (alars). 7/1998 [MASS=106801]/Alanyl-tRNA synthetase, aminoacylates its cognate tRNA with alanine for protein biosynthesis, acts as an autoantigen in patients with polymyositis
SWN:ENT1_HUMAN Q99808 homo sapiens (human). equilibrative nucleoside transporter 1 (equilibrative nitrobenzylmercaptopurine riboside-sensitive nucleoside transporter) (equilibrative nbmpr-sensitive nucle [MASS=50088]/Solute carrier family 29 member 1 (equilibrative nucleoside transporter 1), functions in the transport of physiologic nucleosides and chemotherapeutic nucleoside analog drugs, inhibited by nitrobenzylthioinosine, dipyridamole, and dilazep
SW:CST1_HUMAN Q05048 homo sapiens (human). cleavage stimulation factor, 50 kda subunit (cstf 50 kda subunit) (cf-1 50 kda subunit). 7/1998 [MASS=48358]/Cleavage stimulation factor subunit 1, the 50 kDa subunit of the cleavage stimulation factor complex required for pre-mRNA polyadenylation and 3'-end cleavage, interacts with BARD1 and the C-terminal domain of the RNA polymerase II large subunit
SW:SYQ_HUMAN P47897 homo sapiens (human). glutaminyl-trna synthetase (ec 6.1.1.18) (glutamine--trna ligase) (glnrs). 5/2000 [MASS=87799]/Glutaminyl-tRNA synthetase, aminoacylates cognate tRNAs with glutamine for protein biosynthesis, also suppresses FAS (TNFRSF6)-mediated apoptosis by inhibiting ASK1 (MAP3K5) kinase activity, contains N-terminal appended and C-terminal catalytic domains
SW:IMD2_HUMAN P12268 homo sapiens (human). inosine-5'-monophosphate dehydrogenase 2 (ec 1.1.1.205) (imp dehydrogenase 2) (impdh-ii) (impd 2). 5/2000 [MASS=55805]/Inosine monophosphate dehydrogenase type 2, catalyzes the oxidation of inosine monophosphate to xanthosine monophosphate in GTP biosynthesis, required for T cell activation, a target for immunosuppressive and anticancer chemotherapy
SW:PUR6_HUMAN P22234 homo sapiens (human). multifunctional protein ade2 [includes: phosphoribosylaminoimidazole-succinocarboxamide synthase (ec 6.3.2.6) (saicar synthetase); phosphoribosylaminoimidazol [MASS=47079]/SAICAR (phosphoribosylaminoimidazole-succinocarboxamide) synthetase and AIR (phosphoribosylaminoimidazole) carboxylase, a bifunctional protein required for de novo purine biosynthesis
SW:RINI_HUMAN P13489 homo sapiens (human). placental ribonuclease inhibitor (ribonuclease/angiogenin inhibitor) (rai) (ri). 12/1998 [MASS=49842]/Ribonuclease and angiogenin inhibitor, tightly binds and inhibits alkaline and neutral ribonucleases and angiogenin, functions in mRNA degradation and inhibition of HT-29 human colon adenocarcinoma cell binding to angiogenin (ANG)
GP:AF132941_1 Homo sapiens CGI-07 protein mRNA, complete cds. [MASS=57585]/Protein with moderate similarity to S. cerevisiae Nmd3p, which is a protein involved in the nuclear export of 60S ribosomal subunits
PIR2:A57017 RNase L inhibitor - human [MASS=67559]/Ribonuclease L inhibitor, inhibits the nuclease activity and 2-5A binding ability of RNase L, may be induced by HIV-1 to inhibit the 2-5A/RNase L pathway, can inhibit the antiviral activity of interferon when overexpressed
SW:NPM_HUMAN P06748 homo sapiens (human). nucleophosmin (npm) (nucleolar phosphoprotein b23) (numatrin) (nucleolar protein no38). 5/2000 [MASS=32575]/Nucleophosmin (numatrin), a nucleic acid-binding phosphoprotein involved in apoptosis, abundant in tumor cells; gene fusion with anaplastic lymphoma kinase (ALK) is detected in non-Hodgkin's lymphoma and fusion with MLF1 is seen in acute myeloid leukemia
SW:NDK6_HUMAN O60361 homo sapiens (human). putative nucleoside diphosphate kinase (ec 2.7.4.6) (ndk) (ndp kinase). 12/1998 [MASS=15529]/Nucleoside diphosphate kinase B, a transcription factor and endodeoxyribonuclease that binds to the Myc promoter, may function in DNA repair, may suppress metastasis in some tumors, displays reduced expression in breast carcinoma cells

SW:PAB1_HUMAN P11940 homo sapiens (human). polyadenylate-binding protein 1 (poly(a) binding protein 1) (pabp 1). 7/1998 [MASS=70671]/Poly(A)-binding protein cytoplasmic 1, binds to poly(A) tails of mRNA and plays roles in regulating mRNA stability and translation, also implicated in mRNA transport from the nucleus to the cytoplasm
SWN:SYFB_HUMAN Q9nsd9 homo sapiens (human). phenylalanyl-trna synthetase beta chain (ec 6.1.1.20) (phenylalanine--trna ligase beta chain) (phers) (protein hspc173). 8/2001 [MASS=66130]/Phenylalanyl-tRNA synthetase beta-subunit, regulatory subunit that forms heterodimers with the catalytic alpha subunit (FARSL), involved in protein synthesis, may play a role in tumorigenic events
SW:ROF_HUMAN P52597 homo sapiens (human). heterogeneous nuclear ribonucleoprotein f (hnrnp f). 11/1997 [MASS=45672]/Heterogeneous nuclear ribonucleoprotein F, an RNA binding protein which contains quasi-RRMs (RNA recognition motifs) and plays a role in pre-mRNA splicing
PIR2:T13159 E1B-55kDa-associated protein - human [MASS=95810]/E1B-55kDa-associated protein 5, a heterogeneous nuclear ribonucleoprotein involved in nucleocytoplasmic transport of adenovirus and cellular mRNAs, binds adenovirus early 1B (E1B-55 kD) protein and may regulate viral oncogenic transformation
no_description_avail/Heterogeneous nuclear ribonucleoprotein R, a putative pre-mRNA processing protein that contains three RNA recognition domains and an RGG domain, interacts with survival motor neuron protein and is an autoantigen in autoimmune disease
GP:U85625_1 Homo sapiens ribonuclease 6 precursor, mRNA, complete cds. [MASS=29481]/Ribonuclease 6 precursor, a putative ribonuclease that plays a role in the negative regulation of proliferation, may be involved in senescence, may be a class II tumor suppressor, downregulated in ovarian cancer and in ovarian cancer cell lines
GP:AF037448_1 Homo sapiens RRM RNA binding protein Gry-rbp (GRY-RBP) mRNA, complete cds; RRM RNA binding protein; Glycine, arginine and tyrosine-rich at C-terminus. [MASS=69633]/NS1 associated protein 1, component of the ApoB mRNA editosome involved in apolipoprotein B (APOB) mRNA editing, may bind RNA, may play a role in the regulation of mRNA splicing or transport from the nucleus
SW:PYR1_HUMAN P27708 homo sapiens (human). cad protein [includes: glutamine-dependent carbamoyl-phosphate synthase (ec 6.3.5.5); aspartate carbamoyltransferase (ec 2.1.3.2); dihydroorotase (ec 3.5.2.3)] [MASS=242917]/Carbamoylphosphate synthetase 2-aspartate transcarbamylase-dihydroorotase, a trifunctional enzyme that catalyzes the first three steps of pyrimidine biosynthesis
SW:ROK_HUMAN Q07244 homo sapiens (human), and rattus norvegicus (rat). heterogeneous nuclear ribonucleoprotein k (hnrnp k) (dc-stretch binding protein) (csbp) (transformation upregulated nuclear protein [MASS=50976]/Heterogeneous nuclear ribonucleoprotein K, a transcription factor which binds to poly(C) of RNA and DNA and is involved in RNA processing, gene transcription and translational controls, may induce apoptosis and play a role in viral infection
SW:SMD3_HUMAN P43331 homo sapiens (human). small nuclear ribonucleoprotein sm d3 (snrnp core protein d3) (sm-d3). 10/1996 [MASS=13916]/Small nuclear ribonucleoprotein D3, part of a multimeric complex involved in biogenesis of snRNPs and mRNA splicing, interacts with the spinal muscular atrophy disease protein (SMN); autoantigen for antibodies associated with systemic lupus erythematosus
SW:PSS1_HUMAN P48651 homo sapiens (human). phosphatidylserine synthase i (serine-exchange enzyme i) (ec 2.7.8.-) (kiaa0024). 11/1997 [MASS=55528]/3'-phosphoadenosine 5'-phosphosulfate synthase 1, bifunctional polypeptide with ATP sulfurylase and adenosine 5'-phosphosulfate kinase activites, required for the synthesis of the sulfonate donor 3'-phosphoadenosine 5'-phosphosulfate
SW:ROA0_HUMAN Q13151 homo sapiens (human). heterogeneous nuclear ribonucleoprotein a0 (hnrnp a0). 5/2000 [MASS=30841]/Heterogeneous nuclear ribonucleoprotein A0, has triplet repeats, two consensus sequence-type RNA-binding domains, and a glycine-rich auxiliary domain, found in low abundance hnRNP complexes
SW:ROH1_HUMAN P31943 homo sapiens (human). heterogeneous nuclear ribonucleoprotein h (hnrnp h). 11/1997 [MASS=49229]/Heterogeneous nuclear ribonucleoprotein H1, a pre-mRNA splicing factor that is a component of a complex that mediates post-transcriptional processing of primary transcripts
SW:DDX1_HUMAN Q92499 homo sapiens (human). dead box protein 1 (dead box protein-retinoblastoma) (dbp-rb). 5/2000 [MASS=82432]/DEAD box protein 1, a member of the DEAD-H box ATP-dependent RNA helicase protein family, plays a role in the processing of pre-mRNAs, may interact with CSTF2; corresponding gene is coamplified with MYC in some neuroblastoma and retinoblastoma cell lines
PIR2:JW0079 heterogeneous nuclear ribonucleoprotein homolog JKTBP [imported] - human [MASS=33589]/Heterogeneous nuclear ribonucleoprotein D-like, an RNA- and DNA-binding protein that may play a role in mRNA biogenesis
GP:AC003972_1 Homo sapiens DNA from chromosome 19, cosmid R33485 containing pNORF1, complete sequence; human type 1 RNA helicase; DPS similarity to (U59323) type 1 RNA helicase pNORF1 [Homo sapiens]; Score. [MASS=123036]/regulator of nonsense transcripts 1 (nonsense mrna reducing factor 1) (norf1) (up-frameshift suppressor 1 homolog). 10/2001 [MASS=124345]
SW:RUXF_HUMAN Q15356 homo sapiens (human). small nuclear ribonucleoprotein f (snrnp-f) (sm protein f). 7/1999 [MASS=9725]/Sm protein F, a spliceosomal snRNA-associated Sm core protein that is involved in the biogenesis of the snRNPs; a target of autoantibodies in patients with the autoimmune disease systemic lupus erythematosus
GP:AF177344_1 Homo sapiens clone HC90 unknown mRNA. [MASS=30998]/ weakly similar to a methyltransferase/Member of the RNA methyltransferase family, which catalyze 2'-O-methylation of ribose groups in R

PIR2:T09073 splicing factor Sip1 - human [MASS=128875]/Splicing factor arginine serine rich 2 interacting protein, a SR domain family protein that interacts with the RNA polymerase II C-terminal domain and several splicing factors, is essential in mRNA splicing and possibly spliceosome A-complex formation
PIR2:I55595 splicing factor - human [MASS=58657]/Splicing factor CC1.3, a novel nuclear protein and putative member of the SR family of alternative splicing factors; target of autoantibodies from a patient with hepatocellular carcinoma
PIR2:S78046 ribonuclease 6 (EC 3.1.27.-) precursor - human [MASS=21941]/Ribonuclease k6, a ribonuclease of the ribonuclease A superfamily, possibly functions in host defense
SW:DRN2_HUMAN O00115 homo sapiens (human). deoxyribonuclease ii precursor (ec 3.1.22.1) (dnase ii) (acid dnase) (lysosomal dnase ii) (r31240_2). 7/1999 [MASS=39581]/Deoxyribonuclease II lysosomal, an acid-activated DNA nicking enzyme, may participate in DNA fragmentation during apoptosis, induces apoptotic chromosome condensation when transfected into cell lines
SW:SMD2_HUMAN P43330 homo sapiens (human). small nuclear ribonucleoprotein sm d2 (snrnp core protein d2) (sm-d2). 10/1996 [MASS=13527]/Small nuclear ribonucleoprotein D2 polypeptide, one of seven common core snRNP proteins involved in snRNP biogenesis and pre-mRNA splicing, autoantigen for anti-Sm antibodies produced by individuals with systemic lupus erythematosus
SW:U2AF_HUMAN P26368 homo sapiens (human). splicing factor u2af 65 kda subunit (u2 auxiliary factor 65 kda subunit) (u2 snrnp auxiliary factor large subunit). 12/1998 [MASS=53501]/U2 small nuclear ribonucleoprotein auxiliary factor (65 kDa), a component of U2 small nucleoprotein auxiliary factor, which is necessary for mRNA splicing, binds to pre-mRNA
GP:D21163_1 Human mRNA for KIAA0031 gene, complete cds; similar to human elongation factor 2 mRNA (HSEF2).. [MASS=109436]/U5 snRNP-specific protein 116 kD, a spliceosome component with GTPAse activity, plays a role in mRNA splicing and processing
SW:RU17_HUMAN P08621 homo sapiens (human). u1 small nuclear ribonucleoprotein 70 kda (u1 snrnp 70 kda) (snrp70). 11/1995 [MASS=70081]/U1 small nuclear 70 kDa ribonucleoprotein, involved in pre mRNA splicing, acts as an autoantigen in systemic lupus erythematosus and mixed connective tissue disease
PIR2:A54601 RNA-binding protein AUF1 - human [MASS=31200]/Heterogeneous nuclear ribonucleoprotein D (AU-rich element RNA-binding protein 1 37kD), an RNA and DNA-binding protein which binds to AU-rich elements in the 3' untranslated regions of mRNAs and mediates their degradation
SW:NHPX_HUMAN P55769 homo sapiens (human). nhp2/rs6 family protein yel026w homolog (high mobility group-like nuclear protein 2 homolog) (otk27). 5/2000 [MASS=14174]/Non-histone chromosome protein 2 (S. cerevisiae)-like 1, a member of a family of RNP-associated proteins, a component of the spliceosome and rRNA processing machinery, recognizes a shared stem-internal loop-stem structure in its RNA targets
SW:DDX5_HUMAN P17844 homo sapiens (human). probable rna-dependent helicase p68 (dead-box protein p68) (dead box protein 5). 7/1998 [MASS=69148]/DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 5 (RNA helicase 68kD), a ATP-dependent RNA helicase that has ATP-independent RNA renaturation activity and catalyses branch migration, binds estrogen receptor alpha and function as a transcriptional coactivator
SW:U2AG_HUMAN Q01081 homo sapiens (human). splicing factor u2af 35 kda subunit (u2 auxiliary factor 35 kda subunit) (u2 snrnp auxiliary factor small subunit). 12/1998 [MASS=27872]/U2(RNU2) small nuclear RNA auxiliary factor 1, functions as a pre-mRNA splicing protein, involved in the functional recognition of the 3' splice site AG dinucleotide, interacts with ZNF265 protein involved in alternative splicing
SW:ROU_HUMAN Q00839 homo sapiens (human). heterogenous nuclear ribonucleoprotein u (hnrnp u) (scaffold attachment factor a) (saf-a). 5/2000 [MASS=90479]/Heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A), binds RNA, binds EP300 in a complex that binds scaffold-matrix attachment regions of TOP1, involved in chromatin structure, apoptosis, and perhaps RNA processing and transcription
SW:ROA1_HUMAN P09651 homo sapiens (human). heterogeneous nuclear ribonucleoprotein a1 (helix-destabilizing protein) (single-strand binding protein) (hnrnp core protein a1). 11/1997 [MASS=38715]/Heterogeneous nuclear ribonucleoprotein A1, an RNA-binding protein involved in mRNA splicing and translational control, undergoes nucleocytoplasmic shuttling possibly for mRNA export and telomerase recruitment; an autoantigen in autoimmune disorders
SW:DD17_HUMAN Q92841 homo sapiens (human). probable rna-dependent helicase p72 (dead-box protein p72) (dead box protein 17). 5/2000 [MASS=72371]/DEAD H box protein 17, a member of the DEAD box family of RNA-dependent ATPases and ATP-dependent RNA helicases, a component of an estrogen receptor alpha (ESR) transcriptional coactivator complex
SW:Y017_HUMAN Q15393 homo sapiens (human). hypothetical protein kiaa0017. 5/2000 [MASS=44606]/ Homo sapiens mRNA for SAP 130 spliceosomal protein/Splicing factor 3b subunit 3, a component of the U2 snRNP-associated protein complex SF3b that plays a role in spliceosome assembly, interacts with STAGA and TFTC complexes implicated in DNA repair, chromatin modification, and transcription
SW:NR54_HUMAN Q15233 homo sapiens (human). 54 kda nuclear rna-binding protein (p54(nrb)) (p54nrb) (55 kda nuclear protein) (nmt55). 5/2000 [MASS=54232]/Non-POU-domain-containing octamer-binding nuclear protein, binds DNA and RNA, and implicated in transcription and pre-mRNA splicing; a fusion partner with TFE3 in papillary renal cell carcinoma
SW:SFR7_HUMAN Q16629 homo sapiens (human). splicing factor, arginine/serine-rich 7 (splicing factor 9g8). 5/2000 [MASS=27367]/Splicing factor arginine serine rich 7, a splicing factor of the SR protein family containing an RNA binding domain (RBD) and a serine/arginine (SR) domain that is implicated in alternative pre-mRNA splicing

SW:TRFL_HUMAN P02788 homo sapiens (human). lactotransferrin precursor (lactoferrin). 7/1999 [MASS=78338]/Lactotransferrin, a member of the transferrin family, transports iron in extracellular fluid and may have serine protease activity, has antimicrobial, antifugual, and antiviral activity, potential theraputic or diagnostic target for autoimmune diseases
SW:SAH2_HUMAN O43865 homo sapiens (human). putative adenosylhomocysteinase (ec 3.3.1.1) (s-adenosyl-l-homocysteine hydrolase) (adohcyase). 12/1998 [MASS=55628]/Protein with high similarity to s-adenosylhomocysteine hydrolase (mouse Ahcy), which reversably converts S-adenosylhomocysteine to adenosine and homocysteine and may be associated with epilepsy, member of the S-adenosylhomocysteine hydrolase family
SW:COMT_HUMAN P21964 homo sapiens (human). catechol o-methyltransferase, membrane-bound form (ec 2.1.1.6) (mb-comt) [contains: catechol o-methyltransferase, soluble form (s-comt)]. 5/2000 [MASS=30037]/Catechol-O-methyltransferase, a methyltransferase involved in the degradation of catecholamine neurotransmitters and catechol drugs, variant forms are associated with increased risks for obsessive-compulsive disorder and schizophrenia
SW:ESTD_HUMAN P10768 homo sapiens (human). esterase d (ec 3.1.1.1). 5/2000 [MASS=31463]/Esterase D (formylglutathione hydrolase), a carboxylesterase that may be involved in detoxification
SW:GLNA_HUMAN P15104 homo sapiens (human). glutamine synthetase (ec 6.3.1.2) (glutamate--ammonia ligase). 12/1998 [MASS=42064]/Glutamine synthase, catalyzes the condensation of glutamate and ammonia to form glutamine, may clear L-glutamate from synapses, reduced expression in the brain and abnormal presence in cerebral spinal fluid is associated with Alzheimer disease
SW:MRP1_HUMAN P33527 homo sapiens (human). multidrug resistance-associated protein 1. 5/2000 [MASS=171561]/ATP-binding cassette subfamily C member 1 (multiple drug resistance protein 1), an ATP-binding cassette transporter that acts as a multidrug efflux pump conferring resistance to lipophilic drugs and chemotherapeutic agents
PIR2:T46412 ubiquitin--protein ligase (EC 6.3.2.19) NEDD4 - human (fragment) [MASS=95283]/Neural cell precursor expressed developmentally downregulated 4, ubiquitin-protein ligase with multiple WW domains, binds to and reduces the activity of epithelial sodium channels, may play a role in neural differentiation, regulated by kinase SGK
GP:AC005545_2 Homo sapiens chromosome 19, cosmid R26634, complete sequence; vesicle coat component, similar to alpha and gamma adaptins. [MASS=121170]/Adaptor-related protein complex 3 delta 1 subunit, a component of the AP-3 complex, involved in intracellular vesicle transport
SW:PUR6_HUMAN P22234 homo sapiens (human). multifunctional protein ade2 [includes: phosphoribosylaminoimidazole-succinocarboxamide synthase (ec 6.3.2.6) (saicar synthetase); phosphoribosylaminoimidazol [MASS=47079]/SAICAR (phosphoribosylaminoimidazole-succinocarboxamide) synthetase and AIR (phosphoribosylaminoimidazole) carboxylase, a bifunctional protein required for de novo purine biosynthesis
SW:PON2_HUMAN Q15165 homo sapiens (human). serum paraoxonase/arylesterase 2 (ec 3.1.1.2) (ec 3.1.8.1) (pon 2) (serum aryldiakylphosphatase 2) (a-esterase 2) (aromatic esterase 2). 7/1999 [MASS=39398]/Paraoxonase 2 (arylesterase 2), an antioxidant that protects low density lipoprotein against peroxidation, member of a family of proteins that hydrolyze toxic organophosphates; gene mutations are associated with an increased risk of coronary heart disease
SW:DOPD_HUMAN P30046 homo sapiens (human). d-dopachrome tautomerase (phenylpyruvate tautomerase ii). 5/2000 [MASS=12581]/D-dopachrome tautomerase, a tyrosinase-related zinc metalloenzyme that catalyzes the conversion of D-dopachrome to 5,6-dihydroxyindole in the melanin biosynthetic pathway, specifically expressed in melanin-producing cells, and is a melanoma tumor antigen
SW:HEMZ_HUMAN P22830 homo sapiens (human). ferrochelatase precursor (ec 4.99.1.1) (protoheme ferro-lyase) (heme synthetase). 12/1998 [MASS=47834]/Ferrochelatase (protoheme ferrochelatase), catalyzes the final step in the heme biosynthetic pathway by inserting ferrous iron into protoporphyrin IX to form heme; reduced activity and mutations in the corresponding gene are associated with protoporphyria
GP:AF126782_1 Homo sapiens retinal short-chain dehydrogenase/reductase retSDR4 mRNA, complete cds. [MASS=32268]/Short-chain dehydrogenase-reductase 1, catalyzes the NADPH-dependent reduction of all-trans-retinal to retinol, may play a role in visual system phototransduction; the corresponding gene is deleted in many neuroblastoma cell lines with MYCN amplification
SW:A4_HUMAN P05067 homo sapiens (human). alzheimer's disease amyloid a4 protein precursor (protease nexin-ii) (pn-ii) (appi) [contains: beta-amyloid protein (beta-app) (a-beta)]. 5/2000 [MASS=86943]/Amyloid beta (A4) precursor protein, cell surface protease inhibitor that reduces copper, deposits of proteolytic peptide products are found in Alzheimer's disease and Down syndrome brains, deficiency is associated with early-onset Alzheimer's disease
SW:FLRE_HUMAN P30043 homo sapiens (human). flavin reductase (ec 1.6.99.1) (fr) (nadph-dependent diaphorase) (nadph-flavin reductase) (flr) (biliverdin reductase b) (ec 1.3.1.24) (bvr-b) (biliverdin-ix b [MASS=21988]/Biliverdin-IX beta reductase (NADPH-flavin reductase), catalyzes the conversion of biliverdin-IX beta to bilirubin-IX beta, the major heme catabolite produced during early fetal development; also has NAD(P)H-linked flavin reductase activity
SW:HYEP_HUMAN P07099 homo sapiens (human). epoxide hydrolase (ec 3.3.2.3) (microsomal epoxide hydrolase) (epoxide hydratase). 10/1996 [MASS=52949]/Microsomal epoxide hydrolase, hydrates reactive epoxides to form dihydrodiols, detoxifies cytochrome p450-generated epoxides from the metabolism of xenobiotics; polymorphisms of the gene may affect risk of cancer, lung disease, and preeclampsia

SW:PEBP_HUMAN P30086 homo sapiens (human). phosphatidylethanolamine-binding protein (pebp) (neuropolypeptide h3). 7/1999 [MASS=20926]/Phosphatidylethanolamine-binding protein, binds GTP, may regulate cAMP accumulation, enhance acetylcholine synthesis, and play a role in organizing phospholipids in the myelin sheath
SW:IPYR_HUMAN Q15181 homo sapiens (human). inorganic pyrophosphatase (ec 3.6.1.1) (pyrophosphate phospho-hydrolase) (ppase). 5/2000 [MASS=32660]/Inorganic pyrophosphatase, catalyzes the hydrolysis of pyrophosphate to inorganic phosphate
SW:TRSR_HUMAN P02786 homo sapiens (human). transferrin receptor protein (tr) (antigen cd71) (t9) (p90). 7/1999 [MASS=84901]/Transferrin receptor, binds and internalizes the iron carrier transferrin, involved in iron homeostasis, important for neurologic development and likely erythropoiesis, expression is deregulated in anemia, hemochromatosis, and Friedreich's ataxia
SW:DYL1_HUMAN Q15701 homo sapiens (human), mus musculus (mouse), rattus norvegicus (rat), and oryctolagus cuniculus (rabbit). dynein light chain 1, cytoplasmic (protein inhibitor of neuronal nitric oxid [MASS=10366]/Dynein cytoplasmic light polypeptide (protein inhibitor of nitric oxide synthase), a component of the cytoplasmic dynein motor complex, inhibits neuronal nitric oxide synthase (NOS1), regulates the proapoptotic activity of BCL2-interacting protein BCL2L11
PIR2:I37405 polypeptide N-acetylgalactosaminyltransferase (EC 2.4.1.41) - human [MASS=64733]/N-acetylgalactosaminyltransferase T1, enzyme that initiates O-glycosylation; inhibition affects the sensitivity of tumors cells to immune killer cells
SW:OGT1_HUMAN O15294 homo sapiens (human). udp-n-acetylglucosamine--peptide n-acetylglucosaminyltransferase 100 kda subunit (ec 2.4.1.-) (o-glcnac transferase p100 subunit). 5/2000 [MASS=103012]/O-linked N-acetylglucosamine transferase (UDP-N-acetylglucosamine:polypeptide-N-acetylglucosaminyltransferase), enzyme that functions in O-glycosylation, may be involved in insulin secretion and glucose homeostasis, may play a role in signal transduction
SW:MMSA_HUMAN Q02252 homo sapiens (human). methylmalonate-semialdehyde dehydrogenase [acylating] (ec 1.2.1.27) (mmsdh) (fragment). 12/1998 [MASS=46606]/Methylmalonate-semialdehyde dehydrogenase (2-methyl-3-oxopropanoate:NAD+ oxidoreductase (CoA-propanoylating)), a member of the aldehyde dehydrogenase superfamily; deficiency is associated with developmental delay
SW:AOFB_HUMAN P27338 homo sapiens (human). amine oxidase [flavin-containing] b (ec 1.4.3.4) (monoamine oxidase) (mao-b). 12/1998 [MASS=58763]/Monoamine oxidase B, an oxidase involved in the metabolism of various biologically important amines such as dopamine, requires covalently bound FAD as a cofactor, may play a role in aging and behavior
SW:C1TC_HUMAN P11586 h c-1-tetrahydrofolate synthase, cytoplasmic (c1-thf synthase) [includes: methylenetetrahydrofolate dehydrogenase (ec 1.5.1.5); methenyltetrahydrofolate cyclohydrolase (ec 3.5.4.9); [MASS=101428]/C1-Tetrahydrofolate synthase, a trifunctional enzyme with 10-formyltetrahydrofolate synthetase, 5,10-methenyltetrahydrofolate cyclohydrolase, and 5,10-methylenetetrahydrofolate dehydrogenase activities; mutation associated with risk of neural tube disease
SW:FRIH_HUMAN P02794 homo sapiens (human). ferritin heavy chain (ferritin h subunit). 7/1999 [MASS=21094]/Ferritin heavy polypeptide 1, a ferrioxidase involved in iron storage, heme biosynthesis, cell growth, oxidative stress response, and transcription, may play a role in iron transport, apoptosis, cell differentiation, and response to bacteria
(human). amine oxidase [flavin-containing] a (ec 1.4.3.4) (monoamine oxidase) (mao-a). 12/1998 [MASS=59682]/Monoamine oxidase A, an enzyme involved in degradation of amine neurotransmitters, may be associated with neuropsychiatric disorders, including impulsive aggression and panic disorder, and Parkinson disease
GP:AF277719_1 Homo sapiens 3 beta-hydroxy-delta 5-C27-steroid oxidoreductase mRNA, complete cds. [MASS=40930]/3 beta-hydroxy-delta 5-C27-steroid oxidoreductase, predicted to function in bile acid biosynthesis; variant form is associated with progressive intrahepatic cholestasis
SW:SPHM_HUMAN P51688 homo sapiens (human). n-sulphoglucosamine sulphohydrolase precursor (ec 3.10.1.1) (sulfoglucosamine sulfamidase) (sulphamidase). 5/2000 [MASS=56695]/N-sulfoglucosamine sulfohydrolase (sulfamidase), catalyzes the hydrolysis of the N-linked sulfate group from heparan sulfate; mutation of the corresponding gene causes the lysosomal storage disease Sanfilippo A syndrome (mucopolysaccharidosis type IIIA)
GP:X92689_1 Homo sapiens mRNA for UDP-GalNAc:polypeptide N-acetylgalactosaminyl transferase (GalNAc-T3). [MASS=72638]/N-acetylgalactosaminyltranferase T3 (UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 3), enzyme that initiates O-glycosylation; elevated levels may be associated with differentiation of adenocarcinomas
SW:ATCK_HUMAN P98194 homo sapiens (human). calcium-transporting atpase 2c1 (ec 3.6.1.38) (atp-dependent ca2+ pump pmr1). 5/2000 [MASS=100606]/ATPase (Ca2+ transporting) type 2c member I, a a Ca2+-transporting P-type ATPase involved in Ca2+ homeostasis that may also may play a role in epidermal differentiation; mutations in the gene cause Hailey-Hailey disease, a blistering skin disease
peroxisomal 2,4-dienoyl-CoA reductase /2,4-dienoyl-CoA reductase, an auxiliary beta-oxidation enzyme of the mitochondrion that participates in the metabolism of unsaturated fatty enoyl-CoA esters with double bonds in both odd- and even-numbered positions
SW:SORC_HUMAN P30626 homo sapiens (human). sorcin (22 kda protein) (cp-22) (v19). 11/1997 [MASS=21676]/Sorcin, an EF-hand calcium-binding protein, may be involved in multidrug resistance, a potential modulator of intracellular calcium levels through interaction with the ryanodine receptor

SW:IPYR_HUMAN Q15181 homo sapiens (human). inorganic pyrophosphatase (ec 3.6.1.1) (pyrophosphate phospho-hydrolase) (ppase). 5/2000 [MASS=32660]/Inorganic pyrophosphatase, catalyzes the hydrolysis of pyrophosphate to inorganic phosphate
SW:RO60_HUMAN P10155 homo sapiens (human). 60 kda ro protein (60 kda ribonucleoprotein ro) (rornp) (sjogren syndrome type a antigen (ss-a)). 2/1996 [MASS=60643]/Sjogren syndrome antigen A2, RNA-binding protein that is a component of ribonucleoprotein complexes in association with small cytoplasmic Y RNAs, an autoantigen in systemic rheumatic diseases such as lupus and Sjogren syndrome
SW:PRS8_HUMAN P47210 homo sapiens (human). 26s protease regulatory subunit 8 (proteasome subunit p45) (thyroid hormone receptor interacting protein 1) (trip1). 11/1997 [MASS=45653]/ATPase subunit 5 of the 26S proteasome, which is a multicatalytic proteinase complex involved in cellular protein degradation; may also function as a transcriptional modulator
SW:PLAK_HUMAN P14923 homo sapiens (human). junction plakoglobin (desmoplakin iii). 11/1997 [MASS=81498]/Junction plakoglobin (gamma catenin), links cell-cell adhesion molecules with the cytoskeleton, involved in desmosome organization, cell adhesion, cell prolifiration, apoptosis; loss of heterozygosity is associated with breast and ovarian tumors
GP:BC000441_1 Homo sapiens, junction plakoglobin, clone MGC:8404 IMAGE:2820715, mRNA, complete cds. [MASS=81727]/Junction plakoglobin (gamma catenin), links cell-cell adhesion molecules with the cytoskeleton, involved in desmosome organization, cell adhesion, cell prolifiration, apoptosis; loss of heterozygosity is associated with breast and ovarian tumors
SW:CTNB_HUMAN P35222 homo sapiens (human). beta-catenin. 2/1996 [MASS=85497]/Beta catenin, links cadherins to the cytoskeleton, may act as a component of the Wnt signal transduction pathway transmitting nuclear signals via a complex with LEF1 and TCF transcription factors; mutations in the gene are associated with various cancers
SW:HIP_HUMAN P50502 homo sapiens (human). hsc70-interacting protein (progesterone receptor-associated p48 protein) (putative tumor suppressor st13). 5/2000 [MASS=41332]/Suppression of tumorigenicity 13 (Hsp70-interacting protein), acts as an Hsc70 cochaperone, contains tetratricopeptide repeats, participates in protein complex assembly, heat shock response, and lysosomal transport; downregulated in colorectal carcinoma
PIR2:T46412 ubiquitin--protein ligase (EC 6.3.2.19) NEDD4 - human (fragment) [MASS=95283]/Neural cell precursor expressed developmentally downregulated 4, ubiquitin-protein ligase with multiple WW domains, binds to and reduces the activity of epithelial sodium channels, may play a role in neural differentiation, regulated by kinase SGK
SW:BTF3_HUMAN P20290 homo sapiens (human). transcription factor btf3 (rna polymerase b transcription factor 3). 12/1998 [MASS=22168]/Basic transcription factor 3, a general transcription factor that forms a stable complex with RNA polymerase II and is required for transcriptional initiation by RNA polymerase II, and may be a substrate for protein kinase CK2 (CSNK2B)
SW:ENOA_HUMAN P06733 homo sapiens (human). alpha enolase (ec 4.2.1.11) (2-phospho-d-glycerate hydro-lyase) (non-neural enolase) (nne) (phosphopyruvate hydratase). 7/1998 [MASS=47038]/Enolase 1 (alpha enolase), converts 2-phospho-D-glycerate to phosphoenolpyruvate in glycolysis, an autoantigen in multiple autoimmune diseases, shorter alternative form c-myc promoter binding protein (MPB1) is a transcriptional repressor
SW:TCPD_HUMAN P50991 homo sapiens (human). t-complex protein 1, delta subunit (tcp-1-delta) (cct-delta) (stimulator of tar rna binding). 5/2000 [MASS=57839]/Chaperonin containing T-complex 1 subunit 4 (delta), part of a cytosolic hexadecamer structure involved in ATP-dependent folding of actin, tubulin and other proteins
SWN:PREB_HUMAN Q9hcu5 homo sapiens (human). prolactin regulatory element-binding protein. 3/2002 [MASS=45502]/Prolactin regulatory element binding protein, transcriptional activator, member of the WD-repeat protein family, may have a role in development; chromosomal location of the gene makes this a candidate for the gene mutated in partial trisomy 2p syndrome
SW:CRTC_HUMAN P27797 homo sapiens (human). calreticulin precursor (crp55) (calregulin) (hacbp) (erp60) (52 kda ribonucleoprotein autoantigen ro/ss-a). 7/1998 [MASS=48142]/Calreticulin, an ER-resident Ca2+-binding protein and lectin-binding chaperone involved in protein folding, Ca2+ homeostasis, cell adhesion, and integrin signaling; anti-angiogenic fragment, vasostatin, is a potential anti-cancer agent
SW:TF1B_HUMAN Q13263 homo sapiens (human). transcription intermediary factor 1-beta (nuclear corepressor kap-1) (krab-associated protein 1). 7/1999 [MASS=88550]/KRAB associated protein 1, a member of the transcriptional intermediary factor 1 (TIF1) gene family, acts as a transcriptional corepressor to silence heterochromatin, and as a co-activator in association with HP1-type chromodomain-containing proteins
PIR2:JE0334 nuclear matrix protein NMP 238 - human [MASS=50228]/RuvB like 1, a member of the TIP49 family of proteins, a nuclear protein which contains ATPase-helicase motifs, may interact with the transactivation domain of c-myc (MYC)
GP:AB006572_1 Homo sapiens RMP mRNA for RPB5 meidating protein, complete cds. [MASS=56764]/RPB5-mediating protein, binds to and negatively regulates the function of RNA polymerase II subunit 5 (POLR2E), inhibits transcriptional activation by hepatitis B virus X protein; marker for Reed Sternberg cells in Hodgkin disease

GP:AF000560_1 Homo sapiens TTF-I interacting peptide 20 mRNA, partial cds; TIP20; Transcription Termination Factor I Interacting Peptide 20. [MASS=40770]/TTF-I interacting peptide 20, a protein that contains a putative nucleic acid-binding C2H2 type zinc finger domain
GP:AF084523_1 Homo sapiens cellular repressor of E1A-stimulated genes CREG mRNA, complete cds. [MASS=24075]/Repressor of transcriptional activation and transformation by the adenovirus E1A protein, binds the general transcription factor TBP and the tumor suppressor pRb (RB1), involved in transcriptional control of cell growth and differentiation
SW:P2BA_HUMAN Q08209 homo sapiens (human). serine/threonine protein phosphatase 2b catalytic subunit, alpha isoform (ec 3.1.3.16) (calmodulin-dependent calcineurin a subunit, alpha isoform) (cam-prp cat [MASS=58688]/Calcineurin A alpha, catalytic subunit of calcium/calmodulin regulated protein phosphatase, regulates activity of transcription factors involved in signal transduction and growth control
PIR2:I59405 RNA polymerase II transcription factor SIII p18 subunit - human [MASS=13133]/Transcription elongation factor B (SIII) polypeptide 2, a subunit of the elongin complex that facilitates RNA polymerase II elongation, component of a ubiquitin ligase complex that stabilizes and enhances the tumor suppressor action of the VHL protein
SW:PPOL_HUMAN P09874 homo sapiens (human). poly [adp-ribose] polymerase (ec 2.4.2.30) (parp) (adprt) (nad(+) adp-ribosyltransferase) (poly[adp-ribose] synthetase). 11/1997 [MASS=112953]/ADP-ribosyltransferase, catalyzes formation of ADP ribose polymers attached to proteins using NAD(+) as substrate in response to DNA damage, modulates chromatin structure and plays a role in DNA repair and apoptosis
SW:APE1_HUMAN P27695 homo sapiens (human). dna-(apurinic or apyrimidinic site) lyase (ec 4.2.99.18) (ap endonuclease 1) (apex nuclease) (apen) (ref-1 protein). 12/1998 [MASS=35423]/Apurinic/apyrimidinic endonuclease 1, multifunctional DNA repair enzyme that coordinates the repair of abasic sites and repair synthesis, acts as a transcription regulator; mutations may correlate with inclusion body myositis and colorectal tumorigenesis
SW:CNBP_HUMAN P20694 homo sapiens (human), and rattus norvegicus (rat). cellular nucleic acid binding protein (cnbp). 11/1997 [MASS=19463]/Zinc-finger protein that binds to sterol regulatory element (SRE) and may function in sterol-mediated repression of genes encoding the low density lipoprotein receptor and enzymes of the cholesterol biosynthetic pathway
GP:AF007833_1 Homo sapiens kruppel-related zinc finger protein hcKrox mRNA, complete cds; zinc-finger transcription factor. [MASS=58218]/c-Krox, a zinc-finger domain-containing transcription factor that regulates transcription from the alpha 1(I) procollagen (COL1A1) and fibronectin (FN1) promoters, may play a role in regulating bone formation
SW:RFA1_HUMAN P27694 homo sapiens (human). replication protein a 70 kda dna-binding subunit (rp-a) (rf-a) (replication factor-a protein 1) (single-stranded dna-binding protein). 11/1997 [MASS=68138]/Replication protein A1 (70 kDa), a DNA replication factor A subunit, has roles in DNA replication, recombination, repair, may contribute to latent virus reactivation, inactivated by anti-cancer drug adozelesin
SW:MAZ_HUMAN P56270 homo sapiens (human). myc-associated zinc finger protein (mazi) (purine-binding transcription factor) (pur-1) (zf87) (zif87). 7/1999 [MASS=48608]/MYC-associated zinc finger protein (purine-binding transcription factor), functions both as a positive and a negative regulator of gene expression and may also have roles in initiating and terminating transcription
SW:PUR_HUMAN Q00577 homo sapiens (human). transcriptional activator protein pur-alpha (purine-rich single- stranded dna-binding protein alpha). 7/1998 [MASS=34911]/Purine rich element binding protein A, a single-stranded DNA-RNA binding protein implicated in the control of transcription and DNA replication; interacts with HIV Tat protein and JC virus T antigen to modulate host and viral gene expression
Solute carrier family 9 isoform 3 regulatory factor 1 (sodium-hydrogen exchanger-regulatory factor), a cytoskeleton-linking protein that forms multiprotein complexes with members of the Ezrin-Radixin-Moesin family via two PDZ domains
PIR2:T13151 adapter protein CMS - human [MASS=71451]/CMS: an adapter molecule involved in cytoskeletal rearrangements/CD2-associated protein, an adaptor that may play a role in kidney function and mediate cytoskeletal rearrangement; mouse Cd2ap is associated with congenital nephrotic syndrome and possibly Nail-Patella syndrome nephropathy and polycystic kidney disease
GP:AB008515_1 Homo sapiens mRNA for RanBPM, complete cds. [MASS=55082]/Ran-binding protein 9, plays a role in microtubule nucleation, interacts specifically with RAN guanosine triphosphatase and mediates Ran-dependent centrosomal function
SW:CAPB_HUMAN P47756 homo sapiens (human). f-actin capping protein beta subunit (capz). 5/2000 [MASS=30629]/Capping protein Z-line beta 1, a subunit of an actin-binding protein that caps the barbed end of actin filaments and regulates actin polymerization dynamics, may have a role in cell motility
SW:DAG1_HUMAN Q14118 homo sapiens (human). dystroglycan precursor (dystrophin-associated glycoprotein 1) [contains: alpha-dystroglycan (alpha-dg); beta-dystroglycan (beta- dg)]. 5/2000 [MASS=97581]/Dystroglycan 1, component of a dystrophin-associated glycoprotein complex that binds laminin, may link the extracellular matrix and cytoskeleton, may play a role in synaptic function; deficiency is involved in the pathogenesis of muscular dystrophies
GP:U45976_1 Human clathrin assembly protein lymphoid myeloid leukemia (CALM) mRNA, complete cds. [MASS=70695]/Phosphatidylinositol binding clathrin assembly protein, binds to clathrin heavy chain (CLTC) and plays a role in coated pit internalization; rearrangements in the corresponding gene are associated with acute lymphoblastic and acute myeloid leukemias

GP:AF044670_1 Homo sapiens 33 kDa Vamp-associated protein (VAP33) mRNA, complete cds; VAP-33. [MASS=27318]/Vesicle-associated membrane protein (VAMP)-associated protein A, binds v-SNAREs, t-SNAREs, VAPB, and VAMP, predicted to be involved in vesicle transport and fusion
SW:CAZ2_HUMAN P47755 homo sapiens (human). f-actin capping protein alpha-2 subunit (capz). 12/1998 [MASS=32949]/Capping protein Z-line (alpha 2), subunit of an actin-binding protein that may play a role in cell motility; corresponding gene is amplified in malignant gliomas and may be involved in tumorigenesis
SW:HS9A_HUMAN P07900 homo sapiens (human). heat shock protein hsp 90-alpha (hsp 86). 5/2000 [MASS=84543]/Heat shock 90kD protein 1 alpha, a molecular chaperone that mediates protein folding, activates MAPK1, MAPK3, and caspase, may regulate a G protein-coupled receptor signaling pathway, may promote the proliferation of breast cancer cells
SW:CYP4_HUMAN Q08752 homo sapiens (human). 40 kda peptidyl-prolyl cis-trans isomerase (ec 5.2.1.8) (ppiase) (rotamase) (cyclophilin-40) (cyp-40) (cyclophilin-related protein). 5/2000 [MASS=40764]/Petidylprolyl isomerase D, cyclosporin A and HSPCA -binding peptidylprolyl isomerase, part of steroid receptor and mitochondrial permeability transition pore complexes, may regulate protein trafficking, steroid receptor signal transduction, and apoptosis
PIR2:I59405 RNA polymerase II transcription factor SIII p18 subunit - human [MASS=13133]/Transcription elongation factor B (SIII) polypeptide 2, a subunit of the elongin complex that facilitates RNA polymerase II elongation, component of a ubiquitin ligase complex that stabilizes and enhances the tumor suppressor action of the VHL protein
PIR2:T09073 splicing factor Sip1 - human [MASS=128875]/Splicing factor arginine serine rich 2 interacting protein, a SR domain family protein that interacts with the RNA polymerase II C-terminal domain and several splicing factors, is essential in mRNA splicing and possibly spliceosome A-complex formation
SW:Y017_HUMAN Q15393 homo sapiens (human). hypothetical protein kiaa0017. 5/2000 [MASS=44606]/ Homo sapiens mRNA for SAP 130 spliceosomal protein/Splicing factor 3b subunit 3, a component of the U2 snRNP-associated protein complex SF3b that plays a role in spliceosome assembly, interacts with STAGA and TFTC complexes implicated in DNA repair, chromatin modification, and transcription
GP:AB006537_1 Homo sapiens mRNA for interleukin 1 receptor accessory protein, complete cds. [MASS=65418]/Interleukin-1 receptor accessory protein, a subunit of the interleukin-1 receptor complex, recruits IRAK to the receptor complex in an early stage of interleukin-1 signaling
SW:LMG1_HUMAN P11047 homo sapiens (human). laminin gamma-1 chain precursor (laminin b2 chain). 7/1998 [MASS=177607]/Laminin C1, an extracellular matrix glycoprotein that may be involved in cell-matrix adhesion and the regulation of cell shape
SW:KLK2_HUMAN P20151 homo sapiens (human). glandular kallikrein 2 precursor (ec 3.4.21.35) (tissue kallikrein) (prostate) (hgk-1). 10/1996 [MASS=28671]/Kallikrein 2, arginine selective serine protease, involved in activation of PSA (KLK3), may activate urokinase type plasminogen activator (PLAU), used as a marker with PSA (KLK3) to help discriminate between prostate cancer and benign prostate hyperplasia
SW:PRCE_HUMAN P28074 homo sapiens (human). proteasome epsilon chain precursor (ec 3.4.99.46) (macropain epsilon chain) (multicatalytic endopeptidase complex epsilon chain) (proteasome subunit x) (protea [MASS=22897]/Proteasome (prosome, macropain) subunit beta type 5, which is a multicatalytic proteinase complex involved in cellular protein degradation and antigen processing; may be competitively inhibited by the HIV1 protease inhibitor Ritonavir
PIR2:JC6523 26S proteasome regulatory complex chain p55 - human [MASS=52904]/Proteasome (prosome, macropain) 26S subunit (non-ATPase, 12), a regulatory subunit of the 26S proteasome
GP:AB029020_1 Homo sapiens mRNA for KIAA1097 protein, partial cds. [MASS=110942]/ Similar to ubiquitin specific protease 20/Member of the ubiquitin carboxyl-terminal hydrolase family 2, contains a ubiquitin carboxyl-terminal hydrolases family 2 domain and a Zn-finger in ubiquitin-hydrolases and other proteins domain, has a region of low similarity to a region of human USP4
SW:UBCC_HUMAN Q16781 homo sapiens (human). ubiquitin-conjugating enzyme e2-17 kda (ec 6.3.2.19) (ubiquitin- protein ligase) (ubiquitin carrier protein) (ubc13). 7/1999 [MASS=17138]/Ubiquitin-conjugating enzyme E2N (yeast UBC13 homolog), forms heterodimers with ubiquitin-conjugating enzyme E2 variants 1 or 2 (UBE2V1, UBE2V2), and catalyzes formation of unique lysine 63-linked polyubiquitin chains involved in IkappaB kinase activation
SW:SNAA_HUMAN P54920 homo sapiens (human). alpha-soluble nsf attachment protein (snap-alpha). 5/2000 [MASS=33247]/N-ethylmaleimide-sensitive factor (NSF) attachment protein alpha, binds SNARE complexes and recruits NSF to form the 20s fusion particle, stimulates NSF ATPase activity promoting SNARE complex disassembly and exocytosis, functions in intra-Golgi transport
SW:PRCZ_HUMAN P28066 homo sapiens (human). proteasome zeta chain (ec 3.4.99.46) (macropain zeta chain) (multicatalytic endopeptidase complex zeta chain). 7/1999 [MASS=26469]/Proteasome subunit alpha type 5 (ZETA), component of the 20S catalytic core proteasome that is involved in cellular protein degradation, has ribonuclease activity
GP:U86782_1 Human 26S proteasome-associated pad1 homolog (POH1) mRNA, complete cds; human homolog of fission yeast pad1. [MASS=34577]/26S proteasome-associated pad1 homolog, a subunit of the 26S proteasome, confers multidrug resistance and resistance to ultraviolet light when overexpressed

SW:PRS8_HUMAN P47210 homo sapiens (human). 26s protease regulatory subunit 8 (proteasome subunit p45) (thyroid hormone receptor interacting protein 1) (trip1). 11/1997 [MASS=45653]/ATPase subunit 5 of the 26S proteasome, which is a multicatalytic proteinase complex involved in cellular protein degradation; may also function as a transcriptional modulator
GP:AB012191_1 Homo sapiens mRNA for Nedd8-conjugating enzyme hUbc12, complete cds. [MASS=20900]/Neurally expressed developmentally down-regulated 8, an ubiquitin-like protein that conjugates to CUL proteins to activate ubiquitin ligase complex dependent ubiquitination, possibly involved in cell cycle regulation
SW:NEP_HUMAN P08473 homo sapiens (human). neprilysin (ec 3.4.24.11) (neutral endopeptidase) (nep) (enkephalinase) (common acute lymphocytic leukemia antigen) (calla) (neutral endopeptidase 24.11) (cd10) [MASS=85383]/Enkephalinase; membrane zinc metalloendopeptidase, may inactivate peptide hormones
SW:PRS7_HUMAN P35998 homo sapiens (human). 26s protease regulatory subunit 7 (mss1 protein). 11/1997 [MASS=48634]/26S protease regulatory subunit 7, ATPase subunit of the 26S proteasome, interacts with Tat protein, may be involved in cell cycle control and has a role in the activation of human immunodeficiency virus-1 (HIV-1) gene transcription
SW:PRSX_HUMAN Q92524 homo sapiens (human). 26s protease regulatory subunit s10b (proteasome subunit p42). 12/1998 [MASS=44161]/Proteasome (prosome, macropain) 26S subunit ATPase 6, part of both PA700 and PA700-dependent complexes, which regulate intracellular protease activity, may be involved in spermatogenesis
SW:PRCD_HUMAN P28072 homo sapiens (human). proteasome delta chain precursor (ec 3.4.99.46) (macropain delta chain) (multicatalytic endopeptidase complex delta chain) (proteasome subunit y). 5/2000 [MASS=25316]/Proteasome (prosome, macropain) subunit beta 6 (proteasome delta), putative endopeptidase down-regulated by interferon gamma, may be involved in proteolysis and peptidolysis
SW:PSD2_HUMAN Q13200 homo sapiens (human). 26s proteasome regulatory subunit s2 (p97) (tumor necrosis factor type 1 receptor associated protein 2) (55.11 protein). 7/1999 [MASS=100200]/Proteasome 26S non-ATPase subunit 2, a subunit of the 26S proteasome, likely involved in ubiquitin-dependent proteolysis, binds the type 1 tumor necrosis factor receptor (TNFRSF1A) and may function in TNFR signaling
SW:PRSC_HUMAN P51665 homo sapiens (human). 26s proteasome regulatory subunit s12 (proteasome subunit p40) (mov34 protein). 11/1997 [MASS=37060]/Proteasome (prosome, macropain) 26S subunit non-ATPase 7, a putative regulatory subunit of the 26S proteasome; mutation of the mouse Psdm7 gene results in recessive embryonic lethality
SW:PSD1_HUMAN Q99460 homo sapiens (human). 26s proteasome regulatory subunit s1 (p112). 12/1998 [MASS=105866]/Proteasome (prosome, macropain) 26S subunit (non-ATPase,1), a regulatory subunit of the 26S proteasome
SW:Y253_HUMAN Q92542 homo sapiens (human). hypothetical protein kiaa0253 (fragment). 7/1998 [MASS=78280]/Nicastrin, a transmembrane glycoprotein that may be required for the assembly and transport of presenilin complex that processes amyloid precursor protein (APP), may play a role in notch signaling and abnormal APP processing in Alzheimer disease
SW:PRC5_HUMAN P20618 homo sapiens (human). proteasome component c5 (ec 3.4.99.46) (macropain subunit c5) (proteasome gamma chain) (multicatalytic endopeptidase complex subunit c5). 11/1997 [MASS=26489]/Proteasome subunit alpha type 5 (ZETA), component of the 20S catalytic core proteasome that is involved in cellular protein degradation, has ribonuclease activity
PIR2:JC6524 26S proteasome regulatory complex chain p44.5 - human [MASS=47464]/Subunit 9 of the 26S proteasome (proteasome 26S subunit non-ATPase 11), a non-ATPase subunit of the 19S regulatory unit of the 26S proteasome complex, confers ATP dependency to the 26S proteasome, which mediates ubiquitin-dependent protein degradation
SW:PRC2_HUMAN P25786 homo sapiens (human). proteasome component c2 (ec 3.4.99.46) (macropain subunit c2) (proteasome nu chain) (multicatalytic endopeptidase complex subunit c2) (30 kda prosomal protein) [MASS=29556]/Alpha type 1 proteasome (prosome, macropain) subunit , a component of a multicatalytic proteinase complex that is involved in cellular protein degradation
GP:D38048_1 Human mRNA for proteasome subunit z, complete cds. [MASS=29965]/Proteasome (prosome, macropain) subunit beta 7, a subunit of the 26S proteasome, replaced by PSMB10 upon interferon gamma (IFNG) stimulation
SW:PRC8_HUMAN P25788 homo sapiens (human). proteasome component c8 (ec 3.4.99.46) (macropain subunit c8) (multicatalytic endopeptidase complex subunit c8). 12/1998 [MASS=28302]/Proteasome subunit alpha type 3, the C8 subunit of the 20S core proteasome, which is a multicatalytic proteinase complex involved in cellular protein degradation; expression is increased in skeletal muscle of slim AIDS patients
GP:AB009398_1 Homo sapiens mRNA for 26S proteasome subunit p40.5, complete cds. [MASS=42945]/Proteasome (prosome, macropain) 26S subunit (non-ATPase, 13), a subunit of the PA700 regulatory complex of the 26S proteasome
PIR2:T46412 ubiquitin--protein ligase (EC 6.3.2.19) NEDD4 - human (fragment) [MASS=95283]/Neural cell precursor expressed developmentally downregulated 4, ubiquitin-protein ligase with multiple WW domains, binds to and reduces the activity of epithelial sodium channels, may play a role in neural differentiation, regulated by kinase SGK
SW:UB5A_HUMAN P51668 homo sapiens (human). ubiquitin-conjugating enzyme e2-17 kda 1 (ec 6.3.2.19) (ubiquitin- protein ligase) (ubiquitin carrier protein) (e2(17)kb 1). 12/1998 [MASS=16602]/Ubiquitin-conjugating enzyme E2D1, member of the ubiquitin-conjugating enzyme subfamily that catalyzes the ubiquitination of cellular proteins and marks them for degradation, acts with the ubiquitin protein ligase E6AP (UBE3A) to ubiquitinate p53 (TP53)

SW:PRCI_HUMAN P34062 homo sapiens (human), and rattus norvegicus (rat). proteasome iota chain (ec 3.4.99.46) (macropain iota chain) (multicatalytic endopeptidase complex iota chain) (27 kda prosomal pro [MASS=27399]/Proteasome subunit alpha type 6, a member of the alpha type prosomal gene family, part of a multicatalytic protease complex involved in cellular protein degradation; also binds RNA specifically
SW:PRS4_HUMAN Q03527 homo sapiens (human). 26s protease regulatory subunit 4 (p26s4). 12/1998 [MASS=49185]/Proteasome 26S subunit ATPase 1, an ATPase subunit of the 26S proteasome multicatalytic protease complex, may play a role in ubiquitin-dependent protein degradation, interacts with the papilloma virus oncoprotein E7
SW:TPP2_HUMAN P29144 homo sapiens (human). tripeptidyl-peptidase ii (ec 3.4.14.10) (tpp ii) (tripeptidyl aminopeptidase). 11/1997 [MASS=138449]/Tripeptidyl peptidase II, a serine exopeptidase that may provide an alternative, non-proteasomal mechanism for protein turnover, participates in the apoptotic pathway activated by Shigella, upregulated in Burkitt's lymphoma cells overexpressing MYC
SW:DIAC_HUMAN Q01459 homo sapiens (human). di-n-acetylchitobiase precursor (ec 3.2.1.-). 7/1999 [MASS=43760]/Chitobiase (di-N-acetylchitobiase), a lysosomal glycosidase involved in the degradation of asparagine-linked glycoproteins
GP:U41806_1 Human EBI3-associated protein p60 mRNA, complete cds; EBI3-associated protein. [MASS=47602]/Sequestosome 1 (ubiquitin-binding protein p62), a ubiquitin-binding protein with a zinc finger-like motif, a G protein-binding region and a PEST motif, interacts with several signal transduction pathways, may be involved in endosome to lysosome transport
GP:AB002310_1 Human mRNA for KIAA0312 gene, partial cds. [MASS=209315]/Protein containing a HECT domain, which may confer ubiquitin-protein ligase activity, has high similarity to a region of S. cerevisiae Tom1p, which is a protein required for the G2/M transition
SW:PSD4_HUMAN P55036 homo sapiens (human). 26s proteasome regulatory subunit s5a (multiubiquitin chain binding protein) (antisecretory factor-1) (af) (asf). 12/1998 [MASS=40737]/Proteasome 26S subunit non ATPase 4, an antisecretory factor that is a subunit of the 26S proteasome and may bind to multiubiquitinated proteins; inhibits intestinal fluid secretion induced by cholera toxin
SWN:PSA7_HUMAN O14818 homo sapiens (human). proteasome subunit alpha type 7 (ec 3.4.99.46) (proteasome subunit rc6-1) (proteasome subunit xapc7). 8/2001 [MASS=27887]/Proteasome (prosome, macropain) subunit (alpha type) 7, a subunit of the 20S core proteasome, a target of hepatitis B virus X protein; may be involved in pathogenesis of pancreatic cancer
PIR2:T14762 hypothetical protein DKFZp434A014.1 - human (fragment) [MASS=92341]/Member of the angiotensin-converting enzyme family of dipeptidyl carboxydipeptidases
SW:UBPA_HUMAN Q14694 homo sapiens (human). ubiquitin carboxyl-terminal hydrolase 10 (ec 3.1.2.15) (ubiquitin thiolesterase 10) (ubiquitin-specific processing protease 10) (deubiquitinating enzyme 10) (k [MASS=87134]/Ubiquitin specific protease 10, a member of the ubiquitin-specific cysteine (thiol) protease family, cleaves ubiquitin from ubiquitin-conjugated protein substrates, activity is inhibited upon association with Ras-GAP SH3 domain binding protein
SWN:UBPF_HUMAN Q9y4e8 homo sapiens (human). ubiquitin carboxyl-terminal hydrolase 15 (ec 3.1.2.15) (ubiquitin thiolesterase 15) (ubiquitin-specific processing protease 15) (deubiquitinating enzyme 15) (f [MASS=108965]/Ubiquitin-specific protease 15, a member of the ubiquitin-specific cysteine (thiol) protease family, cleaves ubiquitin from ubiquitin-conjugated protein substrates, may play a role in growth regulation
GP:AF039689_1 Homo sapiens antigen NY-CO-7 (NY-CO-7) mRNA, complete cds; TPR domain protein. [MASS=34791]/STUB1
SW:CATD_HUMAN P07339 homo sapiens (human). cathepsin d precursor (ec 3.4.23.5). 2/1996 [MASS=44552]/Cathepsin D, a lysosomal aspartyl protease that is induced by estrogen and degrades intracellular and endocytosed proteins, a positive mediator of apoptosis; abnormal expression observed in tumor cell proliferation and metastasis
GP:D87684_1 Homo sapiens mRNA for KIAA0242 protein, partial cds; Start codon is not identified. ha03111 cDNA clone for KIAA0242 has a 94-bp deletion at the region from 573 to 666 of the sequence of KIAA0242; similar to a C.elegans ZK353.8 protein (S44655). [MASS=59094]/Protein containing a UBX domain, which are found in ubiquitin regulatory proteins, has low similarity to uncharacterized C. elegans ZK353.8
SW:UBCI_HUMAN P50550 homo sapiens (human), mus musculus (mouse), and xenopus laevis (african clawed frog). ubiquitin-conjugating enzyme e2-18 kda (ec 6.3.2.19) (ubiquitin-protein ligase) (ubiquitin carr [MASS=18007]/Ubiquitin-conjugating enzyme E2I, member of the ubiquitin-conjugating enzyme family that catalyzes the ubiquitination of cellular proteins and marks them for degradation, may play roles in cell cycle progression and repair of TOP1-mediated DNA damage
PIR2:I59405 RNA polymerase II transcription factor SIII p18 subunit - human [MASS=13133]/Transcription elongation factor B (SIII) polypeptide 2, a subunit of the elongin complex that facilitates RNA polymerase II elongation, component of a ubiquitin ligase complex that stabilizes and enhances the tumor suppressor action of the VHL protein
SW:LONM_HUMAN P36776 homo sapiens (human). mitochondrial lon protease homolog precursor (ec 3.4.21.-). 11/1995 [MASS=106467]/Protease serine 15, an ATP-dependent mitochondrial peptidase that binds single-stranded DNA and may play a role in the regulation of mitochondrial DNA replication and gene expression
SW:PRTP_HUMAN P10619 homo sapiens (human). lysosomal protective protein precursor (ec 3.4.16.5) (cathepsin a) (carboxypeptidase c). 12/1998 [MASS=54496]/Protective protein for beta-galactosidase (cathepsin A), has serine carboxypeptidase activity, forms a complex with beta galactosidase (GLB1) and neuraminidase (NEU1), facilitates NEU1 transport and activation; genetic mutation leads to galactosialidosis

SW:PPT_HUMAN P50897 homo sapiens (human). palmitoyl-protein thioesterase precursor (ec 3.1.2.22) (palmitoyl- protein hydrolase). 5/2000 [MASS=34193]/Palmitoyl-protein thioesterase (ceroid-lipofuscinosis, neuronal 1, infantile), catalyzes the hydrolysis of palmitate from S-acetylated cysteine residues, may be involved in apoptosis; gene mutation is detected in infantile neuronal ceroid lipofuscinosis
SW:CATB_HUMAN P07858 homo sapiens (human). cathepsin b precursor (ec 3.4.22.1) (cathepsin b1) (app secretase). 7/1998 [MASS=37808]/Cathepsin B, a cysteine (thiol) protease that degrades cartilage matrix proteins and other proteins, also cleaves APP; commonly overexpressed in tumors, and may be proapoptotic, but also facilitates tumor invasion
SW:CUL2_HUMAN Q13617 homo sapiens (human). cullin homolog 2 (cul-2). 12/1998 [MASS=86956]/Cullin 2, has E3 ubiquitin ligase activity when present in a complex containing von Hippel Lindau tumor suppressor (VHL)- elogin B (TCEB2)- elogin C (TCEB1); modification by ubiquitin-like protein NEDD8 may be important for VHL tumor suppressor function
SW:CATH_HUMAN P09668 homo sapiens (human). cathepsin h precursor (ec 3.4.22.16). 7/1999 [MASS=37404]/Cathepsin H, a cysteine (thiol) protease, member of a family of lysosomal cysteine proteases involved in a variety of proteolytic processes, may serve as a marker of tumor progression in central nervous system and pancreatic neoplasms
SW:RL40_HUMAN P14793 homo sapiens (human), rattus norvegicus (rat), and gallus gallus (chicken). 60s ribosomal protein l40 (cep52). 11/1997 [MASS=6181]/Ubiquitin A-52 residue ribosomal protein fusion product 1, protein consisting of ubiquitin at the N-terminus and ribosomal protein L40 at the C-terminus; the corresponding gene is upregulated in colon cancer but not in gastric cancer
SW:TPP1_HUMAN O14773 homo sapiens (human). tripeptidyl-peptidase i precursor (ec 3.4.14.9) (tpp-i) (tripeptidyl aminopeptidase) (lysosomal pepstatin insensitive protease) (lpic). 5/2000 [MASS=61229]/Tripeptidyl peptidase I (ceroid-lipofuscinosis neuronal 2), a lysosomal serine-type peptidase required for degradation of ATP synthase subunit c (ATP5G1 and ATP5G2); mutations in the corresponding gene cause late infantile neuronal ceroid lipofuscinosis
(matriptase) (membrane- type serine protease 1) (mt-sp1)./Matriptase, a type 2 integral membrane serine protease, degrades extracellular matrix, activates hepatocyte growth factor (HGF) and urokinase plasminogen activator (PLAU), and may play a role in progression and metastasis of epithelial-derived cancers
UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 24 /Member of the ubiquitin carboxyl-terminal hydrolase family 2 that contains a ubiquitin carboxyl-terminal hydrolases family 2 domain, has low similarity to a region of ubiquitin specific protease 9 X chromosome (human USP9X)
SW:TRAL_HUMAN Q12931 homo sapiens (human). tumor necrosis factor type 1 receptor associated protein (trap-1) (fragment). 5/2000 [MASS=75342]/Heat shock protein 75, member of the HSP90 family of molecular chaperones, binds and refolds denatured retinoblastoma (RB1) protein during M phase and after heat shock, binds the intracellular domain of tumor necrosis factor receptor type 1
SW:FKB5_HUMAN Q13451 homo sapiens 51 kda fk506-binding protein (fkbp51) (peptidyl-prolyl cis-trans isomerase) (ec 5.2.1.8) (ppiase) (rotamase) (54 kda progesterone receptor-associated immunophilin) (fkb [MASS=51212]/FK506-binding protein 5, a peptidylprolyl cis-trans isomerase and member of the immunophilin family of FK506-binding proteins, forms a progesterone receptor complex with Hsp90 and p23, serves as a chaperone and mediates inhibition of calcineurin
SW:HS7C_HUMAN P11142 homo sapiens (human). heat shock cognate 71 kda protein. 12/1998 [MASS=70898]/Heat shock 70kD protein 8, a constitutively expressed member of the heat shock HSP70 family of molecular chaperones; expression is elevated in the hearts of patients with hypertrophic cardiomyopathy
PIR2:JC1365 FK506/rapamycin-binding protein FKBP13 precursor - human [MASS=15649]/FK506-binding protein 2 (FKBP13), an ER membrane-associated member of a family of peptidyl-prolyl cis-trans isomerases that bind the macrolide immunosuppressant drugs FK506 and rapamycin, does not play a role in the immunosuppressant action of FK506
SW:TCPE_HUMAN P48643 homo sapiens (human). t-complex protein 1, epsilon subunit (tcp-1-epsilon) (cct-epsilon) (kiaa0098). 11/1997 [MASS=59671]/Chaperonin containing T-complex 1 subunit 5 (epsilon), part of a cytosolic hexadecamer structure involved in ATP-dependent folding of actin, tubulin and other proteins, binds Epstein-Barr Virus-encoded EBNA3 and may mediate its initial folding
GP:AF227905_1 Homo sapiens UDP-glucose:glycoprotein glucosyltransferase 1 precursor, mRNA, complete cds; HUGT1. [MASS=177190]/UDP-glucose:glycoprotein glucosyltransferase; transfers glucose from UDP-glucose to improperly folded glycoproteins
SW:TCPZ_HUMAN P40227 homo sapiens (human). t-complex protein 1, zeta subunit (tcp-1-zeta) (cct-zeta) (cct-zeta-1) (tcp20) (htr3). 7/1999 [MASS=58024]/Chaperonin containing T-complex 1 subunit 6A (zeta), part of a cytosolic hexadecamer structure involved in ATP-dependent folding of actin, tubulin and other proteins, decreased activity may result in misfolded tubulin aggregates in Alzheimers disease
SW:FKB1_HUMAN P20071 homo sapiens (human), and oryctolagus cuniculus (rabbit). fk506-binding protein (fkbp-12) (peptidyl-prolyl cis-trans isomerase) (ec 5.2.1.8) (ppiase) (rotamase) (immunophilin fkbp12 [MASS=11820]/FK506-binding protein 1A, peptidyl prolyl cis-trans isomerase, modulates the Ca2+-release activity of ryanodine receptors, complex with FK506 inhibits calcineurin-dependent lymphokine gene transcription and mediates FK506 immunosuppressive activity

SW:CALX_HUMAN P27824 homo sapiens (human). calnexin precursor (major histocompatibility complex class i antigen-binding protein p88) (p90) (ip90). 11/1995 [MASS=67568]/Calnexin, a calcium and lectin binding protein that functions as a chaperone in the endoplasmic reticulum, involved in protein folding and secretion, mediates retention of misfolded proteins in the endoplasmic reticulum
SW:ER53_HUMAN P49257 homo sapiens (human). ergic-53 protein precursor (er-golgi intermediate compartment 53 kda protein) (gp58) (mr60) (lectin, mannose-binding 1). 7/1998 [MASS=57563]/Mannose-binding lectin 1, involved in the traffic of glycoproteins between endoplasmic reticulum and the Golgi apparatus; mutations of the corresponding gene is associated with combined factor V and VIII coagulation deficiency
SW:DNJ2_HUMAN P31689 homo sapiens (human). dnaj protein homolog 2 (hsj-2). 7/1999 [MASS=44868]/DnaJ homolog subfamily A member 1, heat shock protein, expressed in many tissues
SW:HIP_HUMAN P50502 homo sapiens (human). hsc70-interacting protein (progesterone receptor-associated p48 protein) (putative tumor suppressor st13). 5/2000 [MASS=41332]/Suppression of tumorigenicity 13 (Hsp70-interacting protein), acts as an Hsc70 cochaperone, contains tetratricopeptide repeats, participates in protein complex assembly, heat shock response, and lysosomal transport; downregulated in colorectal carcinoma
SW:TCPB_HUMAN P78371 homo sapiens (human). t-complex protein 1, beta subunit (tcp-1-beta) (cct-beta). 7/1999 [MASS=57488]/Chaperonin containing T-complex polypeptide-1 (TCP1) subunit 2, the beta subunit of the chaperonin containing complex (CCT), plays a role in the folding of cytosolic proteins, may be required for the proper folding of cyclin E
GP:AB015798_1 Homo sapiens HSJ2 mRNA for DnaJ homolog, complete cds; DnaJ homologue HSJ2a. [MASS=36087]/DnaJ homolog subfamily A member 1, heat shock protein, expressed in many tissues
SW:TCPG_HUMAN P49368 homo sapiens (human). t-complex protein 1, gamma subunit (tcp-1-gamma) (cct-gamma). 12/1998 [MASS=60331]/Cytosolic chaperonin containing TCP-1 (CCT) gamma subunit, may act as a chaperonin and assist in the proper folding of tubulin, actin, and centractin
SW:CYPB_HUMAN P23284 homo sapiens (human). peptidyl-prolyl cis-trans isomerase b precursor (ec 5.2.1.8) (ppiase) (rotamase) (cyclophilin b) (s-cyclophilin) (scylp) (cyp-s1). 7/1999 [MASS=22742]/Cyclophilin B, a peptidyl prolyl cis-trans isomerase that binds to and is inhibited by the immunosuppressive drug cyclosporin A, plays a role in protein folding, binds to the human immunodeficiency virus type I Gag polyprotein
SW:TCPH_HUMAN Q99832 homo sapiens (human). t-complex protein 1, eta subunit (tcp-1-eta) (cct-eta) (hiv-1 nef interacting protein). 7/1998 [MASS=59367]/Chaperonin containing T-complex polypeptide-1 (TCP1) subunit 7, the eta subunit of the chaperonin containing complex (CCT), plays a role in protein folding and in the response to chemical stress, may be required for proper folding of cyclin E
SW:TCPA_HUMAN P17987 homo sapiens (human). t-complex protein 1, alpha subunit (tcp-1-alpha) (cct-alpha). 5/2000 [MASS=60344]/T-complex 1, subunit of the cytosolic chaperonin containing TCP-1 (CCT), may assist in the proper folding of tubulin, and may be involved in the response to chemical stressors
SW:TCPD_HUMAN P50991 homo sapiens (human). t-complex protein 1, delta subunit (tcp-1-delta) (cct-delta) (stimulator of tar rna binding). 5/2000 [MASS=57839]/Chaperonin containing T-complex 1 subunit 4 (delta), part of a cytosolic hexadecamer structure involved in ATP-dependent folding of actin, tubulin and other proteins
SW:CYPH_HUMAN P05092 homo sapiens (human), cercopithecus aethiops (green monkey) (grivet), macaca mulatta (rhesus macaque), and papio anubis peptidyl-prolyl cis-trans isomerase a (ec 5.2.1.8) (ppiase) ([MASS=17881]/Peptidylprolyl isomerase A (cyclophilin A), mediates immunosuppressant action of cyclosporin A by inhibiting calcineurin phosphatase activity, has nuclease activity, binds to transcription factors, incorporates into HIV-1 virions and regulates infectivity
PIR2:T00363 hypothetical protein KIAA0674 - human (fragment) [MASS=135179]/Member of the FKBP-type peptidyl-prolyl cis-trans isomerase family
GP:AF039689_1 Homo sapiens antigen NY-CO-7 (NY-CO-7) mRNA, complete cds; TPR domain protein. [MASS=34791]/STUB1
SW:CYP4_HUMAN Q08752 homo sapiens (human). 40 kda peptidyl-prolyl cis-trans isomerase (ec 5.2.1.8) (ppiase) (rotamase) (cyclophilin-40) (cyp-40) (cyclophilin-related protein). 5/2000 [MASS=40764]/Petidylprolyl isomerase D, cyclosporin A and HSPCA -binding peptidylprolyl isomerase, part of steroid receptor and mitochondrial permeability transition pore complexes, may regulate protein trafficking, steroid receptor signal transduction, and apoptosis
SW:HS9B_HUMAN P08238 homo sapiens (human). heat shock protein hsp 90-beta (hsp 84) (hsp 90). 5/2000 [MASS=83163]/Heat shock 90kD protein 1 beta, involved in regulation of both cytochrome c-dependent apoptosis and antiapoptosis via the Akt/PKB (AKT1) serine-threonine kinase, elevated expression is reported in patients with active systemic lupus erythematosus (SLE)
SW:TCPQ_HUMAN P50990 homo sapiens (human). t-complex protein 1, theta subunit (tcp-1-theta) (cct-theta) (kiaa0002). 5/2000 [MASS=59635]/Protein with very strong similarity to murine Mm.17989, which is the theta subunit of the cytosolic chaperonin containing TCP-1 that assists in the proper folding of tubulin, actin and centractin
GP:AF188611_1 Homo sapiens BiP protein (HSPA5) mRNA, partial cds; glucose-regulated protein (grp78). [MASS=70931]/Heat shock 70kD protein 5, chaperone and putative ATPase involved in protein folding in the endoplasmic reticulum, induced in the stress response; autoimmunity may be a factor in rheumatoid arthritis

SW:P60_HUMAN P10809 homo sapiens (human). mitochondrial matrix protein p1 precursor (p60 lymphocyte protein) (60 kda chaperonin) (heat shock protein 60) (hsp-60) (protein cpn60) (groel protein) (hucha60 [MASS=61055]/Chaperonin 60, mitochondrial matrix protein induced by stress, component of the chaperonin complex that is implicated in mitochondrial protein folding and function, induced by inflammatory and immune responses, and implicated in coronary disease
SW:CYPM_HUMAN P30405 homo sapiens (human). peptidyl-prolyl cis-trans isomerase, mitochondrial precursor (ec 5.2.1.8) (ppiase) (rotamase) (cyclophilin). 11/1997 [MASS=22040]/Peptidylprolyl isomerase F (Cyclophilin F), a putative mitochondrial protein that binds the immunosuppressant drug cyclosporin A
STE20/SPS1-RELATED PROLINE-ALANINE RICH PROTEIN KINASE (STE-20RELATED KINASE) (DCHT) /Ste-20-related protein kinase, member of the STE20/SPS1 family, a serine/threonine kinase, activates p38 kinase, may respond to stress activated signals
inhibitor of nuclear factor kappa b kinase beta subunit/Serine kinase that is a subunit of the IkappaB kinase (IKK) complex, phosphorylates IkappaB and activates NF-kappaB (RELA), activated by kinases NIK (MAP3K14) and MEKK1 (MAP3K1)
SW:PRCE_HUMAN P28074 homo sapiens (human). proteasome epsilon chain precursor (ec 3.4.99.46) (macropain epsilon chain) (multicatalytic endopeptidase complex epsilon chain) (proteasome subunit x) (protea [MASS=22897]/Proteasome (prosome, macropain) subunit beta type 5, which is a multicatalytic proteinase complex involved in cellular protein degradation and antigen processing; may be competitively inhibited by the HIV1 protease inhibitor Ritonavir
SWN:AKT3_HUMAN Q9y243 homo sapiens (human). rac-gamma serine/threonine protein kinase (ec 2.7.1.-) (rac-pk-gamma) (protein kinase akt-3) (protein kinase b, gamma) (pkb gamma). 8/2001 [MASS=55775]/Protein kinase B gamma, a serine/threonine protein kinase that is activated by growth factors and 3-phosphoinositide; insulin-induced activity is upregulated in estrogen receptor negative breast cancer and androgen insensitive prostrate carcinoma
SW:AAK1_HUMAN Q13131 homo sapiens (human). 5'-amp-activated protein kinase, catalytic alpha-1 chain (ec 2.7.1.-) (ampk alpha-1 chain) (fragment). 7/1999 [MASS=19837]/AMP-activated protein kinase (alpha 1 catalytic subunit), a metabolic sensor of AMP levels, may have roles in signal transduction, may regulate the cystic fibrosis transmembrane conductance regulator (CFTR)
SW:UBCC_HUMAN Q16781 homo sapiens (human). ubiquitin-conjugating enzyme e2-17 kda (ec 6.3.2.19) (ubiquitin- protein ligase) (ubiquitin carrier protein) (ubc13). 7/1999 [MASS=17138]/Ubiquitin-conjugating enzyme E2N (yeast UBC13 homolog), forms heterodimers with ubiquitin-conjugating enzyme E2 variants 1 or 2 (UBE2V1, UBE2V2), and catalyzes formation of unique lysine 63-linked polyubiquitin chains involved in IkappaB kinase activation
GP:AF024636_1 Homo sapiens STE20-like kinase 3 (mst-3) mRNA, complete cds; protein serine/threonine kinase; similiar to yeast STE20. [MASS=47941]/Serine-threonine kinase 24 (Ste20 yeast homolog), member of the SPS1 subgroup of the STE20-like protein family, a serine-threonine kinase that prefers manganese as a cofactor and uses either GTP or ATP as a phosphate donor
SW:EGFR_HUMAN P00533 homo sapiens (human). epidermal growth factor receptor precursor (ec 2.7.1.112). 12/1998 [MASS=134277]/Epidermal growth factor receptor, a receptor protein tyrosine kinase that binds epidermal growth factor (EGF) and transforming growth factor alpha (TGFA), involved in cell proliferation and differentiation, implicated in tumor invasion and metastasis
SW:TDXN_HUMAN Q13162 homo sapiens (human). thioredoxin peroxidase ao372 (thioredoxin-dependent peroxide reductase a0372) (antioxidant enzyme aoe372) (aoe37-2). 7/1999 [MASS=30540]/Peroxiredoxin 4, a thioredoxin dependent peroxidase that is regulated by interactions with other thiol peroxidases, may mediate hydrogen peroxide activation of NF-kappaB by modulating phosphorylation of cytoplasmic IkappaB-alpha (NFKBIA)
SW:RIB1_HUMAN P04843 homo sapiens (human). dolichyl-diphosphooligosaccharide--protein glycosyltransferase 67 kda subunit precursor (ec 2.4.1.119) (ribophorin i). 7/1999 [MASS=68569]/Ribophorin I, a putative subunit of oligosaccharyltransferase involved in transcription initiation and possibly protein retention in the endoplasmic reticulum
GP:AB012191_1 Homo sapiens mRNA for Nedd8-conjugating enzyme hUbc12, complete cds. [MASS=20900]/Neurally expressed developmentally down-regulated 8, an ubiquitin-like protein that conjugates to CUL proteins to activate ubiquitin ligase complex dependent ubiquitination, possibly involved in cell cycle regulation
GP:AF227905_1 Homo sapiens UDP-glucose:glycoprotein glucosyltransferase 1 precursor, mRNA, complete cds; HUGT1. [MASS=177190]/UDP-glucose:glycoprotein glucosyltransferase; transfers glucose from UDP-glucose to improperly folded glycoproteins
SW:KCCB_HUMAN Q13554 homo sapiens (human). calcium/calmodulin-dependent protein kinase type ii beta chain (cam-kinase ii beta chain) (ec 2.7.1.123) (camk-ii, beta subunit) (fragment). 5/2000 [MASS=15141]/Calcium calmodulin-dependent protein kinase II beta subunit, putative roles in signal transduction and cell growth, increased expression may play a role in schizophrenia; variant forms of the corresponding gene are expressed in tumor cells
SW:PP1B_HUMAN P37140 homo sapiens (human), rattus norvegicus (rat), mus musculus (mouse), oryctolagus cuniculus (rabbit), and gallus gallus (chicken). serine/threonine protein phosphatase pp1-beta catal [MASS=37187]/Protein phosphatase 1 catalytic subunit beta isoform, subunit of a serine-threonine phosphatase that regulates many metabolic processes

SW:P2AA_HUMAN P05323 homo sapiens (human), oryctolagus cuniculus (rabbit), sus scrofa (pig), and bos taurus (bovine). serine/threonine protein phosphatase 2a, catalytic subunit, alpha isoform (ec 3.1.3. [MASS=35594]/Protein phosphatase 2 catalytic subunit alpha, a catalytic subunit of protein phosphatase 2A involved in regulating diverse cellular processes via protein phosphorylation
SW:SRC_HUMAN P12931 homo sapiens (human). proto-oncogene tyrosine-protein kinase src (ec 2.7.1.112) (p60-src) (c-src). 5/2000 [MASS=59704]/V-src avian sarcoma viral oncogene homolog (Schmidt-Ruppin A-2), tyrosine kinase involved in cell proliferation, cell adhesion, and cytoskeletal organization, implicated in the progression of colon cancer and certain breast tumors
SW:KPC1_HUMAN P05771 homo sapiens (human). protein kinase c, beta-i type (ec 2.7.1.-) (pkc-beta-1). 7/1999 [MASS=76839]/Protein kinase C beta 1, conventional PKC expressed as beta I and beta II forms, beta II mediates G2/M phase transition, mitotic nuclear envelope breakdown, neutrophil NADPH oxidase assembly; rat Prkcb1 activity is enhanced in diabetes mellitus
SW:GPS1_HUMAN Q13098 homo sapiens (human). g protein pathway suppressor 1 (gps1 protein) (mfh protein). 11/1997 [MASS=53372]/G protein pathway suppressor 1, suppressor of G protein and MAP kinase-mediated signaling pathways
GP:AB009398_1 Homo sapiens mRNA for 26S proteasome subunit p40.5, complete cds. [MASS=42945]/Proteasome (prosome, macropain) 26S subunit (non-ATPase, 13), a subunit of the PA700 regulatory complex of the 26S proteasome
PIR2:T46412 ubiquitin--protein ligase (EC 6.3.2.19) NEDD4 - human (fragment) [MASS=95283]/Neural cell precursor expressed developmentally downregulated 4, ubiquitin-protein ligase with multiple WW domains, binds to and reduces the activity of epithelial sodium channels, may play a role in neural differentiation, regulated by kinase SGK
SW:UB5A_HUMAN P51668 homo sapiens (human). ubiquitin-conjugating enzyme e2-17 kda 1 (ec 6.3.2.19) (ubiquitin- protein ligase) (ubiquitin carrier protein) (e2(17)kb 1). 12/1998 [MASS=16602]/Ubiquitin-conjugating enzyme E2D1, member of the ubiquitin-conjugating enzyme subfamily that catalyzes the ubiquitination of cellular proteins and marks them for degradation, acts with the ubiquitin protein ligase E6AP (UBE3A) to ubiquitinate p53 (TP53)
SW:G25B_HUMAN P21181 homo sapiens (human), mus musculus (mouse), and bos taurus (bovine). g25k gtp-binding protein, brain isoform (gp) (cdc42 homolog). 12/1998 [MASS=21311]/Cell division cycle 42 (GTP binding protein 25kD), Rho GTPase involved in actin cytoskeleton organization, cell migration, cell cycle progression and apoptosis, downregulated in fibroblasts and macrophages from patients with Tangiers disease
SW:KIME_HUMAN Q03426 homo sapiens (human). mevalonate kinase (ec 2.7.1.36) (mk). 7/1999 [MASS=42451]/Mevalonate kinase (mevalonic aciduria), a peroxisomal enzyme involved in isoprenoid and cholesterol biosynthesis; mutations in the corresponding gene cause mevalonic aciduria, hyperimmunoglobulinemia D and periodic fever syndrome
GP:AB025194_1 Homo sapiens mRNA for protein tyrosine phosphatase HD-PTP, complete cds. [MASS=178974]/Member of the protein-tyrosine phosphatase family, has a region of strong similarity to a region of protein tyrosine phosphatase TD14 (rat Ptpn23), which is a putative tyrosine phosphatase that associates with cytoplasmic vesicles when overexpressed
SW:MK01_HUMAN P28482 homo sapiens (human). mitogen-activated protein kinase 1 (ec 2.7.1.-) (extracellular signal-regulated kinase 2) (erk2) (mitogen-activated protein kinase 2) (map kinase 2) (mapk 2) [MASS=41390]/Mitogen-activated protein kinase 1, a serine-threonine kinase effector of the RAS-MAP kinase pathway, translocates to the nucleus to mediate transcription when activated, involved in the regulation of cell growth, differentiation, migration and apoptosis
SW:LYN_HUMAN P07948 homo sapiens (human). tyrosine-protein kinase lyn (ec 2.7.1.112). 5/2000 [MASS=58443]/ protein tyrosine kinase, a non-receptor tyrosine kinase important in cytokine receptor- and IgE receptor-mediated signal transduction, regulates cell adhesion and apoptosis, plays a role in platelet activation and inflammatory responses
SW:ARP2_HUMAN O15142 homo sapiens (human). actin-like protein 2. 7/1999 [MASS=44761]/Actin-related protein 2 homolog, a component of the Arp2/3 protein complex, which is involved in actin filament nucleation and polymerization, may form the nucleation interface with the pointed end of the actin filament
PIR2:S52920 disintegrin (EC 3.4.24.-) - human (fragment) [MASS=54380]/A disintegrin and metalloproteinase domain 10, an ADAM family disintegrin domain-containing zinc metalloprotease, acts in ectodomain proteolysis of membrane proteins, cleaves cellular prion protein (PRNP), acts as an alpha secretase on APP
SW:KCCD_HUMAN Q13557 homo sapiens (human). calcium/calmodulin-dependent protein kinase type ii delta chain (cam-kinase ii delta chain) (ec 2.7.1.123) (camk-ii, delta subunit) (fragment). 5/2000 [MASS=12846]/Calcium/calmodulin-dependent protein kinase II delta, member of the multifunctional CAMKII family involved in Ca2+ regulated processes; alternative form delta 3 is specifically upregulated in the myocardium of patients with heart failure
SW:KRCB_HUMAN P31751 homo sapiens (human). rac-beta serine/threonine kinase (ec 2.7.1.-) (rac-pk-beta) (akt2 kinase). 11/1995 [MASS=55769]/v-akt murine thymoma viral oncogene homolog 2, protein kinase that is activated by mitogens and survival factors, may regulate cell proliferation and apoptosis, overexpression is associated with ovarian, breast and pancreatic cancers
GP:AB002310_1 Human mRNA for KIAA0312 gene, partial cds. [MASS=209315]/Protein containing a HECT domain, which may confer ubiquitin-protein ligase activity, has high similarity to a region of S. cerevisiae Tom1p, which is a protein required for the G2/M transition

SW:PTN1_HUMAN P18031 homo sapiens (human). protein-tyrosine phosphatase 1b (ec 3.1.3.48) (ptp-1b). 7/1999 [MASS=49967]/Protein tyrosine phosphatase non-receptor type I, likely involved in the negative regulation of insulin receptor signaling, may be associated with type II diabetes and obesity
SW:ERB2_HUMAN P04626 homo sapiens (human). receptor protein-tyrosine kinase erbb-2 precursor (ec 2.7.1.112) (p185erbb2) (neu proto-oncogene) (c-erbb-2) (tyrosine kinase-type cell surface receptor her2) [MASS=137910]/Avian erythroblastosis oncogene B 2, a receptor tyrosine kinase and most oncopotent member of the EGF receptor family, heterodimerizes with other EGFRs; overexpression contributes to growth, metastasis and chemoresistance of epithelial-derived tumors
SW:RAC1_HUMAN P15154 homo sapiens (human), mus musculus (mouse), and canis familiaris (dog). ras-related c3 botulinum toxin substrate 1 (p21-rac1) (ras-like protein tc25). 12/1998 [MASS=21450]/Ras-related C3 botulinum toxin substrate 1, a monomeric GTPase of the Rho family, involved in transducing signals that regulate proliferation, apoptosis, cytoskeletal organization, and response to oxidative stress, contributes to tumor cell invasiveness
PIR2:T00363 hypothetical protein KIAA0674 - human (fragment) [MASS=135179]/Member of the FKBP-type peptidyl-prolyl cis-trans isomerase family
SW:P4HA_HUMAN P13674 homo sapiens (human). prolyl 4-hydroxylase alpha subunit precursor (ec 1.14.11.2). 11/1997 [MASS=61049]/Proline 4-hydroxylase alpha polypeptide I, catalyzes the hydroxylation of proline to form 4-hydroxyproline in collagens in an oxygen-dependent manner, plays an essential role in collagen synthesis
SW:PP1A_HUMAN P08129 homo sapiens (human), mus musculus (mouse), rattus norvegicus (rat), and oryctolagus cuniculus (rabbit). serine/threonine protein phosphatase pp1-alpha 1 catalytic subunit (ec 3.1.3 [MASS=37512]/Protein phosphatase 1 catalytic subunit alpha isoform, plays roles in diverse cellular signal transduction processes that involve protein dephosphorylation, regulates of cell growth and apoptosis and may be a tumor suppressor
PIR2:T14762 hypothetical protein DKFZp434A014.1 - human (fragment) [MASS=92341]/Member of the angiotensin-converting enzyme family of dipeptidyl carboxydipeptidases
SW:UBPA_HUMAN Q14694 homo sapiens (human). ubiquitin carboxyl-terminal hydrolase 10 (ec 3.1.2.15) (ubiquitin thiolesterase 10) (ubiquitin-specific processing protease 10) (deubiquitinating enzyme 10) (k [MASS=87134]/Ubiquitin specific protease 10, a member of the ubiquitin-specific cysteine (thiol) protease family, cleaves ubiquitin from ubiquitin-conjugated protein substrates, activity is inhibited upon association with Ras-GAP SH3 domain binding protein
SWN:UBPF_HUMAN Q9y4e8 homo sapiens (human). ubiquitin carboxyl-terminal hydrolase 15 (ec 3.1.2.15) (ubiquitin thiolesterase 15) (ubiquitin-specific processing protease 15) (deubiquitinating enzyme 15) (f [MASS=108965]/Ubiquitin-specific protease 15, a member of the ubiquitin-specific cysteine (thiol) protease family, cleaves ubiquitin from ubiquitin-conjugated protein substrates, may play a role in growth regulation
SW:PDI_HUMAN P07237 homo sapiens (human). protein disulfide isomerase precursor (pdi) (ec 5.3.4.1) (prolyl 4-hydroxylase beta subunit) (cellular thyroid hormone binding protein) (p55). 5/2000 [MASS=57116]/Procollagen-proline 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase) beta polypeptide (protein disulfide isomerase- thyroid hormone binding protein p55), acts as a protein folding catalyst and promotes protein solubility
SW:GNT2_HUMAN Q10469 h alpha-1,6-mannosyl-glycoprotein beta-1,2-n- acetylglucosaminyltransferase (ec 2.4.1.143) (n-glycosyl- oligosaccharide-glycoprotein n-acetylglucosaminyltransferase ii) (beta-1,2-n- [MASS=51550]/UDP-N-acetylglucosamine: alpha-6-D-mannoside-beta-1,2- N-acetylglucosaminyltransferase II, catalyzes the conversion of oligomannose to complex N-glycans; activity is reduced or absent in type II congenital disorders of glycosylation
SW:EPA7_HUMAN Q15375 homo sapiens (human). ephrin type-a receptor 7 precursor (ec 2.7.1.112) (tyrosine-protein kinase receptor ehk-3) (eph homology kinase-3) (receptor protein- tyrosine kinase hek11). 5 [MASS=112097]/ Ephrin type A receptor 7, an Eph-related receptor tyrosine kinase, interacts with the PDZ domain of the Ras binding protein AF6 (MLLT4), may be involved in cell signaling
SW:INSR_HUMAN P06213 homo sapiens (human). insulin receptor precursor (ec 2.7.1.112) (ir). 5/2000 [MASS=156281]/Insulin receptor, a transmembrane receptor protein tyrosine kinase involved in carbohydrate metabolism, energy pathways, and cell growth; gene mutation is associated with insulin-resistant diabetes mellitus and leprechaunism
GP:AB028128_1 Homo sapiens DPM3 mRNA for dolichol-phosphate-mannose synthase, complete cds. [MASS=10080]/Dolichyl-phosphate mannosyltransferase subunit 3 (prostin 1), part of a complex that produces mannosyl donors for glycoconjugate biosynthesis, stabilizes DPM1 and is stabilized by DPM2; expression is associated with a lack of invasive potential in tumors
SW:UBCI_HUMAN P50550 homo sapiens (human), mus musculus (mouse), and xenopus laevis (african clawed frog). ubiquitin-conjugating enzyme e2-18 kda (ec 6.3.2.19) (ubiquitin-protein ligase) (ubiquitin carr [MASS=18007]/Ubiquitin-conjugating enzyme E2I, member of the ubiquitin-conjugating enzyme family that catalyzes the ubiquitination of cellular proteins and marks them for degradation, may play roles in cell cycle progression and repair of TOP1-mediated DNA damage
SW:KAPA_HUMAN P17612 homo sapiens (human). camp-dependent protein kinase, alpha-catalytic subunit (ec 2.7.1.37) (pka c-alpha). 5/2000 [MASS=40458]/Catalytic subunit C alpha of cAMP-dependent protein kinase, plays a role in transcriptional regulation and may mediate suppression of apoptosis, may also serve as a tumor biomarker; alternative form C alpha 2 may play a role in sperm development
SW:BCR_HUMAN P11274 homo sapiens (human). breakpoint cluster region protein (ec 2.7.1.-). 7/1999 [MASS=142806]/Breakpoint cluster region, GTPase-activating protein for p21rac with serine/threonine kinase activity; translocation of the corresponding gene is associated with Philadelphia chromosome-positive chronic myeloid leukemia

PIR2:I37405 polypeptide N-acetylgalactosaminyltransferase (EC 2.4.1.41) - human [MASS=64733]/N-acetylgalactosaminyltransferase T1, enzyme that initiates O-glycosylation; inhibition affects the sensitivity of tumors cells to immune killer cells
SWN:DUSC_HUMAN Q9uni6 homo sapiens (human). dual specificity protein phosphatase 12 (ec 3.1.3.48) (ec 3.1.3.16) (dual-specificity tyrosine phosphatase yvh1). 8/2001 [MASS=37687]/Dual specificity phosphatase 12, binds zinc via a zinc-finger motif in the carboxyl terminus, may play a role in cell growth; genetic variants may be associated with cancer susceptibility
SW:P2BA_HUMAN Q08209 homo sapiens (human). serine/threonine protein phosphatase 2b catalytic subunit, alpha isoform (ec 3.1.3.16) (calmodulin-dependent calcineurin a subunit, alpha isoform) (cam-prp cat [MASS=58688]/Calcineurin A alpha, catalytic subunit of calcium/calmodulin regulated protein phosphatase, regulates activity of transcription factors involved in signal transduction and growth control
PIR2:JC5938 thioredoxin-like protein - human [MASS=32251]/Thioredoxin-like 32, a thioredoxin related protein that has thioredoxin-like reducing activity
SW:OGT1_HUMAN O15294 homo sapiens (human). udp-n-acetylglucosamine--peptide n-acetylglucosaminyltransferase 100 kda subunit (ec 2.4.1.-) (o-glcnac transferase p100 subunit). 5/2000 [MASS=103012]/O-linked N-acetylglucosamine transferase (UDP-N-acetylglucosamine:polypeptide-N-acetylglucosaminyltransferase), enzyme that functions in O-glycosylation, may be involved in insulin secretion and glucose homeostasis, may play a role in signal transduction
GP:D87116_1 Human mRNA for MAP kinase kinase 3b ,complete cds; MKK3b. [MASS=39318]/Mitogen activated protein kinase kinase 3, phosphorylates MAP kinase p38, involved in stress and inflammatory responses, senescence, and apoptosis, also has roles in ischemic kidney injury, and H. influenzae infection
SW:PPOL_HUMAN P09874 homo sapiens (human). poly [adp-ribose] polymerase (ec 2.4.2.30) (parp) (adprt) (nad(+) adp-ribosyltransferase) (poly[adp-ribose] synthetase). 11/1997 [MASS=112953]/ADP-ribosyltransferase, catalyzes formation of ADP ribose polymers attached to proteins using NAD(+) as substrate in response to DNA damage, modulates chromatin structure and plays a role in DNA repair and apoptosis
SW:PTPF_HUMAN P10586 homo sapiens (human). lar protein precursor (leukocyte antigen related) (ec 3.1.3.48). 10/1994 [MASS=211845]/Protein tyrosine phosphatase receptor-type F (leukocyte common antigen related), regulates insulin receptor signaling and cell migration, inhibits tumor formation in nude mice
SW:PSS1_HUMAN P48651 homo sapiens (human). phosphatidylserine synthase i (serine-exchange enzyme i) (ec 2.7.8.-) (kiaa0024). 11/1997 [MASS=55528]/3'-phosphoadenosine 5'-phosphosulfate synthase 1, bifunctional polypeptide with ATP sulfurylase and adenosine 5'-phosphosulfate kinase activites, required for the synthesis of the sulfonate donor 3'-phosphoadenosine 5'-phosphosulfate
SW:PPT_HUMAN P50897 homo sapiens (human). palmitoyl-protein thioesterase precursor (ec 3.1.2.22) (palmitoyl- protein hydrolase). 5/2000 [MASS=34193]/Palmitoyl-protein thioesterase (ceroid-lipofuscinosis, neuronal 1, infantile), catalyzes the hydrolysis of palmitate from S-acetylated cysteine residues, may be involved in apoptosis; gene mutation is detected in infantile neuronal ceroid lipofuscinosis
SW:PTK7_HUMAN Q13308 homo sapiens (human). tyrosine-protein kinase-like 7 precursor (colon carcinoma kinase-4) (cck-4). 5/2000 [MASS=118260]/Protein tyrosine kinase 7 (colon carcinoma kinase-4), a glycosylated member of the receptor protein tyrosine kinase family that may be involved in tumorigenesis, likely to be catalytically inactive due to alterations within the RTK consensus sequences
PIR2:A57099 DNA-activated protein kinase, catalytic subunit - human [MASS=465428]/DNA-dependent protein kinase catalytic subunit, a DNA-binding protein kinase involved in DNA double-strand break repair and somatic recombination of antibody genes; absence of mouse Prkdc is associated with severe combined immunodeficiency
SW:RB48_HUMAN Q09028 homo sapiens (human). chromatin assembly factor 1 p48 subunit (caf-1 p48 subunit) (retinoblastoma binding protein p48) (retinoblastoma-binding protein 4) (msi1 protein homolog). 12/ [MASS=47656]/Retinoblastoma binding protein 4, a nuclear protein that forms complexes with a variety of proteins including RB1, HDAC1, BRCA1, E2F, which function in histone acetylation, regulation of cell proliferation, or transcriptional repression
SW:RL40_HUMAN P14793 homo sapiens (human), rattus norvegicus (rat), and gallus gallus (chicken). 60s ribosomal protein l40 (cep52). 11/1997 [MASS=6181]/Ubiquitin A-52 residue ribosomal protein fusion product 1, protein consisting of ubiquitin at the N-terminus and ribosomal protein L40 at the C-terminus; the corresponding gene is upregulated in colon cancer but not in gastric cancer
SW:KC2B_HUMAN P13862 homo sapiens (human), mus musculus (mouse), rattus norvegicus (rat), bos taurus (bovine), sus scrofa (pig), oryctolagus cuniculus (rabbit), and gallus gallus (chicken). casein kinase [MASS=24942]/Casein kinase II beta subunit, regulatory subunit of casein kinase II (CK2), confers stability and specificity to CK2 catalytic subunits, may mediate formation of the tetrameric CK2 complex, and may be involved in heat stress response
SW:MA2B_HUMAN O00754 homo sapiens (human). lysosomal alpha-mannosidase precursor (ec 3.2.1.24) (mannosidase, alpha b) (lysosomal acid alpha-mannosidase) (laman). 5/2000 [MASS=113673]/Mannosidase alpha class 2B member 1, catalyzes the hydrolysis of alpha-mannoside linkages in glycoprotein catabolism, enzyme activity is inhibited by azafuranose analogs of mannose, deficiency is associated with alpha-mannosidosis
GP:X92689_1 Homo sapiens mRNA for UDP-GalNAc:polypeptide N-acetylgalactosaminyl transferase (GalNAc-T3). [MASS=72638]/N-acetylgalactosaminyltranferase T3 (UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 3), enzyme that initiates O-glycosylation; elevated levels may be associated with differentiation of adenocarcinomas

GP:AB000449_1 Homo sapiens mRNA for VRK1, complete cds. [MASS=45476]/Vaccinia related kinase 1, nuclear serine/threonine kinase that phosphorylates acidic and basic protein substrates, may activate p53 and function in signal transduction, may regulate cellular proliferation, has similarity to vaccinia virus B1R kinase
SW:CAG4_HUMAN Q11201 h cmp-n-acetylneuraminate-beta-galactosamide-alpha-2,3-sialyltransferase (ec 2.4.99.4) (beta-galactoside alpha-2,3-sialyltransferase) (alpha 2,3-st) (gal-nac6s) (gal-beta-1,3-galnac [MASS=39075]/Sialyltransferase 4A (beta-galactoside alpha-2,3-sialyltransferase), member of a sialyltransferase 4 family, catalyzes the transfer of NeuAc from CMP-NeuAc to asialo-fetuin
SW:RS12_HUMAN P25398 homo sapiens (human). 40s ribosomal protein s12. 5/2000 [MASS=14395]/Ribosomal protein S12, a component of the small 40S ribosomal subunit; overexpressed in colorectal cancer
PIR2:JC4775 p58k protein - human [MASS=57580]/The 58,000-dalton cellular inhibitor of the interferon-induced double-stranded RNA-activated protein kinase (PKR) is a member of the tetratricopeptide repeat family of proteins/DnaJ (Hsp40) homolog subfamily C member 3 (protein kinase inhibitor p58), a member of the tetratricopeptide repeat family of proteins that may act as a cochaperone that inhibits the activity of double-stranded RNA-dependent protein kinase (PRKR)
SW:SYTC_HUMAN P26639 homo sapiens (human). threonyl-trna synthetase, cytoplasmic (ec 6.1.1.3) (threonine--trna ligase) (thrrs). 6/1994 [MASS=82124]/Threonyl-tRNA synthetase, a class II aminoacyl tRNA synthetase which aminoacylates its cognate tRNAs with threonine for protein synthesis, autoantigen in several autoimmune disorders
SW:IF2P_HUMAN O60841 homo sapiens (human). translation initiation factor if-2. 5/2000 [MASS=138755]/Translation initiation factor, member of the Tu elongation factor family, has moderate similarity to yeast YAL035W translation initiation factor 2 (eIF2)
SW:RL7A_HUMAN P11518 homo sapiens (human), and rattus norvegicus (rat). 60s ribosomal protein l7a (surfeit locus protein 3) (pla-x polypeptide). 7/1999 [MASS=29864]/Ribosomal protein L7a (surfeit-3), a putative component of the 60S ribosomal subunit, likely to be involved in protein biosynthesis and in colorectal carcinogenesis; trk-2h fusion oncogene in breast cancer cells comprises a fragment of RPL7A fused to TRK
SW:SYG_HUMAN P41250 homo sapiens (human). glycyl-trna synthetase (ec 6.1.1.14) (glycine--trna ligase) (glyrs). 10/1996 [MASS=77531]/Glycyl-tRNA synthetase; functions in protein biosynthesis, aminoacylates its cognate tRNAs with phenylalanine/Glycyl-tRNA synthetase, a class II aminoacyl-tRNA synthetase that catalyzes aminoacylation of its cognate tRNA with glycine for protein biosynthesis; an autoantigen in dermatomyositis
SW:IF32_HUMAN Q13347 homo sapiens (human). eukaryotic translation initiation factor 3 subunit 2 (eif-3 beta) (eif3 p36) (tgf-beta receptor interacting protein 1) (trip-1). 5/2000 [MASS=36502]/Eukaryotic translation initiation factor 3 subunit 2, an eIF3 subunit with a predicted role in translation initiation, binds transforming growth factor beta receptor II (TGFBR2) and acts as a modulator of TGFBR2 signaling pathways
SW:RS4_HUMAN P12750 homo sapiens (human), rattus norvegicus (rat), mus musculus (mouse), mesocricetus auratus (golden hamster), and felis silvestris catus (cat). 40s ribosomal protein s4, x isoform (sin [MASS=29467]/Ribosomal protein S4 X-linked, a component of the small 40S ribosomal subunit with roles in translation, cell cycle, and cell proliferation; gene is X-linked but escapes X inactivation, and may therefore contribute to haploinsufficency in Turner syndrome
SW:SYD_HUMAN P14868 homo sapiens (human). aspartyl-trna synthetase (ec 6.1.1.12) (aspartate--trna ligase) (asprs). 11/1997 [MASS=57192]/Aspartyl-tRNA synthetase, a class II aminoacyl tRNA synthetase that aminoacylates its cognate tRNA with aspartate for protein biosynthesis, associates with a multisynthetase complex, N-terminus may aid interaction with elongation factor 1 alpha
SW:EF11_HUMAN P04720 homo sapiens (human), and oryctolagus cuniculus (rabbit). elongation factor 1-alpha 1 (ef-1-alpha-1) (elongation factor tu) (ef- tu). 12/1998 [MASS=50141]/Eukaryotic translation elongation factor 1 alpha 1, involved in cytoskeletal rearrangment, has putative roles in translational elongation and senescence and GTP binding; possibly involved in diabetes, Felty syndrome, and HIV life cycle
SW:SYA_HUMAN P49588 homo sapiens (human). alanyl-trna synthetase (ec 6.1.1.7) (alanine--trna ligase) (alars). 7/1998 [MASS=106801]/Alanyl-tRNA synthetase, aminoacylates its cognate tRNA with alanine for protein biosynthesis, acts as an autoantigen in patients with polymyositis
SW:SYR_HUMAN P54136 homo sapiens (human). arginyl-trna synthetase (ec 6.1.1.19) (arginine--trna ligase) (argrs). 5/2000 [MASS=74977]/Arginyl-tRNA synthetase, aminoacylates its cognate tRNAs with arginine for protein biosynthesis
SW:SYM_HUMAN P56192 homo sapiens (human). methionyl-trna synthetase (ec 6.1.1.10) (methionine--trna ligase) (metrs). 12/1998 [MASS=101129]/Methionine-tRNA synthetase, putative tRNA synthetase that is predicted to aminoacylate its cognate tRNAs with methionine for protein biosynthesis, required for rRNA synthesis in the nucleolus
SW:RL8_HUMAN P25120 homo sapiens (human), rattus norvegicus (rat), and mus musculus (mouse). 60s ribosomal protein l8. 5/2000 [MASS=28025]/Ribosomal protein L8, putative component of the large 60S ribosomal subunit
PIR2:B55053 endothelial monocyte-activating protein II precursor - human [MASS=34254]/Endothelial monocyte activating polypeptide II, a proinflammatory cytokine that interacts with ATP synthase and inhibits endothelial cell growth, released during apoptosis, may sensitize tumors to killing by tumor necrosis factor alpha (TNF)
SW:SYEP_HUMAN P07814 homo sapiens (human). multifunctional aminoacyl-trna synthetase [includes: glutamyl-trna synthetase (ec 6.1.1.17) (glutamate--trna ligase); prolyl-trna synthetase (ec 6.1.1.15) (pro [MASS=163026]/Glutamyl-prolyl-tRNA synthetase, a bifunctional enzyme with two functionally separable domains, one that aminoacylates prolyl-tRNA with proline and another that is believed to aminoacylate glutamyl-tRNA with glutamate for protein biosynthesis

SWN:E2BD_HUMAN Q9ui10 homo sapiens (human). translation initiation factor eif-2b delta subunit (eif-2b gdp-gtp exchange factor). 8/2001 [MASS=57599]/Protein with strong similarity to eukaryotic translation initiation factor 2B delta subunit (rat Eif2b), which is a guanine nucleotide-exchange factor subunit of eIF-2B that mediates inhibition of eIF-2B, member of the initiation factor 2 subunit family
SW:SYQ_HUMAN P47897 homo sapiens (human). glutaminyl-trna synthetase (ec 6.1.1.18) (glutamine--trna ligase) (glnrs). 5/2000 [MASS=87799]/Glutaminyl-tRNA synthetase, aminoacylates cognate tRNAs with glutamine for protein biosynthesis, also suppresses FAS (TNFRSF6)-mediated apoptosis by inhibiting ASK1 (MAP3K5) kinase activity, contains N-terminal appended and C-terminal catalytic domains
SW:SYV_HUMAN P26640 homo sapiens (human). valyl-trna synthetase (ec 6.1.1.9) (valine--trna ligase) (valrs). 2/1996 [MASS=140377]/Valyl-tRNA synthetase 2, a putative class I tRNA sythetase, predicted to function in aminoacylation of valyl tRNAs for protein biosynthesis
SW:IF5A_HUMAN P10159 homo sapiens (human). initiation factor 5a (eif-5a) (eif-4d) (rev binding factor). 5/2000 [MASS=16701]/Eukaryotic initiation factor 5A, a translation initiation factor, also an HIV-1 transactivator protein Rev cofactor that exports viral mRNA from the nucleus
SW:RM03_HUMAN P09001 homo sapiens (human). mitochondrial 60s ribosomal protein l3. 8/1992 [MASS=38633]/Mitochondrial ribosomal protein L3, a likely component of the large mitochondrial 60S ribosomal subunit, may be involved in mRNA binding to the ribosome, can interact with the 3' UTR of hepatitis C; elevated levels are associated with hepatocarcinoma
SWN:SU12_HUMAN Q9unq9 homo sapiens (human). protein translation factor sui1 homolog a121. 8/2001 [MASS=12745]/Translation factor sui1 homolog, a translation initiation factor, plays a role in initiating translation, may modulate translation initiation during periods of cell stress such as UV-induced and endoplasmic reticulum stress
SW:RL32_HUMAN P02433 homo sapiens (human), mus musculus (mouse), and rattus norvegicus (rat). 60s ribosomal protein l32. 6/1994 [MASS=15729]/Ribosomal protein L32, an RNA-binding structural component of the large 60S ribosomal subunit that is likely to play a role in protein biosynthesis
GP:AF112214_1 Homo sapiens ribosomal protein L13 mRNA, complete cds; RPL13. [MASS=19917]/Ribosomal protein L13, putative component of the 60S ribosomal subunit, expressed at higher levels in benign breast lesions than in carcinomas
SW:SYK_HUMAN Q15046 homo sapiens (human). lysyl-trna synthetase (ec 6.1.1.6) (lysine--trna ligase) (lysrs) (kiaa0070). 7/1998 [MASS=68034]/Lysyl-tRNA synthetase, a class II aminoacyl tRNA synthetase, aminoacylates its cognate tRNAs with lysine for protein biosynthesis, packaged into HIV virions, exists as cytoplasmic and mitochondrial alternative forms
GP:AB037819_1 Homo sapiens mRNA for KIAA1398 protein, partial cds; Start codon is not identified.. [MASS=170212]/Ribosome binding protein 1, a putative ribosome receptor, may play a role in protein biosynthesis, appears to be involved in cardiac development, may play a role in cardiac remodeling in heart failure
GP:AF132941_1 Homo sapiens CGI-07 protein mRNA, complete cds. [MASS=57585]/Protein with moderate similarity to S. cerevisiae Nmd3p, which is a protein involved in the nuclear export of 60S ribosomal subunits
SW:EF1G_HUMAN P26641 homo sapiens (human). elongation factor 1-gamma (ef-1-gamma). 5/2000 [MASS=50119]/Eukaryotic elongation factor 1 gamma, a likely translation elongation factor 1 (EF-1) complex component that binds cytoplasmic cysteinyl-tRNA synthetase and possibly EF-1 beta; overexpression in gastric carcinoma correlates with vascular permeation
SW:RS8_HUMAN P09058 homo sapiens (human), rattus norvegicus (rat), and mus musculus (mouse). 40s ribosomal protein s8. 2/1996 [MASS=24074]/Ribosomal protein S8, component of the small 40S ribosomal subunit
SW:IF4G_HUMAN Q04637 homo sapiens (human). eukaryotic translation initiation factor 4 gamma (eif-4-gamma) (eif- 4g) (eif4g) (p220). 7/1999 [MASS=153361]/Eukaryotic translation initiation factor 4 gamma 1, gamma subunit of eIF4, functions in translation initiation, binds RNA and forms a bridge between the mRNA cap and polyA tail, cleaved during apoptosis and poliovirus infection
SW:EF2_HUMAN P13639 homo sapiens (human). elongation factor 2 (ef-2). 12/1998 [MASS=95338]/Translation elongation factor 2, member of the superfamily of GTP hydrolases, binds ribosomes, catalyzes the translocation step of peptide elongation in protein biosynthesis, target of ADP-ribosylation by diphteria toxin and Pseudomonas exotoxin
SW:SYI_HUMAN P41252 homo sapiens (human). isoleucyl-trna synthetase, cytoplasmic (ec 6.1.1.5) (isoleucine--trna ligase) (ilers) (irs). 7/1999 [MASS=144959]/Isoleucine-tRNA synthetase, a class I aminoacyl tRNA synthetase, aminoacylates isoleucyl-tRNA with isoleucine for protein biosynthesis, acts as an autoantigen in some autoimmune diseases
GP:AF132939_1 Homo sapiens CGI-04 protein mRNA, complete cds. [MASS=53063]/Member of the class I tryptophanyl and tyrosyl (W and Y) tRNA synthetase family, has low similarity to tyrosyl-tRNA synthetase mitochondrial (S. cerevisiae Msy1p), which is involved in tyrosyl-tRNA aminoacylation
SW:IF38_HUMAN Q99613 homo sapiens (human). eukaryotic translation initiation factor 3 subunit 8 (eif3 p110). 5/2000 [MASS=105344]/Translation initiation factor 3 subunit 8, 110 kDa eIF3 subunit that recruits translation initiation factor 1 (human SUI1) to 40S ribosomes, interacts with viral internal ribosome entry sites, and may be involved in seminoma development
SW:RL3_HUMAN P39023 homo sapiens (human). 60s ribosomal protein l3 (hiv-1 tar rna binding protein b) (tarbp-b). 5/2000 [MASS=45978]/Ribosomal protein L3, component of the large 60S ribosomal subunit; overexpressed in rapidly dividing cells

SW:E2BE_HUMAN Q13144 homo sapiens (human). translation initiation factor eif-2b epsilon subunit (eif-2b gdp-gtp exchange factor) (fragment). 7/1999 [MASS=72237]/Translation initiation factor 2B subunit 5 (epsilon, 82kD), putative guanyl-nucleotide exchange factor component of the translation initiation factor 2B complex, predicted to mediate the exchange of GDP bound to translation initiation factor eIF2 for GTP
SW:RL9_HUMAN P32969 homo sapiens (human). 60s ribosomal protein l9. 5/2000 [MASS=21863]/Ribosomal protein L9, putative component of the large 60S ribosomal subunit
SW:RS5_HUMAN P46782 homo sapiens (human). 40s ribosomal protein s5. 5/2000 [MASS=22777]/Ribosomal protein S5, a component of the 40S ribosomal subunit; gene expression is altered in colorectal carcinoma cells
SW:RS25_HUMAN P25111 homo sapiens (human), and rattus norvegicus (rat). 40s ribosomal protein s25. 10/1993 [MASS=13742]/Ribosomal protein S25, a putative RNA-binding component of the small 40S ribosomal subunit that may play a role in protein biosynthesis
SW:IF2A_HUMAN P05198 homo sapiens (human). eukaryotic translation initiation factor 2 alpha subunit (eif-2- alpha). 7/1999 [MASS=35981]/Eukaryotic translation initiation factor 2 subunit 1 (alpha subunit of eIF2), a translation initiation factor, involved in translational regulation, inhibited by phosphorylation
SW:RS29_HUMAN P30054 homo sapiens (human), mus musculus (mouse), rattus norvegicus (rat), and bos taurus (bovine). 40s ribosomal protein s29. 5/2000 [MASS=6546]Ribosomal protein S29, a component of the small 40S ribosomal subunit, contains a zinc finger-like motif, enhances activity of the tumor suppressor Krev-1 (RAP1A)
SW:RS14_HUMAN P06366 homo sapiens (human), and cricetulus griseus (chinese hamster). 40s ribosomal protein s14. 8/1992 [MASS=16273]/Ribosomal protein S14, a putative component of the small 40S ribosomal subunit, may play a role in protein biosynthesis, may bind RNA, upregulated in prostate carcinoma cell lines
SW:EF12_HUMAN Q05639 homo sapiens (human). elongation factor 1-alpha 2 (ef-1-alpha-2) (statin s1). 12/1998 [MASS=50470]/Eukaryotic translation elongation factor 1 alpha 2, a putative translation elongation factor, upregulated in an estrogen receptor-expressing breast carcinoma cell line; mutation in mouse Eef1a2 causes the multiple-defect wasted phenotype
SW:PAB1_HUMAN P11940 homo sapiens (human). polyadenylate-binding protein 1 (poly(a) binding protein 1) (pabp 1). 7/1998 [MASS=70671]/Poly(A)-binding protein cytoplasmic 1, binds to poly(A) tails of mRNA and plays roles in regulating mRNA stability and translation, also implicated in mRNA transport from the nucleus to the cytoplasm
SW:IF2G_HUMAN P41091 homo sapiens (human). eukaryotic translation initiation factor 2 gamma subunit (eif-2- gamma). 5/2000 [MASS=50978]/Eukaryotic initiation factor 2G, gamma subunit of the heterotrimeric GTP binding protein involved in recruitment of Met-tRNAi to the 40S ribosomal subunit, activity is regulated by herpes simplex virus type 1 gamma 34.5 and by the cellular GADD34 proteins
SW:IF37_HUMAN O15371 homo sapiens (human). eukaryotic translation initiation factor 3 subunit 7 (eif-3 zeta) (eif3 p66). 5/2000 [MASS=63973]/Eukaryotic translation initiation factor 3 subunit 7, mRNA-binding subunit of the tranlation initiation factor 3 complex, which mediates dissociation of 80S ribosomes and stabilizes initiator Met-tRNAi binding to 40S subunits
SW:RL4_HUMAN P36578 homo sapiens (human). 60s ribosomal protein l4 (l1). 12/1998 [MASS=47759]/Ribosomal protein L4, a putative component of the large 60S ribosomal subunit, may bind RNA
SW:RS17_HUMAN P08708 homo sapiens (human). 40s ribosomal protein s17. 8/1992 [MASS=15419]/Ribosomal protein S17, component of the small 40S ribosomal subunit
SW:RS3A_HUMAN P49241 homo sapiens (human), and felis silvestris catus (cat). 40s ribosomal protein s3a. 5/2000 [MASS=29814]/Ribosomal protein S3A (v fos transformation effector), component of the 40S ribosomal subunit, may play roles in apoptosis, cell growth and protein biosynthesis
GP:AF257077_1 Homo sapiens eukaryotic translation initiation factor EIF2B subunit 3 (EIF2B3) mRNA, complete cds; eukaryotic translation initiation factor EIF2Bgamma; guanine nucleotide exchange factor. [MASS=50240]/Eukaryotic translation initiation factor 2B gamma subunit, has a putative role in the initiation of protein synthesis; acts as a cofactor for hepatitis C virus IRES-mediated translation
SWN:SYFB_HUMAN Q9nsd9 homo sapiens (human). phenylalanyl-trna synthetase beta chain (ec 6.1.1.20) (phenylalanine--trna ligase beta chain) (phers) (protein hspc173). 8/2001 [MASS=66130]/Phenylalanyl-tRNA synthetase beta-subunit, regulatory subunit that forms heterodimers with the catalytic alpha subunit (FARSL), involved in protein synthesis, may play a role in tumorigenic events
SW:SR09_HUMAN P49458 homo sapiens (human). signal recognition particle 9 kda protein (srp9). 12/1998 [MASS=9981]/Signal recognition particle 9 kDa, a subunit of the signal recognition particle that forms the Alu RNA-binding protein and binds to Alu RNA with SRP14, involved in translocation of newly synthesized proteins across the membrane of the rough ER
SW:RL23_HUMAN P23131 homo sapiens (human), rattus norvegicus (rat), and sus scrofa (pig). 60s ribosomal protein l23 (l17). 7/1999 [MASS=14865]/Ribosomal protein L23, a putative large ribosomal subunit component that is likely to play a role in protein biosynthesis
SW:RS21_HUMAN P35265 homo sapiens (human), and sus scrofa (pig). 40s ribosomal protein s21. 5/2000 [MASS=9111]/Ribosomal protein S21, component of the small 40S ribosomal subunit
SW:ERF1_HUMAN P46055 homo sapiens (human), mesocricetus auratus (golden hamster), and oryctolagus cuniculus (rabbit). eukaryotic peptide chain release factor subunit 1 (erf1) (tb3-1) (c11 protein). 5/20 [MASS=49031]/ Eukaryotic translation termination factor 1, an RNA binding translation release factor involved in translation termination, expression is increased in H. pylori infected gastric cancer cells; may be candidate gene for certain malignant myeloid diseases

SW:RL5_HUMAN P46777 homo sapiens (human). 60s ribosomal protein l5. 7/1999 [MASS=34317]/Ribosomal protein L5, a putative component of the 60S ribosomal subunit, binds 5S rRNA, undergoes nuclear export, may play a role in rev-mediated HIV-1 RNA nucleocytoplasmic transport; expression is altered in colorectal cancer and astrocytomas
ATP-binding cassette subfamily F member 1, a member of the ATP-binding cassette family that does not contain a transmembrane domain and may play a role in translation
SW:RS11_HUMAN P04643 homo sapiens (human), rattus norvegicus (rat), and mus musculus (mouse). 40s ribosomal protein s11. 5/2000 [MASS=18431]/Ribosomal protein S11, putative component of the small 40S ribosomal subunit
SW:RLA0_HUMAN P05388 homo sapiens (human). 60s acidic ribosomal protein p0 (l10e). 5/2000 [MASS=34274]/Ribosomal protein P0, acidic phosphoprotein component of the large 60S ribosomal subunit; shows increased expression in hepatocellular and colon carcinomas
SW:R27A_HUMAN P14798 homo sapiens (human), and cavia porcellus (guinea pig). 40s ribosomal protein s27a. 5/2000 [MASS=9418]/Ribosomal protein S27a, component of the small ribosomal subunit, consists of ubiquitin at the N-terminus and ribosomal protein S27a at the C-terminus; overexpressed in colon and renal cancers
SW:R10A_HUMAN P53025 homo sapiens (human). 60s ribosomal protein l10a (csa-19). 10/1996 [MASS=24859]/Ribosomal protein L10a, a component of the large 60S ribosomal subunit; expression in the thymus is downregulated by cyclosporin-A
SW:EFTU_HUMAN P49411 homo sapiens (human). elongation factor tu, mitochondrial precursor (p43). 12/1998 [MASS=49542]/Tu translation elongation factor (mitochondrial), a putative translation elongation factor, may be involved in protein biosynthesis, upregulated in some tumors
SW:SYN_HUMAN O43776 homo sapiens (human). asparaginyl-trna synthetase, cytoplasmic (ec 6.1.1.22) (asparagine-- trna ligase) (asnrs). 5/2000 [MASS=62943]/Asparaginyl-tRNA synthetase, a class II aminoacyl tRNA synthetase, aminoacylates its cognate tRNAs with asparagine for protein biosynthesis, acts as an autoantigen in patients with inflammatory myopathy in interstitial lung disease
SW:IF39_HUMAN P55884 homo sapiens (human). eukaryotic translation initiation factor 3 subunit 9 (eif-3 eta) (eif3 p116) (eif3 p110). 5/2000 [MASS=92492]/Eukaryotic translation initiation factor 3 subunit (EIF3 subunit eta), the 116 kDa subunit of the EIF3 complex that plays a role in protein synthesis initiation
SW:RL2A_HUMAN P46776 homo sapiens (human). 60s ribosomal protein l27a. 5/2000 [MASS=16430]/Ribosomal protein L27a, component of the large 60S ribosomal subunit; gene is abnormally expressed in colorectal carcinomas
SW:RSP4_HUMAN P08865 homo sapiens (human). 40s ribosomal protein sa (p40) (34/67 kda laminin receptor) (colon carcinoma laminin-binding protein) (nem/1chd4). 5/2000 [MASS=32854]/Laminin receptor 1, a ribosomal protein of the small 40S ribosomal subunit, plays a role in cancer cell and basement membrane glycoprotein laminin interactions during tumor invasion and metastasis, expression correlates with cancer cell aggressiveness
SW:RL18_HUMAN Q07020 homo sapiens (human). 60s ribosomal protein l18. 5/2000 [MASS=21503]/Ribosomal protein L18, a component of the large 60S ribosomal subunit, a negative regulator of double-stranded RNA-activated protein kinase (PKR) which is involved in control of protein synthesis initiation; gene expression increases in colon cancer
SW:RL3L_HUMAN Q92901 homo sapiens (human). 60s ribosomal protein l3-like. 11/1997 [MASS=46165]/Ribosomal protein L3-like, a putative RNA-binding ribosome structural protein that plays a role in protein biosynthesis
SW:RS6_HUMAN P10660 homo sapiens (human), rattus norvegicus (rat), and mus musculus (mouse). 40s ribosomal protein s6 (phosphoprotein np33). 7/1998 [MASS=28681]/Ribosomal protein S6, structural component of the cytosolic small (40S) ribosomal subunit, functions in RNA binding and protein biosynthesis
SW:IF34_HUMAN O75821 homo sapiens (human). eukaryotic translation initiation factor 3 subunit 4 (eif-3 delta) (eif3 p44) (eif-3 rna-binding subunit) (eif3 p42). 5/2000 [MASS=35696]/Eukaryotic translation initiation factor 3 subunit 4 (delta 44kD), a component of the eIF-3 translation initiation complex which plays a role in formation of the 40S initiator complex containing methionyl-tRNA and 40S subunit, binds RNA
SW:RL10_HUMAN P27635 homo sapiens (human). 60s ribosomal protein l10 (qm protein) (tumor suppressor qm) (laminin receptor homolog). 5/2000 [MASS=24446]/Ribosomal protein L10, a component of the 60S ribosomal subunit; may be involved in the maintenance of the nontumorigenic phenotype in Wilms' microcell hybrid cells
SW:RL12_HUMAN P30050 homo sapiens (human). 60s ribosomal protein l12. 7/1998 [MASS=17819]/Ribosomal protein L12, a likely RNA-binding structural component of the large 60S ribosomal subunit that plays a role in protein biosynthesis; autoantibodies to ribosomal protein L12 are associated with systemic lupus erythematosus
SW:RL14_HUMAN P50914 homo sapiens (human). 60s ribosomal protein l14 (cag-isl 7). 12/1998 [MASS=23158]/Ribosomal protein L14, a putative component of the large 60S ribosomal subunit; transcripts can contain either fixed or variable numbers of CAG triplet repeats depending on cell type
SW:RL17_HUMAN P18621 homo sapiens (human). 60s ribosomal protein l17 (l23). 5/2000 [MASS=21397]/Ribosomal protein L17, an RNA-binding structural component of the large 60S ribosomal subunit that plays a role in protein biosynthesis
SW:DDX1_HUMAN Q92499 homo sapiens (human). dead box protein 1 (dead box protein-retinoblastoma) (dbp-rb). 5/2000 [MASS=82432]/DEAD box protein 1, a member of the DEAD-H box ATP-dependent RNA helicase protein family, plays a role in the processing of pre-mRNAs, may interact with CSTF2; corresponding gene is coamplified with MYC in some neuroblastoma and retinoblastoma cell lines
SW:R37A_HUMAN P12751 homo sapiens (human), rattus norvegicus (rat), and mus musculus (mouse). 60s ribosomal protein l37a. 2/1996 [MASS=10144]/Ribosomal protein L37a, component of the large 60S ribosomal subunit

SW:IF2B_HUMAN P20042 homo sapiens (human). eukaryotic translation initiation factor 2 beta subunit (eif-2-beta). 7/1999 [MASS=38400]/Eukaryotic translation initiation factor 2 subunit 2, the beta subunit of eIF2, a translation initiation factor, involved in the initiation of protein synthesis, binds GDP
SW:RL44_HUMAN P09896 homo sapiens (human), rattus norvegicus (rat), mus musculus (mouse), and sus scrofa (pig). 60s ribosomal protein l44 (l36a). 7/1998 [MASS=12310]/Ribosomal protein L44, a component of the 60S ribosomal subunit; has very strong similarity to Rpl36a, which may be part of the peptidyl transferase center
SW:RL40_HUMAN P14793 homo sapiens (human), rattus norvegicus (rat), and gallus gallus (chicken). 60s ribosomal protein l40 (cep52). 11/1997 [MASS=6181]/Ubiquitin A-52 residue ribosomal protein fusion product 1, protein consisting of ubiquitin at the N-terminus and ribosomal protein L40 at the C-terminus; the corresponding gene is upregulated in colon cancer but not in gastric cancer
SW:RL24_HUMAN P38663 homo sapiens (human), rattus norvegicus (rat), and bos taurus (bovine). 60s ribosomal protein l24 (l30). 5/2000 [MASS=17779]/Ribosomal protein L24, a putative component of the 60S ribosomal subunit
SW:DDX6_HUMAN P26196 homo sapiens (human). probable atp-dependent rna helicase p54 (oncogene rck) (dead box protein 6). 7/1998 [MASS=54418]/DEAD box protein 6, a member of the DEAD/H box ATP-dependent RNA helicase protein family, may be involved in cell proliferation, upregulated in colorectal adenocarcinoma and colonic adenoma; gene is translocated in a diffuse large B-cell lymphoma
SW:RS16_HUMAN P17008 homo sapiens (human), and rattus norvegicus (rat). 40s ribosomal protein s16. 7/1999 [MASS=16314]/Ribosomal protein S16, putative component of the small 40S ribosomal subunit
SW:RS20_HUMAN P17075 homo sapiens (human), and rattus norvegicus (rat). 40s ribosomal protein s20. 5/2000 [MASS=13373]/Ribosomal protein S20, a putative component of the small 40S ribosomal subunit, may play a role in apoptosis
SW:RS2_HUMAN P15880 homo sapiens (human). 40s ribosomal protein s2 (s4) (llrep3 protein). 10/1996 [MASS=31324]/Ribosomal protein S2, a putative component of the small 40S ribosomal subunit, may bind RNA, upregulated in squamous cell carcinoma and in breast and colon tumors
SW:IF4E_HUMAN P06730 homo sapiens (human). eukaryotic translation initiation factor 4e (eif-4e) (eif4e) (mrna cap-binding protein) (eif-4f 25 kda subunit). 5/2000 [MASS=25097]/Eukaryotic translation initiation factor 4E, a subunit of eIF4F, a mRNA cap-binding protein involved in translation initiation, a target of insulin dependent signaling pathway, expression is upregulated in breast carcinomas
SW:IMB3_HUMAN O00410 homo sapiens (human). importin beta-3 subunit (karyopherin beta-3 subunit) (ran-binding protein 5). 12/1998 [MASS=123630]/Karyopherin beta 3, a subunit of the nuclear localization signal receptor complex and plays a role in nuclear import of ribosomal proteins; inhibited by interaction with hepatitis C virus nonstructural protein 5A
SW:IMA1_HUMAN P52294 homo sapiens (human). importin alpha-1 subunit (karyopherin alpha-1 subunit) (srp1-beta) (rag cohort protein 2) (nucleoprotein interactor 1) (npi-1). 12/1998 [MASS=60307]/Karyopherin alpha (importin alpha), a subunit of the nuclear localization sequence (NLS) receptor complex that binds to and mediates the nuclear import of RAG1 and STAT1
Solute carrier family 9 isoform 3 regulatory factor 1 (sodium-hydrogen exchanger-regulatory factor), a cytoskeleton-linking protein that forms multiprotein complexes with members of the Ezrin-Radixin-Moesin family via two PDZ domains
SW:LDLR_HUMAN P01130 homo sapiens (human). low-density lipoprotein receptor precursor (ldl receptor). 5/2000 [MASS=95376]/Low density lipoprotein receptor, mediates uptake of low density lipoproteins, involved in lipid metabolism; gene variations are associated with familial hypercholesterolemia, hypertension, atherosclerosis, and coronary artery disease
SW:IMB1_HUMAN Q14974 homo sapiens (human). importin beta-1 subunit (karyopherin beta-1 subunit) (nuclear factor p97) (importin 90). 12/1998 [MASS=97234]/Importin beta (karyopherin beta 1), a subunit of the NLS (nuclear localization signal) receptor complex, binds to the nuclear pore complex and mediates translocation of the importin alpha-NLS complex into the nucleus
SW:EZRI_HUMAN P15311 homo sapiens (human). ezrin (p81) (cytovillin) (villin-2). 12/1998 [MASS=69268]/Villin 2 (ezrin), a member of the band 4.1 superfamily, links the cytoskeleton to the plasma membrane and thereby regulates cell adhesion and cortical morphogenesis, may play a role in rheumatoid arthritis and retinal degeneration
SW:CALX_HUMAN P27824 homo sapiens (human). calnexin precursor (major histocompatibility complex class i antigen-binding protein p88) (p90) (ip90). 11/1995 [MASS=67568]/Calnexin, a calcium and lectin binding protein that functions as a chaperone in the endoplasmic reticulum, involved in protein folding and secretion, mediates retention of misfolded proteins in the endoplasmic reticulum
SW:ER53_HUMAN P49257 homo sapiens (human). ergic-53 protein precursor (er-golgi intermediate compartment 53 kda protein) (gp58) (mr60) (lectin, mannose-binding 1). 7/1998 [MASS=57563]/Mannose-binding lectin 1, involved in the traffic of glycoproteins between endoplasmic reticulum and the Golgi apparatus; mutations of the corresponding gene is associated with combined factor V and VIII coagulation deficiency
SW:MPRI_HUMAN P11717 homo sapiens (human). cation-independent mannose-6-phosphate receptor precursor (ci man-6-p receptor) (ci-mpr) (insulin-like growth factor ii receptor) (300 kda mannose 6-phosphate [MASS=274309]/Insulin-like growth factor II receptor, functions in transport of mannose 6-phosphate-containing lysosomal enzymes and IGF-II maturation and clearance, mediates granzyme B-induced apoptosis, putative tumor suppressor

SW:VPP1_HUMAN Q93050 homo sapiens (human). clathrin-coated vesicle/synaptic vesicle proton pump 116 kda subunit (ec 3.6.1.34) (vacuolar proton pump subunit 1). 12/1998 [MASS=95751]/ATPase (H+ transporting lysosomal (vacuolar proton pump) noncatalytic accessory protein 1A (110/116 kDa), a component of a multisubunit enzyme which couples ATP hydrolysis to proton translocation
GP:Y18206_1 Homo sapiens mRNA for protein phosphatase 1 (PPP1R6). [MASS=32559]/Protein phosphatase 1 regulatory 6, glycogen targeting subunit of protein phosphatase 1, functions in glycogen metabolism in muscle
GP:AB037819_1 Homo sapiens mRNA for KIAA1398 protein, partial cds; Start codon is not identified.. [MASS=170212]/Ribosome binding protein 1, a putative ribosome receptor, may play a role in protein biosynthesis, appears to be involved in cardiac development, may play a role in cardiac remodeling in heart failure
GP:AF020797_1 Homo sapiens AP-mu chain family member mu1B (HSMU1B) mRNA, complete cds. [MASS=48108]/Adaptor-related protein complex 1 mu 2 subunit, involved in protein sorting
SW:MPRD_HUMAN P20645 homo sapiens (human). cation-dependent mannose-6-phosphate receptor precursor (cd man-6-p receptor) (cd-mpr) (46 kda mannose 6-phosphate receptor) (mpr 46). 5/2000 [MASS=30993]/Cation-dependent mannose-6-phosphate receptor, involved in intracellular sorting and transport of acid hydrolases, transports lysosomal enzymes
GP:AF077032_1 Homo sapiens sec61 homolog mRNA, complete cds. [MASS=52480]/Sec61 alpha form 2, a protein with high similarity to S. cerevisiae Sec61p, which is a component of the Sec61p-Sss1p-Sbh1p complex involved in protein translocation into the endoplasmic reticulum, member of the SecY protein family of protein translocators
SW:IMB2_HUMAN Q92973 homo sapiens (human). importin beta-2 subunit (karyopherin beta-2 subunit) (transportin) (m9 region interaction protein) (mip). 5/2000 [MASS=101310]/Transportin (karyopherin beta 2), a component of the nuclear pore complex, mediates the import of HNRPA1 by binding the M9 nuclear localization sequence, also binds nuclear Ran GTP and nucleoporin Nup153; may mediate mRNA transport
SW:SR19_HUMAN P09132 homo sapiens (human). signal recognition particle 19 kda protein (srp19). 10/1996 [MASS=16156]/Signal recognition particle 19 kDa, a signal recognition particle subunit that binds to 7SL RNA and mediates SRP54 binding to the SRP RNA, may be involved in translocation of newly synthesized proteins across the membrane of the rough ER
GP:AF195951_1 Homo sapiens signal recognition particle 68 mRNA, complete cds; SRP68; subunit of signal recognition particle. [MASS=70242]/Signal recognition particle 68kD, a component of the signal recognition particle complex involved in targeting nascent proteins to the ER; corresponding gene maps to a tumor suppression locus associated with breast, esophageal, and ovarian cancers
SW:SR09_HUMAN P49458 homo sapiens (human). signal recognition particle 9 kda protein (srp9). 12/1998 [MASS=9981]/Signal recognition particle 9 kDa, a subunit of the signal recognition particle that forms the Alu RNA-binding protein and binds to Alu RNA with SRP14, involved in translocation of newly synthesized proteins across the membrane of the rough ER
SW:I13A_HUMAN Q9uhl8 homo sapiens (human), mus musculus (mouse), and rattus norvegicus (rat). mitochondrial import inner membrane translocase subunit tim13 a. 10/2001 [MASS=10458]/Translocase of the mitochondrial inner membrane 13, a mitochondrial translocase subunit that oligomerizes with DDP1 (human TIMM8A) and mediates the translocation of the Tim23 (human TIM23) precursor across the outer mitochondrial membrane
SW:ROM_HUMAN P52272 homo sapiens (human). heterogeneous nuclear ribonucleoprotein m (hnrnp m). 10/1996 [MASS=77469]/Heterogeneous nuclear ribonucleoprotein M, initiates recycling of internalized immature thyroglobulin for further processing through the Golgi back to the apical membrane
SW:CAS_HUMAN P55060 homo sapiens (human). cellular apoptosis susceptibility protein. 11/1997 [MASS=110314]/CSE1 chromosome segregation 1-like (yeast), importin-alpha nuclear export receptor, functions in toxin and TNF resistance and apoptosis, may regulate cell proliferation; corresponding gene is amplified in breast and colon carcinoma cell lines
SW:PKBS_HUMAN P30536 homo sapiens (human). peripheral-type benzodiazepine receptor (pbr) (pkbs) (mitochondrial benzodiazepine receptor). 6/1994 [MASS=18779]/Benzodiazepine receptor (peripheral), involved in steroid biosynthesis, cell proliferation, and may contribute to mitochondrial biogenesis and inhibit oxygen radical induced apoptosis; expression, nuclear location may correlate to breast tumor progression
SW:PXF_HUMAN P40855 homo sapiens (human). peroxisomal farnesylated protein (33 kda housekeeping protein). 12/1998 [MASS=32807]/Peroxisomal farnesylated protein, peroxisomal protein that binds several peroxisomal membrane proteins (PMP), involved in early stages of PMP import and peroxisomal biogenesis; deficiency is associated with Zellweger syndrome complementation group J
GP:U64791_1 Human Golgi membrane sialoglycoprotein MG160 (GLG1) mRNA, complete cds; fibroblast growth factor. [MASS=134593]/Golgi apparatus protein 1, a cysteine-rich membrane sialoglycoprotein that may be a receptor for fibroblast growth factor (FGF), may be involved in cell adhesion
Human cysteine-rich fibroblast growth factor receptor (CFR-1) mRNA/Golgi apparatus protein 1, a cysteine-rich membrane sialoglycoprotein that may be a receptor for fibroblast growth factor (FGF), may be involved in cell adhesion
mitochondrial import inner membrane translocase subunit tim8 b (deafness dystonia protein 2)/Translocase of inner mitochondrial membrane 8 (yeast) homolog A, member of a family of small zinc finger proteins, involved in mitochondrial protein import, may be involved in neurogenesis or X-inactivation; gene mutations cause Mohr Tranebjaerg syndrome

SW:SR14_HUMAN P37108 homo sapiens (human). signal recognition particle 14 kda protein (srp14) (18 kda alu rna binding protein). 5/2000 [MASS=14544]/Signal recognition particle 14 kDa, heterodimer with SRP9 binds Alu-like RNAs, involved in the translocation of newly synthesized proteins across the rough endoplasmic reticulum membrane, may regulate expression and Alu transcript metabolism
SW:SYTC_HUMAN P26639 homo sapiens (human). threonyl-trna synthetase, cytoplasmic (ec 6.1.1.3) (threonine--trna ligase) (thrrs). 6/1994 [MASS=82124]/Threonyl-tRNA synthetase, a class II aminoacyl tRNA synthetase which aminoacylates its cognate tRNAs with threonine for protein synthesis, autoantigen in several autoimmune disorders
SW:SYG_HUMAN P41250 homo sapiens (human). glycyl-trna synthetase (ec 6.1.1.14) (glycine--trna ligase) (glyrs). 10/1996 [MASS=77531]/Glycyl-tRNA synthetase; functions in protein biosynthesis, aminoacylates its cognate tRNAs with phenylalanine/Glycyl-tRNA synthetase, a class II aminoacyl-tRNA synthetase that catalyzes aminoacylation of its cognate tRNA with glycine for protein biosynthesis; an autoantigen in dermatomyositis
SW:SYD_HUMAN P14868 homo sapiens (human). aspartyl-trna synthetase (ec 6.1.1.12) (aspartate--trna ligase) (asprs). 11/1997 [MASS=57192]/Aspartyl-tRNA synthetase, a class II aminoacyl tRNA synthetase that aminoacylates its cognate tRNA with aspartate for protein biosynthesis, associates with a multisynthetase complex, N-terminus may aid interaction with elongation factor 1 alpha
SW:SYA_HUMAN P49588 homo sapiens (human). alanyl-trna synthetase (ec 6.1.1.7) (alanine--trna ligase) (alars). 7/1998 [MASS=106801]/Alanyl-tRNA synthetase, aminoacylates its cognate tRNA with alanine for protein biosynthesis, acts as an autoantigen in patients with polymyositis
SW:SYR_HUMAN P54136 homo sapiens (human). arginyl-trna synthetase (ec 6.1.1.19) (arginine--trna ligase) (argrs). 5/2000 [MASS=74977]/Arginyl-tRNA synthetase, aminoacylates its cognate tRNAs with arginine for protein biosynthesis
SW:SYM_HUMAN P56192 homo sapiens (human). methionyl-trna synthetase (ec 6.1.1.10) (methionine--trna ligase) (metrs). 12/1998 [MASS=101129]/Methionine-tRNA synthetase, putative tRNA synthetase that is predicted to aminoacylate its cognate tRNAs with methionine for protein biosynthesis, required for rRNA synthesis in the nucleolus
SW:SYEP_HUMAN P07814 homo sapiens (human). multifunctional aminoacyl-trna synthetase [includes: glutamyl-trna synthetase (ec 6.1.1.17) (glutamate--trna ligase); prolyl-trna synthetase (ec 6.1.1.15) (pro [MASS=163026]/Glutamyl-prolyl-tRNA synthetase, a bifunctional enzyme with two functionally separable domains, one that aminoacylates prolyl-tRNA with proline and another that is believed to aminoacylate glutamyl-tRNA with glutamate for protein biosynthesis
SW:CST1_HUMAN Q05048 homo sapiens (human). cleavage stimulation factor, 50 kda subunit (cstf 50 kda subunit) (cf-1 50 kda subunit). 7/1998 [MASS=48358]/Cleavage stimulation factor subunit 1, the 50 kDa subunit of the cleavage stimulation factor complex required for pre-mRNA polyadenylation and 3'-end cleavage, interacts with BARD1 and the C-terminal domain of the RNA polymerase II large subunit
SW:SYQ_HUMAN P47897 homo sapiens (human). glutaminyl-trna synthetase (ec 6.1.1.18) (glutamine--trna ligase) (glnrs). 5/2000 [MASS=87799]/Glutaminyl-tRNA synthetase, aminoacylates cognate tRNAs with glutamine for protein biosynthesis, also suppresses FAS (TNFRSF6)-mediated apoptosis by inhibiting ASK1 (MAP3K5) kinase activity, contains N-terminal appended and C-terminal catalytic domains
SW:SYV_HUMAN P26640 homo sapiens (human). valyl-trna synthetase (ec 6.1.1.9) (valine--trna ligase) (valrs). 2/1996 [MASS=140377]/Valyl-tRNA synthetase 2, a putative class I tRNA sythetase, predicted to function in aminoacylation of valyl tRNAs for protein biosynthesis
SW:SYK_HUMAN Q15046 homo sapiens (human). lysyl-trna synthetase (ec 6.1.1.6) (lysine--trna ligase) (lysrs) (kiaa0070). 7/1998 [MASS=68034]/Lysyl-tRNA synthetase, a class II aminoacyl tRNA synthetase, aminoacylates its cognate tRNAs with lysine for protein biosynthesis, packaged into HIV virions, exists as cytoplasmic and mitochondrial alternative forms
SW:SYI_HUMAN P41252 homo sapiens (human). isoleucyl-trna synthetase, cytoplasmic (ec 6.1.1.5) (isoleucine--trna ligase) (ilers) (irs). 7/1999 [MASS=144959]/Isoleucine-tRNA synthetase, a class I aminoacyl tRNA synthetase, aminoacylates isoleucyl-tRNA with isoleucine for protein biosynthesis, acts as an autoantigen in some autoimmune diseases
SW:NPM_HUMAN P06748 homo sapiens (human). nucleophosmin (npm) (nucleolar phosphoprotein b23) (numatrin) (nucleolar protein no38). 5/2000 [MASS=32575]/Nucleophosmin (numatrin), a nucleic acid-binding phosphoprotein involved in apoptosis, abundant in tumor cells; gene fusion with anaplastic lymphoma kinase (ALK) is detected in non-Hodgkin's lymphoma and fusion with MLF1 is seen in acute myeloid leukemia
SW:PCB1_HUMAN Q15365 homo sapiens (human). poly(rc)-binding protein 1 (hnrnp-e1) (nucleic acid binding protein sub2.3) (alpha-cp1). 5/2000 [MASS=37526]/Poly(rC)-binding protein 1, contains KH RNA-binding domains, binds poly(rC) RNA, acts as a translational repressor and plays a role in mRNA stability
SWN:SYFB_HUMAN Q9nsd9 homo sapiens (human). phenylalanyl-trna synthetase beta chain (ec 6.1.1.20) (phenylalanine--trna ligase beta chain) (phers) (protein hspc173). 8/2001 [MASS=66130]/Phenylalanyl-tRNA synthetase beta-subunit, regulatory subunit that forms heterodimers with the catalytic alpha subunit (FARSL), involved in protein synthesis, may play a role in tumorigenic events
GP:AB020880_1 Homo sapiens mRNA for squamous cell carcinoma antigen SART-3, complete cds; squamous cell carcinoma antigen recognized by T cells. [MASS=109935]/Squamous cell carcinoma antigen recognized by T-cells 3, a snRNA binding protein that functions in spliceosome reassembly, acts as a tumor antigen recognized by cytotoxic T lymphocytes, may be a target for immunotherapy in a number of cancers

SW:ROF_HUMAN P52597 homo sapiens (human). heterogeneous nuclear ribonucleoprotein f (hnrnp f). 11/1997 [MASS=45672]/Heterogeneous nuclear ribonucleoprotein F, an RNA binding protein which contains quasi-RRMs (RNA recognition motifs) and plays a role in pre-mRNA splicing
PIR2:T13159 E1B-55kDa-associated protein - human [MASS=95810]/E1B-55kDa-associated protein 5, a heterogeneous nuclear ribonucleoprotein involved in nucleocytoplasmic transport of adenovirus and cellular mRNAs, binds adenovirus early 1B (E1B-55 kD) protein and may regulate viral oncogenic transformation
SW:SYN_HUMAN O43776 homo sapiens (human). asparaginyl-trna synthetase, cytoplasmic (ec 6.1.1.22) (asparagine-- trna ligase) (asnrs). 5/2000 [MASS=62943]/Asparaginyl-tRNA synthetase, a class II aminoacyl tRNA synthetase, aminoacylates its cognate tRNAs with asparagine for protein biosynthesis, acts as an autoantigen in patients with inflammatory myopathy in interstitial lung disease
no_description_avail/Heterogeneous nuclear ribonucleoprotein R, a putative pre-mRNA processing protein that contains three RNA recognition domains and an RGG domain, interacts with survival motor neuron protein and is an autoantigen in autoimmune disease
GP:AF037448_1 Homo sapiens RRM RNA binding protein Gry-rbp (GRY-RBP) mRNA, complete cds; RRM RNA binding protein; Glycine, arginine and tyrosine-rich at C-terminus. [MASS=69633]/NS1 associated protein 1, component of the ApoB mRNA editosome involved in apolipoprotein B (APOB) mRNA editing, may bind RNA, may play a role in the regulation of mRNA splicing or transport from the nucleus
SW:ROK_HUMAN Q07244 homo sapiens (human), and rattus norvegicus (rat). heterogeneous nuclear ribonucleoprotein k (hnrnp k) (dc-stretch binding protein) (csbp) (transformation upregulated nuclear protein [MASS=50976]/Heterogeneous nuclear ribonucleoprotein K, a transcription factor which binds to poly(C) of RNA and DNA and is involved in RNA processing, gene transcription and translational controls, may induce apoptosis and play a role in viral infection
SW:FBRL_HUMAN P22087 homo sapiens (human). fibrillarin (34 kda nucleolar scleroderma antigen). 7/1999 [MASS=33818]/Fibrillarin, a nucleolar RNA-binding protein that is involved in ribosomal RNA processing; recognized by antisera from patients with scleroderma autoimmune disease, systemic sclerosis, and other connective tissue diseases
SW:SMD3_HUMAN P43331 homo sapiens (human). small nuclear ribonucleoprotein sm d3 (snrnp core protein d3) (sm-d3). 10/1996 [MASS=13916]/Small nuclear ribonucleoprotein D3, part of a multimeric complex involved in biogenesis of snRNPs and mRNA splicing, interacts with the spinal muscular atrophy disease protein (SMN); autoantigen for antibodies associated with systemic lupus erythematosus
SW:ROA0_HUMAN Q13151 homo sapiens (human). heterogeneous nuclear ribonucleoprotein a0 (hnrnp a0). 5/2000 [MASS=30841]/Heterogeneous nuclear ribonucleoprotein A0, has triplet repeats, two consensus sequence-type RNA-binding domains, and a glycine-rich auxiliary domain, found in low abundance hnRNP complexes
SW:ROH1_HUMAN P31943 homo sapiens (human). heterogeneous nuclear ribonucleoprotein h (hnrnp h). 11/1997 [MASS=49229]/Heterogeneous nuclear ribonucleoprotein H1, a pre-mRNA splicing factor that is a component of a complex that mediates post-transcriptional processing of primary transcripts
SW:DDX1_HUMAN Q92499 homo sapiens (human). dead box protein 1 (dead box protein-retinoblastoma) (dbp-rb). 5/2000 [MASS=82432]/DEAD box protein 1, a member of the DEAD-H box ATP-dependent RNA helicase protein family, plays a role in the processing of pre-mRNAs, may interact with CSTF2; corresponding gene is coamplified with MYC in some neuroblastoma and retinoblastoma cell lines
PIR2:JW0079 heterogeneous nuclear ribonucleoprotein homolog JKTBP [imported] - human [MASS=33589]/Heterogeneous nuclear ribonucleoprotein D-like, an RNA- and DNA-binding protein that may play a role in mRNA biogenesis
SW:PCB2_HUMAN Q15366 homo sapiens (human). poly(rc)-binding protein 2 (hnrnp-e2). 5/2000 [MASS=38580]/Poly(rC)-binding protein 2, poly(rC) and poly(U)-binding protein, involved in the translational regulation of poliovirus, papillomavirus, and hepatitis C virus transcripts
GP:AC003972_1 Homo sapiens DNA from chromosome 19, cosmid R33485 containing pNORF1, complete sequence; human type 1 RNA helicase; DPS similarity to (U59323) type 1 RNA helicase pNORF1 [Homo sapiens]; Score. [MASS=123036]/regulator of nonsense transcripts 1 (nonsense mrna reducing factor 1) (norf1) (up-frameshift suppressor 1 homolog). 10/2001 [MASS=124345]
SW:RUXF_HUMAN Q15356 homo sapiens (human). small nuclear ribonucleoprotein f (snrnp-f) (sm protein f). 7/1999 [MASS=9725]/Sm protein F, a spliceosomal snRNA-associated Sm core protein that is involved in the biogenesis of the snRNPs; a target of autoantibodies in patients with the autoimmune disease systemic lupus erythematosus
GP:AF177344_1 Homo sapiens clone HC90 unknown mRNA. [MASS=30998]/ weakly similar to a methyltransferase/Member of the RNA methyltransferase family, which catalyze 2'-O-methylation of ribose groups in R
PIR2:I55595 splicing factor - human [MASS=58657]/Splicing factor CC1.3, a novel nuclear protein and putative member of the SR family of alternative splicing factors; target of autoantibodies from a patient with hepatocellular carcinoma
SW:ROA3_HUMAN P51991 homo sapiens (human). heterogeneous nuclear ribonucleoprotein a3 (hnrnp a3) (fbrnp) (d10s102). 7/1999 [MASS=39686]/Protein with similarity to heterogeneous ribonucleoproteins, contains RRM (RNA recognition motif) domains
SW:SMD2_HUMAN P43330 homo sapiens (human). small nuclear ribonucleoprotein sm d2 (snrnp core protein d2) (sm-d2). 10/1996 [MASS=13527]/Small nuclear ribonucleoprotein D2 polypeptide, one of seven common core snRNP proteins involved in snRNP biogenesis and pre-mRNA splicing, autoantigen for anti-Sm antibodies produced by individuals with systemic lupus erythematosus

SW:U2AF_HUMAN P26368 homo sapiens (human). splicing factor u2af 65 kda subunit (u2 auxiliary factor 65 kda subunit) (u2 snrnp auxiliary factor large subunit). 12/1998 [MASS=53501]/U2 small nuclear ribonucleoprotein auxiliary factor (65 kDa), a component of U2 small nucleoprotein auxiliary factor, which is necessary for mRNA splicing, binds to pre-mRNA
GP:D21163_1 Human mRNA for KIAA0031 gene, complete cds; similar to human elongation factor 2 mRNA (HSEF2).. [MASS=109436]/U5 snRNP-specific protein 116 kD, a spliceosome component with GTPAse activity, plays a role in mRNA splicing and processing
SW:RU17_HUMAN P08621 homo sapiens (human). u1 small nuclear ribonucleoprotein 70 kda (u1 snrnp 70 kda) (snrp70). 11/1995 [MASS=70081]/U1 small nuclear 70 kDa ribonucleoprotein, involved in pre mRNA splicing, acts as an autoantigen in systemic lupus erythematosus and mixed connective tissue disease
PIR2:A54601 RNA-binding protein AUF1 - human [MASS=31200]/Heterogeneous nuclear ribonucleoprotein D (AU-rich element RNA-binding protein 1 37kD), an RNA and DNA-binding protein which binds to AU-rich elements in the 3' untranslated regions of mRNAs and mediates their degradation
SW:NHPX_HUMAN P55769 homo sapiens (human). nhp2/rs6 family protein yel026w homolog (high mobility group-like nuclear protein 2 homolog) (otk27). 5/2000 [MASS=14174]/Non-histone chromosome protein 2 (S. cerevisiae)-like 1, a member of a family of RNP-associated proteins, a component of the spliceosome and rRNA processing machinery, recognizes a shared stem-internal loop-stem structure in its RNA targets
SW:DDX5_HUMAN P17844 homo sapiens (human). probable rna-dependent helicase p68 (dead-box protein p68) (dead box protein 5). 7/1998 [MASS=69148]/DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 5 (RNA helicase 68kD), a ATP-dependent RNA helicase that has ATP-independent RNA renaturation activity and catalyses branch migration, binds estrogen receptor alpha and function as a transcriptional coactivator
SW:U2AG_HUMAN Q01081 homo sapiens (human). splicing factor u2af 35 kda subunit (u2 auxiliary factor 35 kda subunit) (u2 snrnp auxiliary factor small subunit). 12/1998 [MASS=27872]/U2(RNU2) small nuclear RNA auxiliary factor 1, functions as a pre-mRNA splicing protein, involved in the functional recognition of the 3' splice site AG dinucleotide, interacts with ZNF265 protein involved in alternative splicing
SW:ROU_HUMAN Q00839 homo sapiens (human). heterogenous nuclear ribonucleoprotein u (hnrnp u) (scaffold attachment factor a) (saf-a). 5/2000 [MASS=90479]/Heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A), binds RNA, binds EP300 in a complex that binds scaffold-matrix attachment regions of TOP1, involved in chromatin structure, apoptosis, and perhaps RNA processing and transcription
SW:ROA1_HUMAN P09651 homo sapiens (human). heterogeneous nuclear ribonucleoprotein a1 (helix-destabilizing protein) (single-strand binding protein) (hnrnp core protein a1). 11/1997 [MASS=38715]/Heterogeneous nuclear ribonucleoprotein A1, an RNA-binding protein involved in mRNA splicing and translational control, undergoes nucleocytoplasmic shuttling possibly for mRNA export and telomerase recruitment; an autoantigen in autoimmune disorders
SW:DD17_HUMAN Q92841 homo sapiens (human). probable rna-dependent helicase p72 (dead-box protein p72) (dead box protein 17). 5/2000 [MASS=72371]/DEAD H box protein 17, a member of the DEAD box family of RNA-dependent ATPases and ATP-dependent RNA helicases, a component of an estrogen receptor alpha (ESR) transcriptional coactivator complex
SW:Y017_HUMAN Q15393 homo sapiens (human). hypothetical protein kiaa0017. 5/2000 [MASS=44606]/ Homo sapiens mRNA for SAP 130 spliceosomal protein/Splicing factor 3b subunit 3, a component of the U2 snRNP-associated protein complex SF3b that plays a role in spliceosome assembly, interacts with STAGA and TFTC complexes implicated in DNA repair, chromatin modification, and transcription
SW:NR54_HUMAN Q15233 homo sapiens (human). 54 kda nuclear rna-binding protein (p54(nrb)) (p54nrb) (55 kda nuclear protein) (nmt55). 5/2000 [MASS=54232]/Non-POU-domain-containing octamer-binding nuclear protein, binds DNA and RNA, and implicated in transcription and pre-mRNA splicing; a fusion partner with TFE3 in papillary renal cell carcinoma
SW:SFR7_HUMAN Q16629 homo sapiens (human). splicing factor, arginine/serine-rich 7 (splicing factor 9g8). 5/2000 [MASS=27367]/Splicing factor arginine serine rich 7, a splicing factor of the SR protein family containing an RNA binding domain (RBD) and a serine/arginine (SR) domain that is implicated in alternative pre-mRNA splicing
GP:AF037448_1 Homo sapiens RRM RNA binding protein Gry-rbp (GRY-RBP) mRNA, complete cds; RRM RNA binding protein; Glycine, arginine and tyrosine-rich at C-terminus. [MASS=69633]/NS1 associated protein 1, component of the ApoB mRNA editosome involved in apolipoprotein B (APOB) mRNA editing, may bind RNA, may play a role in the regulation of mRNA splicing or transport from the nucleus
SW:SMD3_HUMAN P43331 homo sapiens (human). small nuclear ribonucleoprotein sm d3 (snrnp core protein d3) (sm-d3). 10/1996 [MASS=13916]/Small nuclear ribonucleoprotein D3, part of a multimeric complex involved in biogenesis of snRNPs and mRNA splicing, interacts with the spinal muscular atrophy disease protein (SMN); autoantigen for antibodies associated with systemic lupus erythematosus
SW:RUXF_HUMAN Q15356 homo sapiens (human). small nuclear ribonucleoprotein f (snrnp-f) (sm protein f). 7/1999 [MASS=9725]/Sm protein F, a spliceosomal snRNA-associated Sm core protein that is involved in the biogenesis of the snRNPs; a target of autoantibodies in patients with the autoimmune disease systemic lupus erythematosus

PIR2:T09073 splicing factor Sip1 - human [MASS=128875]/Splicing factor arginine serine rich 2 interacting protein, a SR domain family protein that interacts with the RNA polymerase II C-terminal domain and several splicing factors, is essential in mRNA splicing and possibly spliceosome A-complex formation
PIR2:I55595 splicing factor - human [MASS=58657]/Splicing factor CC1.3, a novel nuclear protein and putative member of the SR family of alternative splicing factors; target of autoantibodies from a patient with hepatocellular carcinoma
SW:SMD2_HUMAN P43330 homo sapiens (human). small nuclear ribonucleoprotein sm d2 (snrnp core protein d2) (sm-d2). 10/1996 [MASS=13527]/Small nuclear ribonucleoprotein D2 polypeptide, one of seven common core snRNP proteins involved in snRNP biogenesis and pre-mRNA splicing, autoantigen for anti-Sm antibodies produced by individuals with systemic lupus erythematosus
SW:U2AF_HUMAN P26368 homo sapiens (human). splicing factor u2af 65 kda subunit (u2 auxiliary factor 65 kda subunit) (u2 snrnp auxiliary factor large subunit). 12/1998 [MASS=53501]/U2 small nuclear ribonucleoprotein auxiliary factor (65 kDa), a component of U2 small nucleoprotein auxiliary factor, which is necessary for mRNA splicing, binds to pre-mRNA
GP:D21163_1 Human mRNA for KIAA0031 gene, complete cds; similar to human elongation factor 2 mRNA (HSEF2).. [MASS=109436]/U5 snRNP-specific protein 116 kD, a spliceosome component with GTPAse activity, plays a role in mRNA splicing and processing
SW:RU17_HUMAN P08621 homo sapiens (human). u1 small nuclear ribonucleoprotein 70 kda (u1 snrnp 70 kda) (snrp70). 11/1995 [MASS=70081]/U1 small nuclear 70 kDa ribonucleoprotein, involved in pre mRNA splicing, acts as an autoantigen in systemic lupus erythematosus and mixed connective tissue disease
SW:U2AG_HUMAN Q01081 homo sapiens (human). splicing factor u2af 35 kda subunit (u2 auxiliary factor 35 kda subunit) (u2 snrnp auxiliary factor small subunit). 12/1998 [MASS=27872]/U2(RNU2) small nuclear RNA auxiliary factor 1, functions as a pre-mRNA splicing protein, involved in the functional recognition of the 3' splice site AG dinucleotide, interacts with ZNF265 protein involved in alternative splicing
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SW:Y017_HUMAN Q15393 homo sapiens (human). hypothetical protein kiaa0017. 5/2000 [MASS=44606]/ Homo sapiens mRNA for SAP 130 spliceosomal protein/Splicing factor 3b subunit 3, a component of the U2 snRNP-associated protein complex SF3b that plays a role in spliceosome assembly, interacts with STAGA and TFTC complexes implicated in DNA repair, chromatin modification, and transcription
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SW:SFR7_HUMAN Q16629 homo sapiens (human). splicing factor, arginine/serine-rich 7 (splicing factor 9g8). 5/2000 [MASS=27367]/Splicing factor arginine serine rich 7, a splicing factor of the SR protein family containing an RNA binding domain (RBD) and a serine/arginine (SR) domain that is implicated in alternative pre-mRNA splicing
SW:HS71_HUMAN P08107 homo sapiens (human). heat shock 70 kda protein 1 (hsp70.1) (hsp70-1/hsp70-2). 5/2000 [MASS=70052]/Heat shock 70 kDa protein 1A, a member of the HSP70 chaperone family involved in protein folding, translocation, and complex assembly, blocks AU-rich mRNA decay by nuclear sequestering of AU-rich binding protein, may contribute to celiac disease
SW:RINI_HUMAN P13489 homo sapiens (human). placental ribonuclease inhibitor (ribonuclease/angiogenin inhibitor) (rai) (ri). 12/1998 [MASS=49842]/Ribonuclease and angiogenin inhibitor, tightly binds and inhibits alkaline and neutral ribonucleases and angiogenin, functions in mRNA degradation and inhibition of HT-29 human colon adenocarcinoma cell binding to angiogenin (ANG)
GP:AF132941_1 Homo sapiens CGI-07 protein mRNA, complete cds. [MASS=57585]/Protein with moderate similarity to S. cerevisiae Nmd3p, which is a protein involved in the nuclear export of 60S ribosomal subunits
PIR2:A57017 RNase L inhibitor - human [MASS=67559]/Ribonuclease L inhibitor, inhibits the nuclease activity and 2-5A binding ability of RNase L, may be induced by HIV-1 to inhibit the 2-5A/RNase L pathway, can inhibit the antiviral activity of interferon when overexpressed
SW:PAB1_HUMAN P11940 homo sapiens (human). polyadenylate-binding protein 1 (poly(a) binding protein 1) (pabp 1). 7/1998 [MASS=70671]/Poly(A)-binding protein cytoplasmic 1, binds to poly(A) tails of mRNA and plays roles in regulating mRNA stability and translation, also implicated in mRNA transport from the nucleus to the cytoplasm
GP:U85625_1 Homo sapiens ribonuclease 6 precursor, mRNA, complete cds. [MASS=29481]/Ribonuclease 6 precursor, a putative ribonuclease that plays a role in the negative regulation of proliferation, may be involved in senescence, may be a class II tumor suppressor, downregulated in ovarian cancer and in ovarian cancer cell lines

GP:AC003972_1 Homo sapiens DNA from chromosome 19, cosmid R33485 containing pNORF1, complete sequence; human type 1 RNA helicase; DPS similarity to (U59323) type 1 RNA helicase pNORF1 [Homo sapiens]; Score. [MASS=123036]/regulator of nonsense transcripts 1 (nonsense mrna reducing factor 1) (norf1) (up-frameshift suppressor 1 homolog). 10/2001 [MASS=124345]

PIR2:S78046 ribonuclease 6 (EC 3.1.27.-) precursor - human [MASS=21941]/Ribonuclease k6, a ribonuclease of the ribonuclease A superfamily, possibly functions in host defense

PIR2:A54601 RNA-binding protein AUF1 - human [MASS=31200]/Heterogeneous nuclear ribonucleoprotein D (AU-rich element RNA-binding protein 1 37kD), an RNA and DNA-binding protein which binds to AU-rich elements in the 3' untranslated regions of mRNAs and mediates their degradation

SW:IMA1_HUMAN P52294 homo sapiens (human). importin alpha-1 subunit (karyopherin alpha-1 subunit) (srp1-beta) (rag cohort protein 2) (nucleoprotein interactor 1) (npi-1). 12/1998 [MASS=60307]/Karyopherin alpha (importin alpha), a subunit of the nuclear localization sequence (NLS) receptor complex that binds to and mediates the nuclear import of RAG1 and STAT1

SW:FRAP_HUMAN P42345 homo sapiens (human). fkbp-rapamycin associated protein (frap) (rapamycin target protein). 7/1999 [MASS=288892]/FK506 binding protein 12-rapamycin associated protein 1, serine/threonine and 1-phosphatidylinositol 4-kinase, regulates translation, cell cycle and p53 (TP53) -dependent apoptosis; altered expression is associated with recurrent prostate tumors

PIR2:JE0334 nuclear matrix protein NMP 238 - human [MASS=50228]/RuvB like 1, a member of the TIP49 family of proteins, a nuclear protein which contains ATPase-helicase motifs, may interact with the transactivation domain of c-myc (MYC)

SW:HMG1_HUMAN P09429 homo sapiens (human). high mobility group protein hmg1 (hmg-1). 5/2000 [MASS=24763]/High-mobility group (nonhistone chromosomal) protein 1, induces DNA bending, binds damaged DNA, activates and represses transcription, involved in the DNA damage response and V(D)J recombination, may be a target for therapeutic intervention of sepsis

SW:KU86_HUMAN P13010 h atp-dependent dna helicase ii, 80 kda subunit (lupus ku autoantigen protein p86) (ku86) (ku80) (86 kda subunit of ku antigen) (thyroid- lupus autoantigen) (tlaa) (ctc box binding [MASS=82573]/X-ray repair complementing defective repair in Chinese hamster cells 5, binds ds-DNA free ends, binds Ku70 (G22P1) to regulate DNA-PK, involved in DNA repair, V(D)J recombination, cell adhesion, and enzyme activation, may play a role in tumor progression

SW:RFA3_HUMAN P35244 homo sapiens (human). replication protein a 14 kda subunit (rp-a) (rf-a) (replication factor-a protein 3). 11/1997 [MASS=13569]/Replication protein A 3, a subunit of replication protein A, which is a single-stranded DNA-binding protein complex with roles in DNA replication, repair, and recombination

PIR2:A57099 DNA-activated protein kinase, catalytic subunit - human [MASS=465428]/DNA-dependent protein kinase catalytic subunit, a DNA-binding protein kinase involved in DNA double-strand break repair and somatic recombination of antibody genes; absence of mouse Prkdc is associated with severe combined immunodeficiency

SW:RFA1_HUMAN P27694 homo sapiens (human). replication protein a 70 kda dna-binding subunit (rp-a) (rf-a) (replication factor-a protein 1) (single-stranded dna-binding protein). 11/1997 [MASS=68138]/Replication protein A1 (70 kDa), a DNA replication factor A subunit, has roles in DNA replication, recombination, repair, may contribute to latent virus reactivation, inactivated by anti-cancer drug adozelesin

inhibitor of nuclear factor kappa b kinase beta subunit/Serine kinase that is a subunit of the IkappaB kinase (IKK) complex, phosphorylates IkappaB and activates NF-kappaB (RELA), activated by kinases NIK (MAP3K14) and MEKK1 (MAP3K1)

GP:U35146_1 Human p56 protein kinase (KKIAMRE), complete cds; similar to human p42 KKIALRE gene, GenBank Accession Number X66358; these protein kinases have mutually exclusive expression in testis (p56 KKIAMRE) and ovary (p42 KKIALRE). [MASS=56019]/Cyclin-dependent kinase-like 2, putative protein kinase whose activity is stimulated by epidermal growth factor (EGF), may play a role in sex differentiation

SW:FKB5_HUMAN Q13451 homo sapiens 51 kda fk506-binding protein (fkbp51) (peptidyl-prolyl cis-trans isomerase) (ec 5.2.1.8) (ppiase) (rotamase) (54 kda progesterone receptor-associated immunophilin) (fkb [MASS=51212]/FK506-binding protein 5, a peptidylprolyl cis-trans isomerase and member of the immunophilin family of FK506-binding proteins, forms a progesterone receptor complex with Hsp90 and p23, serves as a chaperone and mediates inhibition of calcineurin

SW:143E_HUMAN P42655 homo sapiens (human), mus musculus (mouse), rattus norvegicus (rat), bos taurus (bovine), and ovis aries 14-3-3 protein epsilon (mitochondrial import stimulation factor l subunit) ([MASS=29174]/14-3-3 epsilon, may regulate the cell cycle by binding cdc25 phosphatases and linking cell cycle machinery with mitogenic signaling, binds DNA topoisomerase II alpha (TOP2A), prevents TOP2A binding of DNA and renders cells resistant to anticancer drugs

SW:RIN1_HUMAN Q13671 homo sapiens (human). ras interaction/interference protein 1 (ras inhibitor jc99) (fragment). 11/1997 [MASS=52857]/Ras inhibitor 1, inhibits Ras (HRAS) - mediated transformation and may be regulated by serine phosphorylation and 14-3-3 protein binding; augments BCR-ABL oncogenic activity and is amplified in some oral squamous cell carcinomas
SW:TNRC_HUMAN P36941 homo sapiens (human). lymphotoxin-beta receptor precursor (tumor necrosis factor receptor 2 related protein) (tumor necrosis factor c receptor). 11/1997 [MASS=46709]/Lymphotoxin beta receptor, member of the tumor necrosis factor receptor family that specifically binds lymphotoxin-alpha/beta heterotrimers and mediates cytotoxic responses, may be involved in lymph gland development or organization
SWN:AKT3_HUMAN Q9y243 homo sapiens (human). rac-gamma serine/threonine protein kinase (ec 2.7.1.-) (rac-pk-gamma) (protein kinase akt-3) (protein kinase b, gamma) (pkb gamma). 8/2001 [MASS=55775]/Protein kinase B gamma, a serine/threonine protein kinase that is activated by growth factors and 3-phosphoinositide; insulin-induced activity is upregulated in estrogen receptor negative breast cancer and androgen insensitive prostrate carcinoma
SW:RRAS_HUMAN P10301 homo sapiens (human). ras-related protein r-ras (p23). 11/1997 [MASS=23480]/Related RAS viral oncogene homolog, inhibits apoptosis through BCL2 or Bcl-xl (BCL2L1), mediates myoblast differentiation, acts as a downstream effector of GRF2 in the activation of JNK, enhances cell-matrix adhesion by modulating integrins
SW:ATS1_HUMAN Q9uhi8 homo sapiens (human). adam-ts 1 precursor (ec 3.4.24.-) (a disintegrin and metalloproteinase with thrombospondin motifs 1) (adamts-1) (adam-ts1) (meth-1). 5/2000 [MASS=103498]/A disintegrin metalloprotease with a thrombospondin type 1 motif 1, a putative heparin-binding metalloprotease that inhibits endothelial cell proliferation, involved in angiogenesis; mouse Adamts1 may play a role in the pathogenesis of cancer cachexia
SW:AAK1_HUMAN Q13131 homo sapiens (human). 5'-amp-activated protein kinase, catalytic alpha-1 chain (ec 2.7.1.-) (ampk alpha-1 chain) (fragment). 7/1999 [MASS=19837]/AMP-activated protein kinase (alpha 1 catalytic subunit), a metabolic sensor of AMP levels, may have roles in signal transduction, may regulate the cystic fibrosis transmembrane conductance regulator (CFTR)
GP:AF061258_1 Homo sapiens LIM protein mRNA, complete cds. [MASS=64028]/ similar to rat protein kinase C-binding enigma/Enigma homolog, contains LIM domains, binds oncoprotein Ret and may bind protein kinase C, may mediate Ret mitogenic signaling
PIR2:JC4775 p58k protein - human [MASS=57580]/The 58,000-dalton cellular inhibitor of the interferon-induced double-stranded RNA-activated protein kinase (PKR) is a member of the tetratricopeptide repeat family of proteins/DnaJ (Hsp40) homolog subfamily C member 3 (protein kinase inhibitor p58), a member of the tetratricopeptide repeat family of proteins that may act as a cochaperone that inhibits the activity of double-stranded RNA-dependent protein kinase (PRKR)
SW:COF1_HUMAN P23528 homo sapiens (human). cofilin, non-muscle isoform. 11/1997 [MASS=18502]/Non-muscle cofilin, an actin-binding protein that assists translocation of actin from the cytoplasm to the nucleus; inactivation through phosphorylation by LIM-kinase leads to actin depolymerization
GP:AF100757_1 Homo sapiens COP9 complex subunit 4 mRNA, complete cds. [MASS=46198]/COP9 (constitutive photomorphogenic Arabidopsis homolog) subunit 4, a subunit of a complex related to the 26S proteasome regulatory complex, and possibly involved in regulating protein degradation
PIR2:T13151 adapter protein CMS - human [MASS=71451]/CMS: an adapter molecule involved in cytoskeletal rearrangements/CD2-associated protein, an adaptor that may play a role in kidney function and mediate cytoskeletal rearrangement; mouse Cd2ap is associated with congenital nephrotic syndrome and possibly Nail-Patella syndrome nephropathy and polycystic kidney disease
GP:AF024636_1 Homo sapiens STE20-like kinase 3 (mst-3) mRNA, complete cds; protein serine/threonine kinase; similiar to yeast STE20. [MASS=47941]/Serine-threonine kinase 24 (Ste20 yeast homolog), member of the SPS1 subgroup of the STE20-like protein family, a serine-threonine kinase that prefers manganese as a cofactor and uses either GTP or ATP as a phosphate donor
SW:RAPB_HUMAN P09526 homo sapiens (human), and bos taurus (bovine). ras-related protein rap-1b (gtp-binding protein smg p21b). 7/1993 [MASS=20825]/Ras related protein 1b, member of the Ras superfamily of low molecular weight GTP-binding proteins, regulates cell cycle progression and cellular proliferation, may play a role in cAMP-responsive tumorigenesis
SW:MOES_HUMAN P26038 homo sapiens (human). moesin (membrane-organizing extension spike protein). 6/1994 [MASS=67689]/Moesin, putative receptor that may link the cytoskeleton and plasma membrane and play roles in microvillus assembly and cell morphogenesis, may be an autoantigen in rheumatoid arthritis and may play a role in impaired brain development in Down syndrome
SW:CAP1_HUMAN Q01518 homo sapiens (human). adenylyl cyclase-associated protein 1 (cap 1). 10/1996 [MASS=51673]/Adenylyl cyclase-associated protein 1, putative homolog of bifunctional S. cerevisiae Srv2p, C-terminus mediates actin binding and may play a role in regulating cell growth and morphogenesis, the N-terminal domain may bind and-or regulate adenylyl cyclase
GP:AF001628_1 Homo sapiens interactor protein AblBP4 (AblBP4) mRNA, complete cds; member of the Abl interactor protein family; contains an SH3 domain and an SH3 binding domain. [MASS=49305]/Spectrin SH3 domain binding protein 1, has an SH3 domain, binds SH3 domains of EPS8, ABL1, and spectrin (SPTA1), acts in pinocytosis, inhibits cell proliferation; fusion of the corresponding gene with the MLL gene is linked to acute myelogenous leukemia

SW:EGFR_HUMAN P00533 homo sapiens (human). epidermal growth factor receptor precursor (ec 2.7.1.112). 12/1998 [MASS=134277]/Epidermal growth factor receptor, a receptor protein tyrosine kinase that binds epidermal growth factor (EGF) and transforming growth factor alpha (TGFA), involved in cell proliferation and differentiation, implicated in tumor invasion and metastasis
GP:AB014718_1 Homo sapiens DR5 gene, exon 9 and complete cds. [MASS=47894]/Tumor necrosis factor receptor superfamily member 10b, receptor that binds the ligand TRAIL (TNFSF10), induces apoptosis through interaction with FADD and activation of caspase 8 (CASP8), loss of apoptotic function is associated with cancer
SW:TDXN_HUMAN Q13162 homo sapiens (human). thioredoxin peroxidase ao372 (thioredoxin-dependent peroxide reductase a0372) (antioxidant enzyme aoe372) (aoe37-2). 7/1999 [MASS=30540]/Peroxiredoxin 4, a thioredoxin dependent peroxidase that is regulated by interactions with other thiol peroxidases, may mediate hydrogen peroxide activation of NF-kappaB by modulating phosphorylation of cytoplasmic IkappaB-alpha (NFKBIA)
SW:RAC3_HUMAN O14658 homo sapiens (human). ras-related c3 botulinum toxin substrate 3 (p21-rac3). 12/1998 [MASS=21379]/Ras-related C3 botulinum toxin substrate 3, a Rho family GTPase involved in integrin signaling via alphaIIb-beta3 (ITGA2B, ITGB3), binds CIB1, regulates cell-matrix adhesion and may activate the JNK pathway and stimulate tumor cell growth
SW:RHOB_HUMAN P01121 homo sapiens (human), mus musculus (mouse), and rattus norvegicus (rat). transforming protein rhob (h6). 12/1998 [MASS=22123]/Ras-related GTP binding protein of the rho subfamily, member B; may regulate assembly of actin stress fibers and focal adhesions; very strongly similar to murine Arhb
GP:AF091035_1 Homo sapiens GTP-binding protein RAB21 (RAB21) mRNA, complete cds. [MASS=24348]/Ras related GTP binding protein, member of the Rab subfamily of the Ras superfamily of small GTP binding proteins, may be involved in apically directed vesicle-mediated transport in polarized intestinal epithelium
SW:CTN1_HUMAN P35221 homo sapiens (human). alpha-1 catenin (cadherin-associated protein) (alpha e-catenin). 11/1997 [MASS=100071]/Catenin alpha 1 (cadherin-associated protein); binds cadherins and links them with the actin cytoskeleton
GP:AB018358_1 Homo sapiens mRNA for ABP125, complete cds; This sequence is a product of alternative splicing of human ABP130. [MASS=129053]/Secretion 31 homolog, a putative component of the COPII coat of secretory pathway vesicles involved in endoplasmic reticulum to Golgi transport, plays a role in intracellular protein trafficking
SW:RGP1_HUMAN P46060 homo sapiens (human). ran-gtpase activating protein 1. 7/1999 [MASS=63542]/Ran GTPase activating protein 1, a GTPase activator for ras family GTP binding protein RAN, ubiquitin-like SUMO-1 modification results in localization to the nuclear pore complex, required for nuclear protein import when bound to RANBP2
SW:KCCB_HUMAN Q13554 homo sapiens (human). calcium/calmodulin-dependent protein kinase type ii beta chain (cam-kinase ii beta chain) (ec 2.7.1.123) (camk-ii, beta subunit) (fragment). 5/2000 [MASS=15141]/Calcium calmodulin-dependent protein kinase II beta subunit, putative roles in signal transduction and cell growth, increased expression may play a role in schizophrenia; variant forms of the corresponding gene are expressed in tumor cells
SW:ITAV_HUMAN P06756 homo sapiens (human). vitronectin receptor alpha subunit precursor (integrin alpha-v) (cd51). 12/1998 [MASS=116052]/Alpha V subunit integrin, a subunit of the vitronectin receptor that is involved in cell-matrix interactions, chemotaxis, phagocytosis and angiogenesis, may contribute to the tumorigenicity of cutaneous malignant melanoma and invasive breast cancer
SW:IQGA_HUMAN P46940 homo sapiens (human). ras gtpase-activating-like protein iqgap1 (p195) (kiaa0051). 7/1999 [MASS=189252]/IQ motif-containing GTPase activating protein 1, an actin-associated calmodulin (CALM1)-regulated protein that serves as an effector for CDC42 and RAC1, modulates E-cadherin (CDH1)-mediation cellular adhesion, upregulated in colon carcinomas
SW:GBAK_HUMAN P08754 homo sapiens (human). guanine nucleotide-binding protein g(k), alpha subunit (g(i) alpha-3). 11/1997 [MASS=40401]/G protein alpha i3 subunit, a component of pertussis toxin sensitive heterotrimeric G protein complexes, transduces signals from G protein-coupled receptors to intracellular effectors, inhibits forskolin-stimulated cAMP production
SW:P2AA_HUMAN P05323 homo sapiens (human), oryctolagus cuniculus (rabbit), sus scrofa (pig), and bos taurus (bovine). serine/threonine protein phosphatase 2a, catalytic subunit, alpha isoform (ec 3.1.3. [MASS=35594]/Protein phosphatase 2 catalytic subunit alpha, a catalytic subunit of protein phosphatase 2A involved in regulating diverse cellular processes via protein phosphorylation
SW:FKB1_HUMAN P20071 homo sapiens (human), and oryctolagus cuniculus (rabbit). fk506-binding protein (fkbp-12) (peptidyl-prolyl cis-trans isomerase) (ec 5.2.1.8) (ppiase) (rotamase) (immunophilin fkbp12 [MASS=11820]/FK506-binding protein 1A, peptidyl prolyl cis-trans isomerase, modulates the Ca2+-release activity of ryanodine receptors, complex with FK506 inhibits calcineurin-dependent lymphokine gene transcription and mediates FK506 immunosuppressive activity
SW:CTNB_HUMAN P35222 homo sapiens (human). beta-catenin. 2/1996 [MASS=85497]/Beta catenin, links cadherins to the cytoskeleton, may act as a component of the Wnt signal transduction pathway transmitting nuclear signals via a complex with LEF1 and TCF transcription factors; mutations in the gene are associated with various cancers
SW:Y253_HUMAN Q92542 homo sapiens (human). hypothetical protein kiaa0253 (fragment). 7/1998 [MASS=78280]/Nicastrin, a transmembrane glycoprotein that may be required for the assembly and transport of presenilin complex that processes amyloid precursor protein (APP), may play a role in notch signaling and abnormal APP processing in Alzheimer disease

GP:U70735_1 Homo sapiens 34 kDa Mov34 homolog mRNA, complete cds; similar to Mov34. [MASS=33576]/COP9 subunit 6, putative translation initiation factor and a subunit of COP9 signalosome, which mediates p53 (human TP53) degradation, may be involved in G2-M phase transition of cell cycle
SW:BASI_HUMAN P35613 homo sapiens (human). basigin precursor (leukocyte activation antigen m6) (collagenase stimulatory factor) (extracellular matrix metalloproteinase inducer) (emmprin) (5f7) (cd147 an [MASS=29221]/Basigin (OK blood group), a cyclophilin receptor of the immunoglobulin family, enhances cancer progression by increasing the production and activation of MMP2 and enhances infectivity of HIV 1 virions
SW:SRC_HUMAN P12931 homo sapiens (human). proto-oncogene tyrosine-protein kinase src (ec 2.7.1.112) (p60-src) (c-src). 5/2000 [MASS=59704]/V-src avian sarcoma viral oncogene homolog (Schmidt-Ruppin A-2), tyrosine kinase involved in cell proliferation, cell adhesion, and cytoskeletal organization, implicated in the progression of colon cancer and certain breast tumors
SW:ITA6_HUMAN P23229 homo sapiens (human). integrin alpha-6 precursor (vla-6) (cd49f). 5/2000 [MASS=119462]/Integrin alpha 6, a laminin receptor and component of hemidesmosomes, participates in the maintenance of epidermal integrity; gene mutations are responsible for epidermolysis bullosa and overexpression is correlated with carcinoma invasiveness
SW:ABP2_HUMAN P21333 homo sapiens (human). endothelial actin-binding protein (abp-280) (nonmuscle filamin) (filamin 1). 11/1997 [MASS=280761]/Filamin A (alpha), an actin crosslinking phosphoprotein involved in actin cytoskeletal organization, signal transduction, and mechanical stimulus response, may contribute to cell adhesion; genetic mutations are associated with periventricular heterotopia
SWN:P23_HUMAN Q15185 homo sapiens (human). telomerase-binding protein p23 (hsp90 co-chaperone) (progesterone receptor complex p23). 8/2001 [MASS=18697]/Inactive progesterone receptor (23kD), cochaperone with prostaglandin E synthase activity that is a component of the unstimulated progesterone receptor complex and that enhances receptor complex formation through interactions with Hsp90 (HSPCA)
SW:KPC1_HUMAN P05771 homo sapiens (human). protein kinase c, beta-i type (ec 2.7.1.-) (pkc-beta-1). 7/1999 [MASS=76839]/Protein kinase C beta 1, conventional PKC expressed as beta I and beta II forms, beta II mediates G2/M phase transition, mitotic nuclear envelope breakdown, neutrophil NADPH oxidase assembly; rat Prkcb1 activity is enhanced in diabetes mellitus
SW:GPS1_HUMAN Q13098 homo sapiens (human). g protein pathway suppressor 1 (gps1 protein) (mfh protein). 11/1997 [MASS=53372]/G protein pathway suppressor 1, suppressor of G protein and MAP kinase-mediated signaling pathways
SW:MPRI_HUMAN P11717 homo sapiens (human). cation-independent mannose-6-phosphate receptor precursor (ci man-6-p receptor) (ci-mpr) (insulin-like growth factor ii receptor) (300 kda mannose 6-phosphate [MASS=274309]/Insulin-like growth factor II receptor, functions in transport of mannose 6-phosphate-containing lysosomal enzymes and IGF-II maturation and clearance, mediates granzyme B-induced apoptosis, putative tumor suppressor
GP:AF124145_1 Homo sapiens autocrine motility factor receptor (AMFR) mRNA, complete cds. [MASS=73022]/Autocrine motility factor receptor, a cell surface transmembrane glycoprotein involved in cell motility signaling and metastasis, acts as a ubiqiuitin ligase involved in protein degradation, associated with tumor progression in various carcinomas
GP:AF087020_1 Homo sapiens protein zero related protein (PZR) mRNA, complete cds; immunoglobulin superfamily member. [MASS=29082]/Myelin protein zero-like 1, a member of the immunoglobulin superfamily that is a concanavalin A (ConA) receptor, mediates ConA and c-Src (SRC) signaling, may be a plasma membrane anchor for SHP-2 (PTPN11) type I, contains two ITIM motifs
GP:AB002382_1 Human mRNA for KIAA0384 gene, complete cds. [MASS=104952]/Catenin delta 1, a member of the catenin family of cadherin-binding proteins that link cadherins to the cytoskeleton, acts in cell signaling, plays a role in cell migration, loss of expession is correlated with bladder, colorectal and other cancer
PIR2:B55053 endothelial monocyte-activating protein II precursor - human [MASS=34254]/Endothelial monocyte activating polypeptide II, a proinflammatory cytokine that interacts with ATP synthase and inhibits endothelial cell growth, released during apoptosis, may sensitize tumors to killing by tumor necrosis factor alpha (TNF)
SW:RHOG_HUMAN P35238 homo sapiens (human), and cricetus cricetus (black-bellied hamster). rho-related gtp-binding protein rhog. 11/1995 [MASS=21309]/Aplysia ras-related homolog G (RhoG), a Ras-related GTP-binding protein of the rho-subfamily which regulates reorganization of the actin cytoskeleton and may be involved in the regulation of cholesterol excretion in patients with Tangier disease
SW:G25B_HUMAN P21181 homo sapiens (human), mus musculus (mouse), and bos taurus (bovine). g25k gtp-binding protein, brain isoform (gp) (cdc42 homolog). 12/1998 [MASS=21311]/Cell division cycle 42 (GTP binding protein 25kD), Rho GTPase involved in actin cytoskeleton organization, cell migration, cell cycle progression and apoptosis, downregulated in fibroblasts and macrophages from patients with Tangiers disease
SW:ITA5_HUMAN P08648 homo sapiens (human). integrin alpha-5 precursor (fibronectin receptor alpha subunit) (integrin alpha-f) (vla-5) (cd49e). 7/1999 [MASS=114508]/Integrin alpha 5, acts as a receptor for fibronectin, mediates binding of the cell to the extracellular matrix, involved in cell migration and trophoblast invasion; upregulation is associated with metastatic melanomas and carcinomas

GP:AB006534_1 Homo sapiens mRNA for hepatocyte growth factor activator inhibitor type 2, complete cds. [MASS=28169]/Serine protease inhibitor Kunitz type 2 (bikunin), inhibits hepatocyte growth factor activator (HGFAC) and serine proteases involved in coagulation and fibrinolysis, overexpressed in pancreatic cancer, may play roles in urolithiasis and glioma progression
SW:143T_HUMAN P27348 homo sapiens (human). 14-3-3 protein tau (14-3-3 protein theta) (14-3-3 protein t-cell) (hs1 protein). 11/1997 [MASS=27764]/14-3-3 theta (14-3-3 tau in T-cells), may modulate T-cell signaling and cytokine expression through interaction with and inhibition of protein kinase C and phosphatidylinositol 3-kinase, may promote cell survival during amyotrophic lateral sclerosis (ALS)
GP:AC002306_1 Homo sapiens DNA from chromosome 19-cosmid R33799, genomic sequence, complete sequence; hypothetical human G-protein coupled receptor on 19p; hypothetical human protein with BLASTX similarity to G protein-coupled receptor Rec1.3 [Mus musculus],(U4823 [MASS=39084]/Endothelial differentiation lysophosphatidic acid (LPA) G protein-coupled receptor 4, activated by saturated and unsaturated LPA, elevates intracellular Ca2+ and cAMP levels, activates MAP kinase, may mediate LPA-induced tumor growth in ovarian cancer
SW:GBB2_HUMAN P11016 homo sapiens (human). guanine nucleotide-binding protein g(i)/g(s)/g(t) beta subunit 2 (transducin beta chain 2). 5/2000 [MASS=37331]/Guanine nucleotide binding protein beta 2, component of heterotrimeric G protein complexes that transduce signals from G protein-coupled receptors to intracellular effectors, complex with Ggamma mediates inhibition of N- and PQ-type calcium channels
GP:AF151793_1 Homo sapiens ALG-2 interacting protein 1 (AIP1) mRNA, complete cds. [MASS=96079]/Protein with very strong similarity to murine Mm.28049, which interacts with the activin type IIA receptor and signaling molecule Smad3, has very strong similarity to rat Rn.29998, which is a synaptic scaffolding protein, contains PDZ and WW domains
GP:AB025194_1 Homo sapiens mRNA for protein tyrosine phosphatase HD-PTP, complete cds. [MASS=178974]/Member of the protein-tyrosine phosphatase family, has a region of strong similarity to a region of protein tyrosine phosphatase TD14 (rat Ptpn23), which is a putative tyrosine phosphatase that associates with cytoplasmic vesicles when overexpressed
GP:D87930_1 Homo sapiens mRNA for myosin phosphatase target subunit 1 (MYPT1); MYPT1. [MASS=115281]/Myosin phosphatase target subunit 1, a signal transducer that is involved in Rho-mediated regulation of myosin light chain dephosphorylation, may function in muscle contraction
PIR2:T46270 hypothetical protein DKFZp564N1563.1 - human (fragment) [MASS=77321]/Filamin B (beta, actin-binding protein-278), may be involved in actin cytoskeleton organization through interaction with the cytoplasmic domain of glycoprotein Ib alpha (GP1BA) and mediation of thyrotropin-induced actin microfilament disruption
SW:RHOA_HUMAN P06749 homo sapiens (human), and bos taurus (bovine). transforming protein rhoa (h12). 7/1998 [MASS=21768]/Ras homolog gene family member A, monomeric GTPase of the Rho family that mediates cell surface receptor and integrin signaling, induces actin stress fiber and focal adhesion formation, activity may contribute to cellular transformation and tumor invasion
SW:APP2_HUMAN Q06481 homo sapiens (human). amyloid-like protein 2 precursor (amyloid protein homolog) (apph) (cdei-box binding protein) (cdebp). 5/2000 [MASS=86956]/Amyloid precursor-like protein 2, a nuclear protein whcih may contribute to neurogenesis and cell cycle control
PIR2:I38176 ras-related GTPase rag, splice form A [imported] - human [MASS=36566]/Ras-related GTP binding protein, a GTP-binding protein that lacks GTPase activity, interacts with RAGC (GTR2), RAGD, and the adenovirus 14.7 kDa E3 protein, may be part of the tumor necrosis factor alpha (TNF) signaling pathway
GP:AF092130_1 Homo sapiens GTP-binding protein Sara mRNA, complete cds. [MASS=22410]/Mothers against decapentaplegic homolog interacting protein receptor activation anchor (Smad anchor for receptor activation), an early endosomal protein involved in activin- and TGF beta-mediated Smad activation, binds phosphatidylinositol 3-phosphate
PIR2:S29815 N-ras upstream protein NRU - human [MASS=88885]/Pyrimidinergic receptor P2Y4, a G protein-coupled nucleotide receptor activated by UTP and ATP and insensitive to inhibition by suramin, signals through stimulation of phosphoinositide hydrolysis and elevation of intracellular calcium
SW:MK01_HUMAN P28482 homo sapiens (human). mitogen-activated protein kinase 1 (ec 2.7.1.-) (extracellular signal-regulated kinase 2) (erk2) (mitogen-activated protein kinase 2) (map kinase 2) (mapk 2) [MASS=41390]/Mitogen-activated protein kinase 1, a serine-threonine kinase effector of the RAS-MAP kinase pathway, translocates to the nucleus to mediate transcription when activated, involved in the regulation of cell growth, differentiation, migration and apoptosis
SW:PRO1_HUMAN P07737 homo sapiens (human). profilin i. 12/1998 [MASS=14923]/Profilin I, a protein that regulates actin polymerization in response to extracellular signals and may suppress breast cancer cell tumorigenicity
SW:LYN_HUMAN P07948 homo sapiens (human). tyrosine-protein kinase lyn (ec 2.7.1.112). 5/2000 [MASS=58443]/ protein tyrosine kinase, a non-receptor tyrosine kinase important in cytokine receptor- and IgE receptor-mediated signal transduction, regulates cell adhesion and apoptosis, plays a role in platelet activation and inflammatory responses
SW:RAPA_HUMAN P10113 homo sapiens (human), rattus norvegicus (rat), and bos taurus (bovine). ras-related protein rap-1a (c21kg) (krev-1 protein) (gtp-binding protein smg-p21a) (g-22k). 12/1998 [MASS=20987]/RAP1A member of RAS oncogene family (Ras-related protein 1a), a member of the Ras superfamily of low molecular weight GTPases that is involved in cell cycle control and negative regulation of cellular proliferation, acts as a tumor suppressor

SW:RAN_HUMAN P17080 homo sapiens (human). gtp-binding nuclear protein ran (tc4). 12/1998 [MASS=24354]/RAN, member of the ras family of GTP binding proteins, couples completion of DNA synthesis to mitosis and induces mitotic spindle formation, involved in nuclear transport of RNA and proteins, interacts with polyglutamate repeats of the androgen receptor
SW:EFA5_HUMAN P52803 homo sapiens (human). ephrin-a5 precursor (eph-related receptor tyrosine kinase ligand 7) (lerk-7) (al-1). 5/2000 [MASS=26297]/Ephrin A5, a ligand of Eph-related receptor tyrosine kinases that is attached to the membrane via glycosylphosphatidylinositol linkage and is developmentally regulated in the brain, and may play a role during neurogenesis
SW:CD59_HUMAN P13987 homo sapiens (human). cd59 glycoprotein precursor (membrane attack complex inhibition factor) (macif) (mac-inhibitory protein) (mac-ip) (mem43 antigen) (protectin) (membrane inhibit [MASS=14177]/CD59 antigen (protectin), plasma membrane-secreted protein, inhibits formation of the membrane attack complex and protects against complement-mediated cell lysis, acts as a T-cell co-activator, may contribute to tumor cell escape from immune surveillance
SW:SRD6_HUMAN O15173 homo sapiens (human). steroid receptor protein dg6. 5/2000 [MASS=23818]/Progesterone receptor membrane component 2, putative transmembrane steroid hormone receptor, preferentially expressed in placenta
GP:U41806_1 Human EBI3-associated protein p60 mRNA, complete cds; EBI3-associated protein. [MASS=47602]/Sequestosome 1 (ubiquitin-binding protein p62), a ubiquitin-binding protein with a zinc finger-like motif, a G protein-binding region and a PEST motif, interacts with several signal transduction pathways, may be involved in endosome to lysosome transport
SW:KAP2_HUMAN P13861 homo sapiens (human). camp-dependent protein kinase type ii-alpha regulatory chain. 5/2000 [MASS=45387]/cAMP-dependent Protein kinase A regulatory subunit alpha (type II), binds A-kinase anchoring proteins to mediate holoenzyme localization and plays important roles in sperm motility and in trophoblast cell differentiation
SW:KCCD_HUMAN Q13557 homo sapiens (human). calcium/calmodulin-dependent protein kinase type ii delta chain (cam-kinase ii delta chain) (ec 2.7.1.123) (camk-ii, delta subunit) (fragment). 5/2000 [MASS=12846]/Calcium/calmodulin-dependent protein kinase II delta, member of the multifunctional CAMKII family involved in Ca2+ regulated processes; alternative form delta 3 is specifically upregulated in the myocardium of patients with heart failure
SW:KRCB_HUMAN P31751 homo sapiens (human). rac-beta serine/threonine kinase (ec 2.7.1.-) (rac-pk-beta) (akt2 kinase). 11/1995 [MASS=55769]/v-akt murine thymoma viral oncogene homolog 2, protein kinase that is activated by mitogens and survival factors, may regulate cell proliferation and apoptosis, overexpression is associated with ovarian, breast and pancreatic cancers
SW:PTN1_HUMAN P18031 homo sapiens (human). protein-tyrosine phosphatase 1b (ec 3.1.3.48) (ptp-1b). 7/1999 [MASS=49967]/Protein tyrosine phosphatase non-receptor type I, likely involved in the negative regulation of insulin receptor signaling, may be associated with type II diabetes and obesity
SW:FASA_HUMAN P25445 homo sapiens (human). fasl receptor precursor (apoptosis-mediating surface antigen fas) (apo-1 antigen) (cd95 antigen). 11/1997 [MASS=37732]/Apoptosis antigen ligand 1, a tumor necrosis factor alpha related cytokine that binds Fas and induces apoptosis, plays important roles in immune system development, immune response and tumorigenesis, may be a prognostic tumor marker
SW:FK38_HUMAN Q14318 homo sapiens (human). 38 kda fk-506 binding protein homolog (fkbpr38). 5/2000 [MASS=38408]/FK506 binding protein, member of a subclass of immunophilins, contains tetratricopeptide repeat and a consensus leucine zipper domains
GP:AF260566_1 Homo sapiens hepatocyte growth factor-regulated tyrosine kinase substrate HRS isoform 2 (HRS) mRNA, complete cds. [MASS=76362]/Hepatocyte growth factor regulated tyrosine kinase substrate, zinc-finger protein with ATPase activity, tyrosine phosphorylated upon growth factor stimulation, involved in endosome trafficking and mediates FOS transcription via cytokine signaling
SW:ERB2_HUMAN P04626 homo sapiens (human). receptor protein-tyrosine kinase erbb-2 precursor (ec 2.7.1.112) (p185erbb2) (neu proto-oncogene) (c-erbb-2) (tyrosine kinase-type cell surface receptor her2) [MASS=137910]/Avian erythroblastosis oncogene B 2, a receptor tyrosine kinase and most oncopotent member of the EGF receptor family, heterodimerizes with other EGFRs; overexpression contributes to growth, metastasis and chemoresistance of epithelial-derived tumors
SW:RAC1_HUMAN P15154 homo sapiens (human), mus musculus (mouse), and canis familiaris (dog). ras-related c3 botulinum toxin substrate 1 (p21-rac1) (ras-like protein tc25). 12/1998 [MASS=21450]/Ras-related C3 botulinum toxin substrate 1, a monomeric GTPase of the Rho family, involved in transducing signals that regulate proliferation, apoptosis, cytoskeletal organization, and response to oxidative stress, contributes to tumor cell invasiveness
PIR2:T47172 hypothetical protein DKFZp762H186.1 - human (fragment) [MASS=55769]/Coronin actin-binding protein 1C, a member of the coronin-like protein family, has five WD repeats and a coiled-coil motif, a putative actin binding protein that may play a role in mitosis, cytokinesis, cell motility, signal transduction, and phagocytosis
GP:AK022871_1 Homo sapiens cDNA FLJ12809 fis, clone NT2RP2002408, highly similar to Homo sapiens mRNA for TOLLIP protein; unnamed protein product. [MASS=22813]/Tollip, mediates interleukin-1 receptor signaling through interaction with serine/threonine kinase IRAK, inhibits the activity of IRAK1, inhibits lipopolysaccharide-induced activation of macrophages and TLR2 and TLR4 induced activation of NF-KB

SW:A4_HUMAN P05067 homo sapiens (human). alzheimer's disease amyloid a4 protein precursor (protease nexin-ii) (pn-ii) (appi) [contains: beta-amyloid protein (beta-app) (a-beta)]. 5/2000 [MASS=86943]/Amyloid beta (A4) precursor protein, cell surface protease inhibitor that reduces copper, deposits of proteolytic peptide products are found in Alzheimer's disease and Down syndrome brains, deficiency is associated with early-onset Alzheimer's disease
PIR1:JC5394 DJ-1 protein - human [MASS=19847]/RNA-binding protein regulatory subunit, a putative oncogene that may regulate the androgen receptor, play a role in RAS protein signal transduction, and is predicted to play a role in fertilization
GP:AB011126_1 Homo sapiens mRNA for KIAA0554 protein, partial cds. [MASS=77448]/Formin binding protein 17, contains a Src homology 3 (SH3) domain and a Fes/CIP4 homology domain, binds SNX2 and may mediate the assembly of protein signaling complexes; gene is a fusion partner with MLL in acute myelogeneous leukemia
SW:143Z_HUMAN P29312 homo sapiens (human), and bos taurus (bovine). 14-3-3 protein zeta/delta (protein kinase c inhibitor protein-1) (kcip-1) (factor activating exoenzyme s) (fas). 7/1999 [MASS=27745]/14-3-3 zeta, mediates various signal transduction pathways, including inhibition of protein kinase C and activation of inositol polyphosphate 5-phosphatase, phospholipase A2 activity is questionable; may be associated with Alzheimer's disease
GP:AL096767_2 Human DNA sequence from clone 579N16 on chromosome 22. Contains the 3' part of the gene for KIAA0685, the SBF1 gene for SET binding factor 1, a novel gene, ESTs, an STS, GSSs and three putative CpG islands, complete sequence; owing to approximately 7 [MASS=182476]/SET binding factor 1, a pseudo phosphatase that is inactive as a phosphatase and may act as a competitive inhibitor of other protein phosphatases, regulates cellular growth and may have a role in signal transduction
SW:NTC1_HUMAN P46531 homo sapiens (human). neurogenic locus notch protein homolog 1 precursor (translocation-associated notch protein tan-1) (fragment). 2/1996 [MASS=260649]/Notch homolog 1, a transcriptional regulator involved in different types of cell proliferation and differentiation (especially blood cells), may play a role in cell cycle control; gene translocation is associated with T-cell leukemia
SW:GBI2_HUMAN P04899 homo sapiens (human). guanine nucleotide-binding protein g(i), alpha-2 subunit (adenylate cyclase-inhibiting g alpha protein). 12/1998 [MASS=40320]/G protein alpha subunit i2, a component of pertussis toxin sensitive heterotrimeric G protein complexes that transduces signals to effectors and inhibits adenylyl cyclase; mutations in the gene are associated with tachycardia and endocrine tumors
SW:EPA7_HUMAN Q15375 homo sapiens (human). ephrin type-a receptor 7 precursor (ec 2.7.1.112) (tyrosine-protein kinase receptor ehk-3) (eph homology kinase-3) (receptor protein- tyrosine kinase hek11). 5 [MASS=112097]/ Ephrin type A receptor 7, an Eph-related receptor tyrosine kinase, interacts with the PDZ domain of the Ras binding protein AF6 (MLLT4), may be involved in cell signaling
GP:AB002313_1 Human mRNA for KIAA0315 gene, partial cds. [MASS=205412]/Plexin B2, putative semaphorin receptor that may be involved in mediating cell guidance
SW:ER60_HUMAN P30101 homo sapiens (human). probable protein disulfide isomerase er-60 precursor (ec 5.3.4.1) (erp60) (58 kda microsomal protein) (p58) (grp58) (erp57). 7/1998 [MASS=56782]/Glucose regulated 58kDa protein, acts as a protein disulfide isomerase and possibly a protease, involved in folding and maturation of N-linked glycoproteins and MHC class I antigen processing; identified as a sperm antigen in immunological infertility
SW:INSR_HUMAN P06213 homo sapiens (human). insulin receptor precursor (ec 2.7.1.112) (ir). 5/2000 [MASS=156281]/Insulin receptor, a transmembrane receptor protein tyrosine kinase involved in carbohydrate metabolism, energy pathways, and cell growth; gene mutation is associated with insulin-resistant diabetes mellitus and leprechaunism
SW:PI52_HUMAN P48426 homo sapiens (human). phosphatidylinositol-4-phosphate 5-kinase type ii alpha (ec 2.7.1.68) (pip5kii-alpha) (1-phosphatidylinositol-4-phosphate kinase) (ptdins(4)p-5-kinase b isofor [MASS=46193]/Phosphatidylinositol-4-phosphate 5-kinase type II, alpha, a member of a family of kinases responsible for the synthesis of PtdIns(4,5)P2
GP:BC018192_1 Homo sapiens, inositol 1,3,4-triphosphate 5/6 kinase, clone MGC:21491 IMAGE:3867269, mRNA, complete cds. [MASS=45621]/Inositol 1,3,4-triphosphate 5-6 kinase, phosphorylates Ins(1,3,4)P3 to form Ins(1,3,4,5)P4 and Ins(1,3,4,6)P4, regulates inositol phosphate metabolism; variant form phosphorylates Ins(3,4,5,6)P4 to yield Ins(1,3,4,5,6)P5
SW:TRA2_HUMAN Q12933 homo sapiens (human). tnf receptor associated factor 2 (traf2) (tumor necrosis factor type 2 receptor associated protein 3). 5/2000 [MASS=55794]/TNF receptor-associated factor 2, interacts with and mediates tumor necrosis factor signaling through activation of NF-kappaB cascade, functions as an apoptosis inhibitor
SW:GBB1_HUMAN P04901 homo sapiens (human), mus musculus (mouse), bos taurus (bovine), and canis familiaris (dog). guanine nucleotide-binding protein g(i)/g(s)/g(t) beta subunit 1 (transducin beta chain [MASS=37377]/Guanine nucleotide binding protein (G protein) beta 1, a component of heterotrimeric G protein complexes, plays a role in signal transduction
SW:KAPA_HUMAN P17612 homo sapiens (human). camp-dependent protein kinase, alpha-catalytic subunit (ec 2.7.1.37) (pka c-alpha). 5/2000 [MASS=40458]/Catalytic subunit C alpha of cAMP-dependent protein kinase, plays a role in transcriptional regulation and may mediate suppression of apoptosis, may also serve as a tumor biomarker; alternative form C alpha 2 may play a role in sperm development
GP:AF020202_1 Homo sapiens Munc13 mRNA, complete cds; contains C2 domains; similar to R. norvegicus Munc13-2 encoded by GenBank Accession Number U24071. [MASS=180684]/UNC13 (C. elegans)-like, a diacylglycerol receptor that may function in a PKC-independent, diacylglycerol-activated signaling pathway that induces apoptosis, may be involved in renal cell injury in hyperglycemia

SW:BCR_HUMAN P11274 homo sapiens (human). breakpoint cluster region protein (ec 2.7.1.-). 7/1999 [MASS=142806]/Breakpoint cluster region, GTPase-activating protein for p21rac with serine/threonine kinase activity; translocation of the corresponding gene is associated with Philadelphia chromosome-positive chronic myeloid leukemia
GP:AB037857_1 Homo sapiens mRNA for KIAA1436 protein, partial cds; Start codon is not identified.. [MASS=102996]/Prostaglandin F2 alpha receptor regulatory protein, a putative transmembrane glycoprotein that copurifies with and negatively regulates the prostaglandin F2 alpha receptor by inhibiting ligand-binding
SW:P2BA_HUMAN Q08209 homo sapiens (human). serine/threonine protein phosphatase 2b catalytic subunit, alpha isoform (ec 3.1.3.16) (calmodulin-dependent calcineurin a subunit, alpha isoform) (cam-prp cat [MASS=58688]/Calcineurin A alpha, catalytic subunit of calcium/calmodulin regulated protein phosphatase, regulates activity of transcription factors involved in signal transduction and growth control
PIR2:JC5938 thioredoxin-like protein - human [MASS=32251]/Thioredoxin-like 32, a thioredoxin related protein that has thioredoxin-like reducing activity
SW:OGT1_HUMAN O15294 homo sapiens (human). udp-n-acetylglucosamine--peptide n-acetylglucosaminyltransferase 100 kda subunit (ec 2.4.1.-) (o-glcnac transferase p100 subunit). 5/2000 [MASS=103012]/O-linked N-acetylglucosamine transferase (UDP-N-acetylglucosamine:polypeptide-N-acetylglucosaminyltransferase), enzyme that functions in O-glycosylation, may be involved in insulin secretion and glucose homeostasis, may play a role in signal transduction
GP:AK001521_1 Homo sapiens cDNA FLJ10659 fis, clone NT2RP2006071; unnamed protein product. [MASS=36277]/Protein with unknown function, has high similarity to a region of APPL, an adaptor protein with a PH domain, a PTB domain and a leucine zipper motif, and which binds to AKT2 and PI3 kinase catalytic subunit p110alpha
SW:KG3B_HUMAN P49841 homo sapiens (human). glycogen synthase kinase-3 beta (ec 2.7.1.37) (gsk-3 beta). 7/1999 [MASS=46768]/Glycogen synthase kinase-3 beta, a serine threonine protein kinase that phosphorylates several cytoplasmic and nuclear proteins, involved in embryonic development, and may hyperphosporylate tau (MAPT) in
GP:D87116_1 Human mRNA for MAP kinase kinase 3b ,complete cds; MKK3b. [MASS=39318]/Mitogen activated protein kinase kinase 3, phosphorylates MAP kinase p38, involved in stress and inflammatory responses, senescence, and apoptosis, also has roles in ischemic kidney injury, and H. influenzae infection
SW:EBI2_HUMAN P32249 homo sapiens (human). ebv-induced g protein-coupled receptor 2 (ebi2). 7/1998 [MASS=41224]/Epstein-Barr virus induced gene 2, a lymphocyte specific G protein-coupled receptor that may mediate the effects of Epstein-Barr virus on B lymphocytes
SW:THIO_HUMAN P10599 homo sapiens (human). thioredoxin (atl-derived factor) (adf) (surface associated sulphydryl protein) (sasp). 7/1998 [MASS=11606]/Thioredoxin, has dithiol-disulfide oxidoreductase activity and is upregulated in activated monocytes and in established dividing cell lines, promotes neutrophil migration
SW:OCRL_HUMAN Q01968 homo sapiens (human). lowe's oculocerebrorenal syndrome protein. 7/1998 [MASS=111485]/Oculocerebrorenal syndrome of Lowe, phosphatidylinositol-4,5-bisphosphate 5-phosphatase, may play a role in intracellular protein trafficking; mutation of the corresponding gene causes Lowe oculocerebrorenal syndrome
PIR2:I38026 MLN 62 protein - human [MASS=53444]/TNF receptor-associated factor 4, a member of a family of proteins that interact with the cytoplasmic domain of TNF receptors, plays a role in apoptosis, may function in TNF-related signal transduction associated with breast cancer
SW:GBLP_HUMAN P25388 homo sapiens (human), mus musculus (mouse), rattus norvegicus (rat), sus scrofa (pig), and gallus gallus guanine nucleotide-binding protein beta subunit-like protein 12.3 (p205) (re [MASS=35077]/Guanine nucleotide binding protein beta 2 related sequence 1, protein kinase C (PKC) anchoring system subunit, homologous to G protein beta subunits, deficit is associated with impaired activation of PKC in the aging brain, contributing to Alzheimers
GP:AB033078_1 Homo sapiens mRNA for KIAA1252 protein, partial cds; Start codon is not identified.. [MASS=64962]/Protein with strong similarity to sphingosine phosphate lyase 1 (mouse Sgpl1), which is a member of the carbon-carbon lyase subclass of aldehyde-lyases that catalyzes cleavage of sphingosine phosphate and is involved in proliferative signal transduction
SW:RSP4_HUMAN P08865 homo sapiens (human). 40s ribosomal protein sa (p40) (34/67 kda laminin receptor) (colon carcinoma laminin-binding protein) (nem/1chd4). 5/2000 [MASS=32854]/Laminin receptor 1, a ribosomal protein of the small 40S ribosomal subunit, plays a role in cancer cell and basement membrane glycoprotein laminin interactions during tumor invasion and metastasis, expression correlates with cancer cell aggressiveness
SW:OBRG_HUMAN O15243 homo sapiens (human). leptin receptor gene-related protein (ob-r gene related protein) (ob- rgrp). 7/1999 [MASS=14254]/Leptin receptor, member of the gp130 (IL6ST) cytokine-receptor family, signals through the JAK/STAT cascade and functions in regulation of appetite, body fat, bone formation, and reproduction; mutations in the gene cause obesity and pituitary dysfunction
SW:PTPF_HUMAN P10586 homo sapiens (human). lar protein precursor (leukocyte antigen related) (ec 3.1.3.48). 10/1994 [MASS=211845]/Protein tyrosine phosphatase receptor-type F (leukocyte common antigen related), regulates insulin receptor signaling and cell migration, inhibits tumor formation in nude mice
SW:GBI1_HUMAN P04898 homo sapiens (human), and bos taurus (bovine). guanine nucleotide-binding protein g(i), alpha-1 subunit (adenylate cyclase-inhibiting g alpha protein). 7/1999 [MASS=40230]/Guanine nucleotide binding protein alpha inhibiting activity polypeptide 1 (Gi alpha 1), pertussis toxin-sensitive heterotrimeric G protein subunit downregulated at the membrane by increased cholesterol, mediates adenylyl cyclase inhibition

SW:C166_HUMAN Q13740 homo sapiens (human). cd166 antigen precursor (activated leukocyte-cell adhesion molecule) (alcam). 7/1999 [MASS=65132]/Activated leukocyte cell adhesion molecule, an immunoglobulin superfamily member and ligand for CD6, involved in hematopoietic cell adhesion, may play a role in osteogenesis, marker for tumor progression in malignant melanoma
SW:PTK7_HUMAN Q13308 homo sapiens (human). tyrosine-protein kinase-like 7 precursor (colon carcinoma kinase-4) (cck-4). 5/2000 [MASS=118260]/Protein tyrosine kinase 7 (colon carcinoma kinase-4), a glycosylated member of the receptor protein tyrosine kinase family that may be involved in tumorigenesis, likely to be catalytically inactive due to alterations within the RTK consensus sequences
GP:U17032_1 Human p190-B (p190-B) mRNA, complete cds; member of the Rho GAP family. [MASS=171569]/Rho GTPase activating protein 5/Rho GTPase-activating protein (GAP) 5, has GAP activity for ARHA, RAC1 and CDC42, which are ras-related GTP binding proteins of the rho subfamily; may be involved in the integrin receptor signaling pathway and in cell adhesion
SW:CAN1_HUMAN P07384 homo sapiens (human). calpain 1, large [catalytic] subunit (ec 3.4.22.17) (calcium-activated neutral proteinase) (canp) (mu-type). 10/1996 [MASS=81890]/Calpain I, catalytic subunit of mu-calpain, a calcium-dependent cysteine (thiol) protease that requires micromolar concentrations of calcium in vitro
SW:ITB1_HUMAN P05556 homo sapiens (human). fibronectin receptor beta subunit precursor (integrin beta-1) (cd29) (integrin vla-4 beta subunit). 7/1999 [MASS=88465]/Integrin beta 1, involved in extracellular matrix interactions and signal transduction, plays roles in cell adhesion, migration, proliferation and development, may be involved in tumor metastasis
GP:AB007867_1 Homo sapiens KIAA0407 mRNA, complete cds. [MASS=232298]/Plexin B1 (plexin 5), a member of the plexin family of semaphorin receptors which are involved in axon guidance, receptor for semaphorin 4D (SEMA4D), functions in RAC and RHO signal transduction pathways and in actin cytoskeleton reorganization
GP:AL023805_1 Human DNA sequence from clone RP4-811H13 on chromosome 20p12. Contains part of the PLCB4 gene for Phospholipase C beta 4, STSs, GSSs and a CpG island, complete sequence; combines with dJ1119D9.2.1 and .2 in Em:AL031652 to form isoforms 5 and 6; may a [MASS=61433]/1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase beta 4/Phospholipase C beta 4, member of a G protein-regulated family of phospholipases that hydrolyze phosphatidylinositol 4,5-bisphosphate to the second messengers inositol 1,4,5-trisphosphate and diacylglycerol
Homo sapiens pleiotropic regulator 1 (PLRG1) mRNA/Member of the WD repeat protein family, interacts with a nuclear protein kinase C-beta II isoenzyme that is involved in insulin signaling
SW:KC2B_HUMAN P13862 homo sapiens (human), mus musculus (mouse), rattus norvegicus (rat), bos taurus (bovine), sus scrofa (pig), oryctolagus cuniculus (rabbit), and gallus gallus (chicken). casein kinase [MASS=24942]/Casein kinase II beta subunit, regulatory subunit of casein kinase II (CK2), confers stability and specificity to CK2 catalytic subunits, may mediate formation of the tetrameric CK2 complex, and may be involved in heat stress response
SW:NRP_HUMAN O14786 homo sapiens (human). neuropilin precursor (vascular endothelial cell growth factor 165 receptor). 5/2000 [MASS=103121]/Neuropilin 1, a receptor for VEGF (165) and the axonal chemorepellent Semaphorin III, involved in organogenesis, axon guidance and angiogenesis, may regulate cell proliferation and response to wounding, upregulated in neuroblastoma vascular endothelium
GP:X92689_1 Homo sapiens mRNA for UDP-GalNAc:polypeptide N-acetylgalactosaminyl transferase (GalNAc-T3). [MASS=72638]/N-acetylgalactosaminyltranferase T3 (UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 3), enzyme that initiates O-glycosylation; elevated levels may be associated with differentiation of adenocarcinomas
SW:GST3_HUMAN O14880 homo sapiens (human). microsomal glutathione s-transferase 3 (ec 2.5.1.18) (microsomal gst- 3) (microsomal gst-iii). 5/2000 [MASS=16516]/Microsomal glutathione S-transferase 3, a microsomal membrane protein that has glutathione-dependent transferase and peroxidase activities, member of a family that includes 5-lipoxygenase activating protein (ALOX5AP) and leukotriene-C4 synthase (LTC4S)
SW:POR1_HUMAN P21796 homo sapiens (human). voltage-dependent anion-selective channel protein 1 (hvdac1) (outer mitochondrial membrane protein porin 1) (plasmalemmal porin) (porin 31hl) (porin 31hm). 5/2 [MASS=30641]/Voltage-dependent anion channel 1, mitochondrial outer membrane anion channel that mediates apoptotic signals from Bcl-2 (BCL2) and related proteins; deficiency of protein in skeletal muscle causes mitochondrial encephalomyopathy
SW:MAZ_HUMAN P56270 homo sapiens (human). myc-associated zinc finger protein (mazi) (purine-binding transcription factor) (pur-1) (zf87) (zif87). 7/1999 [MASS=48608]/MYC-associated zinc finger protein (purine-binding transcription factor), functions both as a positive and a negative regulator of gene expression and may also have roles in initiating and terminating transcription
SW:IBP2_HUMAN P18065 homo sapiens (human). insulin-like growth factor binding protein 2 precursor (igfbp-2) (ibp-2) (igf-binding protein 2). 12/1998 [MASS=35138]/Insulin like growth factor binding protein 2, binds to and modulates insulin-like growth factor activity, regulates cell proliferation, may be involved in apoptosis; associated with the malignant phenotype, may play a role in prostatic involution
SW:GRBA_HUMAN Q13322 homo sapiens (human). growth factor receptor-bound protein 10 (grb10 adaptor protein) (insulin receptor binding protein grb-ir) (kiaa0207). 5/2000 [MASS=67231]/Growth factor receptor bound protein 10, an adaptor protein with PH and SH2 domains that binds to various receptor and cytosolic kinases and may mediate growth factor and Src family kinase signaling; variants may be associated with Russell-Silver Syndrome

SW:SORC_HUMAN P30626 homo sapiens (human). sorcin (22 kda protein) (cp-22) (v19). 11/1997 [MASS=21676]/Sorcin, an EF-hand calcium-binding protein, may be involved in multidrug resistance, a potential modulator of intracellular calcium levels through interaction with the ryanodine receptor
SW:LU_HUMAN P50895 homo sapiens (human). lutheran blood group glycoprotein precursor (b-cam cell surface glycoprotein) (auberger b antigen) (f8/g253 antigen). 11/1997 [MASS=67375]/Precursor of Lutheran blood group glycoprotein and B-CAM, laminin receptors and cell adhesion molecules, have a role in the blood-brain barrier, contribute to vasoocculsion in sickle cell disease and possibly tumorigenesis
GP:D63481_1 Human mRNA for KIAA0147 gene, partial cds; The KIAA0147 gene product is related to adenylyl cyclase.. [MASS=166187]/Protein containing PDZ (DHR, GLGF) domains, which target signaling proteins to membranes, contains leucine rich repeats, which mediate protein-protein interactions
GP:AB006537_1 Homo sapiens mRNA for interleukin 1 receptor accessory protein, complete cds. [MASS=65418]/Interleukin-1 receptor accessory protein, a subunit of the interleukin-1 receptor complex, recruits IRAK to the receptor complex in an early stage of interleukin-1 signaling
GP:AF002668_1 Homo sapiens putative fatty acid desaturase MLD mRNA, complete cds; putative fatty acid desaturase. [MASS=37866]/Degenerative spermatocyte homolog (Drosophila), member of the membrane fatty acid desaturase family, regulates the biosynthesis of the epidermal growth factor receptor (EGFR)
SW:RDC1_HUMAN P25106 homo sapiens (human). g protein-coupled receptor rdc1 homolog. 7/1998 [MASS=41474]/Chemokine orphan receptor 1, protein with strong similarity to murine Rdc1, which is a member of the G protein-coupled receptor family and related to chemokine receptors of the CXC family, acts as a coreceptor for HIV strains that infect brain cells
SW:PA2M_HUMAN P14555 homo sapiens (human). phospholipase a2, membrane associated precursor (ec 3.1.1.4) (phosphatidylcholine 2-acylhydrolase) (group ii phospholipase a2) (non-pancreatic secretory phosph [MASS=16083]/Group IIA phospholipase A2, a secreted member of the phospholipase A2 family that hydrolyzes the phospholipid sn-2 ester bond, plays roles in phospholipid metabolism, host defense, and inflammation; gene loss reported in a sporadic colorectal tumor
SW:KDGG_HUMAN P49619 homo sapiens (human). diacylglycerol kinase, gamma (ec 2.7.1.107) (diglyceride kinase) (dgk-gamma) (dag kinase gamma). 5/2000 [MASS=88997]/Diacylglycerol kinase gamma, member of diacylglycerol kinase family, contains EF-hand motifs, zinc finger and ATP-binding site, converts diacylglycerol to phosphatidic acid in a phosphatidylserine-dependent manner, may regulate phospholipid turnover
SW:TRFL_HUMAN P02788 homo sapiens (human). lactotransferrin precursor (lactoferrin). 7/1999 [MASS=78338]/Lactotransferrin, a member of the transferrin family, transports iron in extracellular fluid and may have serine protease activity, has antimicrobial, antifugual, and antiviral activity, potential theraputic or diagnostic target for autoimmune diseases
SW:FLOH_HUMAN O60779 homo sapiens (human). folate-like transporter dj206d15.1 on chromosome 1 (fragment). 7/1999 [MASS=52323]/Solute carrier family 19 member 2, functions as a thiamine transporter; mutations in the gene are associated with thiamine responsive megaloblastic anemia (TRMA) often combined with diabetes mellitus and deafness
SW:Y274_HUMAN Q92562 homo sapiens (human). hypothetical protein kiaa0274. 7/1998 [MASS=103635]/Protein containing two SacI homology domains, has a region of low similarity to suppressor of actin 1 (rat Sacm1l), which is an integral membrane lipid phosphatase that acts on PI 3 phosphate, PI 4 phosphate, and PI 3,5 bisphosphate
Solute carrier family 9 isoform 3 regulatory factor 1 (sodium-hydrogen exchanger-regulatory factor), a cytoskeleton-linking protein that forms multiprotein complexes with members of the Ezrin-Radixin-Moesin family via two PDZ domains
SW:AAAT_HUMAN Q15758 homo sapiens (human). neutral amino acid transporter b(0) (atb(0)). 12/1998 [MASS=56621]/Solute carrier family 1 member 5, a sodium-dependent neutral amino acid transporter that comprises the amino acid transport system B(0), acts as a cell-surface receptor for RD114/simian type D
SW:ATND_HUMAN P54709 homo sapiens (human). sodium/potassium-transporting atpase beta-3 chain (sodium/potassium-dependent atpase beta-3 subunit) (atpb-3). 7/1999 [MASS=31513]/ATPase (Na+/K+ transporting beta 3 subunit), proposed to actively transport sodium and potassium across the cell membrane to produce electrochemical gradients
SW:MRP1_HUMAN P33527 homo sapiens (human). multidrug resistance-associated protein 1. 5/2000 [MASS=171561]/ATP-binding cassette subfamily C member 1 (multiple drug resistance protein 1), an ATP-binding cassette transporter that acts as a multidrug efflux pump conferring resistance to lipophilic drugs and chemotherapeutic agents
SW:NC5R_HUMAN P00387 homo sapiens (human). nadh-cytochrome b5 reductase (ec 1.6.2.2) (b5r). 11/1997 [MASS=34104]/NADH-dependent cytochrome b5 reductase (diaphorase), soluble erythrocyte-specific form functions in methemoglobin reduction, ubiquitous membrane-bound form functions in lipid metabolism; mutations in the gene cause methemoglobinemia types I and II
SW:MRP4_HUMAN O15439 homo sapiens (human). multidrug resistance-associated protein 4 (fragment). 5/2000 [MASS=18448]/Multidrug resistance protein 4, a member of the ATP-binding cassette transporter superfamily, transports cAMP, cGMP, and estradiol 17-beta-D-glucuronide, acts as a multidrug efflux pump, may be involved in cellular detoxification and xenobiotic resistance/Multidrug resistance protein 4, a member of the ATP-binding cassette transporter superfamily, transports cAMP, cGMP, and estradiol 17-beta-D-glucuronide, acts as a multidrug efflux pump, may be involved in cellular detoxification and xenobiotic resistance

SW:CLI1_HUMAN O00299 homo sapiens (human). chloride intracellular channel protein 1 (nuclear chloride ion channel 27) (ncc27) (p64 clcp). 5/2000 [MASS=26924]/Chloride intracellular channel 1 (nuclear chloride channel-27), an intracellular chloride channel that localizes predominantly to the nucleus, member of the glutathione transferase structural family
SW:GBAK_HUMAN P08754 homo sapiens (human). guanine nucleotide-binding protein g(k), alpha subunit (g(i) alpha-3). 11/1997 [MASS=40401]/G protein alpha i3 subunit, a component of pertussis toxin sensitive heterotrimeric G protein complexes, transduces signals from G protein-coupled receptors to intracellular effectors, inhibits forskolin-stimulated cAMP production
SW:ATHA_HUMAN P20648 homo sapiens (human). potassium-transporting atpase alpha chain (ec 3.6.1.36) (proton pump) (gastric h+/k+ atpase alpha subunit). 5/2000 [MASS=114091]/H+/K+ transporting ATPase alpha polypeptide, a putative gastric heterodimeric proton pump responsible for acidification of the stomach lumen
SWN:ENT1_HUMAN Q99808 homo sapiens (human). equilibrative nucleoside transporter 1 (equilibrative nitrobenzylmercaptopurine riboside-sensitive nucleoside transporter) (equilibrative nbmpr-sensitive nucle [MASS=50088]/Solute carrier family 29 member 1 (equilibrative nucleoside transporter 1), functions in the transport of physiologic nucleosides and chemotherapeutic nucleoside analog drugs, inhibited by nitrobenzylthioinosine, dipyridamole, and dilazep
SW:ANX7_HUMAN P20073 homo sapiens (human). annexin vii (synexin). 5/2000 [MASS=50316]/Annexin A7 (synexin), a calcium-dependent GTPase that acts as a voltage-dependent calcium channel, interaction with galectin 3 (LGALS3) suggests roles in apoptosis and exocytosis, may function as a tumor suppressor
PIR2:T46412 ubiquitin--protein ligase (EC 6.3.2.19) NEDD4 - human (fragment) [MASS=95283]/Neural cell precursor expressed developmentally downregulated 4, ubiquitin-protein ligase with multiple WW domains, binds to and reduces the activity of epithelial sodium channels, may play a role in neural differentiation, regulated by kinase SGK
SW:VATX_HUMAN Q02547 homo sapiens (human). vacuolar atp synthase subunit ac39 (ec 3.6.1.34) (v-atpase ac39 subunit) (32 kda accessory protein) (p39). 11/1997 [MASS=31704]/Vacuolar H+-ATPase proton pump (subunit D), an accessory subunit in the peripheral catalytic V1 complex, may be involved in coupling ATP hydrolysis (V1 complex) and proton transport (V0 complex)
SW:VPP1_HUMAN Q93050 homo sapiens (human). clathrin-coated vesicle/synaptic vesicle proton pump 116 kda subunit (ec 3.6.1.34) (vacuolar proton pump subunit 1). 12/1998 [MASS=95751]/ATPase (H+ transporting lysosomal (vacuolar proton pump) noncatalytic accessory protein 1A (110/116 kDa), a component of a multisubunit enzyme which couples ATP hydrolysis to proton translocation
GP:AF284422_1 Homo sapiens cation-chloride cotransporter-interacting protein mRNA, complete cds; cation-chloride cotransporter family; CIP1; 96.2 kDa; predicted to contain 12 transmembrane domains and cytoplasmic N-and C-termini. [MASS=96171]/Cation-chloride cotransporter-interacting protein 1, inhibits Na+-K+-Cl- cotransporter 1-mediated transport activity, may modulate cation-chloride cotransporter activity or kinetics through heterodimer formation
SW:MOT4_HUMAN O15374 homo sapiens (human). monocarboxylate transporter 4 (mct 4). 5/2000 [MASS=54022]/Monocarboxylate transporter, member of a family of proton-linked monocarboxylate transporters, may transport monocarboxylates such as lactate across the plasma membrane
SWN:STX8_HUMAN Q9unk0 homo sapiens (human). syntaxin 8. 8/2001 [MASS=26907]/Syntaxin 8, member of the soluble NSF attachment protein receptor (SNARE) family, plays a role in endosome trafficking, may mediate vesicle docking and fusion, may regulate CFTR -mediated chloride currents
GP:AK022853_1 Homo sapiens cDNA FLJ12791 fis, clone NT2RP2001991, highly similar to SODIUM- AND CHLORIDE-DEPENDENT TRANSPORTER NTT73; unnamed protein product. [MASS=32264]/Orphan transporter V7-3, a member of the sodium:neurotransmitter symporter family with an unknown substrate specificity, predominantly expressed in neuronal tissues
SW:ICLN_HUMAN P54105 homo sapiens (human). chloride conductance regulatory protein icln (chloride channel, nucleotide sensitive 1a) (chloride ion current inducer protein) (clci) (reticulocyte picln). 12 [MASS=26215]/Chloride channel nucleotide-sensitive 1A, a putative chloride channel regulator, binds beta-actin, may regulate chloride transport and cell volume (especially in young red blood cells), may play a role in aqueous humor formation in the eye
SW:MK01_HUMAN P28482 homo sapiens (human). mitogen-activated protein kinase 1 (ec 2.7.1.-) (extracellular signal-regulated kinase 2) (erk2) (mitogen-activated protein kinase 2) (map kinase 2) (mapk 2) [MASS=41390]/Mitogen-activated protein kinase 1, a serine-threonine kinase effector of the RAS-MAP kinase pathway, translocates to the nucleus to mediate transcription when activated, involved in the regulation of cell growth, differentiation, migration and apoptosis
SW:IEFS_HUMAN P31948 homo sapiens (human). transformation-sensitive protein ief ssp 3521. 10/1996 [MASS=62639]/Stress-induced phosphoprotein 1, a cochaperone that inhibits protein folding and may stabilize a heat shock protein complex on the lysosomal membrane, contains nine TPR (tetratricopeptide repeat) domains, which may mediate protein-protein interactions
GP:AJ131612_1 Homo sapiens dic gene, exons 1-11. [MASS=31325]/Solute carrier family 25 member 10 (dicarboxylate carrier), a putative dicarboxylic acid transporter predicted to reside in the inner mitochondrial membrane, may be involved in gluconeogenesis
GP:AF288687_1 Homo sapiens CGI-152 protein mRNA, complete cds. [MASS=121110]/Member of the haloacid dehalogenase or epoxide hydrolase family and the E1-E2 (P-type) ATPase family, which are cation transporters, has moderate similarity to S. cerevisiae Spf1p, which functions in cell wall organization and xenobiotic response

SW:CLC3_HUMAN P51790 homo sapiens (human). chloride channel protein 3 (clc-3). 7/1998 [MASS=84793]/Chloride channel 3, chloride channel of the voltage-gated family, plays a role in chloride transport, may be responsible for outwardly rectifying chloride currents, regulated by calcium/calmodulin dependent protein kinase II (CAMK2A), binds to SLC9A3R1
SW:ATN1_HUMAN P05023 homo sapiens (human). sodium/potassium-transporting atpase alpha-1 chain precursor (ec 3.6.1.37) (sodium pump) (na+/k+ atpase). 7/1999 [MASS=112896]/Alpha 1 subunit of the Na+-K+-transporting ATPase, required for active transport of sodium in the kidney and other tissues, may function in blood pressure regulation; mutations may be associated with essential hypertension and diabetic neuropathy
GP:U81006_1 Human p76 mRNA, complete cds; predicted molecular weight is 76kD; contains nine potential membrane spanning domains; similar to yeast p24a precursor protein encoded by GenBank Accession Number X67316. [MASS=75776]/Transmembrane 9 superfamily member 2, an endosomal protein with membrane spanning domains, may be a channel or transporter of small molecules
SW:CPT2_HUMAN P23786 homo sapiens (human). carnitine o-palmitoyltransferase ii, mitochondrial precursor (ec 2.3.1.21) (cpt ii). 5/2000 [MASS=73777]/Carnitine palmitoyltransferase II, a mitochondrial long-chain fatty acid oxidation enzyme; mutations are associated with a lipid metabolism disorder that includes recurrent myopathy with progressive rhabdomyolysis, muscle weakness and myoglobinuria
SW:ATCS_HUMAN P23634 homo sapiens (human). calcium-transporting atpase plasma membrane, isoform 4 (ec 3.6.1.38) (calcium pump) (pmca4). 5/2000 [MASS=133931]/ATPase Ca++ transporting plasma membrane 4, a calcium pump that regulates levels of cytosolic free Ca2+, binds calmodulin
SW:HBP_HUMAN Q00341 homo sapiens (human). high density lipoprotein binding protein (hdl-binding protein). 12/1998 [MASS=141440]/High density lipoprotein binding protein, binds and inhibits cleavage of the 3' UTR of vitellogenin mRNA, binds and promotes nuclear export of tRNA, binds high density lipoproteins and may have roles in cholesterol metabolism and atherogenesis
SW:ATHL_HUMAN P54707 homo sapiens (human). potassium-transporting atpase alpha-like chain (ec 3.6.1.36) (proton pump) (non-gastric h+/k+ atpase alpha subunit). 5/2000 [MASS=115511]/Alpha subunit of non-gastric H,K ATPase, the catalytic subunit of the non-gastric nongastric hydrogen:potassium-exchanging ATPase, likely mediates Na+,K+ exchange, activity is pH dependent and sensitive to inhibition by ouabain and vanadate
SW:NPC1_HUMAN O15118 homo sapiens (human). niemann-pick c1 protein precursor. 5/2000 [MASS=142149]/Niemann-Pick disease type C1, a lysosomal sterol transporter involved in cholesterol metabolism; mutation of the corresponding gene causes Niemann-Pick type C1 disease and mutation of mouse Npc1 causes a disease like Niemann-Pick type C1 disease
SW:COXS_HUMAN Q14061 homo sapiens (human). cytochrome c oxidase copper chaperone. 7/1999 [MASS=6784]/Cytochrome c oxidase assembly protein 17, a putative copper binding protein, may function to transport copper to mitochondria for assembly into cytochrome oxidase complex; mutation does not appear to be a common cause of COX deficiency disorders
SW:VAB1_HUMAN P15313 homo sapiens (human). vacuolar atp synthase subunit b, kidney isoform (ec 3.6.1.34) (endomembrane proton pump 58 kda subunit) (v-atpase b subunit). 5/2000 [MASS=56980]/Vacuolar H+-ATPase proton pump (B1 kidney isoform of the B subunit), mediates distal nephron acid secretion and the interaction between V-ATPase and F-actin; variants are associated with renal tubular acidosis accompanied with sensorineural deafness
SW:TRSR_HUMAN P02786 homo sapiens (human). transferrin receptor protein (tr) (antigen cd71) (t9) (p90). 7/1999 [MASS=84901]/Transferrin receptor, binds and internalizes the iron carrier transferrin, involved in iron homeostasis, important for neurologic development and likely erythropoiesis, expression is deregulated in anemia, hemochromatosis, and Friedreich's ataxia
SW:ATC2_HUMAN P16615 h sarcoplasmic/endoplasmic reticulum calcium atpase isoform 2 (ec 3.6.1.38) (calcium pump 2) (serca2) (sr ca(2+)-atpase 2) (calcium- transporting atpase sarcoplasmic reticulum type, [MASS=114757]/Sarcoplasmic reticulum Ca2+-ATPase 2 (slow twitch muscle, cardiac, and nonmuscle form), pumps calcium from the cytoplasm to the ER; reduced activity in the heart is implicated in dilated cardiomyopathy and gene mutations are associated with Darier disease
SW:SAP_HUMAN P07602 h proactivator polypeptide precursor [contains: saposin a (protein a); saposin b (sphingolipid activator protein 1) (sap-1) (dispersin) (sulfatide/gm1 activator); saposin c (co-beta- [MASS=58113]/Prosaposin, precursor of saposins A, B, C, and D which transport gangliosides and activate sphingolipid hydrolysis, stimulates neurite growth and inhibits apoptosis; variants are associated with metachromatic leukodystrophy and Gaucher disease
GP:AF149418_1 Oryctolagus cuniculus duodenal sodium bicarbonate cotransport protein NBC1 mRNA, complete cds; transmembrane protein; belongs to the functional superfamily of HCO3- transporters; similar to human and mouse pancreatic NBC1 proteins. [MASS=121427]/Solute carrier family 4 (sodium bicarbonate cotransporter) member 4, acts in cellular pH regulation and maintenance of cornea and lens transparency and intraocular pressure; mutations cause proximal renal tubular acidosis with ocular abnormalities
SW:TXTP_HUMAN P53007 homo sapiens (human). tricarboxylate transport protein precursor (citrate transport protein) (ctp) (tricarboxylate carrier protein). 5/2000 [MASS=34085]/Solute carrier family 25 (mitochondrial carrier citrate transporter) member 1, a putative mitochondrial membrane citrate transporter; gene is localized to a region deleted in DiGeorge:velocardiofacial syndromes
SW:ATNB_HUMAN P05026 homo sapiens (human). sodium/potassium-transporting atpase beta-1 chain (sodium/potassium-dependent atpase beta-1 subunit). 7/1999 [MASS=35061]/Beta 1 subunit of Na+:K+-ATPase, a putative sodium:potassium-exchanging ATPase

SW:VAB2_HUMAN P21281 homo sapiens (human). vacuolar atp synthase subunit b, brain isoform (ec 3.6.1.34) (endomembrane proton pump 58 kda subunit) (v-atpase b subunit) (ho57). 7/1999 [MASS=56517]/Vacuolar-type H(+)-ATPase (beta isoform 2), 56 kDa subunit of the ATPase catalytic domain which may assist in transepithelial H+ transport in the kidney, may effect vacuolar acidification, and may play a role in the polarization of osteoclasts
SW:NLTP_HUMAN P22307 homo sapiens (human). nonspecific lipid-transfer protein precursor (nsl-tp) (sterol carrier protein 2) (scp-2) (sterol carrier protein x) (scp-x) (scpx). 5/2000 [MASS=58994]/Sterol carrier protein 2, catalyzes the exchange of phospholipids between membranes, stimulates cholesterol metabolism and may regulate steroidogenesis; alternative form, SCPX, is a 3 oxoacyl CoA thiolase
SW:ATCP_HUMAN P20020 homo sapiens (human). calcium-transporting atpase plasma membrane, isoform 1b (ec 3.6.1.38) (calcium pump) (pmca1b). 5/2000 [MASS=134685]/ATPase Ca++ transporting plasma membrane 1, a member of the P type primary ion transport ATPase family, a housekeeping gene, alternatively spliced isoforms show differential tissue expression; candidate gene for hereditary hearing impairment
SW:ADT1_HUMAN P12235 homo sapiens (human). adp,atp carrier protein, heart/skeletal muscle isoform t1 (adp/atp translocase 1) (adenine nucleotide translocator 1) (ant 1). 10/1994 [MASS=33064]/Solute carrier family 25 member 4, an ADP:ATP transporter that may act in mitochondrial genome stability, altered transport capacity due to autoimmune response leads to myocarditis and cardiomyopathy; mutation causes progressive external ophthalmoplegia
SW:ECHB_HUMAN P55084 homo sapiens (human). trifunctonal enzyme beta subunit, mitochondrial precursor (tp-beta) [includes: 3-ketoacyl-coa thiolase (ec 2.3.1.16) (acetyl-coa acyltransferase) (beta-ketothi [MASS=51294]/3-hydroxyacyl-CoA dehydrogenase, 3-ketoacyl-CoA thiolase trifunctional protein beta subunit, involved in fatty acid beta-oxidation; variants are associated with trifunctional protein deficiency, sudden infant death syndrome and liver failure
SW:ECHA_HUMAN P40939 homo sapiens (human). mitochondrial trifunctional enzyme alpha subunit precursor (tp-alpha) [includes: long-chain enoyl-coa hydratase (ec 4.2.1.17); long chain 3-hydroxyacyl-coa deh [MASS=82960]/Mitochondrial long-chain enoyl-CoA hydratase/3-hydroxyacyl-CoA dehydrogenase/3-ketoacyl-CoA thiolase alpha subunit, involved in fatty acid beta-oxidation, mutations are associated with trifuctional protein deficiency and Reye-like syndrome
SW:POR2_HUMAN P45880 homo sapiens (human). voltage-dependent anion-selective channel protein 2 (hvdac2) (outer mitochondrial membrane protein porin 2). 5/2000 [MASS=38093]/Voltage-dependent anion channel 2, a voltage-gated pore of the outer mitochondrial membrane, may bind hexokinase
PIR2:B53737 phosphate carrier protein precursor, mitochondrial, splice form B - human [MASS=39959]/Mitochondrial phosphate carrier (solute carrier family 25 member 3), catalyzes the transport of phosphate from the cytoplasm to the mitochondrial matrix for ATP synthesis during oxidative phosphorylation
SW:ATPG_HUMAN P36542 homo sapiens (human). atp synthase gamma chain, mitochondrial precursor (ec 3.6.1.34). 5/2000 [MASS=32996]/ATP synthase H+ transporting mitochondrial F1 complex gamma 1, putative component of multisubunit enzyme that synthesizes ATP during oxidative phosphorylation, exists in tissue-specific alternative forms that are spliced in response to acidic conditions
GP:AC002540_1 Human BAC clone GS1-25M2 from 7q21-q22, complete sequence; [MASS=25323]//Solute carrier family 25 member 13 (citrin), a calcium-dependent mitochondrial solute transporter that may play a role in urea cycle function; mutation of the corresponding gene result in neonatal:infantile and adult onset forms of type II citrullinemia
SW:POR1_HUMAN P21796 homo sapiens (human). voltage-dependent anion-selective channel protein 1 (hvdac1) (outer mitochondrial membrane protein porin 1) (plasmalemmal porin) (porin 31hl) (porin 31hm). 5/2 [MASS=30641]/Voltage-dependent anion channel 1, mitochondrial outer membrane anion channel that mediates apoptotic signals from Bcl-2 (BCL2) and related proteins; deficiency of protein in skeletal muscle causes mitochondrial encephalomyopathy
SW:ATPA_HUMAN P25705 homo sapiens (human). atp synthase alpha chain, mitochondrial precursor (ec 3.6.1.34). 12/1998 [MASS=59751]/ATP synthase H+ transporting mitochondrial F1 complex alpha subunit isoform 1 cardiac muscle, part of the synthase enzymatic complex that catalyzes the synthesis of ATP during oxidative phosphorylation
SWN:POR3_HUMAN Q9y277 homo sapiens (human). voltage-dependent anion-selective channel protein 3 (vdac-3) (hvdac3) (outer mitochondrial membrane protein porin 3). 8/2001 [MASS=30659]/Voltage-dependent anion channel 3, may function as a voltage-gated pore of the outer mitochondrial membrane that binds hexokinase and glycerol kinase and transports adenine nucleotides
SW:ADT2_HUMAN P05141 homo sapiens (human). adp,atp carrier protein, fibroblast isoform (adp/atp translocase 2) (adenine nucleotide translocator 2) (ant 2). 7/1999 [MASS=32895]/Solute carrier family 25 member 5 (adenine nucleotide translocator 2), may mediate the exchange of ADP and ATP between the cytosol and mitochondria, expression is altered in dilated cardiomyopathy
SW:ADT3_HUMAN P12236 homo sapiens (human). adp,atp carrier protein, liver isoform t2 (adp/atp translocase 3) (adenine nucleotide translocator 3) (ant 3). 11/1995 [MASS=32866]/Solute carrier family 25 member 6 (adenine nucleotide translocator), member of the ADP/ATP translocase family
SW:ATCK_HUMAN P98194 homo sapiens (human). calcium-transporting atpase 2c1 (ec 3.6.1.38) (atp-dependent ca2+ pump pmr1). 5/2000 [MASS=100606]/ATPase (Ca2+ transporting) type 2c member I, a a Ca2+-transporting P-type ATPase involved in Ca2+ homeostasis that may also may play a role in epidermal differentiation; mutations in the gene cause Hailey-Hailey disease, a blistering skin disease
SW:SORC_HUMAN P30626 homo sapiens (human). sorcin (22 kda protein) (cp-22) (v19). 11/1997 [MASS=21676]/Sorcin, an EF-hand calcium-binding protein, may be involved in multidrug resistance, a potential modulator of intracellular calcium levels through interaction with the ryanodine receptor

SW:B3A2_HUMAN P04920 homo sapiens (human). anion exchange protein 2 (non-erythroid band 3-like protein) (bnd3l). 10/1996 [MASS=136814]/Solute carrier family 4 member 2 (anion exchanger 2), a chloride and bicarbonate exchanger that may play a role in pH regulation, binds ankyrin and links the basolateral membrane to the cytoskeleton
SW:AT2A_HUMAN O75110 homo sapiens (human). potential phospholipid-transporting atpase iia (ec 3.6.1.-) (fragment). 5/2000 [MASS=116933]/Member of the haloacid dehalogenase or epoxide hydrolase family, has moderate similarity to S. cerevisiae Neo1p, which is an ATPase whose overproduction confers neomycin resistance
SW:SNAG_HUMAN Q99747 homo sapiens (human). gamma-soluble nsf attachment protein (snap-gamma). 7/1999 [MASS=34746]/N-ethylmaleimide-sensitive factor (NSF) attachment protein gamma, member of a family of proteins involved in membrane fusion during exocytosis, may have roles in platelet exocytosis and in the attachment of mitochondria to the cytoskeleton
sec24-related protein D (human)/Protein with high similarity to SEC24 (S. cerevisiae) related gene family member C (human SEC24C), which is a putative COPII vesicle coat protein that forms a complex with Sec23Ap (human SEC23) and functions in ER-Golgi transport
SW:RB3B_HUMAN P20337 homo sapiens (human). ras-related protein rab-3b. 10/1994 [MASS=24760]/Ras-related GTP-binding protein 3b, a GTP-binding protein and GTPase that is involved in exocytosis
SW:ADG_HUMAN O43747 homo sapiens (human). gamma-adaptin (golgi adaptor ha1/ap1 adaptin gamma subunit) (clathrin assembly protein complex 1 gamma large chain). 7/1999 [MASS=91592]/Adaptor-related protein complex 1 gamma 1 subunit, promotes the formation of clathrin coated vesicles and pits for intracellular transport; deletion of the corresponding gene occurs in Wilm's tumor, prostate adenocarcinomas, and hepatocellular carcinomas
SW:LDLR_HUMAN P01130 homo sapiens (human). low-density lipoprotein receptor precursor (ldl receptor). 5/2000 [MASS=95376]/Low density lipoprotein receptor, mediates uptake of low density lipoproteins, involved in lipid metabolism; gene variations are associated with familial hypercholesterolemia, hypertension, atherosclerosis, and coronary artery disease
SW:RB4A_HUMAN P20338 homo sapiens (human). ras-related protein rab-4a. 10/1996 [MASS=23902]/GTP-binding protein, a member of the rab family of proteins, involved in early endosome trafficking and receptor recycling
PIR2:A53016 myosin heavy chain VA - human (fragment) [MASS=96052]/Class V myosin (Myoxin), a member of the myosin family of proteins, a motor protein that may be involved in vesicle transport and epidermal differentiation; mutation of the corresponding genge is associated with Griscelli syndrome
SW:EGFR_HUMAN P00533 homo sapiens (human). epidermal growth factor receptor precursor (ec 2.7.1.112). 12/1998 [MASS=134277]/Epidermal growth factor receptor, a receptor protein tyrosine kinase that binds epidermal growth factor (EGF) and transforming growth factor alpha (TGFA), involved in cell proliferation and differentiation, implicated in tumor invasion and metastasis
SW:STB3_HUMAN O00186 homo sapiens (human). syntaxin binding protein 3 (unc-18 homolog 3) (unc-18c) (unc-18-3). 5/2000 [MASS=67574]/Syntaxin binding protein 3, binds syntaxin 4 (STX4), predicted to be involved in vesicle transport and docking and in neurotransmitter release
SW:CLH2_HUMAN P53675 homo sapiens (human). clathrin heavy chain 2 (clh-22). 5/2000 [MASS=187030]/Clathrin heavy polypeptide-like 1, may play roles in vesicle budding and in cytoskeleton-dependent trans-Golgi network membrane sorting; gene is among those deleted in velocardiofacial and DiGeorge syndromes, and is a fusion partner with ALK in lymphoma
SW:S23B_HUMAN Q15437 homo sapiens (human). protein transport protein sec23 homolog isoform b. 11/1997 [MASS=86470]/Member of the SEC23 family of vesicle trafficking proteins
GP:AF038535_1 Homo sapiens synaptotagmin VII mRNA, partial cds; similar to rat synaptotagmin VII. [MASS=47195]/Very strongly similar to synaptotagmin 7 (Rn.10193); may be a phospholipid-binding calcium sensor protein
SW:KINH_HUMAN P33176 homo sapiens (human). kinesin heavy chain (ubiquitous kinesin heavy chain) (ukhc). 7/1999 [MASS=109685]/Kinesin family member 5B (kinesin heavy chain), a microtubule-associated motor protein that may function in intracellular organelle transport and may play a role in susceptibility and resistance
SW:RB35_HUMAN Q15286 homo sapiens (human). ras-related protein rab-35 (rab-1c) (gtp-binding protein ray). 5/2000 [MASS=23025]/Ras-related GTP-binding protein 35, member of the Rab family of GTP-binding proteins, may function in vesicular transport
SW:COPG_HUMAN Q9y678 homo sapiens (human). coatomer gamma subunit (gamma-coat protein) (gamma-cop). 10/2001 [MASS=97718]/Coatomer protein complex subunit gamma 1, a subunit of the coat of COP I-coated vesicles, predicted to be involved in retrograde Golgi to endoplasmic reticulum transport, contains two clathrin-associated adaptin N-terminal domains
SW:SN23_HUMAN O00161 homo sapiens (human). synaptosomal associated protein 23 (snap-23) (vesicle-membrane fusion protein snap-23). 5/2000 [MASS=23354]/Synaptosomal-associated protein 23, a member of the SNARE family of proteins that regulate membrane fusion during exocytosis, a t-SNARE that binds to syntaxins and is involved in docking and fusion of transport vesicles during exocytosis
SW:RB3D_HUMAN O95716 homo sapiens (human). ras-related protein rab-3d. 5/2000 [MASS=24267]/Ras-related GTP-binding protein 3d, putative small monomeric GTP-binding protein and GTPase that plays a role in regulated secretion

SW:RAB2_HUMAN P08886 homo sapiens (human), and canis familiaris (dog). ras-related protein rab-2. 10/1994 [MASS=23546]/Ras-related GTP-binding protein 2, a GTPase which plays a role in vesicle transport from the ER to the Golgi complex; overexpression in nonmalignant peripheral blood lymphocytes is associated with Searzy syndrome
SW:GBAK_HUMAN P08754 homo sapiens (human). guanine nucleotide-binding protein g(k), alpha subunit (g(i) alpha-3). 11/1997 [MASS=40401]/G protein alpha i3 subunit, a component of pertussis toxin sensitive heterotrimeric G protein complexes, transduces signals from G protein-coupled receptors to intracellular effectors, inhibits forskolin-stimulated cAMP production
GP:AF091079_1 Homo sapiens clone 560 SNARE protein Ykt6 mRNA, partial cds. [MASS=21607]/Homolog of S. cerevisiae Ykt6p, which is a v-SNARE required for ER to Golgi transport, likely involved in trafficking proteins from the ER to the Golgi
SW:CLH1_HUMAN Q00610 homo sapiens (human). clathrin heavy chain 1 (clh-17) (kiaa0034). 5/2000 [MASS=191615]/Clathrin heavy polypetide c, involved in endocytosis, may bind to endocytic proteins through an LLDLD consensus sequence, interacts with huntingtin interacting protein 1 (HIP1), amino terminus folds into a seven-bladed beta-propeller
GP:AJ131245_1 Homo sapiens mRNA for Sec24 protein (Sec24B isoform). [MASS=137789]/SEC24 related gene family member B, a member of the SEC24 family of vesicle trafficking proteins, interacts with SEC23A, predicted to be localized to COPII-coated vesicles and to be involved in the export of proteins from the endoplasmic reticulum
SW:DYN2_HUMAN P50570 homo sapiens (human). dynamin 2. 10/1996 [MASS=98018]/Dynamin II, member of a family of 100-kD guanosine triphosphatases, regulates budding of endocytic vesicles at the plasma membrane and may function in the formation of transport vesicles at the trans-Golgi
GP:D31886_1 Human mRNA for KIAA0066 gene, partial cds. [MASS=110524]/RAB3 GTPase-activating protein, GTPase-activating protein specific for lipid-modified members of the Rab3 subfamily, may influence calcium-dependent exocytosis of synaptic vesicles
SW:CALX_HUMAN P27824 homo sapiens (human). calnexin precursor (major histocompatibility complex class i antigen-binding protein p88) (p90) (ip90). 11/1995 [MASS=67568]/Calnexin, a calcium and lectin binding protein that functions as a chaperone in the endoplasmic reticulum, involved in protein folding and secretion, mediates retention of misfolded proteins in the endoplasmic reticulum
SW:ER53_HUMAN P49257 homo sapiens (human). ergic-53 protein precursor (er-golgi intermediate compartment 53 kda protein) (gp58) (mr60) (lectin, mannose-binding 1). 7/1998 [MASS=57563]/Mannose-binding lectin 1, involved in the traffic of glycoproteins between endoplasmic reticulum and the Golgi apparatus; mutations of the corresponding gene is associated with combined factor V and VIII coagulation deficiency
GP:U45976_1 Human clathrin assembly protein lymphoid myeloid leukemia (CALM) mRNA, complete cds. [MASS=70695]/Phosphatidylinositol binding clathrin assembly protein, binds to clathrin heavy chain (CLTC) and plays a role in coated pit internalization; rearrangements in the corresponding gene are associated with acute lymphoblastic and acute myeloid leukemias
SW:ADB_HUMAN P21851 homo sapiens (human), rattus norvegicus (rat), and bos taurus (bovine). beta-adaptin (plasma membrane adaptor ha2/ap2 adaptin beta subunit) (clathrin assembly protein complex 2 beta [MASS=104553]/Adaptor-related protein complex 2 beta 1 subunit, a large subunit of the AP2 adaptor complex, involved in clathrin coat assembly at the plasma membrane; may bind to the transmembrane envelope protein of HIV-1 and HTLV retroviruses
SW:MPRI_HUMAN P11717 homo sapiens (human). cation-independent mannose-6-phosphate receptor precursor (ci man-6-p receptor) (ci-mpr) (insulin-like growth factor ii receptor) (300 kda mannose 6-phosphate [MASS=274309]/Insulin-like growth factor II receptor, functions in transport of mannose 6-phosphate-containing lysosomal enzymes and IGF-II maturation and clearance, mediates granzyme B-induced apoptosis, putative tumor suppressor
GP:AF044670_1 Homo sapiens 33 kDa Vamp-associated protein (VAP33) mRNA, complete cds; VAP-33. [MASS=27318]/Vesicle-associated membrane protein (VAMP)-associated protein A, binds v-SNAREs, t-SNAREs, VAPB, and VAMP, predicted to be involved in vesicle transport and fusion
GP:AF128536_1 Homo sapiens cytoplasmic phosphoprotein PACSIN2 mRNA, complete cds; related to PACSIN1; contains CDC15 N-terminal domain, 3 EH domain-binding NPF motifs, and a C-terminal SH3 domain. [MASS=55905]/Protein kinase C and casein kinase substrate in neurons 2, member of the PACSIN family of cytoplasmic adapter proteins, may function to organize the actin cytoskeleton and regulate vesicular traffic
GP:AF004563_1 Homo sapiens hUNC18b alternatively-spliced mRNA, complete cds; alternatively-spliced; similar to rat n-Sec1. [MASS=68736]/Syntaxin-binding protein 1, binds syntaxins, may be involved in synaptic vesicle exocytosis
SW:G25B_HUMAN P21181 homo sapiens (human), mus musculus (mouse), and bos taurus (bovine). g25k gtp-binding protein, brain isoform (gp) (cdc42 homolog). 12/1998 [MASS=21311]/Cell division cycle 42 (GTP binding protein 25kD), Rho GTPase involved in actin cytoskeleton organization, cell migration, cell cycle progression and apoptosis, downregulated in fibroblasts and macrophages from patients with Tangiers disease
SW:143T_HUMAN P27348 homo sapiens (human). 14-3-3 protein tau (14-3-3 protein theta) (14-3-3 protein t-cell) (hs1 protein). 11/1997 [MASS=27764]/14-3-3 theta (14-3-3 tau in T-cells), may modulate T-cell signaling and cytokine expression through interaction with and inhibition of protein kinase C and phosphatidylinositol 3-kinase, may promote cell survival during amyotrophic lateral sclerosis (ALS)

SW:ACTZ_HUMAN P42024 homo sapiens (human), mus musculus (mouse), and canis familiaris (dog). alpha-centractin (centractin) (centrosome-associated actin homolog) (actin-rpv) (arp1). 7/1999 [MASS=42614]/Actin-related protein 1, a component of the dynactin complex involved in transport along microtubules, associates with centrophilin NUMA1 at nuclear envelope breakdown, expression is significantly reduced in Down syndrome fetal brain
SWN:STX8_HUMAN Q9unk0 homo sapiens (human). syntaxin 8. 8/2001 [MASS=26907]/Syntaxin 8, member of the soluble NSF attachment protein receptor (SNARE) family, plays a role in endosome trafficking, may mediate vesicle docking and fusion, may regulate CFTR -mediated chloride currents
GP:AC005545_2 Homo sapiens chromosome 19, cosmid R26634, complete sequence; vesicle coat component, similar to alpha and gamma adaptins. [MASS=121170]/Adaptor-related protein complex 3 delta 1 subunit, a component of the AP-3 complex, involved in intracellular vesicle transport
SW:S23A_HUMAN Q15436 homo sapiens (human). protein transport protein sec23 homolog isoform a. 11/1997 [MASS=86147]/Sec23 homolog A, a putative intracellular transporter that plays a role in protein trafficking, interacts with SEC24B and SEC24C
SW:ADB1_HUMAN Q10567 homo sapiens (human). beta-adaptin 1 (plasma membrane adaptor ha2/ap2 adaptin beta subunit) (clathrin assembly protein complex 2 beta large chain) (ap105a). 7/1999 [MASS=104607]/Adaptor-related protein complex 1 beta 1, likely participates in clathrin-coated vesicle endocytosis and intracellular receptor transport; loss is associated with meningioma tumors
SW:TERA_HUMAN P55072 homo sapiens (human). transitional endoplasmic reticulum atpase (ter atpase) (15s mg(2+)-atpase p97 subunit) (valosin containing protein) (vcp) [contains: valosin]. 7/1999 [MASS=89322]/Valosin-containing protein, a putative clathrin-binding ATPase involved in cell cycle control, ubiquitin-dependent protein degradation, and JAK-STAT signaling, may be involved in DNA repair via BRCA1, may be involved in receptor-mediated endocytosis
GP:AC006942_1 Homo sapiens chromosome 19, cosmid R31181, complete sequence CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-A LARGE CHAIN); Non- consensussplice junction found at position 18996. [MASS=90046]/Adaptor-related protein complex 2 alpha 1 subunit, component of the clathrin adaptor complex, involved in vesicle transport
GP:AF020797_1 Homo sapiens AP-mu chain family member mu1B (HSMU1B) mRNA, complete cds. [MASS=48108]/Adaptor-related protein complex 1 mu 2 subunit, involved in protein sorting
SW:MPRD_HUMAN P20645 homo sapiens (human). cation-dependent mannose-6-phosphate receptor precursor (cd man-6-p receptor) (cd-mpr) (46 kda mannose 6-phosphate receptor) (mpr 46). 5/2000 [MASS=30993]/Cation-dependent mannose-6-phosphate receptor, involved in intracellular sorting and transport of acid hydrolases, transports lysosomal enzymes
GP:AC006378_1 Homo sapiens BAC clone RP11-455I9 from 7q21.2-q22, complete sequence; match to AAB62941.1 (PID:2253426); H_NH0455I09.1. [MASS=13289]/S. cerevisiae Bet1 homolog, may be involved in ER to Golgi transport
PIR2:I53171 pantophysin - human [MASS=28565]/Synaptophysin-like protein (pantophysin), a protein that has similarity to the synaptic vesicle protein synaptophysin (SYP), may play a role in vesicle transport
GP:AF260566_1 Homo sapiens hepatocyte growth factor-regulated tyrosine kinase substrate HRS isoform 2 (HRS) mRNA, complete cds. [MASS=76362]/Hepatocyte growth factor regulated tyrosine kinase substrate, zinc-finger protein with ATPase activity, tyrosine phosphorylated upon growth factor stimulation, involved in endosome trafficking and mediates FOS transcription via cytokine signaling
SW:COPB_HUMAN P53618 homo sapiens (human). coatomer beta subunit (beta-coat protein) (beta-cop) (fragment). 11/1997 [MASS=33444]/Coatomer protein beta, component of non-clathrin-coated vesicles essential for membrane trafficking, binds to HIV-1 Nef protein
SWN:SNX3_HUMAN O60493 homo sapiens (human). sorting nexin 3 (sdp3 protein). 8/2001 [MASS=18762]/Sorting nexin 3, involved in intracellular protein trafficking
SW:ARF6_HUMAN P26438 homo sapiens (human), mus musculus (mouse), and rattus norvegicus (rat). adp-ribosylation factor 6. 12/1998 [MASS=19951]/ADP-ribosylation factor 6, GTP-binding protein that stimulates cholera toxin activity and is involved in endocytosis, exocytosis, membrane trafficking, and possibly regulation of glucose transport
GP:AF151858_1 Homo sapiens CGI-100 protein mRNA, complete cds. [MASS=26005]/Protein with high similarity to T1-ST2 receptor binding protein (human IL1RL1LG), which binds to the T1/ST2 receptor (human IL1RL1), member of the emp24 family, which are involved in protein transport from endoplasmic reticulum to Golgi
GP:AF032922_1 Homo sapiens syntaxin 4 binding protein UNC-18c (UNC-18c) mRNA, complete cds. [MASS=67764]/Syntaxin binding protein 3, binds syntaxin 4 (STX4), predicted to be involved in vesicle transport and docking and in neurotransmitter release
SW:STB2_HUMAN Q15833 homo sapiens (human). syntaxin binding protein 2 (unc-18 homolog 2) (unc-18b). 5/2000 [MASS=66439]/Syntaxin-binding protein 2, a member of the Sec1 family of proteins involved in synaptic transmission and secretion, may be involved in intracellular vesicular transport
SW:AP50_HUMAN P20172 homo sapiens clathrin coat assembly protein ap50 (clathrin coat associated protein ap50) (plasma membrane adaptor ap-2 50 kda protein) (ha2 50 kda subunit) (clathrin assembly protei [MASS=49655]/Medium chain subunit of the clathrin associated protein complex AP2, involved in vesicle transport, endocytosis, and required for V-ATPase complex activity
SW:NSF_HUMAN P46459 homo sapiens (human). vesicular-fusion protein nsf (n-ethylmaleimide-sensitive fusion protein) (nem-sensitive fusion protein). 12/1998 [MASS=82654]/N-ethylmaleimide-sensitive factor, an ATPase involved in membrane fusion during exocytosis

no_description_avail/Coatomer protein complex subunit gamma 2, putative intracellular transporter that may be involved in non-selective vesicle transport
SW:COPP_HUMAN P35606 homo sapiens (human). coatomer beta' subunit (beta'-coat protein) (beta'-cop) (p102). 12/1998 [MASS=102356]/Coatomer protein (COP) complex subunit beta 2 (COP beta prime), part of a Golgi coatomer complex that comprises the coat of non-clathrin coated vesicles, likely to play a role in exocytosis
SW:RAB7_HUMAN P51149 homo sapiens (human). ras-related protein rab-7. 7/1998 [MASS=23490]/Ras-related GTP-binding protein 7, a member of the rab family of proteins that is involved in vesicle transport, membrane fusion, and vacuole formation; implicated in Chediak Higashi Syndrome
GP:AB019435_1 Homo sapiens mRNA for putative phospholipase, complete cds; putative. [MASS=111076]/Sec23-interacting protein p125, a proline rich protein containing a phospholipase motif, binds to the COPII vesicle coat protein Sec23p (mouse Sec23a), may play a role in protein transport between the endoplasmic reticulum and Golgi
GP:U85946_1 Homo sapiens brain secretory protein hSec10p (HSEC10) mRNA, complete cds; similar to S. cerevisiae Sec10p. [MASS=81853]/SEC10 (S. cerevisiae)-like 1, a component of the exocyst complex, involved in the synthesis and delivery of secretory proteins in epithelial cells, involved in the development of epithelial cysts and tubules
Homo sapiens, vacuolar protein sorting 35/Maternal-embryonic 3, may be a component of the sorting machinery required for vesicle to Golgi retrieval
PIR2:S33377 P63 protein - human [MASS=65793]/Cytoskeleton-associated protein 4, type II membrane protein of the endoplasmic reticulum, binds to microtubules and links them to the endoplasmic reticulum, promotes tubulin polymerization and endoplasmic reticulum reorganization
SW:TM21_HUMAN P49755 homo sapiens (human). transmembrane protein tmp21 precursor (s31iii125) (s31i125). 12/1998 [MASS=24976]/Transmembrane protein Mr 21,000, involved in biosynthetic protein transport from the ER to Golgi, regulates Rac-GTP levels through interaction with beta 2-chimaerin (CHN2); corresponding gene is located in the AD3 region mutated in Alzheimer's Disease
SWN:CNE3_HUMAN O75131 homo sapiens (human). copine iii. 8/2001 [MASS=60131]/Copine III, a member of the copine family of phospholipid binding proteins, contains C2 and integrin A domains, may play a role in membrane trafficking, displays protein kinase activity, however, it does not contain a traditional kinase catalytic domain
SW:RB13_HUMAN P51153 homo sapiens (human). ras-related protein rab-13. 12/1998 [MASS=22774]/Ras-related GTP-binding protein 13, a putative RAB small monomeric GTPase that is likely to play a role in intracellular protein trafficking and cell adhesion
SW:GDIB_HUMAN P50395 homo sapiens (human). rab gdp dissociation inhibitor beta (rab gdi beta) (gdi-2). 7/1998 [MASS=50664]/Guanosine diphosphate dissociation inhibitor 2, one of a family proteins that regulate GDP/GTP cycle and are involved in intracellular vesicular trafficking, associates with RAB1B, RAB5 and RAB6 and may play a role in their intracellular targeting
PIR2:I53799 CG1 protein - human [MASS=149611]/human kinectin/Kinectin, functions as a receptor for the microtubule-motor protein kinesin and plays a role in intracellular movement of organelles; mutations in the corresponding gene are associated with childhood papillary thyroid carcinoma
PIR2:A55575 ankyrin 3, long splice form - human [MASS=480403]/Ankyrin 3 (ankyrin G), may link integral membrane proteins to the cytoskeleton, may play a role in localizing sodium channels to the axonal initial segment and nodes of Ranvier, may play a role in vesicle transport
SW:COPA_HUMAN P53621 homo sapiens (human). coatomer alpha subunit (alpha-coat protein) (alpha-cop) (hepcop) (hep-cop) [contains: xenin (xenopsin-related peptide); proxenin]. 5/2000 [MASS=138332]/ Coatomer protein complex subunit alpha, involved in transport between the endoplasmic reticulum and the Golgi apparatus, binds to RNA, N-terminal 25 amino acids may be cleaved to release the peptide xenin, which stimulates pancreatic secretion
SW:PRS7_HUMAN P35998 homo sapiens (human). 26s protease regulatory subunit 7 (mss1 protein). 11/1997 [MASS=48634]/26S protease regulatory subunit 7, ATPase subunit of the 26S proteasome, interacts with Tat protein, may be involved in cell cycle control and has a role in the activation of human immunodeficiency virus-1 (HIV-1) gene transcription
SW:VE1_HPV14 P36721 human papillomavirus type 14. replication protein e1. 7/1998 [MASS=69302]/ATP-DEPENDENT DNA HELICASE REQUIRED FOR INITIATION OF VIRAL DNA REPLICATION. IT FORMS A COMPLEX WITH THE VIRAL E2 PROTEIN. THE E1-E2 COMPLEX BINDS TO THE REPLICATION ORIGIN WHICH CONTAINS BINDING SITES FOR BOTH PROTEINS
SW:EBI2_HUMAN P32249 homo sapiens (human). ebv-induced g protein-coupled receptor 2 (ebi2). 7/1998 [MASS=41224]/Epstein-Barr virus induced gene 2, a lymphocyte specific G protein-coupled receptor that may mediate the effects of Epstein-Barr virus on B lymphocytes
SW:MCP_HUMAN P15529 homo sapiens (human). membrane cofactor protein precursor (cd46 antigen) (trophoblast leucocyte common antigen) (tlx). 5/2000 [MASS=42248]/Membrane cofactor protein (CD46), a cofactor for factor I-mediated cleavage of C3B and C4B, a T-cell coactivator with signal transduction properties, and a receptor for viruses and bacteria, protects host cells against complement-mediated cytolysis

SW:TMS2_HUMAN O15393 homo sapiens (human). transmembrane protease, serine 2 (ec 3.4.21.-). 7/1998 [MASS=53847]/Transmembrane protease serine 2 (epitheliasin), a putative serine endopeptidase with transmembrane, LDLRA (LDL receptor class A) and SRCR (scavenger receptor cysteine-rich) domains; highly expressed in androgen-dependent prostate cancer
GP:AC005278_12 Arabidopsis thaliana chromosome 1 BAC F15K9 sequence, complete sequence; Contains similarity to transcription initiation factor IIE, alpha subunit gb|X63468 from Homo sapiens.. [MASS=57306]
GP:AK000542_1 Homo sapiens cDNA FLJ20535 fis, clone KAT11013; unnamed protein product. [MASS=75854] contains a Tetratricopeptide repeats Domain/Protein containing three TPR (tetratrico peptide repeat) domains, which may mediate protein-protein interactions
SW:CD9_HUMAN P21926 homo sapiens (human). cd9 antigen (p24) (leukocyte antigen mic3) (motility-related protein) (mrp-1). 7/1999 [MASS=25285]/ CD9
SW:PROS_HUMAN P07288 homo sapiens (human). prostate specific antigen precursor (ec 3.4.21.77) (psa) (gamma-seminoprotein) (semenogelase) (seminin) (p-30 antigen). 7/1999 [MASS=28741]/Kallikrein 3, (prostate specific antigen), serine protease, dissolves seminal coagulum, may play a role in regulation of cell growth, may be involved in prostate cancer invasion and metastasis, used as marker to test for and monitor prostate cancer
PIR2:T34532 hypothetical protein DKFZp434B1517.1 - human (fragment) [MASS=71502]CH, Calponin homology domain; Actin binding domains present in duplicate at the N-termini of spectrin-like proteins (including dystrophin, alpha-actinin/LIM, Zinc binding domain present in Lin-11, Isl-1, Mec-3.; Zinc-binding domain family. Some LIM domains bind protein partners via tyrosine-containing motifs. LIM domains are found in many key regulators of developmental pathways/Protein containing a calponin homology (CH) domain and LIM domains, has a region of moderate similarity to a region of beta spectrin (beta-fodrin, human SPTB), which is a component of the erythrocyte membrane-associated cytoskeleton
GP:AB037745_1 Homo sapiens mRNA for KIAA1324 protein, partial cds; Start codon is not identified.. [MASS=63365]
[FUNCTION] AFFECTS PLASMA MEMBRANE H+-ATPASE ACTIVITY. MAY ACT ON A GLUCOSE-SIGNALING PATHWAY THAT CONTROLS THE EXPRESSION OF SEVERAL GENES THAT ARE TRANSCRIPTIONALLY REGULATED BY GLUCOSE SUCH AS PMA1,HXT3 AND SNF3.[SUBCELLULAR LOCATION] INTEGRAL MEMBRANE PROTEIN (PROBABLE).[SIMILARITY] BELONGS TO GNS1/SUR4/YJL196C/C40H1.4 FAMILY./Elongation of very long chain fatty acids-like 2, protein with strong similarity to murine Ssc2, which is a member of a family of enzymes involved in tissue specific biosynthesis of very long chain fatty acids and sphingolipids
diminuto-like protein /24-dehydrocholesterol reductase, catalyzes the reduction of the delta (24) double bond of sterols in cholesterol biosynthesis, blocks apoptosis after oxidative stress and APP -induced toxicity; gene mutation is detected in desmosterolosis
GP:AK022527_1 Homo sapiens cDNA FLJ12465 fis, clone NT2RM1000802; unnamed protein product. [MASS=103079] similar to Peptidase_C2, Calpain family cysteine protease/A Novel Gene ' Niban ' Upregulated in Renal Carcinogenesis/Protein of unknown function, has high similarity to uncharacterized rat Niban
GP:AK025588_1 Homo sapiens cDNA: FLJ21935 fis, clone HEP04373; unnamed protein product. [MASS=83792]/ contains a SH3 domain/ similar to epidermal growth factor receptor pathway substrate 8 /Protein containing an Src homology 3 (SH3) domain, which bind proline-rich peptides, has moderate similarity to human EPS8, which is tyrosine-phosphorylated by epidermal growth factor receptor (human EGFR) and enhances EGF -dependent mitogenic signals
GP:AJ245222_1 Homo sapiens mRNA for immunoglobulin gamma heavy chain variable region, partial, clone 2A-3G17. [MASS=13498]
contains a repeated domain in ubiquitin activating enzyme E1 and members of the bacterial ThiF/MoeB/HesA family/Member of the UBA-THIF-type NAD-FAD binding fold family, has a region of low similarity to a region of S. pombe Uba2p, which is required for the activation of the ubiquitin-like S. pombe Ubl2p for conjugation to other enzymes
GP:AJ239387_1 Homo sapiens mRNA for immunoglobulin heavy chain variable region, ID 81; ID 81. [MASS=13150]
GP:AB020706_1 Homo sapiens mRNA for KIAA0899 protein, partial cds. [MASS=102986]/ADAPTER-RELATED PROTEIN COMPLEX 2 ALPHA 2 SUBUNIT"/Alpha-adaptin-C, a protein that interacts with the polyglutamine-containing protein called huntingtin (HD) which is associated with Huntington's disease
GP:AC011001_19 Arabidopsis thaliana chromosome I BAC F4H5 genomic sequence, complete sequence; Putative membrane protein; Similar to predicted proteins in yeast, human and Drosophila. Predicted to be a membrane protein. [MASS=130186]/similar to GASTRIN/CHOLECYSTOKININ TYPE B RECEPTOR (CCK-B RECEPTOR) (CCK-BR)
GP:AB040955_1 Homo sapiens mRNA for KIAA1522 protein, partial cds; Start codon is not identified. fh14706 cDNA clone for KIAA1522 has a 241-bp deletion at the position between 1701 and 1943 of the sequence of KIAA1522.. [MASS=107934]/Protein of unknown function, has a region of weak similarity to a region of heavy polypeptide of neurofilament (mouse Nfh), which is a cytoskeleton structural protein that may regulate axon caliber, synaptic transmission and intermediate filament assembly
PIR2:S71949 metalloproteinase 12 (EC 3.4.24.-) precursor - human [MASS=72759]/Meltrin alpha, member of the metalloproteinase-disintegrin family, metalloproteinase involved in cell adhesion and muscle cell differentiation and fusion
GP:U85992_1 Human clone IMAGE:35527 unknown protein mRNA, partial cds. [MASS=19006]/ similar to ryanodine receptor, calcium release channel

PIR2:T17320 hypothetical protein DKFZp564J0863.1 - human (fragment) [MASS=61969]/ similar to Mus musculus ARL-6 interacting protein-2 (Aip-2)/ similar to GBP, Guanylate-binding protein, N-terminal domain. Transcription of the anti-viral guanylate-binding protein (GBP) is induced by interferon-gamma during macrophage induction. This family contains GBP1 and GPB2, both GTPases capable of binding GTP, GDP and GMP.
PIR2:A49674 flightless-I homolog - human (fragment) [MASS=144620]/Flightless I homolog (Drosophila), actin binding protein of the gelsolin family, interacts with other proteins including the repressor LRRFIP1, may function in signal transduction; gene maps within Smith Magenis syndrome microdeletion critical region
SW:CRP2_HUMAN P52943 homo sapiens (human). cysteine-rich protein 2 (crp2) (esp1 protein). 11/1997 [MASS=22493]/: CONTAINS 2 LIM DOMAINS. THE LIM DOMAIN BINDS 2 ZINC IONS
PIR2:T00261 hypothetical protein KIAA0603 - human [MASS=146606]/ contains a Phosphotyrosine-binding domain, phosphotyrosine-interaction (PI) domain; PTB/PI domain structure similar to those of pleckstrin homology (PH) and IRS-1-like PTB domains. / contains a TBC, TBC domain. Identification of a TBC domain in GYP6_YEAST and GYP7_YEAST, which are GTPase activator proteins of yeast Ypt6 and Ypt7, imply that these domains are GTPase activator proteins of Rab-like small GTPases/KIAA0603 gene product, contains a TBC domain similar to that found in the deubiquitinating enzyme USP6 oncogene
SW:B2MG_HUMAN P01884 homo sapiens (human), pan troglodytes (chimpanzee), and gorilla gorilla gorilla (lowland gorilla). beta-2-microglobulin precursor. 5/2000 [MASS=13715]/Beta 2-microglobulin, component of class I major histocompatibility antigen that bind and present antigenic peptides to cytotoxic T lymphocytes (CTLs), major component of hemodialysis-associated amyloid fibrils, associated with cancer progression
SW:ANX4_HUMAN P09525 homo sapiens (human). annexin iv (lipocortin iv) (endonexin i) (chromobindin 4) (protein ii) (p32.5) (placental anticoagulant protein ii) (pap-ii) (pp4-x) (35-beta calcimedin) (carb [MASS=35752]/ membrane aggregation/Annexin IV, a calcium-dependent phospholipid-binding protein involved in regulation of transmembrane conductance and endocytosis, inhibits phospholipase A2, and has in vitro anticoagulation activity, may confer paclitaxel resistance to cancer cell lines
LYST-interacting protein LIP5;"Interactions of the Chediak-Higashi lysosomal-trafficking regulator protein with SNARE complex and signal transduction proteins"; dopamine responsive protein DRG-1/Protein containing a beige or BEACH domain and five WD domains (WD-40 repeats), has a region of moderate similarity to a region of lysosomal trafficking regulator protein (mouse Lyst), which is required for vesicular transport to and from lysosomes
contains a DEXDc, DEAD-like helicases superfamily domains/Member of the DEAD or DEAH box ATP-dependent RNA helicase family, contains two helicase conserved C-terminal domains, has low similarity to C. elegans MOG-4, which is involved in oogenesis and development/
SW:PLSL_HUMAN P13796 homo sapiens (human). l-plastin (lymphocyte cytosolic protein 1) (lcp-1) (lc64p). 11/1997 [MASS=70289]/Lymphocyte cytosolic protein 1, member of the fibrin family, binds calcium and bundles actin, binds to the Ca2+ binding protein grancalcin (GCA), binds to the HLA-DR53 molecule, which is linked to autoimmune diseases; may contribute to tumorigenesis
The human TDE gene homologue: localization to 20q13.1-13.3 and variable expression in human tumor cell lines and tissue/ membrane protein/Tumor differentially expressed 1, a putative membrane protein that is overexpressed in lung tumors and colorectal tumor cells
GP:AB029025_1 Homo sapiens mRNA for KIAA1102 protein, partial cds. [MASS=95613]/ contains a LIM domain/ EST/Protein containing a LIM domain, which may mediate protein-protein interactions
GP:AB033001_1 Homo sapiens mRNA for KIAA1175 protein, partial cds; Start codon is not identified.. [MASS=70419]/ humun homologue of cytosolic sorting protein PACS-1a /Cytosolic sorting protein 1, may control the subcellular localization of proteins between the Golgi and endosomal compartments; may play a role in the pathogenesis of HIV-1
GP:AK024639_1 Homo sapiens cDNA: FLJ20986 fis, clone CAE01156; unnamed protein product. [MASS=69591]/ contains a domain similar to a hydrolase/ PROBABLE CATION-TRANSPORTING ATPASE/Member of the haloacid dehalogenase or epoxide hydrolase family, has weak similarity to a region of sodium- and potassium-transporting ATPase alpha 4 (rat Atp1a4), which is an ATPase that is sensitive to inhibition by ouabain and vanadate
PIR2:JE0350 Anterior gradient-2 - human [MASS=19979]/hAG-2, the human homologue of the Xenopus laevis cement gland gene XAG-2, is coexpressed with estrogen receptor in breast cancer cell lines/Anterior gradient 2 (Xenopus laevis) homolog, putative protein coexpressed with estrogen receptor in some breast cancer cell lines, expression in a colon carcinoma cell line may be regulated by the peroxisome proliferator-activated receptor gamma (PPARG)
SW:ARGR_HUMAN P55145 homo sapiens (human). arginine-rich protein. 10/1996 [MASS=26906]/A gene from human chromosomal band 3p21.1 encodes a highly conserved arginine-rich protein and is mutated in renal cell carcinomas/Arginine-rich mutated in early stage tumors, may be involved in cell growth or maintenance; point mutations of the gene are seen in renal cell carcinoma, pancreatic cancer, squamous cell carcinoma and other cancers of the lung, breast, and prostate
SW:MGD2_HUMAN Q9unf1 homo sapiens (human). melanoma-associated antigen d2 (mage-d2 antigen) (breast cancer associated gene 1 protein) (bcg-1) (11b6). 10/2001 [MASS=64954]/Member of the MAGE (melanoma antigen-encoding gene) family, which are expressed in a variety of tumors, has moderate similarity to neurotrophin-receptor interacting MAGE homolog (rat Maged1), which positively regulates LNGFR -mediated apoptosis
GP:AC004839_2 [MASS=28320/B-cell antigen receptor-associated protein 29, protein with strong similarity to murine Bcap29p, a B-cell receptor-associated protein that associates preferentially with IgD and weakly with IgM]

SW:XIP_HUMAN O43504 homo sapiens (human). hepatitis b virus x interacting protein (hbx-interacting protein) (hbv x interacting protein). 5/2000 [MASS=9614]/Hepatitis B virus x-interacting protein, an antiviral response protein that interacts with hepatitis B virus protein x (HBx), inhibits hepatitis B viral replication and disrupts the viral life cycle by negatively regulating HBx transactivation activity
SW:CYSR_HUMAN P21291 homo sapiens (human). cysteine-rich protein 1 (crp1) (crp). 7/1999 [MASS=20436]/Cysteine and glycine-rich protein, a two zinc finger/LIM domain protein which interacts with alpha actinin (ACTN1); capable of homodimerization, may also be a DNA-binding protein
PIR2:T46901 hypothetical protein DKFZp761C10121.1 - human [MASS=44684]/Protein with high similarity to GTP-binding proteins
GP:AK026010_1 Homo sapiens cDNA: FLJ22357 fis, clone HRC06404; unnamed protein product. [MASS=97371]/Member of the rhomboid family of integral membrane proteins, has high similarity to uncharacterized human FLJ22341
PIR2:T08684 hypothetical protein DKFZp564L2123.1 - human (fragment) [MASS=60751]/Member of the ZIP zinc transporter family, which may be metal transporters, has moderate similarity to uncharacterized human LIV-1
SW:2AAA_HUMAN P30153 homo sapiens (human). serine/threonine protein phosphatase 2a, 65 kda regulatory subunit a, alpha isoform (pp2a, subunit a, pr65-alpha isoform) (pp2a, subunit a, r1-alpha isoform) ([MASS=65092]/Protein phosphatase 2 regulatory subunit A alpha isoform, a regulatory subunit of the PP2 enzyme complex, binds CTLA-4 (Cd152), CD28 and RelA (RELA); mutations in the gene are occasionally detected in cancer cells
SW:DYI2_HUMAN Q13409 homo sapiens (human). dynein intermediate chain 2, cytosolic (dh ic-2) (cytoplasmic dynein intermediate chain 2) (fragment). 5/2000 [MASS=39236]/Protein with strong similarity to cytoplasmic dynein intermediate polypeptide 2 (rat Dnci2), which may interact with p150Glued (rat Dctn1) subunit of dynactin
GP:D38549_1 Human mRNA for KIAA0068 gene, partial cds; ha1025 is new. [MASS=147136]/Cytoplasmic FMRP interacting protein 1, a member of the CYFIP protein family, binds F-actin and active, GTP-bound RAC1, predicted to play a role in membrane ruffling formation and may be necessary for neuronal structure development or maintenance
GP:AB002366_1 Human mRNA for KIAA0368 gene, partial cds. [MASS=159478]/Protein of unknown function, has low similarity to a region of S. cerevisiae Ecm29p, which is involved in cell wall structure or biosynthesis
SW:ZO1_HUMAN Q07157 homo sapiens (human). tight junction protein zo-1 (zona occludens 1 protein) (tight junction protein 1). 5/2000 [MASS=194723]/Tight junction protein 1, component of the blood brain barrier that may play roles in the organization and attachment of tight junction components, cellular differentiation, placental development, breast cancer progression, and pancreatic cancer
PIR2:T17218 hypothetical protein DKFZp434P1750.1 - human [MASS=26577]/Protein of unknown function, has moderate similarity to a region of EBP50-PDZ interactor of 64 kD (human EPI64), which is a putative RAB GTPase activator that binds the PDZ domains of ERM-binding phosphoprotein 50 (SLC9A3R1) and E3KARP (SLC9A3R2)
SW:DYJ2_HUMAN O43237 homo sapiens (human). dynein light intermediate chain 2, cytosolic (lic53/55) (lic-2). 7/1998 [MASS=54099]/Cytoplasmic dynein light intermediate chain 2, a putative subunit of cytoplasmic dynein that may have ATPase activity
SW:9123_HUMAN P51808 homo sapiens (human). protein 91/23. 11/1997 [MASS=13062]/T-complex-associated-testis-expressed 1-like, protein with similarity to murine Tctex1, which is a dynein light chain expressed in retina and in germ cells of the testis
PIR2:T46394 hypothetical protein DKFZp434H0820.1 - human (fragment) [MASS=78344]/Protein of unknown function, has moderate similarity to uncharacterized human C1ORF24
GP:AB040884_1 Homo sapiens mRNA for KIAA1451 protein, partial cds; Start codon is not identified.. [MASS=56449]/Member of the oxysterol-binding protein (OSBP) family, which are involved in sterol biosynthesis and possibly regulation, contains a pleckstrin homology (PH) domain, has a region of moderate similarity to S. cerevisiae Osh7p
GP:U21252_1 Human rearranged Ig gamma heavy chain V region (VH3-JH4b) mRNA, partial cds, clone JGpFv3-06 VH; from VH3 family gene and JH4b. [MASS=13752]
GP:D87438_1 Human mRNA for KIAA0251 gene, partial cds; Similar to a C.elegans protein in cosmid C14H10. [MASS=90027]/Protein containing two pyridoxal-dependent group II decarboxylase conserved domains, which bind pyridoxal-phosphate groups, has strong similarity to uncharacterized mouse Kiaa0251-hp
GP:AB032997_1 Homo sapiens mRNA for KIAA1171 protein, partial cds; Start codon is not identified.; hh05501 cDNA clone for KIAA1171 has 960-bp and 414-bp insertions (may be introns) after the positions 1275 and 1339 of the sequence of KIAA1171, respectively.. [MASS=66540]/Protein of unknown function
SW:ENP2_HUMAN Q9y5l3 homo sapiens (human). ectonucleoside triphosphate diphosphohydrolase 2 (ec 3.6.1.3) (ntpdase2) (ecto-atpase) (cd39 antigen-like 1). 10/2001 [MASS=53665]/Ectonucleoside triphosphate diphosphohydrolase 2, a member of the CD39-like family that functions as a ecto-ATPase
GP:AK023914_1 Homo sapiens cDNA FLJ13852 fis, clone THYRO1000934, weakly similar to PYRROLINE-5-CARBOXYLATE REDUCTASE (EC 1.5.1.2); unnamed protein product. [MASS=28663]/Protein with high similarity to pyrroline-5-carboxylate reductase 1 (human PYCR1), which catalyzes the NAD(P)H dependent reduction of pyrroline-5-carboxylate to proline, member of the delta 1-pyrroline-5-carboxylate reductase (P5CR) family
SW:AMP1_HUMAN P53582 homo sapiens (human). putative methionine aminopeptidase 1 (ec 3.4.11.18) (metap 1) (peptidase m 1) (kiaa0094) (fragment). 11/1997 [MASS=44046]/Methionine aminopeptidase 1, metallopeptidase that cleaves N-terminal methionine when the adjacent residue is small and uncharged, enzymatic activity may not be inhibited by the angiogenesis inhibitor fungal fumagillin

GP:AB020637_1 Homo sapiens mRNA for KIAA0830 protein, partial cds. [MASS=57202]/Protein of unknown function
GP:AB040887_1 Homo sapiens mRNA for KIAA1454 protein, partial cds; Start codon is not identified.. [MASS=142702]/Protein of unknown function
PIR2:T46299 hypothetical protein DKFZp434J0310.1 - human [MASS=38923]/Three prime repair exonuclease 1, member of the exonuclease family, displays 3'-5' exodeoxyribonuclease activity and may be involved in DNA repair
GP:AB046798_1 Homo sapiens mRNA for KIAA1578 protein, partial cds; Start codon is not identified.. [MASS=132841]
GP:AF155652_1 Human potassium channel modulatory factor mRNA; PCMF. [MASS=41973]/Protein containing a ZZ zinc finger and a C2H2 type zinc finger domain, which bind nucleic acids, has high similarity to uncharacterized mouse 1700094M07Rik
GP:AF167438_1 Homo sapiens androgen-regulated short-chain dehydrogenase/reductase 1 (ARSDR1) mRNA, complete cds; short-chain dehydrogenase/reductase family member./Member of the short-chain dehydrogenase-reductase family, has moderate similarity to a region of WW domain-containing oxidoreductase (mouse Wwox), which is an apoptosis activator
SWN:DB83_HUMAN P57088 homo sapiens (human). db83 protein. 8/2001 [MASS=27951]/Member of the UPF0121 uncharacterized protein family, has very strong similarity to uncharacterized rat LOC59303
SW:WDR1_HUMAN O75083 homo sapiens (human). wd-repeat protein 1 (actin interacting protein 1) (nori-1). 10/2001 [MASS=66194]/WD repeat domain 1, contains WD40 repeats which are believed to be involved in protein-protein interactions, may bind actin, and may be involved in hearing
SW:GC5L_HUMAN P78537 homo sapiens (human). gcn5-like protein 1 (rt14 protein). 7/1999 [MASS=14311]/General control of amino acid synthesis-like 1 (yeast), a widely expressed protein that may be a transcriptional activator
GP:AB011145_1 Homo sapiens mRNA for KIAA0573 protein, partial cds. [MASS=51859]/Member of the thioredoxin family, which are small enzymes involved in redox reactions, has low similarity to S. cerevisiae Pdi1p, which is a protein disulfide isomerase and oxidoreductase
SW:CC4H_HUMAN P50851 homo sapiens (human). cdc4-like protein (fragment). 7/1998 [MASS=213599]/Lipopolysaccharide-responsive and beige-like anchor, a putative protein-binding protein that contains WD-like repeats and a BEACH (BEige And CHS) domain, may play a role in vesicle transport
SW:LMO6_HUMAN O43900 homo sapiens (human). lim-only protein 6 (triple lim domain protein 6). 12/1998 [MASS=46098]/LIM domain only 6, a member of the LIM family of proteins which are involved in regulating development, protein-protein interactions and perhaps binding to nucleic acids, contains three LIM domains
GPN:AF239156_1 Homo sapiens peptide deformylase-like protein mRNA, complete cds; huPD. [MASS=27013]/
SW:G100_HUMAN Q16186 homo sapiens (human). 110 kda cell membrane glycoprotein. 11/1997 [MASS=42167]/Cell membrane glycoprotein 110 kDa, putative integral plasma membrane glycoprotein, putative tumor antigen and is expressed on human gastric carcinoma cells; upregulated in response to IFNgamma (IFNG)
1 Homo sapiens mRNA for nuclear protein containing a WW domain (Npw38), complete cds. [MASS=30472]/Npw38-binding protein, interacts with the WW domain of Npw38 (PQBP1), binds poly(rG) and G-rich single-stranded DNA, interacts with nuclear or perinuclear filaments and may play a role in regulation of pre-mRNA processing
GP:AF151867_1 Homo sapiens CGI-109 protein mRNA, complete cds. [MASS=24354
SW:ME18_HUMAN P35227 homo sapiens (human). dna-binding protein mel-18 (zinc finger protein 144). 11/1995 [MASS=37788]/Zinc finger protein 144, member of the Drosophila polycomb gene group, contains a helix-loop-helix like structure and a proline and serine-rich region, putative transcription factor that may be involved in hematopoiesis
GP:U06631_1 Human (H326) mRNA, complete cds; homologous to mouse gene PC326:GenBank Accession Number M95564. [MASS=66385]/Protein containing seven WD domains (WD-40 repeats), which may mediate protein-protein interactions, has a region of low similarity to a region of breakpoint cluster region protein uterine leiomyoma 2 (human BCRP2), which may have a housekeeping function
GP:AC003956_1 Homo sapiens DNA from chromosome 19, cosmid R34078, complete sequence; human homolog of acetolactate synthase; DPS similarity to Accession: gi|1730288 (U61263) acetolactate synthase homolog [Homo sapiens. [MASS=67868]
SW:SC13_HUMAN P55735 homo sapiens (human). sec13-related protein. 7/1998 [MASS=35569]/SEC13 (S. cerevisiae)-like 1, a serine- and threonine-rich WD40 repeat-containing protein that plays a role in protein transport from the endoplasmic reticulum to the Golgi
PIR2:T46292 hypothetical protein DKFZp434E0610.1 - human (fragment) [MASS=65841]/BCL2-associated athanogene 3, interacts with the Hsc70 ATPase domain to regulate its chaperone activity, interacts with BCL2 to modulate cellular antiapoptosis , and participates in the EGF signaling pathway
GP:AF293335_1 Homo sapiens p30 DBC mRNA, complete cds; putative protein from MH0802201. [MASS=30451]
GP:AK000303_1 Homo sapiens cDNA FLJ20296 fis, clone HEP05890; unnamed protein product. [MASS=36853]/Protein of unknown function
PIR2:JC7515 vesicle protein sorting 29 protein - human [MASS=20506]/Vacuolar sorting protein 29, putative transporter that may play a role in retrograde transport from endosomes to the trans-Golgi network
GP:AF068297_1 Homo sapiens HDCMD45P mRNA, partial cds. [MASS=17895]
GP:AB037807_1 Homo sapiens mRNA for KIAA1386 protein, partial cds; Start codon is not identified.. [MASS=135444]/Protein containing ankyrin repeats, an IBR domain, which are found in zinc finger proteins, and a C3HC4 type (RING) zinc finger, which may mediate protein-protein interactions
PIR2:T08753 hypothetical protein DKFZp586H2219.1 - human [MASS=53489]/Protein of unknown function, has strong similarity to uncharacterized rat Sca10

GP:AK022499_1 Homo sapiens cDNA FLJ12437 fis, clone NT2RM1000118, weakly similar to CALCINEURIN B SUBUNIT; unnamed protein product. [MASS=26041]
SW:EF1D_HUMAN P29692 homo sapiens (human). elongation factor 1-delta (ef-1-delta). 6/1994 [MASS=31221]/Eukaryotic translation elongation factor 1 delta, a guanine nucleotide exchange protein that gets hyperphosphorylated in cells infected with herpesviruses, binds HIV-1 protein Tat and causes a reduction of host mRNA translation efficiency
GP:AB037856_1 Homo sapiens mRNA for KIAA1435 protein, partial cds; Start codon is not identified.. [MASS=46908]/Protein containing two FYVE zinc finger domains, which bind phosphatidylinositol 3-phosphate, and 12 WD domains (WD-40 repeats), has a region of low similarity to a region of F-box/WD-repeat protein (C. elegans LIN-23), which regulates cell proliferation
GP:AF284574_1 Homo sapiens Nit protein 2 (NIT2) mRNA, complete cds; Nit2; similar to the Nit domains of Caenorhabditis elegans NitFhit and Drosophila melanogaster NitFhit. [MASS=30608]/NIT2
GP:AK022868_1 Homo sapiens cDNA FLJ12806 fis, clone NT2RP2002235; unnamed protein product. [MASS=34951]/Protein of unknown function
PIR2:T46298 hypothetical protein DKFZp434I1110.1 - human (fragment) [MASS=18088]
SW:FA5_HUMAN P12259 homo sapiens (human). coagulation factor v precursor (activated protein c cofactor). 11/1997 [MASS=251701]/Coagulation factor V, a cofactor in the prothrombinase complex that plays a role in the regulation of blood coagulation; alterations of corresponding gene are associated with activated protein C (APC) resistance, parahemophilia, and thrombosis
SW:SR72_HUMAN O76094 homo sapiens (human). signal recognition particle 72 kda protein (srp72). 12/1998 [MASS=74475]/Signal recognition particle 72, a ribonucleoprotein that undergoes cleavage by caspase during apoptosis; protein is an autoantigen in patients with dermatomyositis and systemic lupus erythematosus
GP:AF236056_1 Homo sapiens golgi membrane protein GP73 mRNA, complete cds. [MASS=45202]/Golgi phosphoprotein 2, an integral membrane Golgi protein that is epithelial cell-specific in healthy liver, upregulated in hepatocytes in both nonviral- and viral-associated liver disease including adult giant-cell hepatitis
GP:AF250859_1 Homo sapiens UDP-GlcNAc:a-3-D-mannoside b1,2-N-acetylglucosaminyltransferase I.2 (MGAT1.2) mRNA, partial cds; glycosyltransferase; similar to b1,2-N-acetylglucosaminyltransferase I; GnTI.2. [MASS=65499]/O-linked mannose beta1,2-N-acetylglucosaminyltransferase, has specific activity for alpha-linked terminal Man residues and is predicted to be involved in glycoprotein metabolism
SW:ROH2_HUMAN P55795 homo sapiens (human). heterogeneous nuclear ribonucleoprotein h' (hnrnp h') (ftp-3). 11/1997 [MASS=49264]/Heterogeneous nuclear ribonucleoprotein H2, a putative heterogeneous nuclear ribonucleoprotein that contains three repeats that resemble the RNA recognition motif (RRM)
GP:AF130092_1 Homo sapiens clone FLB9715 PRO2620 mRNA, complete cds; predicted protein of HQ2620. [MASS=53655]/Protein of unknown function, has low similarity to uncharacterized S. pombe Spac1142.01p
SW:CN37_HUMAN P09543 homo sapiens (human). 2',3'-cyclic nucleotide 3'-phosphodiesterase (ec 3.1.4.37) (cnp) (cnpase). 5/2000 [MASS=47579]/2'3'-Cyclic nucleotide 3' phosphodiesterase, a myelin-associated phosphodiesterase that is involved in regulation of central nervous system myelination
GP:AK021647_1 Homo sapiens cDNA FLJ11585 fis, clone HEMBA1003692; unnamed protein product. [MASS=16310]/Metallophosphoesterase 1, a putative transmembrane phosphoesterase expressed only in brain
SW:PPAL_HUMAN P11117 homo sapiens (human). lysosomal acid phosphatase precursor (ec 3.1.3.2) (lap). 12/1992 [MASS=48344]/Lysosomal acid phosphatase, a tartrate-inhibitable lysosomal enzyme; mice lacking Acp2 are more susceptible to seizures
SW:EF1B_HUMAN P24534 homo sapiens (human). elongation factor 1-beta (ef-1-beta). 6/1994 [MASS=24633]/Eukaryotic translation elongation factor 1 beta 2, putative component of the eukaryotic translation elongation complex
GP:AF226054_1 Homo sapiens GK001 (GK001) mRNA, complete cds. [MASS=55816]/Protein of unknown function, has moderate similarity to uncharacterized C. elegans ZK1058.4
GP:AC005067_2 Homo sapiens BAC clone CTB-122E10 from 7q11.23-q21.1, complete sequence; Supported by Human EST H08032.1 (NID:g872854), mouse EST AA870042.1 (NID:g2965487), and genscan; H_RG122E10.2b. [MASS=39202]/Member of the rhomboid family of integral membrane proteins
PIR2:T47174 hypothetical protein DKFZp762I166.1 - human (fragment) [MASS=31436]/Protein with high similarity to coronin 1a (human CORO1A), which is an actin-binding protein that binds to phagocyte oxidases and may transport them to the phagosome membrane, contains three WD domains (WD-40 repeat)
GP:AB032993_1 Homo sapiens mRNA for KIAA1167 protein, partial cds; Start codon is not identified.; hj01786 cDNA clone for KIAA1167 has 1412-bp and 708-bp insertions (may be introns) after the positions 850 and 2258 of the sequence of KIAA1167, respectively.. [MASS=95259]/Protein of unknown function/Protein of unknown function
GP:AJ245820_1 Homo sapiens mRNA for type I transmembrane receptor (psk-1 gene). [MASS=92455]/Protein with high similarity to murine Sez6, which is expressed in the brain and may play a role in seizure, contains five sushi or short consensus repeat domains, which are found in complement and adhesion proteins, and an extracellular CUB domain
GP:BC011524_1 Homo sapiens, Similar to hypothetical protein, clone MGC:8793 IMAGE:3872837, mRNA, complete cds. [MASS=42196]/Protein of unknown function, has moderate similarity to uncharacterized human LOC90268
GP:AK023834_1 Homo sapiens cDNA FLJ13772 fis, clone PLACE4000300; unnamed protein product. [MASS=72580]/Protein of unknown function

SW:LYII_HUMAN Q14108 homo sapiens (human). lysosome membrane protein ii (limp ii) (85 kda lysosomal membrane sialoglycoprotein) (lgp85) (cd36 antigen-like 2). 7/1998 [MASS=54159]/Lysosomal integral membrane protein II, a lysosomal membrane sialoglycoprotein with similarity to CD36 antigen
PIR2:T47160 hypothetical protein DKFZp762K0911.1 - human [MASS=23897]/Ras-related GTP-binding protein 14, putative GTP binding protein and GTPase, induced in lung fibroblasts in response to endothelin treatment
GP:AJ293573_1 Homo sapiens mRNA for zinc finger protein Cezanne (CEZANNE gene). [MASS=94401]/of unknown function, has a region of low similarity to a region of tumor necrosis factor alpha-induced protein 3 (mouse Tnfaip3), which is a cytoplasmic protein that blocks NF-kappaB activation and inhibits Tnf -induced apoptosis and necrosis
GP:AK025999_1 Homo sapiens cDNA: FLJ22346 fis, clone HRC06158; unnamed protein product. [MASS=81877]/Member of the ubiquitin-conjugating enzyme (E2) family, which catalyze the covalent attachment of ubiquitin to target proteins, has a region of moderate similarity to a region of mouse Birc6, which is a ubiquitin-conjugating enzyme
SW:SP02_HUMAN Q92796 homo sapiens (human). presynaptic protein sap102 (synapse-associated protein 102) (neuroendocrine-dlg) (ne-dlg). 5/2000 [MASS=90344]/Discs large (Drosophila) homolog 3 (neuroendocrine-dlg), putative guanylate kinase, inhibits cell proliferation, acts in neuronal cell adhesion, may facilitate neoplasm development or progression; corresponding gene is upregulated in ovarian carcinomas
GP:AB037728_1 Homo sapiens mRNA for KIAA1307 protein, partial cds; Start codon is not identified.. [MASS=186192]/Protein containing two putative zinc finger in N-recognition domains
SW:SPC1_HUMAN Q15005 homo sapiens (human). microsomal signal peptidase 25 kda subunit (ec 3.4.-.-) (spc25) (kiaa0102). 5/2000 [MASS=25003]/Protein of unknown function
PIR2:G01447 GP36b glycoprotein - human [MASS=40229]/Protein of unknown function, has moderate similarity to a region of human LMAN1, which is a mannose-binding lectin involved in the traffic of glycoproteins between endoplasmic reticulum and the Golgi apparatus, and associated with a coagulation disorder
SW:TGT_HUMAN P54578 homo sapiens (human). queuine trna-ribosyltransferase (ec 2.4.2.29) (trna-guanine transglycosylase) (guanine insertion enzyme). 5/2000 [MASS=55938]/tRNA-guanine transglycosylase, catalyses the exchange of queuine for guanine in the first position of the anticodon of tRNAs for asparagine, aspartic acid, histidine and tyrosine
GP:AB014555_1 Homo sapiens mRNA for KIAA0655 protein, partial cds. [MASS=120902]/Huntingtin interacting protein 1 related protein, putative actin-binding protein predicted to be involved in actin polymerization, interacts with HIP1 but not Huntingtin (HD)
PIR2:T46375 hypothetical protein DKFZp434D1319.1 - human [MASS=49166]
PIR2:I52882 autoantigen - human [MASS=131858]/Protein of unknown function
GP:AB037773_1 Homo sapiens mRNA for KIAA1352 protein, partial cds; Start codon is not identified.. [MASS=138362]/
GP:AB020697_1 Homo sapiens mRNA for KIAA0890 protein, complete cds. [MASS=133938]/Protein containing two helicase conserved C-terminal domains and four double-stranded RNA binding domains, 6), has a region of low similarity to a region of S. pombe Cdc28p, which is an ATP-dependent RNA helicase involved in cell cycle progression
GP:AK022827_1 Homo sapiens cDNA FLJ12765 fis, clone NT2RP2001511, moderately similar to Homo sapiens putative RNA-binding protein Q99 mRNA; unnamed protein product. [MASS=97330]/Protein with high similarity to C. elegans ALG-1, which is a piwi-related protein involved in the production of stRNA (small temporal RNA) of LIN-4, contains a PAZ (Piwi, Argonaut and Zwille) domain, which may mediate protein-protein interactions
GP:U25756_1 Human Ki nuclear autoantigen gene, partial cds; region of similarity to Ki nuclear autoantigen mRNA sequence, GenBank Accession Number U11292. [MASS=6323]
SW:CYTC_HUMAN P01034 homo sapiens (human). cystatin c precursor (neuroendocrine basic polypeptide) (gamma-trace) (post-gamma-globulin). 5/2000 [MASS=15799]/Cystatin C, a cysteine protease inhibitor regulated by TGFB1, may have roles in vascular remodeling and disease; mutations in the gene cause hereditary cystatin C amyloid angiopathy, in which amyloid aggregates form in the brain
GP:AK023618_1 Homo sapiens cDNA FLJ13556 fis, clone PLACE1007705, moderately similar to Mus musculus mRNA for Ndr1 related protein Ndr3; unnamed protein product. [MASS=31484]/Protein with high similarity to human NDRG1, which is induced by nickel, homocysteine, 2-mercaptoethanol, and tunicamycin and is induced during colon carcinoma cell line differentiation
SW:TBA4_HUMAN P05215 homo sapiens (human), macaca fascicularis (crab eating macaque) (cynomolgus monkey), and mus musculus (mouse). tubulin alpha-4 chain. 7/1999 [MASS=49924]/Member of the tubulin-FtzA family, which are involved in polymer formation, has strong similarity to a region of mouse Tuba6, which is a structural protein that polymerizes to form microtubules
GP:AF129332_1 Homo sapiens MUM2 (MUM2) gene, complete cds; similar to Saccharomyces cerevisiae bet5. [MASS=16832]/Protein with low similarity to S. cerevisiae Bet5p, which is a subunit of both the Transport Protein Particle I complex involved in vesicular transport from endoplasmic reticulum to Golgi and the Transport Protein Particle II involved in Golgi trafficking
PIR2:T17237 hypothetical protein DKFZp434P106.1 - human (fragment) [MASS=28268]/Protein of unknown function, has high similarity to uncharacterized mouse 6330583M11Rik
SW:ANX6_HUMAN P08133 homo sapiens (human). annexin vi (lipocortin vi) (p68) (p70) (protein iii) (chromobindin 20) (67 kda calelectrin) (calphobindin-ii) (cpb-ii). 5/2000 [MASS=75742]/Annexin VI, member of the annexin family of calcium-dependent phospholipid binding proteins that shift between soluble and membrane associated states; involved in the budding of clathrin coated pits and may play a role in tumor suppression

GP:BC012058_1 Homo sapiens, hypothetical protein FLJ12701, clone MGC:19885 IMAGE:4554033, mRNA, complete cds. [MASS=37535]/Protein containing a double-stranded RNA binding domain
GP:AB033097_1 Homo sapiens mRNA for KIAA1271 protein, partial cds; Start codon is not identified.. [MASS=56670]/Protein of unknown function
GP:AK002163_1 Homo sapiens cDNA FLJ11301 fis, clone PLACE1009908, weakly similar to HYPOTHETICAL GTP-BINDING PROTEIN IN SEH1-PRP20 INTERGENIC REGION; unnamed protein product. [MASS=73142]/Member of an uncharacterized GTPase family, has moderate similarity to yeast YGL099W, which is required for normal growth, morphology, mating, and sporulation
PIR2:T00050 hypothetical protein KIAA0400 - human [MASS=111651]/Development and differentiation enhancing factor 2 (Pyk2 C terminus-associated protein), phosphatidylinositol-4,5-bisphosphate-dependent ARF GTPase activator, binds Src kinases and PYK2 (PTK2B), inhibits paxillin (PXN) recruitment to focal adhesions
SW:ACTY_HUMAN P42025 homo sapiens (human). beta-centractin. 7/1999 [MASS=42293]/Beta centractin, a member of the centractin family of actin-related proteins, a subunit of the dynactin complex which functions in the cytoplasmic dynein-driven organelle movement along microtubules
PIR2:T46333 hypothetical protein DKFZp434J1813.1 - human (fragment) [MASS=53778]
SW:LEGU_HUMAN Q99538 homo sapiens (human). legumain precursor (ec 3.4.22.34) (asparaginyl endopeptidase). 12/1998 [MASS=49411]/Protease cysteine 1 (legumain), a lysosomal cysteine endopeptidase that hydrolyzes asparaginyl bonds, inhibits osteoclast differentiation, may play a role in antigen processing for MHC class II presentation
GP:AK025520_1 Homo sapiens cDNA: FLJ21867 fis, clone HEP02419; unnamed protein product. [MASS=60579]/Protein with strong similarity to peripheral benzodiazepine receptor associated protein 7 (mouse Pap7), which binds peripheral-type benzodiazepine receptor (Bzrp) and functions in regulation of steroidogenesis, contains an acyl CoA binding domain
GPN:AF060511_1 Homo sapiens clone 016b10 My016 protein mRNA, complete cds.[MASS=10117]
PIR2:PH0268 epidermal autoantigen 450K (clone pE450-C/D) - human (fragment) [MASS=73263]/Epiplakin 1, a member of the plakin family of proteins that bind to cytoplasmic intermediate filaments; autoantigens to the protein are present in patients with a subepidermal blistering disease that resembles bullous pemphigoid
GP:Z74021_1 Human DNA sequence from clone SC22CB-1E7 on chromosome 22 Contains the RPS17L4 gene for Ribosomal protein S17-like 4, exons 1 and 2 of the SLC5A1 gene for solute carrier family 5 (sodium/glucose cotransporter) member 1 (High Affinity Sodium-Glucose C [MASS=15602]
GP:AJ245621_1 Homo sapiens CTL2 gene. [MASS=80138]/Protein of unknown function, has high similarity to uncharacterized mouse 2210409B01Rik
GP:AC005154_1/Protein of unknown function, has moderate similarity to uncharacterized C. elegans C44B7.7
GP:X87832_1 Homo sapiens mRNA for partial NOV/plexin-A1 protein. [MASS=194818]/Plexin A1, acts as a coreceptor with neuropilin (NRP1) for semaphorins, which are signaling molecules controlling cell repulsion
SW:YCE7_HUMAN Q9y3e5 homo sapiens (human). hypothetical protein cgi-147. 5/2000 [MASS=19194]
GP:AF137372_1 Homo sapiens ras-related protein RAB18 mRNA, complete cds. MASS=22977]/Ras-related GTP-binding protein 18, putative GTP binding protein and GTPase, may be involved in vesicle transport and may play a role in inflammation
SW:ANXA_HUMAN P50995 homo sapiens (human). annexin xi (calcyclin-associated annexin 50) (cap-50) (56 kda autoantigen). 5/2000 [MASS=54390]/Annexin A10, a liver-specific member of the annexin family of calcium-dependent phospholipid-binding proteins that typically have a role in inositol phosphate metabolism; downregulation correlates with high grade and high stage hepatocellular carcinoma
GP:AK001243_1 Homo sapiens cDNA FLJ10381 fis, clone NT2RM2002055; unnamed protein product. [MASS=49582]/Protein of unknown function
SWN:RTN4_HUMAN Q9nqc3 homo sapiens (human). reticulon 4 (neurite outgrowth inhibitor) (nogo protein) (foocen) (neuroendocrine-specific protein)(nsp) (neuroendocrine specific protein c homolog) (rtn-x) ([MASS=129931]/Reticulon 4, ligand for RTN4R, inhibits axon regeneration in adult CNS but not PNS, yet peptide derivative NEP1-40 acts as an antagonist and promotes axonal regeneration and may have therapeutic potential
PIR2:T46272 hypothetical protein DKFZp564L0864.1 - human (fragment) [MASS=20191]/Protein with high similarity to uncharacterized mouse Hiat1
PIR2:T46254 hypothetical protein DKFZp761H171.1 - human [MASS=28611]/Protein with high similarity to S. cerevisiae Gtr2p, which is a putative small GTPase involved in nucleocytoplasmic transport
SW:DSR3_HUMAN O14972 homo sapiens (human). down syndrome critical region protein 3. 5/2000 [MASS=33010]/Down syndrome criticial region gene 3, a ubiquitously expressed protein; the corresponding gene is located in the Down syndrome critical region of chromosome 21
SW:SKP1_HUMAN P34991 homo sapiens (human), and cavia porcellus (guinea pig). cyclin a/cdk2-associated protein p19 (rna polymerase ii elongation factor-like protein) (organ of corti protein 2) (ocp-ii pr [MASS=18527]/S-phase kinase-associated protein 1A (p19A), component of Cbf3 kinetochore and SCF (Skp1p-cullin-F-box) complexes which target many cell cycle dependent proteins for ubiquitin-dependent degradation, deregulation may lead to tumorigenesis
SW:TBB1_HUMAN P07437 homo sapiens (human). tubulin beta-1 chain. 7/1999 [MASS=49759]/Protein with high similarity to beta-2 tubulin (rat Tubb2), which plays a role in the response to wounding and possibly in axonal outgrowth and regeneration, member of the tubulin-FtzA family, which are involved in polymer formation

SW:TBL2_HUMAN Q9y4p3 homo sapiens (human). transducin beta-like 2 protein (ws beta-transducin repeats protein) (ws-betatrp). 10/2001 [MASS=49798]/Protein containing five WD domains (WD-40 repeat), which may mediate protein-protein interactions, has weak similarity to human CIAO1, which interacts with and inhibits Wilms tumor suppressor protein (human WT1) transactivation activity
GP:AL049795_2 Human DNA sequence from clone RP4-622L5 on chromosome 1p34.2-36.11. Contains the gene for importin alpha 7 (karyopherin), up to six novel genes and the 5' end of the EIF3S2 gene for eukaryotic translation initiation factor 3 beta. Contains ESTs, STSs [MASS=41648]
GP:AB011163_1 Homo sapiens mRNA for KIAA0591 protein, partial cds. [MASS=151594]/Kinesin family member 1B, a putative motor protein involved in synaptic vesicle transnport; mutation of the gene underlies Charcot-Marie-Tooth type 2A peripheral neuropathy
SW:KNLC_HUMAN Q07866 homo sapiens (human). kinesin light chain (klc). 10/1996 [MASS=64786]/Kinesin light chain, member of a family of microtubule-associated motor proteins that function in intracellular transport and mitosis; has very strong similarity to murine Klc1, which is abundantly expressed in the axons of sciatic nerve
GP:AF272357_1 Homo sapiens NPDC1-like protein (NPDC1) mRNA, complete cds; similar to mouse NPDC1. [MASS=34507]/Protein of unknown function, has a region of low similarity to a region of C. elegans CAB-1, which is a component of a neuronal transmission pathway that affects defecation and locomotion
GP:AB040882_1 Homo sapiens mRNA for KIAA1449 protein, partial cds; Start codon is not identified.. [MASS=68085]/Protein containing six WD domains (WD-40 repeats), which may mediate protein-protein interactions, has a region of low similarity to a region of platelet-activating factor acetylhydrolase isoform 1b alpha subunit (45kD) (human PAFAH1B1)
GP:AF226045_1 Homo sapiens GK002 (GK002) mRNA, complete cds. [MASS=41280]/Mitochondrial ribosomal protein S22, a putative component of the mitochondrial small 28S ribosomal subunit
GP:D42085_1 Human mRNA for KIAA0095 gene, complete cds; KIAA0095 gene is related to S.cerevisiae NIC96 gene.. [MASS=93488]/Protein with low similarity to S. cerevisiae Nic96p, which is a nuclear pore protein (nucleoporin) that acts in a complex with S. cerevisiae Nsp1p, Nup57p, and Nup49p
GP:AF151069_1 Homo sapiens HSPC235 mRNA, complete cds. [MASS=40152]/Mitochondrial ribosomal protein L37, putative component of the large subunit (39S) of the mitochondrial ribosome
PIR2:T50639 synaptic glycoprotein SC2, spliced variant [imported] - human [MASS=36061]/Member of the 3-oxo-5-alpha-steroid 4-dehydrogenase family, which are involved in dihydrotestosterone biosynthesis
SW:PHB_HUMAN P35232 homo sapiens (human). prohibitin. 12/1998 [MASS=29804]/Prohibitin, mitochondrial suppressor of cell proliferation that binds to Rb family members RB1 , RBL1 , and RBL2 , represses E2F-induced transcription; gene is mutated in sporadic breast cancer and expression is elevated in endometrial adenocarcinoma
PIR2:T00345 hypothetical protein KIAA0590 - human [MASS=165197]/Protein containing two WD domains (WD-40 repeats), which may mediate protein-protein interactions, has low similarity to C. elegans CHE-11, which is required for normal cilial development, dauer larva formation, and chemotaxis
GP:AK001718_1 Homo sapiens cDNA FLJ10856 fis, clone NT2RP4001547; unnamed protein product. [MASS=40684]/Protein with moderate similarity to S. cerevisiae Cdc50p, which is a protein that functions in cell cycle control, transcription regulation from the Pol II promoter, and is associated with a cell-division-cycle (CDC) phenotype when mutated
GP:AB018270_1 Homo sapiens mRNA for KIAA0727 protein, partial cds. [MASS=78790]/Protein containing two IQ calmodulin-binding motifs and a myosin head (motor domain), has very strong similarity to a region of rat Myo1c, which is an unconventional Class I myosin heavy chain that binds calmodulin and may be involved in neurogenesis
GP:AB015631_1 Homo sapiens mRNA for type II membrane protein, complete cds, clone:HP10390. [MASS=20652]/Transmembrane protein 4, a putative type II membrane protein
GP:AF155658_1 Homo sapiens putative 55 kDa protein mRNA, complete cds. [MASS=55003]/Member of the uncharacterized protein family UPF0027, has high similarity to uncharacterized C. elegans F16A11.2
SW:TRM1_HUMAN Q9nxh9 homo sapiens (human). probable n2,n2-dimethylguanosine trna methyltransferase (ec 2.1.1.32) (trna(guanine-26,n2-n2) methyltransferase) (trna 2,2- dimethylguanosine-26 methyltransfer [MASS=72234]
GP:AL451015_9 Neurospora crassa DNA linkage group V BAC clone B13O20; weak similarity to g-alpha interacting protein, homo sapiens, SWISSPROT:GAIP_HUMAN contains EST gb:AW708419, AW708418, AI330099, AI330098. [MASS=16236]
GP:AB033011_1 Homo sapiens mRNA for KIAA1185 protein, partial cds; Start codon is not identified.. [MASS=44499]/Protein containing a leucine rich repeat, which mediates protein-protein interactions, has a region of low similarity to a region of phenylalanyl-tRNA synthetase beta-subunit (human PheHB), which is involved in protein synthesis and possibly tumurigenesis
SW:HEXB_HUMAN P07686 homo sapiens (human). beta-hexosaminidase beta chain precursor (ec 3.2.1.52) (n-acetyl-beta-glucosaminidase) (beta-n-acetylhexosaminidase) (hexosaminidase a). 5/2000 [MASS=63111]/Hexosaminidase B beta polypeptide, a subunit of a lysosomal enzyme that hydrolyzes the ganglioside GM2; mutations in the gene cause Sandhoff disease, a lysosomal stroage disorder
GP:AF151062_1 Homo sapiens HSPC228 mRNA, complete cds. [MASS=33677]
SW:VATG_HUMAN O75348 homo sapiens (human). vacuolar atp synthase subunit g (ec 3.6.1.34) (v-atpase 13 kda subunit) (vacuolar h(+)-atpase subunit g) (vacuolar atp synthase subunit m16). 5/2000 [MASS=13758]/Member of the vacuolar (H+)-ATPase G subunit family, which may couple ATP degradation to H+ translocation, has high similarity to uncharacterized human ATP6G2

SW:RS3_HUMAN P23396 homo sapiens (human). 40s ribosomal protein s3. 2/1996 [MASS=26688]/Ribosomal protein S3, a putative component of the small 40S ribosomal subunit, has DNA endonuclease activity, endonuclease activity is absent in Xeroderma pigmentosum group D patients, expression is increased in colorectal cancer
GP:AK022956_1 Homo sapiens cDNA FLJ12894 fis, clone NT2RP2004170, moderately similar to Homo sapiens mRNA for transducin (beta) like 1 protein; unnamed protein product. [MASS=55569]/Protein with strong similarity to transducin (beta)-like 1 (human TBL1), which binds histone H3 and is part of the SMRT corepressor complex and may be involved in vision and hearing, contains eight WD domains (WD-40 repeats)
PIR2:S55474 Human giant larvae homolog - human [MASS=112908]/Protein with high similarity to lethal giant larvae (Drosophila) homolog 1 (human LLGL1), which is a nonmuscle myosin II heavy chain-associating cytoskeletal protein that may be linked to Smith-Magenis Syndrome, contains three WD domains (WD-40 repeats)
SW:1A01_HUMAN P30443 homo sapiens (human). hla class i histocompatibility antigen, a-1 alpha chain precursor. 5/2000 [MASS=40846]/Major histocompatibility complex class I-A, binds antigenic peptides, associates with beta 2-microglobulin (B2M) to form a complex that contributes to self-recognition by cytotoxic T lymphocytes
GP:AB038995_1 Homo sapiens mRNA for RAB-8b protein, complete cds. [MASS=23584]/Member of the Ras superfamily of GTP-binding proteins, has very strong similarity to rat Rn.10995 (Rab8b), which is a member of the Rab family of small GTP binding proteins
GP:AK001050_1 Homo sapiens cDNA FLJ10188 fis, clone HEMBA1004693; unnamed protein product. [MASS=30704]/Protein of unknown function
SW:2ABA_HUMAN Q00007 h serine/threonine protein phosphatase 2a, 55 kda regulatory subunit b, alpha isoform (pp2a, subunit b, b-alpha isoform) (pp2a, subunit b, b55-alpha isoform) (pp2a, subunit b, pr55- [MASS=51692]/Protein phosphatase 2 regulatory subunit B alpha isoform, determines the substrate affinity and regulates the kinetics of protein phosphatase 2, expression is decreased in the hippocampus of Alzheimer's disease patients
GP:AK024781_1 Homo sapiens cDNA: FLJ21128 fis, clone CAS06258; unnamed protein product. [MASS=56106]/Member of the YjeF-related protein N-terminus containing family, has weak similarity to uncharacterized C. albicans Orf6.
GP:AB018790_1 Homo sapiens gene, complete cds, similar to Caenorhabditis elegans C42C1.9 gene sequence; similar to Caenorhabditis elegans C42C1.9 gene sequence in GenBank Accession Number AF043695. [MASS=37840]
GP:AK002135_1 Homo sapiens cDNA FLJ11273 fis, clone PLACE1009338; unnamed protein product. [MASS=31113]/Protein of unknown function, has high similarity to uncharacterized human MGC5576
GP:AF271388_1 Homo sapiens CMP-N-acetylneuraminic acid synthase mRNA, complete cds. [MASS=48379]/Protein with strong similarity to cytidine monophospho-N-acetylneuraminic acid synthetase (mouse Cmas), which generates the activated sugar nucleotide CMP-N-acetylneuraminic acid for use by sialyltransferases, member of the cytidylyltransferase
GP:AB033767_1 Homo sapiens BSCv mRNA, partial cds; brain-selective and closely mapped on the counter allele of CMAP in cystatin cluster. [MASS=47746]/Member of the strictosidine synthase family, which catalyze the condensation of tryptamine with secologanin to form strictosidine, has low similarity to uncharacterized C. elegans F57C2.5
SWN:TALI_HUMAN Q9y490 homo sapiens (human). talin. 8/2001 [MASS=269718]/Talin 1, a component of focal adhesion sites, links integrins to the actin cytoskeleleton, binds phospholipids, and mediates other interactions at the cytoplasmic face of cell/matrix contacts, important for cell spreading and motility
SWN:PM5P_HUMAN Q15155 homo sapiens (human). protein pm5 precursor. 8/2001 [MASS=134321]/Protein of unknown function, has low similarity to uncharacterized C. elegans C02E11.1
GPN:AL136131_4 Human DNA sequence from clone RP1-261G23 on chromosome 6p12.2-21.1 Contains ESTs, STSs, GSSs and CpG islands. Contains the KIAA0110 gene, two novel genes, a novel pseudogene similar to OPA-interacting protein (OIP1), a putative novel gene, and the VE [MASS=22184]/Mitochondrial ribosomal protein S18A, component of the small (28S) ribosomal subunit of mitochondria
PIR2:T42646 hypothetical protein DKFZp727K171.1 - human (fragment) [MASS=64691]/Protein of unknown function, has a region of moderate similarity to a region of Sjogren syndrome antigen B (human SSB), which is an RNA-binding protein that regulates translation and is associated with Sjogren syndrome and systemic lupus erythematosus
GP:AB014729_1 Homo sapiens mRNA for SMAP-1, complete cds; tetratricopeptide repeat(TPR motif). [MASS=101675]/Protein containing two putative arf GTPase activation (GAP) domains, which have C-4 class zinc fingers, has a region of moderate similarity to a region of centaurin-alpha (human CENTA1), which is a PtdIns(3,4,5)P3-binding protein
SW:COPD_HUMAN P48444 homo sapiens (human). coatomer delta subunit (delta-coat protein) (delta-cop) (archain). 11/1997 [MASS=57210]/Archain 1, a putative structural protein that is ubiquitously expressed and may play a role in intracellular protein trafficking
GP:AB046829_1 Homo sapiens mRNA for KIAA1609 protein, partial cds; Start codon is not identified.. [MASS=52735]/Protein of unknown function
SW:PTPA_HUMAN P18433 homo sapiens (human). protein-tyrosine phosphatase alpha precursor (ec 3.1.3.48) (r-ptp- alpha). 5/2000 [MASS=90600]/Phosphotyrosyl phosphatase activator, regulatory subunit of protein phosphatase 2A, involved in cell cycle control and may protect against oxidative DNA damage
SWN:UNRI_HUMAN Q9y3f4 homo sapiens (human). unr-interacting protein (wd-40 repeat protein pt-wd). 8/2001 [MASS=38438]/Unr-interacting protein, has WD domain, interacts with unr (NR1H2) protein and may function in the transforming growth receptor signaling pathway; upregulated in breast cancer and may contribute to tumor progression

GP:AC005788_1 Homo sapiens chromosome 19, cosmid R26652, complete sequence; protein tyrosine phosphatase sigma. [MASS=157056]
GP:AK000330_1 Homo sapiens cDNA FLJ20323 fis, clone HEP09648; unnamed protein product. [MASS=64016]/Protein containing three WD domains (WD-40 repeats), which likely mediate protein-protein interactions
GP:AB037855_1 Homo sapiens mRNA for KIAA1434 protein, partial cds; Start codon is not identified.. [MASS=76634]/Member of the glycerophosphoryl diester phosphodiesterase family, which are involved in lipid metabolism, contains a starch binding domain, which are found in glycosyl hydrolases, has low similarity to uncharacterized C. elegans T05H10.7
PIR2:T08729 RING zinc finger protein homolog DKFZp566H073.1 - human (fragment) [MASS=35718]/Protein containing a C3HC4 type (RING) zinc finger and a PA (protease associated) domain, has a region of moderate similarity to a region of RING finger protein 12 (mouse Rnf12), which is a corepressor of LIM that binds to LIM domains
GPN:AK017745_1 Mus musculus 8 days embryo whole body cDNA, RIKEN full-length enriched library, clone:5730502D15:homolog to human DJ402G11.4 (NOVEL PROTEIN SIMILAR TO C. ELEGANS F38A5.2 (ISOFORM 2)) (FRAGMENT), full insert sequence; data source:SPTR, source key:Q9UG [MASS=46538]
GP:AF005888_1 Homo sapiens COX4AL mRNA, complete cds. [MASS=23773]/Neighbor of COX4, ubiquitously expressed, contains potential binding sites for Sp1 and NRF-2/GABP
SW:T9S3_HUMAN Q9hd45 homo sapiens (human). transmembrane 9 superfamily protein member 3 precursor (sm-11044 binding protein) (ep70-p-iso). 10/2001 [MASS=67888]/SM-11044 binding protein, member of the transmembrane protein 9 superfamily, a predicted integral membrane protein which has functional ligand binding properties
GP:AB020694_1 Homo sapiens mRNA for KIAA0887 protein, partial cds. [MASS=52421]/Protein containing a UBX domain, which are found in ubiquitin regulatory proteins
GP:U47924_19 Human chromosome 12p13 sequence, complete sequence; similar to S. cerevisiae ORF YOR175c, encoded by GenBank Accession Number Z75083. [MASS=44122]/Member of the membrane bound O-acyl transferase (MBOAT) family, which are found in acyltransferase enzymes, has strong similarity to uncharacterized mouse Grcc3f
GP:AF161380_1 Homo sapiens HSPC262 mRNA, partial cds. [MASS=20619]
SW:DDX3_HUMAN O00571 homo sapiens (human). dead box protein 3 (helicase-like protein 2) (hlp2) (dead box, x isoform). 7/1999 [MASS=73243]/DEAD box protein 3, a member of the DEAD/H box ATP-dependent RNA helicase protein family, interacts with Hepatitis C virus core protein; corresponding gene is found on X chromosomes and escapes X-inactivation
PIR2:T08769 hypothetical protein DKFZp586K011.1 - human (fragment) [MASS=81441]/Protein with strong similarity to rat Mbc2, which localizes to microsomes and plasma membranes and is expressed ubiquitously
PIR2:T08787 probable testin DKFZp586B2022.1 - human (fragment) [MASS=15593]/Protein containing three LIM domains, has a region of low similarity to a region of four and a half LIM domains 2 (human FHL2), which is a apoptosis and transcription regulator that is downregulated in rhabdomyosarcoma cell lines
SW:Y041_HUMAN Q15057 homo sapiens (human). hypothetical protein kiaa0041 (fragment). 7/1999 [MASS=71243]/Centaurin beta 2, a GTPase activating protein for ARF6, stimulated by phosphatidic acid and PIP2, and acts in the cell periphery to affect the actin cytoskeleton
GP:AF078860_1 Homo sapiens PTD007 mRNA, complete cds. [MASS=16661]/Mitochondrial ribosomal protein L42, component of the large ribosomal subunit
no_description_avail/Protein containing many ankyrin (Ank) repeats, which may mediate protein-protein interactions, has low similarity to a region of ankyrin (rat Ank3), which binds Na+/K+-ATPase and links integral membrane proteins to the cytoskeleton
GP:AK000325_1 Homo sapiens cDNA FLJ20318 fis, clone HEP08704; unnamed protein product. [MASS=62816]/Protein of unknown function
GP:AB046774_1 Homo sapiens mRNA for KIAA1554 protein, partial cds; Start codon is not identified.. [MASS=150426]/Protein containing a C3HC4 type (RING) zinc finger, which may mediate protein-protein interactions
no_description_avail/Protein of unknown function, has low similarity to a region of threonyl-tRNA synthetases
GP:U97519_1 Homo sapiens podocalyxin-like protein mRNA, complete cds. [MASS=55596]/Podocalyxin like, a transmembrane sialomucin that is an L selectin ligand and important for lymphocyte adhesion and homing
GP:AJ011129_1 Homo sapiens mRNA for 17kD fetal brain protein; ORF1. [MASS=17218]/Member of the SCP-like extracellular protein family, has moderate similarity to a region of S. cerevisiae Pry3p, which shows daughter-specific expression and may have a role in mating efficiency
GP:AC007055_5 Homo sapiens chromosome 14 clone BAC 201F1 map 14q24.3, complete sequence; unknown; This gene is predicted by Genscan and supported by ESTs AA836348 and AI077817. The closes. [MASS=35283]
GP:AJ131186_1 Homo sapiens mRNA for nuclear matrix protein NMP200; related to splicing factor PRP19. [MASS=55181]/Protein containing six WD domains (WD-40 repeats), which may mediate protein-protein interactions, has weak similarity to non-snRNP spliceosome component (S. cerevisiae Prp19p), which is involved in mitotic recombination and gene conversion
no_description_avail/Reticulon 3, member of the reticulon (neuroendocrine-specific, NSP) family of proteins that associate with the endoplasmic reticulum, most highly expressed in brain
PIR2:T12456 hypothetical protein DKFZp564M2423.1 - human [MASS=42427]
no_description_avail/Zinc-finger protein-like 1, a putative transcription regulator with zinc-finger-like domains and leucine-zipper-like motifs, expressed strongly (and perhaps exclusively) in the exocrine (but not the endocrine) pancreas

SW:RBP2_HUMAN P49792 homo sapiens (human). ran-binding protein 2 (nuclear pore complex protein nup358) (nucleoporin nup358) (358 kda nucleoporin) (p270). 5/2000 [MASS=358218]/RAN binding protein 2, binds RAN-GTP at the cytoplasmic face of nuclear pores, also functions as a chaperone for red and green opsin molecules
SW:HEPS_HUMAN P05981 homo sapiens (human). serine protease hepsin (ec 3.4.21.-) (transmembrane protease, serine 1). 11/1997 [MASS=45011]/Hepsin, a transmembrane serine protease implicated in cell growth control and initiation of blood coagulation; overexpressed in prostate and ovarian tumors
no_description_avail/Serine protease inhibitor (Kunitz type 1), a Kunitz type serine protease inhibitor that may inhibit hepatocyte growth factor activator (HGFAC), involved in the progression of hepatocellular carcinoma, downregulated in colorectal adenocarcinomas
GP:AK000512_1 Homo sapiens cDNA FLJ20505 fis, clone KAT09459; unnamed protein product. [MASS=37773]/Protein of unknown function
SW:RL30_HUMAN P04645 homo sapiens (human), rattus norvegicus (rat), and mus musculus (mouse). 60s ribosomal protein l30. 2/1995 [MASS=12653]/Ribosomal protein L30, a putative component of the large 60S ribosomal subunit
no_description_avail/Protein of unknown function
GP:S82470_1 BB1=malignant cell expression-enhanced gene/tumor progression-enhanced gene [human, UM-UC-9 bladder carcinoma cell line, mRNA, 1897 nt]; malignant cell expression-enhanced gene/tumor progression-enhanced gene; This sequence comes from Fig. 4A. [MASS=38164]/Member of the membrane bound O-acyl transferase (MBOAT) family, which are found in acyltransferase enzymes
GP:AF055016_1 Homo sapiens clone 24774 unknown mRNA, partial cds. [MASS=23711]/Protein containing a SPRY (SPla and RYanodine Receptor) domain, has high similarity to uncharacterized C. elegans F18H3.1
GP:U52426_1 Homo sapiens GOK (STIM1) mRNA, complete cds. [MASS=77492]/Stromal interaction molecule 1, a protein involved in both positive and negative control of cell proliferation; loss of expression is associated with rhabdomyosarcoma and may be involved in Beckwith Wiedemann syndrome
GP:AF177377_1 Homo sapiens cytoplasmic protein mRNA, complete cds; 120kDa; strongly overexpressed during mitosis. [MASS=108903]/Restrictedly overexpressed proliferation-associated protein, a cytoplasmic protein containing WD repeats and a serine protease motif, highly expressed only during mitosis
GP:AK022722_1 Homo sapiens cDNA FLJ12660 fis, clone NT2RM4002174, moderately similar to MRP PROTEIN; unnamed protein product. [MASS=31130]/Protein of unknown function, has high similarity to uncharacterized C. albicans Orf6.5982p
GP:AF157325_1 Homo sapiens sterol regulatory element binding protein 3 (SREBP3) mRNA, complete cds. [MASS=51277]/Epithelial protein lost in neoplasm, a component of actin cytoskeleton, exists as alternative splice forms alpha and beta, and contributes to cell growth regulation; downregulation of EPLIN alpha may promote cancer progression
GP:AL096857_1 Novel human mRNA from chromosome 1, which has similarities to BAT2 genes. [MASS=295830]
GP:AB018313_1 Homo sapiens mRNA for KIAA0770 protein, partial cds. [MASS=83943]/Vam6-Vps39-like, contains a citron homology (CNH) domain and a clathrin heavy chain repeat domain, forms homooligomers and may act as a tethering or docking factor that promotes lysosome clustering and fusion
SWN:Z272_HUMAN Q14592 homo sapiens (human). zinc finger protein 272 (zinc finger protein hzf8) (fragment). 8/2001 [MASS=19678]/Zinc finger protein 272, a protein that contains tandem zinc fingers, may be involved in hemopoiesis
GP:U16406_1 Human immunodeficiency virus type 1 patient I01, clone D, envelope glycoprotein (env) gene, V3 region, partial cds. [MASS=10815]
GP:D87453_1 Human mRNA for KIAA0264 gene, partial cds. [MASS=47798]/Protein of unknown function
PIR2:T17219 hypothetical protein DKFZp566H1924.1 - human (fragment) [MASS=32002]/Stromal cell derived factor receptor 1, contains an immunoglobulin domain
GP:AK025859_1 Homo sapiens cDNA: FLJ22206 fis, clone HRC01431; unnamed protein product. [MASS=49620]/Protein containing ten ankyrin (Ank) repeats, which may mediate protein-protein interactions, has moderate similarity to a region of ankyrin 3 (human ANK3, ankyrin G), which may link integral membrane proteins to the cytoskeleton
SW:L130_HUMAN P42704 homo sapiens (human). 130 kda leucine-rich protein (lrp 130) (gp130). 10/1996 [MASS=145201]/Leucine-rich PPR-motif containing, a leucine-rich protein associated with multiprotein complexes, binds mRNA and is likely involved in nuclear export of mRNA, may be involved in cytoskeletal organization
GP:AK001207_1 Homo sapiens cDNA FLJ10345 fis, clone NT2RM2000984; unnamed protein product. [MASS=38193]
no_description_avail/Esp-15 homology domain-containing 4, may be involved in type VI collagen filament formation or stabilization, contains an N-terminal nucleotide-binding site, a bipartite nuclear localization signal, and a C-terminal EH protein-binding domain
SW:SMN1_HUMAN Q16637 homo sapiens (human). survival motor neuron protein 1. 5/2000 [MASS=31849]/Survival of motor neuron 2 centromeric, involved in neuromuscular function and may be required for neurogenesis; deletion of the corresponding gene is associated with spinal muscular atrophy (SMA) and adult progressive muscular atrophy
GP:U52111_2 Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protei [MASS=20867]/ribosomal protein L18a/Ribosomal protein L18a, a component of the 60S ribosomal subunit that is likely to play a role in protein synthesis; murine Rpl18a may play a role in squamous cell carcinoma progression

SW:PCP_HUMAN P42785 homo sapiens (human). lysosomal pro-x carboxypeptidase precursor (ec 3.4.16.2) (prolylcarboxypeptidase) (prcp) (proline carboxypeptidase) (angiotensinase c) (lysosomal carboxypeptida [MASS=55800]/Prolylcarboxypeptidase (angiotensinase C), a serine carboxypeptidase that catalyzes the cleavage of C-terminal amino acid residues linked to proline; corresponding gene may be a candidate locus for essential hypertension
SW:EP1_HUMAN Q15668 homo sapiens (human), pan troglodytes (chimpanzee), and macaca fascicularis (crab eating macaque) (cynomolgus monkey). epididymal secretory protein e1 precursor (epi-1) (he1) (epidid [MASS=16570]/Neimann-Pick disease type C2 (epididymal secretory protein 1), putative lysosomal protein that may play a role in cholesterol transport; mutations of the corresponding gene cause Niemann-Pick type C2 disease
PIR2:T46250 hypothetical protein DKFZp761A051.1 - human (fragment) [MASS=58084]
SW:HE47_HUMAN Q13838 homo sapiens (human). probable atp-dependent rna helicase p47. 11/1997 [MASS=48991]/HLA-B associated transcript 1, a putative DEAD/H box ATP-dependent RNA helicase, involved in immune response and may negatively regulate inflammation by repressing cytokine production; corresponding gene lies within the major histocompatibility complex
GP:AF161494_1 Homo sapiens HSPC145 mRNA, complete cds. [MASS=33420]/mitochondrial ribosomal protein L15/Protein containing a ribosomal protein L15 family amino terminal domain, has a region of moderate similarity to a region of S. cerevisiae Mrpl10p, which is a mitochondrial ribosomal protein of the large subunit (YmL10)
GP:AL035413_5 Human DNA sequence from clone RP4-657E11 on chromosome 1p35.1-36.23 Contains 3' part of the CAPZB (capping protein (actin filament) muscle Z-line, beta) gene, genes for aldo-keto reductase family 7 (aflatoxin aldehyde reductase) members A2 (AKR7A2) a [MASS=95553]/ EST/Protein of unknown function
EST/Protein of unknown function, has moderate similarity to uncharacterized C. elegans C01G10.8
PIR2:T42692 hypothetical protein DKFZp434D0428.1 - human (fragment) [MASS=51316]
homo sapiens (human). protein c9orf10/EST/Protein of unknown function, has weak similarity to uncharacterized human KIAA1838
GP:AK024512_1 Homo sapiens cDNA: FLJ20859 fis, clone ADKA01617; unnamed protein product. [MASS=50734]/ probable ATPase/ EST/Protein of unknown function, has low similarity to uncharacterized C. elegans F32A7.4
GP:AF157317_1 Homo sapiens AD-015 protein mRNA, complete cds; protein x 0008. [MASS=22864]/ similar to mouse minor histocompatibility antigen precursor/Protein of unknown function
GP:AF161507_1 Homo sapiens HSPC158 mRNA, complete cds. [MASS=26192]/mitochondrial ribosomal protein L22/Mitochondrial ribosomal protein L22, a putative structural protein of the mitochondrial large 39S ribosomal subunit, may play a role in protein biosynthesis
SWN:ZH10_HUMAN Q14585 homo sapiens (human). zinc finger protein hzf10. 8/2001 [MASS=55383]/Zinc finger protein 345, a Kruppel-related zinc protein
GP:AB039669_1 Homo sapiens mRNA for ALEX3, complete cds; similar to ALEX1 protein. [MASS=42501]/a novel human armadillo repeat containing protein/Arm proteins lost in epithelial cancers on chromosome X 3, a member of the ALEX protein family, contains a single armadillo-like (Arm) repeat and N-terminal hydrophobic residues that suggests it may be a membrane-associated protein
SW:DDX9_HUMAN Q08211 homo sapiens (human). atp-dependent rna helicase a (nuclear dna helicase ii) (ndh ii) (dead box protein 9). 12/1998 [MASS=140877]/DEAD box protein 9 (RNA helicase A), ATP-dependent RNA and DNA helicase, involved in HIV replication and transcription, and retroviral mRNA nuclear export; present as an autoantigen in patients with systemic lupus erythematosus
GP:AB043007_1 Homo sapiens SDF2L1 mRNA for SDF2 like protein 1, complete cds. [MASS=23511]/Stromal cell-derived factor 2-like 1, a member of the protein-O-mannosyltransferase-rotated abdomen (pmt-rt) family, contains three MIR (protein mannosyltransferase, IP3R and RyR) domains and a C-terminal ER retention signal
Similar to dipeptidyl peptidase 7/Dipeptidyl peptidase 7 (quiescent cell proline dipeptidase), a serine protease that cleaves N-terminal Xaa-Pro dipeptides, member of a family of post proline cleaving exopeptidases, may play a role in inhibition of apoptosis in quiescent lymphocytes
similar to neuronal protein 15.6/Protein of unknown function, has high similarity to uncharacterized mouse Np15.6
SW:G732_HUMAN P16422 homo sapiens major gastrointestinal tumor-associated protein ga733-2 precursor (epithelial cell surface antigen) (epithelial glycoprotein) (egp) (adenocarcinoma-associated antigen) [MASS=34920]/Tumor-associated calcium signal transducer 1 (Epithelial cell adhesion molecule), a surface glycoprotein that mediates homotypic calcium-independent cell adhesion, acts in pancreas morphogenesis, present on most carcinomas
estrogen-responsive finger protein/Zinc finger protein 147, an estrogen-responsive zinc-finger transcription factor required for estrogen induced cell proliferation and may mediate estrogen action
GP:AL035689_4 Human DNA sequence from clone RP1-187J11 on chromosome 6q11.1-22.33. Contains the gene for a novel protein similar to S. pombe and S. cerevisiae predicted proteins, the gene for a novel protein similar to protein kinase C inhibitors, the 3' end of th [MASS=20361]/Member of the histidine triad (HIT) family
GP:S69272_1 cytoplasmic antiproteinase=38 kda intracellular serine proteinase inhibitor [human, placenta, mRNA, 1465 nt]; 38 kda intracellular serine proteinase inhibitor; This sequence comes from Fig. 1; CAP. [MASS=42590]/Serine proteinase inhibitor clade B member 6 (placental thrombin inhibitor), member of the serine proteinase inhibitor (serpin) superfamily, may play roles in keratinocyte differentiation and platelet activat
GP:AB046803_1 Homo sapiens mRNA for KIAA1583 protein, partial cds; Start codon is not identified.. [MASS=46775]/ EST
mesenchymal stem cell protein DSCD75

SWN:U123_HUMAN Q9uh06 homo sapiens (human). hypothetical 12.4 kda protein bk223h9.2. 8/2001 [MASS=12405]/Member of the UPF0123 uncharacterized protein family, has very strong similarity to uncharacterized rat Loc192246
GP:AK025822_1 Homo sapiens cDNA: FLJ22169 fis, clone HRC00632; unnamed protein product. [MASS=74624]/EST/Protein of unknown function, has low similarity to a region of S. cerevisiae Apg9p, which is required for starvation-induced autophagy
GP:AJ245620_1 Homo sapiens CTL1 gene. [MASS=73349]/CDW92 antigen; mutations in the corresponding gene may result in familial dysautonomia
SWN:NDR2_HUMAN Q9un36 homo sapiens (human). ndrg2 protein (syld709613 protein). 8/2001 [MASS=39289]/N-myc downstream-regulated gene 2, a member of the Ndr family, which are involved in cell differentiation
GP:AK022590_1 Homo sapiens cDNA FLJ12528 fis, clone NT2RM4000155, moderately similar to THREONYL-TRNA SYNTHETASE, CYTOPLASMIC (EC 6.1.1.3); unnamed protein product. [MASS=66372]/Protein containing a tRNA synthetase class II core domain (G, H, P, S and T), a TGS (ThrRS, GTPase, and SpoT) domain, and an anticodon binding domain, has moderate similarity to threonyl-tRNA synthetase (human TARS)/Protein containing a tRNA synthetase class II core domain (G, H, P, S and T), a TGS (ThrRS, GTPase, and SpoT) domain, and an anticodon binding domain, has moderate similarity to threonyl-tRNA synthetase (human TARS)
GP:D26361_1 Human mRNA for KIAA0042 gene, complete cds. [MASS=186492]/EST/Protein containing two kinesin motor domains, which bind ATP and microtubules, and two forkhead associated (FHA) domains, which bind phosphopeptides, has a region of moderate similarity to a region of plus-end directed motor kinesin (C. elegans UNC-104)
SW:TISB_HUMAN Q07352 homo sapiens (human). tis11b protein (butyrate response factor 1) (egf-response factor 1) (erf-1). 7/1999 [MASS=36314]/TATA box binding protein-associated factor RNA polymerase III C 90, a subunit of RNA polymerase III transcription factor TFIIIB that is required for transcription of genes encoding tRNA, 5S rRNA, and small nuclear RNAs
GP:AF220049_1 Homo sapiens uncharacterized hematopoietic stem/progenitor cells protein MDS029 mRNA, complete cds. [MASS=12199]/Protein of unknown function, has high similarity to a region of C. elegans KLP-17, which is a C-terminal motor kinesin that is involved in chromosome movement during early embryonic and germ line development
SW:MA32_HUMAN Q07021 homo sapiens (human). complement component 1, q subcomponent binding protein, mitochondrial precursor (glycoprotein gc1qbp) (gc1q-r protein) (hyaluronan-binding protein 1) (pre-mrna [MASS=31362]/Complement component 1 q subcomponent binding protein, binds the globular heads of complement subcomponent C1q, interacts with a wide array of proteins, involved in regulation of complement activation, may be associated with sperm motility
mitochondrial ribosomal protein S30; PAP protein; programmed cell death 9; bone marrow protein BM04/Mitochondrial ribosomal protein S30 (programmed cell death 9), a putative structural protein of the mitochondrial small 28S ribosomal subunit, may play a role in protein biosynthesis and apoptosis
GP:U96114_1 Homo sapiens Nedd-4-like ubiquitin-protein ligase WWP2 mRNA, complete cds; Nedd-4-like ubiquitin-protein ligase; WW domain-containing protein. [MASS=99070]/Atrophin 1 interacting protein 2, putative Nedd4-like ubiquitin ligase, may play a role in the ubiquitination and endocytosis of C1C 5 protein (CLCN5), may be involved in the ubiquitin-dependent degradation of LMP2A and Lyn
SW:Z142_HUMAN P52746 homo sapiens (human). zinc finger protein 142 (kiaa0236) (ha4654). 5/2000 [MASS=187866]/Zinc finger protein 142, a putative transcription factor, member of the Kruppel zinc-finger protein family
SW:ES1_HUMAN P30042 homo sapiens (human). es1 protein homolog precursor (protein knp-i) (gt335). 5/2000 [MASS=28142]/Protein with similarity to zebrafish ES1 and E. coli SCRP-27A, highly expressed in skeletal muscle and heart
GP:AF151817_1 Homo sapiens CGI-59 protein mRNA, complete cds. [MASS=45695]/weakly similar to SPLICING FACTOR, ARGININE/SERINE-RICH 4/Member of the DUF259 protein of unknown function family, has strong similarity to uncharacterized human LUC7L
GP:AK001714_1 Homo sapiens cDNA FLJ10852 fis, clone NT2RP4001498, weakly similar to ANKYRIN REPEAT-CONTAINING PROTEIN AKR1; unnamed protein product. [MASS=54514]/Protein contains five ankyrin (Ank) repeats, which may mediate protein-protein interactions, and a DHHC-type zinc finger or NEW1 domain
SW:MIF_HUMAN P14174 homo sapiens (human). macrophage migration inhibitory factor (mif) (glycosylation-inhibiting factor) (gif). 5/2000 [MASS=12345]/Macrophage migration inhibitory factor, an immunoregulatory cytokine involved in monocyte migration and chemotaxis, T cell activation, delayed type hypersensitivity, and the response to lipopolysaccharide, counteracts glucocorticoid suppression
GP:AF042284_1 Homo sapiens unknown mRNA; similar to fission yeast sulfide dehydrogenase. [MASS=49961]/CGI-44 protein (sulfide dehydrogenase like yeast), a putative oxidoreductase homolog of Schizosaccharomyces pombe hmt2
SW:TFPI_HUMAN P10646 homo sapiens (human). tissue factor pathway inhibitor precursor (tfpi) (lipoprotein- associated coagulation inhibitor) (laci) (extrinsic pathway inhibitor) (epi). 12/1998 [MASS=35015]/Tissue factor pathway inhibitor, a Kunitz-type protease inhibitor that inhibits fibrin clot formation by directly inhibiting factor Xa and indirectly inhibiting the factor VIIa/tissue factor complex
GP:AF151809_1 Homo sapiens CGI-51 protein mRNA, complete cds. [MASS=52160]/similar to GASTRIN/CHOLECYSTOKININ TYPE BRECEPTOR (CCK-B RECEPTOR) (CCK-BR) (H. sapiens)/Protein of unknown function, has low similarity to uncharacterized C. elegans GOP-3

GP:AF085361_1 Homo sapiens HSPC032 mRNA, complete cds. [MASS=33331]/mitochondrial carrier homolog 2 /Member of the mitochondrial carrier protein family of membrane transporters, has strong similarity to uncharacterized mouse Mtch2
GP:AJ001258_1 Homo sapiens mRNA for NIPSNAP1 protein. [MASS=33324]/NIPSNAP C. elegans homolog 1, a member of the NIPSNAP family of proteins, may have a vesicle transport-related function
GP:AC004528_1 Homo sapiens chromosome 19, cosmid R32184, complete sequence; Hypothetical human protein (partial CDS); CDS constructed from combination of BLASTX, EST matches and Xgrail predictions. N-terminus of protein likely encoded in flanking cosmid R29942. Pr [MASS=47306]/Protein containing four WD domains (WD-40 repeat), which may mediate protein-protein interactions, has a region of low similarity to a region of TATA box binding protein associated factor 2d 100 kD (human TAF5), which functions in transcription initiation
GP:AC004957_1 Homo sapiens PAC clone RP5-1093O17 from 7q11.23-q21, complete sequence; heterogeneous ribonuclear particle protein A1; similar to P49312 (PID:g1350822); H_DJ1093O17.1. [MASS=33911]
GP:AK024450_1 Homo sapiens mRNA for FLJ00042 protein, partial cds; For this clone, GeneMark analysis triggered an alert for spurious CDS split. The result of GeneMark analysis of the nucleotide sequence of this clone i. [MASS=48320]/Protein of unknown function, has a region of low similarity to aplysia Ras-related homolog B (human ARHB), which functions in actin cytoskeleton assembly and is the pharmacological target of certain anti-cancer drugs that inhibit cell growth
SW:PSS8_HUMAN Q16651 homo sapiens (human). prostasin precursor (ec 3.4.21.-). 7/1998 [MASS=36431]/Protease serine 8 (prostasin), a serine protease that plays a role in regulation of the amiloride-sensitive epithelial sodium channel, may act as a suppressor of invasive prostate and breast cancer, overexpressed in ovarian cancer cells
SW:SBP1_HUMAN Q13228 homo sapiens (human). selenium-binding protein 1. 5/2000 [MASS=52313]/Selenium binding protein 1, may have a role in negative regulation of cell growth; mouse Selenbp1 may play a role in mediating the anticarcinogenic effects of selenium
PIR2:T08789 hypothetical protein DKFZp586C1622.1 - human (fragment) [MASS=16138]/Homo sapiens testis-specific chromodomain Y-like protein (CDYL) mRNA/Chromodomain protein Y chromosome-like, a ubiquitously-expressed autosomal protein with similarity to chromodomain-containing proteins located on the Y chromosome
GP:AK022587_1 Homo sapiens cDNA FLJ12525 fis, clone NT2RM4000030, weakly similar to LAS1 PROTEIN; unnamed protein product. [MASS=83065]/Protein of unknown function, has a region of low similarity to a region of S. cerevisiae Las1p, which is involved in cell morphogenesis, cytoskeletal regulation, and bud formation
immunoglobulin light chain variable region (human)
PIR2:S12444 hypothetical protein 458 - human [MASS=49127]/human immunoglobulin lambda genes

Panel 5, pgs. 239-242

Cellular Process	Gene	Functional Group	XPRESS Count	d0:d8 ratio	d0:d8 StdDev	Description
Lipid, Fat, and Sterol Metabolism						
SW:FDFT_HUMAN	FDFT1	19	1	0.22	0.00	SW:FDFT_HUMAN P37268 homo sapiens (human). farnesyl-diphosphate farnesyltransferase (ec 2.5.1.21) (squalene synthetase) (sqs) (ss) (fpp:fpp farnesyltransferase). 10/1996 [MASS=48115]/Squalene synthase (farnesyl-diphosphate farnesyltransferase 1), catalyzes the conversion of farnesyl diphosphate to squalene in cholesterol biosynthesis, may be a potential target for cholesterol lowering therapy
GPN:Y14436_1	PPAP2A	19	2	0.27	0.02	type-2 phosphatidic acid phosphatase alpha-1 /Phosphatidic acid phosphatase type 2a, catalyzes the dephosphorylation of various lipid phosphates, regulates the level of lipid phosphates which are involved in signal transduction
GP:D89053_1	FACL3	19	13	0.29	0.13	fatty-acid-Coenzyme A ligase, long-chain 3 /Fatty acid Coenzyme A ligase long chain 3, a putative long-chain fatty-acyl-CoA synthetase that may function in lipid synthesis and fatty acid degradation
SW:ACDV_HUMAN	ACADVL	19	1	0.32	0.00	SW:ACDV_HUMAN P49748 homo sapiens (human). acyl-coa dehydrogenase, very-long-chain specific, mitochondrial precursor (ec 1.3.99.-) (vlcad). 5/2000 [MASS=70390]/Very long chain acyl-coenzyme A dehydrogenase, oxidizes straight chain acyl-CoAs in the initial step of fatty acid beta-oxidation, severe deficiency results in infant cardiomyopathy with high mortality, mild deficiency results in hypoketotic hypoglycemia
SW:FAS_HUMAN	FASN	19	90	0.34	0.15	SW:FAS_HUMAN P49327 homo sapiens (human). fatty acid synthase (ec 2.3.1.85) [includes: ec 2.3.1.38; ec 2.3.1.39; ec 2.3.1.41; ec 1.1.1.100; ec 4.2.1.61; ec 1.3.1.10; ec 3.1.2.14]. 7/1999 [MASS=273102]/Fatty acid synthase, multifunctional enzyme that synthesizes fatty acids from dietary proteins and carbohydrates; increased expression is associated with tumor growth and development, expression may serve as a prognostic maker for breast cancer
SW:ERG7_HUMAN	LSS	19	1	0.37	0.00	SW:ERG7_HUMAN P48449 homo sapiens (human). lanosterol synthase (ec 5.4.99.7) (oxidosqualene--lanosterol cyclase) (2,3-epoxysqualene--lanosterol cyclase) (osc). 5/2000 [MASS=83309]/Lanosterol synthase, catalyzes the cyclization of (S)-2,3-oxidosqualene forming lanosterol in sterol biosynthesis
SW:COA1_HUMAN	ACACA	19	2	0.41	0.05	SW:COA1_HUMAN Q13085 homo sapiens (human). acetyl-coa carboxylase 1 (ec 6.4.1.2) (acc-alpha) [includes: biotin carboxylase (ec 6.3.4.14)]. 7/1999 [MASS=265040]/Acetyl-Coenzyme A carboxylase alpha, catalyzes the rate-limiting step in long-chain fatty acid biogenesis; deficiency leads to defects in fatty acid synthesis
SW:ACLY_HUMAN	ACLY	19	6	0.44	0.09	SW:ACLY_HUMAN P53396 homo sapiens (human). atp-citrate (pro-s-)-lyase (ec 4.1.3.8) (citrate cleavage enzyme). 10/1996 [MASS=121420]/ATP citrate lyase, catalyzes the formation of acetyl-CoA and oxaloacetate from citrate and CoA with the concomitant hydrolysis of ATP to ADP and phosphate, involved in cholesterol and fatty acid synthesis, nutritionally regulated
SW:LDLR_HUMAN	LDLR	19	3	0.55	0.04	SW:LDLR_HUMAN P01130 homo sapiens (human). low-density lipoprotein receptor precursor (ldl receptor). 5/2000 [MASS=95376]/Low density lipoprotein receptor, mediates uptake of low density lipoproteins, involved in lipid metabolism; gene variations are associated with familial hypercholesterolemia, hypertension, atherosclerosis, and coronary artery disease
SW:NSDL_HUMAN	NSDHL	19	6	0.58	0.16	SW:NSDL_HUMAN Q15738 homo sapiens (human). nad(p)-dependent steroid dehydrogenase-like protein (h105e3 protein). 5/2000 [MASS=41900]/NAD(P)H steroid dehydrogenase-like protein, a 3 beta-hydroxysteroid dehydrogenase that functions in cholesterol biosynthesis; mutations in the corresponding gene cause CHILD syndrome
SW:CP51_HUMAN	CYP51	19	3	0.71	0.04	SW:CP51_HUMAN Q16850 homo sapiens (human). cytochrome p450 51 (ec 1.14.14.1) (cypl1) (p450l1) (sterol 14-alpha demethylase) (lanosterol 14-alpha demethylase) (ldm) (p450-14dm). 5/2000 [MASS=56806]/Lanosterol 14-alpha-demethylase (sterol 14alpha-demethylase); cytochrome P450 enzyme involved in sterol biosynthesis
SW:LCFA_HUMAN	FACL1	19	14	0.81	0.13	SW:LCFA_HUMAN P41215 homo sapiens (human). long-chain-fatty-acid--coa ligase 1 (ec 6.2.1.3) (long-chain acyl-coa synthetase 1) (lacs 1) (palmitoyl-coa ligase). 10/1996 [MASS=78348]/Long chain fatty acid-Coenzyme A ligase (palmitoyl-CoA ligase), a member of the long chain acyl-CoA synthetase family required for lipid synthesis and fatty acid degradation
SW:LCB2_HUMAN	SPTLC2	19	1	0.82	0.00	SW:LCB2_HUMAN O15270 homo sapiens (human). serine palmitoyltransferase 2 (ec 2.3.1.50) (long chain base biosynthesis protein 2) (lcb 2) (serine-palmitoyl-coa transferase 2) (spt 2) (kiaa0526). 5/2000 [MASS=62924]/Serine palmitoyltransferase long chain base subunit 2, member of the aminolevulinate synthase superfamily, catalyzes the first step in ceramide formation, involved in epidermal cell response to UV exposure and in leukemia cell ectopside-induced apoptosis
SW:DRS1_HUMAN	PECI	19	9	0.83	0.22	SW:DRS1_HUMAN O75521 homo sapiens (human). dbi-related protein 1 (drs-1). 5/2000 [MASS=40151]/Peroxisomal D3,D2-enoyl-CoA isomerase, catalyzes the isomerization of 3-cis-octenoyl-CoA to 2-trans-octenoyl-CoAm, a step in the beta oxidation of fatty acids in peroxisomes
SWN:P23_HUMAN	p23	19	2	0.85	0.01	SWN:P23_HUMAN Q15185 homo sapiens (human). telomerase-binding protein p23 (hsp90 co-chaperone) (progesterone receptor complex p23). 8/2001 [MASS=18697]/Inactive progesterone receptor (23kD), cochaperone with prostaglandin E synthase activity that is a component of the unstimulated progesterone receptor complex and that enhances receptor complex formation through interactions with Hsp90 (HSPCA)
SW:KIME_HUMAN	MVK	19	1	0.91	0.00	SW:KIME_HUMAN Q03426 homo sapiens (human). mevalonate kinase (ec 2.7.1.36) (mk). 7/1999 [MASS=42451]/Mevalonate kinase (mevalonic aciduria), a peroxisomal enzyme involved in isoprenoid and cholesterol biosynthesis; mutations in the corresponding gene cause mevalonic aciduria, hyperimmunoglobulinemia D and periodic fever syndrome
GP:U66669_1	HIBCH	19	1	0.91	0.00	GP:U66669_1 Homo sapiens 3-hydroxyisobutyryl-coenzyme A hydrolase mRNA, complete cds. [MASS=42908]/Beta-hydroxyisobutyryl-coenzyme A hydrolase, enzyme that hydrolyzes 3-hydroxyisobutyryl CoA, an intermediate of valine catabolism

SW:ASAH_HUMAN	ASAH	19	1	0.99	0.00	SW:ASAH_HUMAN Q13510 homo sapiens (human). acid ceramidase precursor (ec 3.5.1.23) (acylsphingosine deacylase) (n-acylsphingosine amidohydrolase) (ac) (putative 32 kda heart protein) (php32). 5/2000 [MASS=44650]/N-acylsphingosine amidohydrolase (acid ceramidase), catalyzes hydrolysis of ceramide to sphingosine and free fatty acid, inhibits apoptosis, upregulated in prostate cancer, deficiency is associated with Farber disease
GP:AF126782_1	RETSDR1	19	8	1.06	0.21	GP:AF126782_1 Homo sapiens retinal short-chain dehydrogenase/reductase retSDR4 mRNA, complete cds. [MASS=32268]/Short-chain dehydrogenase-reductase 1, catalyzes the NADPH-dependent reduction of all-trans-retinal to retinol, may play a role in visual system phototransduction; the corresponding gene is deleted in many neuroblastoma cell lines with MYCN amplification
SW:OXYB_HUMAN	OSBP	19	3	1.08	0.26	SW:OXYB_HUMAN P22059 homo sapiens (human). oxysterol-binding protein. 11/1995 [MASS=89421]/Oxysterol binding protein, member of a family of intracellular lipid receptors, contains a pleckstrin domain and an oxysterol binding domain, binds oxysterols, may play a role in the regulation of cholesterol metabolism and oxysterol-induced cell death
SW:CPT2_HUMAN	CPT2	19	1	1.08	0.00	SW:CPT2_HUMAN P23786 homo sapiens (human). carnitine o-palmitoyltransferase ii, mitochondrial precursor (ec 2.3.1.21) (cpt ii). 5/2000 [MASS=73777]/Carnitine palmitoyltransferase II, a mitochondrial long-chain fatty acid oxidation enzyme; mutations are associated with a lipid metabolism disorder that includes recurrent myopathy with progressive rhabdomyolysis, muscle weakness and myoglobinuria
SW:FAAH_HUMAN	FAAH	19	3	1.10	0.22	SW:FAAH_HUMAN O00519 homo sapiens (human). fatty-acid amide hydrolase (ec 3.1.-.-) (oleamide hydrolase). 5/2000 [MASS=63038]/Fatty acid amide hydrolase, degrades neuromodulatory fatty acid amides, including anandamide, predicted to have a role in a wide variety of physiologic efffects such as voluntary movement, pain, sleep, and fertility, may have a role in Parkinson disease
SW:HBP_HUMAN	HDLBP	19	3	1.11	0.27	SW:HBP_HUMAN Q00341 homo sapiens (human). high density lipoprotein binding protein (hdl-binding protein). 12/1998 [MASS=141440]/High density lipoprotein binding protein, binds and inhibits cleavage of the 3' UTR of vitellogenin mRNA, binds and promotes nuclear export of tRNA, binds high density lipoproteins and may have roles in cholesterol metabolism and atherogenesis
SW:NPC1_HUMAN	NPC1	19	1	1.16	0.00	SW:NPC1_HUMAN O15118 homo sapiens (human). niemann-pick c1 protein precursor. 5/2000 [MASS=142149]/Niemann-Pick disease type C1, a lysosomal sterol transporter involved in cholesterol metabolism; mutation of the corresponding gene causes Niemann-Pick type C1 disease and mutation of mouse Npc1 causes a disease like Niemann-Pick type C1 disease
SW:PEBP_HUMAN	PBP	19	2	1.17	0.15	SW:PEBP_HUMAN P30086 homo sapiens (human). phosphatidylethanolamine-binding protein (pebp) (neuropolypeptide h3). 7/1999 [MASS=20926]/Phosphatidylethanolamine-binding protein, binds GTP, may regulate cAMP accumulation, enhance acetylcholine synthesis, and play a role in organizing phospholipids in the myelin sheath
SW:GLCM_HUMAN	GBA	19	2	1.21	0.09	SW:GLCM_HUMAN P04062 homo sapiens (human). glucosylceramidase precursor (ec 3.2.1.45) (beta-glucocerebrosidase) (acid beta-glucosidase) (d-glucosyl-n-acylsphingosine glucohydrolase) (alglucerase) (imigl [MASS=59697]/Acid beta glucosidase (beta-glucocerebrosidase), a lysosomal membrane protein that hydrolyzes glucosylceramide and glucosylsphingosine, may play a role in epidermal differentiation; mutations in the corresponding gene cause Gaucher's disease
SW:PI52_HUMAN	PIP5K2A	19	1	1.24	0.00	SW:PI52_HUMAN P48426 homo sapiens (human). phosphatidylinositol-4-phosphate 5-kinase type ii alpha (ec 2.7.1.68) (pip5kii-alpha) (1-phosphatidylinositol-4-phosphate kinase) (ptdins(4)p-5-kinase b isofor [MASS=46193]/Phosphatidylinositol-4-phosphate 5-kinase type II, alpha, a member of a family of kinases responsible for the synthesis of PtdIns(4,5)P2
GP:AF034544_1	DHCR7	19	6	1.25	0.30	GP:AF034544_1 Homo sapiens delta7-sterol reductase mRNA, complete cds; D7SR. [MASS=54516]/7-dehydrocholesterol reductase, catalyzes the reduction of the C7-C8 (delta 7) double bond of 7-dehydrocholesterol in the last step of cholesterol biosynthesis; mutations in the corresponding gene are associated with Smith-Lemli-Opitz
SW:THIK_HUMAN	ACAA1	19	15	1.26	0.25	SW:THIK_HUMAN P09110 homo sapiens (human). 3-ketoacyl-coa thiolase, peroxisomal precursor (ec 2.3.1.16) (beta-ketothiolase) (acetyl-coa acyltransferase) (peroxisomal 3-oxoacyl- coa thiolase). 7/1999 [MASS=44292]/Peroxisomal 3-oxoacyl-coenzyme A thiolase (peroxisomal 3-ketoacyl-Coenzyme A thiolase), functions in peroxisomal beta-oxidation of fatty acids, deficiency is associated with rhizomelic chondrodysplasia punctata (RCDP)
SW:CPT1_HUMAN	CPT1A	19	1	1.30	0.00	SW:CPT1_HUMAN P50416 homo sapiens (human). carnitine o-palmitoyltransferase i, mitochondrial liver isoform (ec 2.3.1.21) (cpt i) (cpti-l). 7/1999 [MASS=88429]/Liver carnitine palmitoyltransferase I, enzyme of long-chain fatty acid beta-oxidation pathway; mutations in the corresponding gene are associated with carnitine palmitoyltransferase I deficiency
SW:D3D2_HUMAN	DCI	19	3	1.31	0.20	SW:D3D2_HUMAN P42126 homo sapiens (human). 3,2-trans-enoyl-coa isomerase, mitochondrial precursor (ec 5.3.3.8) (dodecenoyl-coa delta-isomerase). 7/1999 [MASS=32816]/Dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenzyme A isomerase), catalyzes the isomerization of 3-cis and 3-trans enoyl CoA esters to 2-trans enoyl CoA esters, functions in mitochondrial beta-oxidation of unsaturated fatty acids
SW:SAP_HUMAN	PSAP	19	14	1.31	0.91	SW:SAP_HUMAN P07602 h proactivator polypeptide precursor [contains: saposin a (protein a); saposin b (sphingolipid activator protein 1) (sap-1) (dispersin) (sulfatide/gm1 activator); saposin c (co-beta- [MASS=58113]/Prosaposin, precursor of saposins A, B, C, and D which transport gangliosides and activate sphingolipid hydrolysis, stimulates neurite growth and inhibits apoptosis; variants are associated with metachromatic leukodystrophy and Gaucher disease
GP:AB037108_1	TPRA40	19	2	1.36	0.09	GP:AB037108_1 Homo sapiens mRNA for seven transmembrane domain orphan receptor, complete cds; seven transmembrane domain containing protein. [MASS=41090]/Protein with strong similarity to murine Tpra40, which is a seven transmembrane domain protein expressed in 3T3 adipocytes, and that has elevated expression in epididymal fat of genetically diabetic and obese mice

SW:ECH1_HUMAN	ECH1	19	28	1.36	0.24	SW:ECH1_HUMAN Q13011 homo sapiens (human). delta3,5-delta2,4-dienoyl-coa isomerase precursor (ec 5.3.3.-). 7/1999 [MASS=35994]/Enoyl Coenzyme A hydratase 1 (peroxisomal), putative enzyme that may play a role in peroxisomal beta-oxidation
SW:SAP3_HUMAN	GM2A	19	3	1.39	0.14	SW:SAP3_HUMAN P17900 homo sapiens (human). ganglioside gm2 activator precursor (cerebroside sulfate activator protein) (shingolipid activator protein 3) (sap-3). 7/1999 [MASS=20822]/GM2 ganglioside activator protein, binds glycolipids and is a cofactor for GM2 ganglioside hydrolysis by beta hexosaminidase A, activates phospholipase D, and inhibits platelet activating factor; mutation of the gene causes GM2-gangliosidosis variant AB
GP:AF035959_1	PPAP2C	19	1	1.42	0.00	GP:AF035959_1 Homo sapiens type-2 phosphatidic acid phosphatase-gamma (PAP2-g) mRNA, complete cds; phosphatidate phosphohydrolase; phospholipid phosphatase. [MASS=32574]/Phosphatidic acid phosphatase 2c, hydrolyzes phospholipids, may play a role in signal transduction
SW:OCRL_HUMAN	OCRL	19	2	1.42	1.00	SW:OCRL_HUMAN Q01968 homo sapiens (human). lowe's oculocerebrorenal syndrome protein. 7/1998 [MASS=111485]/Oculocerebrorenal syndrome of Lowe, phosphatidylinositol-4,5-bisphosphate 5-phosphatase, may play a role in intracellular protein trafficking; mutation of the corresponding gene causes Lowe oculocerebrorenal syndrome
GP:AB033078_1	SGPL1	19	2	1.44	0.06	GP:AB033078_1 Homo sapiens mRNA for KIAA1252 protein, partial cds; Start codon is not identified.. [MASS=64962]/Protein with strong similarity to sphingosine phosphate lyase 1 (mouse Sgpl1), which is a member of the carbon-carbon lyase subclass of aldehyde-lyases that catalyzes cleavage of sphingosine phosphate and is involved in proliferative signal transduction
SWN:CNE3_HUMAN	CPN3	19	28	1.47	0.27	SWN:CNE3_HUMAN O75131 homo sapiens (human). copine iii. 8/2001 [MASS=60131]/Copine III, a member of the copine family of phospholipid binding proteins, contains C2 and integrin A domains, may play a role in membrane trafficking, displays protein kinase activity, however, it does not contain a traditional kinase catalytic domain
SW:NLTP_HUMAN	SCP2	19	2	1.50	0.06	SW:NLTP_HUMAN P22307 homo sapiens (human). nonspecific lipid-transfer protein precursor (nsl-tp) (sterol carrier protein 2) (scp-2) (sterol carrier protein x) (scp-x) (scpx). 5/2000 [MASS=58994]/Sterol carrier protein 2, catalyzes the exchange of phospholipids between membranes, stimulates cholesterol metabolism and may regulate steroidogenesis; alternative form, SCPX, is a 3 oxoacyl CoA thiolase
SW:CAOP_HUMAN	ACOX1 or ACOX	19	1	1.53	0.00	SW:CAOP_HUMAN Q15067 homo sapiens (human). acyl-coenzyme a oxidase, peroxisomal (ec 1.3.3.6) (palmitoyl-coa oxidase) (aox). 11/1997 [MASS=74502]/Peroxisomal acyl-coenzyme A oxidase, catalyzes the first step in very long chain fatty acid beta-oxidation, desaturates acyl-CoA to 2-trans-enoyl-CoA and produces hydrogen peroxide
SW:PKBS_HUMAN	BZRP	19	2	1.57	0.04	SW:PKBS_HUMAN P30536 homo sapiens (human). peripheral-type benzodiazepine receptor (pbr) (pkbs) (mitochondrial benzodiazepine receptor). 6/1994 [MASS=18779]/Benzodiazepine receptor (peripheral), involved in steroid biosynthesis, cell proliferation, and may contribute to mitochondrial biogenesis and inhibit oxygen radical induced apoptosis; expression, nuclear location may correlate to breast tumor progression
SW:PXF_HUMAN	PXF	19	1	1.61	0.00	SW:PXF_HUMAN P40855 homo sapiens (human). peroxisomal farnesylated protein (33 kda housekeeping protein). 12/1998 [MASS=32807]/Peroxisomal farnesylated protein, peroxisomal protein that binds several peroxisomal membrane proteins (PMP), involved in early stages of PMP import and peroxisomal biogenesis; deficiency is associated with Zellweger syndrome complementation group J
SW:DHA4_HUMAN	ALDH3A2	19	2	1.62	0.67	SW:DHA4_HUMAN P51648 homo sapiens (human). fatty aldehyde dehydrogenase (ec 1.2.1.3) (aldehyde dehydrogenase, microsomal) (aldh class 3). 7/1999 [MASS=54848]/Aldehyde dehyrogenase 3 family member A2, catalyzes the oxidation of long chain fatty aldehydes and leukotrienes; mutation of the corresponding gene causes Sjogren Larsson syndrome, a disorder marked by mental retardation, spasticity, and ichthyosis
SW:HCD2_HUMAN	HADH2	19	4	1.67	0.12	SW:HCD2_HUMAN Q99714 homo sapiens (human). 3-hydroxyacyl-coa dehydrogenase type ii (ec 1.1.1.35) (endoplasmic reticulum-associated amyloid beta-peptide binding protein) (short- chain type dehydrogenase/ [MASS=26923]/Hydroxyacyl-Coenzyme A dehydrogenase (type II), catalyzes the oxidation of steroids and alcohols, binds amyloid-beta protein; overexpressed and mediates neurotoxicity of Alzheimer's disease, mutation in the corresponding gene causes hyperinsulinism
SW:DHB4_HUMAN	HSD17B4	19	12	1.74	0.52	SW:DHB4_HUMAN P51659 homo sapiens (human). estradiol 17 beta-dehydrogenase 4 (ec 1.1.1.62) (17-beta-hsd 4) (17-beta-hydroxysteroid dehydrogenase 4). 11/1997 [MASS=79686]/Type IV 17 beta-hydroxysteroid dehydrogenase, a peroxisomal multifunctional enzyme with estradiol 17 beta-dehydrogenase and D-3 hydroxyacyl CoA dehydratase activities, involved in steroid and bile acid metabolism
SW:AGAL_HUMAN	GLA	19	1	1.80	0.00	SW:BDH_HUMAN P06280 homo sapiens (human). alpha-galactosidase a precursor (ec 3.2.1.22) (melibiase) (alpha-d-galactoside galactohydrolase) (alpha-d-galactosidase a). 7/1998 [MASS=48767]/Alpha-galactosidase A (alpha-D-galactoside galactohydrolase), hydrolyzes glycosphingolipids to release alpha-D-galactosyl residues; mutation of the corresponding gene causes Fabry disease
SW:ADRO_HUMAN	FDXR	19	1	1.82	0.00	SW:ADRO_HUMAN P22570 homo sapiens (human). nadph:adrenodoxin oxidoreductase precursor (ec 1.18.1.2) (adrenodoxin reductase) (ferredoxin-nadp(+) reductase). 7/1999 [MASS=53809]/Ferredoxin reductase, mitochondrial flavoprotein that mediates electron transport from NADPH to cytochrome P450scc
SW:ECHB_HUMAN	HADHB	19	4	1.87	0.07	SW:ECHB_HUMAN P55084 homo sapiens (human). trifunctonal enzyme beta subunit, mitochondrial precursor (tp-beta) [includes: 3-ketoacyl-coa thiolase (ec 2.3.1.16) (acetyl-coa acyltransferase) (beta-ketothi [MASS=51294]/3-hydroxyacyl-CoA dehydrogenase, 3-ketoacyl-CoA thiolase trifunctional protein beta subunit, involved in fatty acid beta-oxidation; variants are associated with trifunctional protein deficiency, sudden infant death syndrome and liver failure

SW:CNBP_HUMAN	ZNF9	19	2	1.87	0.27	SW:CNBP_HUMAN P20694 homo sapiens (human), and rattus norvegicus (rat). cellular nucleic acid binding protein (cnbp). 11/1997 [MASS=19463]/Zinc-finger protein that binds to sterol regulatory element (SRE) and may function in sterol-mediated repression of genes encoding the low density lipoprotein receptor and enzymes of the cholesterol biosynthetic pathway
SW:MAOM_HUMAN	ME2	19	2	1.96	0.04	SW:MAOM_HUMAN P23368 homo sapiens (human). nad-dependent malic enzyme, mitochondrial precursor (ec 1.1.1.38) (nad-me). 5/2000 [MASS=65444]/Malic enzyme 2, a NAD(+)-dependent mitochondrial form of malic enzyme, catalyzes the oxidative decarboxylation of malate to form pyruvate
SW:ECHA_HUMAN	HADHA	19	13	1.97	0.65	SW:ECHA_HUMAN P40939 homo sapiens (human). mitochondrial trifunctional enzyme alpha subunit precursor (tp-alpha) [includes: long-chain enoyl-coa hydratase (ec 4.2.1.17); long chain 3-hydroxyacyl-coa deh [MASS=82960]/Mitochondrial long-chain enoyl-CoA hydratase/3-hydroxyacyl-CoA dehydrogenase/3-ketoacyl-CoA thiolase alpha subunit, involved in fatty acid beta-oxidation, mutations are associated with trifuctional protein deficiency and Reye-like syndrome
SW:ETFB_HUMAN	ETFB	19	2	1.99	0.48	SW:ETFB_HUMAN P38117 homo sapiens (human). electron transfer flavoprotein beta-subunit (beta-etf). 5/2000 [MASS=27844]/Electron transfer flavoprotein beta subunit, shuttles electrons between primary flavoprotein dehydrogenases involved in mitochondrial fatty acid metabolism and ubiquinone oxidoreductase; genetic variants are associated with type II glutaric acidemia
GP:AL023805_1	PLCB4	19	6	2.00	0.24	GP:AL023805_1 Human DNA sequence from clone RP4-811H13 on chromosome 20p12. Contains part of the PLCB4 gene for Phospholipase C beta 4, STSs, GSSs and a CpG island, complete sequence; combines with dJ1119D9.2.1 and .2 in Em:AL031652 to form isoforms 5 and 6; may a [MASS=61433]/1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase beta 4/Phospholipase C beta 4, member of a G protein-regulated family of phospholipases that hydrolyze phosphatidylinositol 4,5-bisphosphate to the second messengers inositol 1,4,5-trisphosphate and diacylglycerol
SW:GST3_HUMAN	MGST3	19	2	2.31	0.83	SW:GST3_HUMAN O14880 homo sapiens (human). microsomal glutathione s-transferase 3 (ec 2.5.1.18) (microsomal gst-3) (microsomal gst-iii). 5/2000 [MASS=16516]/Microsomal glutathione S-transferase 3, a microsomal membrane protein that has glutathione-dependent transferase and peroxidase activities, member of a family that includes 5-lipoxygenase activating protein (ALOX5AP) and leukotriene-C4 synthase (LTC4S)
SW:ETFA_HUMAN	ETFA	19	1	2.36	0.00	SW:ETFA_HUMAN P13804 homo sapiens (human). electron transfer flavoprotein alpha-subunit precursor (alpha-etf). 5/2000 [MASS=35080]/Electron transfer flavoprotein alpha subunit, shuttles electrons between flavoprotein dehydrogenases of mitochondrial fatty acid metabolism and ubiquinone oxidoreductase, deficiency associated with Type II glutaricaciduria
SW:MAZ_HUMAN	MAZ	19	1	2.37	0.00	SW:MAZ_HUMAN P56270 homo sapiens (human). myc-associated zinc finger protein (mazi) (purine-binding transcription factor) (pur-1) (zf87) (zif87). 7/1999 [MASS=48608]/MYC-associated zinc finger protein (purine-binding transcription factor), functions both as a positive and a negative regulator of gene expression and may also have roles in initiating and terminating transcription
SW:THIL_HUMAN	ACAT1	19	2	2.44	0.44	SW:THIL_HUMAN P24752 homo sapiens (human). acetyl-coa acetyltransferase, mitochondrial precursor (ec 2.3.1.9) (acetoacetyl-coa thiolase) (t2). 7/1999 [MASS=45200]/Acetyl-Coenzyme A acetyltransferase 1 (mitochondrial acetoacetyl-coenzyme A thiolase); mutations in the corresponding gene are associated with 3-ketothiolase deficiency
GP:AF161397_1	HPCL2	19	2	2.53	0.16	GP:AF161397_1 Homo sapiens HSPC279 mRNA, partial cds. [MASS=64199]/Homo sapiens mRNA for 2-hydroxyphytanoyl-CoA lyase; thiamine pyrophosphate dependent enzyme/2-Hydroxyphytanoyl-CoA lyase (peroxisomal 2-hydroxyphytanoyl-CoA lyase), catalyzes the thiamine pyrophosphate-dependent cleavage of C-C bonds during alpha-oxidation of 3-methyl-branched fatty acids to form formyl-CoA and 2-methyl-branched fatty aldehyde
SW:TPP1_HUMAN	CLN2	19	1	2.62	0.00	SW:TPP1_HUMAN O14773 homo sapiens (human). tripeptidyl-peptidase i precursor (ec 3.4.14.9) (tpp-i) (tripeptidyl aminopeptidase) (lysosomal pepstatin insensitive protease) (lpic). 5/2000 [MASS=61229]/Tripeptidyl peptidase I (ceroid-lipofuscinosis neuronal 2), a lysosomal serine-type peptidase required for degradation of ATP synthase subunit c (ATP5G1 and ATP5G2); mutations in the corresponding gene cause late infantile neuronal ceroid lipofuscinosis
GP:AF002668_1	DEGS	19	1	3.29	0.00	GP:AF002668_1 Homo sapiens putative fatty acid desaturase MLD mRNA, complete cds; putative fatty acid desaturase. [MASS=37866]/Degenerative spermatocyte homolog (Drosophila), member of the membrane fatty acid desaturase family, regulates the biosynthesis of the epidermal growth factor receptor (EGFR)
SW:PA2M_HUMAN	PLA2G2A	19	3	3.94	1.93	SW:PA2M_HUMAN P14555 homo sapiens (human). phospholipase a2, membrane associated precursor (ec 3.1.1.4) (phosphatidylcholine 2-acylhydrolase) (group ii phospholipase a2) (non-pancreatic secretory phosph [MASS=16083]/Group IIA phospholipase A2, a secreted member of the phospholipase A2 family that hydrolyzes the phospholipid sn-2 ester bond, plays roles in phospholipid metabolism, host defense, and inflammation; gene loss reported in a sporadic colorectal tumor
GP:AJ002744_1	GALNT7	19	1	4.00	0.00	GP:AJ002744_1 Homo sapiens mRNA for UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase 7. [MASS=75402]/UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 7, enzyme that functions in O-glycosylation and is specific for partially glycosylated substrates

Cellular Process #	Incyte Groups	# proteins in each class above 1.6 ICAT ratio	# proteins in each class observed (irrespective of ICAT ratio)	# of proteins in each class according to Incyte	# of observed proteins with ICAT ratio > 1.6	# of observed proteins	representation of class compared to random expectation	-log10p-value for deviation from random expectation
38	RNA Splicing	12	14	99	350	1064	over	4.22804
18	Energy Generation	38	74	292	350	1064	over	3.52166
25	Nucleotide Metabolism	30	55	375	350	1064	over	3.45137
43	Vesicular Transport	12	68	347	350	1064	under	2.72852
19	Lipid, Fat, and Sterol Metabolism	31	63	468	350	1064	over	2.63834
37	RNA Processing/Modification	25	48	279	350	1064	over	2.63503
35	Protein Synthesis	17	85	219	350	1064	under	2.59070
42	Small Molecule Transport	26	61	649	350	1064	over	1.55238
7	Cell Cycle Control	9	42	482	350	1064	under	1.42875
34	Protein Modification	17	67	882	350	1064	under	1.35576
26	Other Metabolism	15	33	362	350	1064	over	1.35386
41	Signal Transduction	44	145	2194	350	1064	under	1.22140
29	Pol II Transcription	5	25	883	350	1064	under	1.15959
5	Carbohydrate Metabolism	21	54	317	350	1064	over	1.13892
2	Amino Acid Metabolism	6	28	169	350	1064	under	1.13757
32	Protein Degradation	14	52	344	350	1064	under	1.09526
21	Membrane Fusion	3	17	60	350	1064	under	1.04515
11	Cell Structure	22	71	429	350	1064	under	1.00464
23	Mitosis	2	13	194	350	1064	under	0.98223
16	Differentiation	18	51	1103	350	1064	over	0.95353
33	Protein Folding	7	28	92	350	1064	under	0.94442
15	DNA Synthesis	4	7	154	350	1064	over	0.90786
10	Cell Stress	11	29	248	350	1064	over	0.88650
6	Cell Adhesion	11	33	423	350	1064	over	0.82934
36	Protein Translocation	9	28	91	350	1064	under	0.79253
40	Recombination	4	8	61	350	1064	over	0.77904
31	Protein Complex Assembly	6	15	90	350	1064	over	0.75467
24	Nuclear-Cytoplasmic Transport	7	20	82	350	1064	over	0.73878
12	Chromatin/Chromosome Structure	4	9	237	350	1064	over	0.69617
39	RNA Turnover	4	9	31	350	1064	over	0.69617
44	Virulence	0	4	21	350	1064	under	0.69418
14	DNA Repair	4	10	166	350	1064	over	0.64693
13	Cytokinesis	1	1	14	350	1064	over	0.48287
8	Cell Elongation	1	5	10	350	1064	under	0.47645
9	Cell Polarity	1	3	19	350	1064	over	0.35162
20	Meiosis	0	2	41	350	1064	under	0.34669
1	Aging	0	1	4	350	1064	under	0.17324
4	Axonal Transport	0	1	5	350	1064	under	0.17324
17	Dosage Compensation	0	1	1	350	1064	under	0.17324
27	Phosphate Metabolism	0	1	34	350	1064	under	0.17324
28	Pol III Transcription	0	1	30	350	1064	under	0.17324
3	Asymmetric cell division	0	0	1				
22	Mitochondrial Transcription	0	0	2				
30	Pol I Transcription	0	0	16				

Panel 7, pg. 244

Cellular Process #	Incyte Groups	# proteins in each class above 1.8 ICAT ratio	# proteins in each class observed (irrespective of ICAT ratio)	# of proteins in each class according to Incyte	# of observed proteins with ICAT ratio > 1.8	# of observed proteins	representation of class compared to random expectation	-log10p-value for deviation from random expectation
18	Energy Generation	36	74	292	265	1064	over	5.57096
38	RNA Splicing	11	14	99	265	1064	over	4.50842
43	Vesicular Transport	7	68	347	265	1064	under	2.93280
19	Lipid, Fat, and Sterol Metabolism	26	63	468	265	1064	over	2.85080
7	Cell Cycle Control	3	42	482	265	1064	under	2.66078
35	Protein Synthesis	11	85	219	265	1064	under	2.62610
25	Nucleotide Metabolism	22	55	375	265	1064	over	2.33556
37	RNA Processing/Modification	18	48	279	265	1064	over	1.76290
23	Mitosis	0	13	194	265	1064	under	1.62779
42	Small Molecule Transport	21	61	649	265	1064	over	1.59088
5	Carbohydrate Metabolism	19	54	317	265	1064	over	1.58108
41	Signal Transduction	33	145	2194	265	1064	under	1.16502
34	Protein Modification	13	67	882	265	1064	under	1.16481
33	Protein Folding	4	28	92	265	1064	under	1.09479
26	Other Metabolism	11	33	362	265	1064	over	1.09089
32	Protein Degradation	10	52	344	265	1064	under	1.06311
11	Cell Structure	15	71	429	265	1064	under	1.05522
16	Differentiation	15	51	1103	265	1064	over	1.02412
21	Membrane Fusion	2	17	60	265	1064	under	0.94304
12	Chromatin/Chromosome Structure	4	9	237	265	1064	over	0.93698
2	Amino Acid Metabolism	5	28	169	265	1064	under	0.88677
6	Cell Adhesion	9	33	423	265	1064	over	0.82593
36	Protein Translocation	8	28	91	265	1064	over	0.81978
10	Cell Stress	6	29	248	265	1064	under	0.80291
31	Protein Complex Assembly	5	15	90	265	1064	over	0.78286
29	Pol II Transcription	5	25	883	265	1064	under	0.77824
24	Nuclear-Cytoplasmic Transport	6	20	82	265	1064	over	0.77179
8	Cell Elongation	0	5	10	265	1064	under	0.62333
13	Cytokinesis	1	1	14	265	1064	over	0.60370
14	DNA Repair	2	10	166	265	1064	under	0.54782
39	RNA Turnover	2	9	31	265	1064	under	0.52021
15	DNA Synthesis	2	7	154	265	1064	over	0.50565
40	Recombination	2	8	61	265	1064	over	0.50496
44	Virulence	0	4	21	265	1064	under	0.49839
9	Cell Polarity	0	3	19	265	1064	under	0.37359
20	Meiosis	0	2	41	265	1064	under	0.24893
1	Aging	0	1	4	265	1064	under	0.12439
4	Axonal Transport	0	1	5	265	1064	under	0.12439
17	Dosage Compensation	0	1	1	265	1064	under	0.12439
27	Phosphate Metabolism	0	1	34	265	1064	under	0.12439
28	Pol III Transcription	0	1	30	265	1064	under	0.12439
3	Asymmetric cell division	0	0	1				
22	Mitochondrial Transcription	0	0	2				
30	Pol I Transcription	0	0	16				

Cellular Process #	Incyte Groups	# proteins in each class above 2.0 ICAT ratio	# proteins in each class observed (irrespective of ICAT ratio)	# of proteins in each class according to Incyte	# of observed proteins with ICAT ratio > 2.0	# of observed proteins	representation of class compared to random expectation	-log10p-value for deviation from random expectation
43	Vesicular Transport	2	68	347	203	1064	under	4.31178
18	Energy Generation	27	74	292	203	1064	over	3.88873
38	RNA Splicing	9	14	99	203	1064	over	3.67911
7	Cell Cycle Control	1	42	482	203	1064	under	2.92983
2	Amino Acid Metabolism	0	28	169	203	1064	under	2.61137
35	Protein Synthesis	8	85	219	203	1064	under	2.23742
25	Nucleotide Metabolism	17	55	375	203	1064	over	1.93243
19	Lipid, Fat, and Sterol Metabolism	18	63	468	203	1064	over	1.70628
11	Cell Structure	8	71	429	203	1064	under	1.55380
37	RNA Processing/Modification	14	48	279	203	1064	over	1.53325
5	Carbohydrate Metabolism	15	54	317	203	1064	over	1.45556
16	Differentiation	14	51	1103	203	1064	over	1.37354
42	Small Molecule Transport	16	61	649	203	1064	over	1.35148
23	Mitosis	0	13	194	203	1064	under	1.20277
26	Other Metabolism	9	33	362	203	1064	over	1.09619
41	Signal Transduction	28	145	2194	203	1064	over	1.04659
10	Cell Stress	3	29	248	203	1064	under	0.99077
21	Membrane Fusion	1	17	60	203	1064	under	0.96511
34	Protein Modification	11	67	882	203	1064	under	0.94544
6	Cell Adhesion	4	33	423	203	1064	under	0.93432
32	Protein Degradation	9	52	344	203	1064	under	0.85372
24	Nuclear-Cytoplasmic Transport	5	20	82	203	1064	over	0.78265
33	Protein Folding	4	28	92	203	1064	under	0.77086
31	Protein Complex Assembly	4	15	90	203	1064	over	0.75169
13	Cytokinesis	1	1	14	203	1064	over	0.71945
36	Protein Translocation	5	28	91	203	1064	under	0.71401
29	Pol II Transcription	4	25	883	203	1064	under	0.70268
15	DNA Synthesis	2	7	154	203	1064	over	0.57497
40	Recombination	2	8	61	203	1064	over	0.54164
12	Chromatin/Chromosome Structure	2	9	237	203	1064	over	0.52419
14	DNA Repair	2	10	166	203	1064	over	0.51907
39	RNA Turnover	1	9	31	203	1064	under	0.50014
8	Cell Elongation	0	5	10	203	1064	under	0.46066
44	Virulence	0	4	21	203	1064	under	0.36833
9	Cell Polarity	0	3	19	203	1064	under	0.27610
20	Meiosis	0	2	41	203	1064	under	0.18397
1	Aging	0	1	4	203	1064	under	0.09194
4	Axonal Transport	0	1	5	203	1064	under	0.09194
17	Dosage Compensation	0	1	1	203	1064	under	0.09194
27	Phosphate Metabolism	0	1	34	203	1064	under	0.09194
28	Pol III Transcription	0	1	30	203	1064	under	0.09194
3	Asymmetric cell division	0	0	1				
22	Mitochondrial Transcription	0	0	2				
30	Pol I Transcription	0	0	16				

Panel 9, pgs. 246-269

Cellular Process	Gene	Functional Group	XPRESS Count	d0:d8 ratio	d0:d8 StdDev	Description
Energy Generation						
SW:ACDV_HUMAN	ACADVL	18	1	0.32	0.00	SW:ACDV_HUMAN P49748 homo sapiens (human). acyl-coa dehydrogenase, very-long-chain specific, mitochondrial precursor (ec 1.3.99.-) (vlcad). 5/2000 [MASS=70390]/Very long chain acyl-coenzyme A dehydrogenase, oxidizes straight chain acyl-CoAs in the initial step of fatty acid beta-oxidation, severe deficiency results in infant cardiomyopathy with high mortality, mild deficiency results in hypoketotic hypoglycemia
SW:PHS2_HUMAN	PYGM	18	1	0.36	0.00	SW:PHS2_HUMAN P11217 homo sapiens (human). glycogen phosphorylase, muscle form (ec 2.4.1.1) (myophosphorylase). 5/2000 [MASS=97092]/Muscle glycogen phosphorylase, participates in glycogen catabolism; mutation of corresponding gene is associated with McArdle disease
SW:PHS3_HUMAN	PYGB	18	10	0.48	0.06	SW:PHS3_HUMAN P11216 homo sapiens (human). glycogen phosphorylase, brain form (ec 2.4.1.1). 10/1996 [MASS=96683]/Brain glycogen phosphorylase, catalyzes the rate-limiting step in glycogen catabolism, activated by AMP and phosphorylation, may play a role in intestinal development; associated with gastric carcinomas displaying a differentiated intestinal phenotype
SW:GLYG_HUMAN	GYG	18	6	0.51	0.11	SW:GLYG_HUMAN P46976 homo sapiens (human). glycogenin-1 (ec 2.4.1.186). 7/1999 [MASS=37347]Glycogenin (glycogenin glucosyltransferase), autocatalytic and self-glucosylating enzyme that primes de novo glycogen synthesis
SW:NC5R_HUMAN	DIA1	18	2	0.60	0.02	SW:NC5R_HUMAN P00387 homo sapiens (human). nadh-cytochrome b5 reductase (ec 1.6.2.2) (b5r). 11/1997 [MASS=34104]/NADH-dependent cytochrome b5 reductase (diaphorase), soluble erythrocyte-specific form functions in methemoglobin reduction, ubiquitous membrane-bound form functions in lipid metabolism; mutations in the gene cause methemoglobinemia types I and II
SW:GFA1_HUMAN	GFPT1	18	5	0.72	0.06	SW:GFA1_HUMAN Q06210 homo sapiens (human). glucosamine--fructose-6-phosphate aminotransferase [isomerizing] 1 (ec 2.6.1.16) (hexosephosphate aminotransferase 1) (d-fructose-6- phosphate amidotransferase [MASS=76616]/Glutamine-fructose-6-phosphate transaminase 1, catalyzes the first step in glucosamine formation, modulates glucose flux and functions in development of insulin resistance, upregulation in kidney associated with diabetic nephropathy
SW:UGS1_HUMAN	GYS1	18	5	0.73	0.15	SW:UGS1_HUMAN P13807 homo sapiens (human). glycogen [starch] synthase, muscle (ec 2.4.1.11). 5/2000 [MASS=83786]/Glycogen synthase 1 (muscle), catalyzes transfer of a glucosyl residue from UDP-glucose to glycogen, stimulated by insulin, Acipimox and Flouxetine; mutations in the corresponding gene may be associated with non-insulin-dependent diabetes mellitus
SW:WFS1_HUMAN	WFS1	18	1	0.75	0.00	SW:WFS1_HUMAN O76024 homo sapiens (human). wolframin. 5/2000 [MASS=100306]/Wolfram syndrome 1 (wolframin), may play a role in islet beta cell and neuron survival, may influence normal hearing and vision; gene mutation is detected in Wolfram syndrome and some types of hearing loss and may influence type 2 diabetes susceptibility
SW:G3P2_HUMAN	GAPD	18	2	0.85	0.01	SW:G3P2_HUMAN P04406 homo sapiens (human). glyceraldehyde 3-phosphate dehydrogenase, liver (ec 1.2.1.12). 7/1999 [MASS=35922]/Glyceraldehyde-3-phosphate dehydrogenase, catalyzes reversible oxidation and phosphorylation of glyceraldehyde-3-phosphate to 1,3-diphosphoglycerate in glycolysis, involved in apoptosis, may play a role in neurodegeneration in diseases like Alzheimer's
SW:ENOB_HUMAN	ENO3	18	4	0.86	0.13	SW:ENOB_HUMAN P13929 homo sapiens (human). beta enolase (ec 4.2.1.11) (2-phospho-d-glycerate hydro-lyase) (skeletal muscle enolase) (mse). 7/1998 [MASS=46856]/Enolase 3 (muscle-specific enolase, beta enolase), a putative enolase which catalyzes the conversion of 2-phospho-D-glycerate to phosphoenolpyruvate in muscle glycolysis, deficiency is associated with exercise intolerance and myalgias
SW:KCRB_HUMAN	CKB	18	3	0.88	0.26	SW:KCRB_HUMAN P12277 homo sapiens (human). creatine kinase, b chain (ec 2.7.3.2) (b-ck). 7/1999 [MASS=42644]/Brain creatine kinase, involved in energy homeostasis, expression is elevated in some forms of cancer; CK-MB is a dimer of subunits CKM and CKB, and is an important serum marker for acute myocardial infarction
SW:GDE_HUMAN	AGL	18	18	0.92	0.22	SW:GDE_HUMAN P35573 homo sapiens (human). glycogen debranching enzyme (glycogen debrancher) [includes: 4-alpha-glucanotransferase (ec 2.4.1.25) (oligo-1,4-1,4-glucantransferase); amylo-1,6-glucosidase [MASS=172497]/Glycogen debranching enzyme, (amylo-1,6-glucosidase 4-alpha-glucanotransferase), catalyzes glycantransferase and glucosidase activities required for glycogen degradation; mutations and dysregulation are associated with type III glycogen storage diseases
SW:PGK1_HUMAN	PGK1	18	16	0.93	0.18	SW:PGK1_HUMAN P00558 homo sapiens (human). phosphoglycerate kinase 1 (ec 2.7.2.3) (primer recognition protein 2) (prp 2). 7/1999 [MASS=44597]/Phosphoglycerate kinase 1, catalyzes conversion of 1,3-diphosphoglycerate to 3-phosphoglycerate in glycolysis, forming one molecule of ATP; PGK1 gene transcription is induced by hypoxia and mutation is associated with non-spherocytic hemolytic anemia
SW:ODO1_HUMAN	OGDH	18	9	0.94	0.18	SW:ODO1_HUMAN Q02218 homo sapiens (human). 2-oxoglutarate dehydrogenase e1 component, mitochondrial precursor (ec 1.2.4.2) (alpha-ketoglutarate dehydrogenase). 7/1999 [MASS=113475]/2-Oxoglutarate dehydrogenase (alpha-ketoglutarate dehydrogenase), E1 component of the complex that converts alpha-ketoglutarate to succinyl coenzyme A in the Krebs cycle; deficiency has been observed in Alzheimer and Parkinson disease
SW:K6PL_HUMAN	PFKL	18	8	0.97	0.17	SW:K6PL_HUMAN P17858 homo sapiens (human). 6-phosphofructokinase, liver type (ec 2.7.1.11) (phosphofructokinase 1) (phosphohexokinase) (phosphofructo-1-kinase isozyme b). 10/1996 [MASS=85148]/Liver phosphofructokinase, catalyses the phosphorylation of fructose-6-phosphate to fructose-1,6-bisphosphate in glycolysis, deficiency is linked to glycogenosis type VII while overexpression may lead to the cognitive diabilites of Down's syndrome

SW:KPB1_HUMAN	PHKA1	18	3	1.00	0.09	SW:KPB1_HUMAN P46020 homo sapiens (human). phosphorylase b kinase alpha regulatory chain, skeletal muscle isoform (phosphorylase kinase alpha m subunit). 2/1996 [MASS=137338]/Phosphorylase kinase regulatory subunit alpha-1 (muscle), which phosphorylates and thereby activates muscle-specific glycogen phosphorylase (PYGM); mutations in the corresponding gene are associated with muscle glycogenosis, a glycogen storage disease
SW:TPIS_HUMAN	TPI1	18	9	1.00	0.18	SW:TPIS_HUMAN P00938 homo sapiens (human), and pan troglodytes (chimpanzee). triosephosphate isomerase (ec 5.3.1.1) (tim). 7/1998 [MASS=26538]/Triosephosphate isomerase 1, catalyzes the reversible interconversion of glyceraldehyde 3-phosphate and dihydroxyacetone phosphate in glycolysis; variant forms cause hemolytic anemia and neurodegeneration; variant form is an antigen on melanoma cells
SW:ENOA_HUMAN	ENO1	18	3	1.01	0.08	SW:ENOA_HUMAN P06733 homo sapiens (human). alpha enolase (ec 4.2.1.11) (2-phospho-d-glycerate hydro-lyase) (non-neural enolase) (nne) (phosphopyruvate hydratase). 7/1998 [MASS=47038]/Enolase 1 (alpha enolase), converts 2-phospho-D-glycerate to phosphoenolpyruvate in glycolysis, an autoantigen in multiple autoimmune diseases, shorter alternative form c-myc promoter binding protein (MPB1) is a transcriptional repressor
GP:AJ131612_1	Slc25a10	18	1	1.02	0.00	GP:AJ131612_1 Homo sapiens dic gene, exons 1-11. [MASS=31325]/Solute carrier family 25 member 10 (dicarboxylate carrier), a putative dicarboxylic acid transporter predicted to reside in the inner mitochondrial membrane, may be involved in gluconeogenesis
SW:ODPB_HUMAN	PDHB	18	1	1.05	0.00	SW:ODPB_HUMAN P11177 homo sapiens (human). pyruvate dehydrogenase e1 component beta subunit, mitochondrial precursor (ec 1.2.4.1) (pdhe1-b). 7/1999 [MASS=39219]/E1 beta subunit of pyruvate dehydrogenase complex, oxidatively decarboxylates pyruvate to acetyl-CoA
SW:HEMZ_HUMAN	FECH	18	8	1.06	0.19	SW:HEMZ_HUMAN P22830 homo sapiens (human). ferrochelatase precursor (ec 4.99.1.1) (protoheme ferro-lyase) (heme synthetase). 12/1998 [MASS=47834]/Ferrochelatase (protoheme ferrochelatase), catalyzes the final step in the heme biosynthetic pathway by inserting ferrous iron into protoporphyrin IX to form heme; reduced activity and mutations in the corresponding gene are associated with protoporphyria
SW:HXK1_HUMAN	HK1	18	5	1.07	0.11	SW:HXK1_HUMAN P19367 homo sapiens (human). hexokinase, type i (ec 2.7.1.1) (hk i) (brain form hexokinase). 12/1998 [MASS=102503]/Hexokinase Type I (ATP:D-hexose 6-phosphotransferase), catalyzes ATP-dependent conversion of glucose to glucose 6 phosphate in glycolysis, deficiency may lead to non-spherocytic hemolytic anemia
SW:CPT2_HUMAN	CPT2	18	1	1.08	0.00	SW:CPT2_HUMAN P23786 homo sapiens (human). carnitine o-palmitoyltransferase ii, mitochondrial precursor (ec 2.3.1.21) (cpt ii). 5/2000 [MASS=73777]/Carnitine palmitoyltransferase II, a mitochondrial long-chain fatty acid oxidation enzyme; mutations are associated with a lipid metabolism disorder that includes recurrent myopathy with progressive rhabdomyolysis, muscle weakness and myoglobinuria
SW:KPY1_HUMAN	PKM2	18	19	1.09	0.24	SW:KPY1_HUMAN P14618 homo sapiens (human). pyruvate kinase, m1 isozyme (ec 2.7.1.40) (pyruvate kinase muscle isozyme) (cytosolic thyroid hormone-binding protein) (cthbp) (thbp1). 12/1998 [MASS=57747]/Pyruvate kinase muscle (pyruvate kinase 3), glycolytic enzyme that converts phosphoenolpyruvate to pyruvate with phosphorylation of ADP to ATP, exists as M1 and M2 alternative forms, may have roles in viral transformation and cell differentiation
SW:FLRE_HUMAN	BLVRB	18	3	1.12	0.12	SW:FLRE_HUMAN P30043 homo sapiens (human). flavin reductase (ec 1.6.99.1) (fr) (nadph-dependent diaphorase) (nadph-flavin reductase) (flr) (biliverdin reductase b) (ec 1.3.1.24) (bvr-b) (biliverdin-ix b [MASS=21988]/Biliverdin-IX beta reductase (NADPH-flavin reductase), catalyzes the conversion of biliverdin-IX beta to bilirubin-IX beta, the major heme catabolite produced during early fetal development; also has NAD(P)H-linked flavin reductase activity
SW:COXS_HUMAN	COX17	18	1	1.18	0.00	SW:COXS_HUMAN Q14061 homo sapiens (human). cytochrome c oxidase copper chaperone. 7/1999 [MASS=6784]/Cytochrome c oxidase assembly protein 17, a putative copper binding protein, may function to transport copper to mitochondria for assembly into cytochrome oxidase complex; mutation does not appear to be a common cause of COX deficiency disorders
SW:INSR_HUMAN	INSR	18	2	1.22	0.02	SW:INSR_HUMAN P06213 homo sapiens (human). insulin receptor precursor (ec 2.7.1.112) (ir). 5/2000 [MASS=156281]/Insulin receptor, a transmembrane receptor protein tyrosine kinase involved in carbohydrate metabolism, energy pathways, and cell growth; gene mutation is associated with insulin-resistant diabetes mellitus and leprechaunism
SW:THIK_HUMAN	ACAA1	18	15	1.26	0.25	SW:THIK_HUMAN P09110 homo sapiens (human). 3-ketoacyl-coa thiolase, peroxisomal precursor (ec 2.3.1.16) (beta-ketothiolase) (acetyl-coa acyltransferase) (peroxisomal 3-oxoacyl- coa thiolase). 7/1999 [MASS=44292]/Peroxisomal 3-oxoacyl-coenzyme A thiolase (peroxisomal 3-ketoacyl-Coenzyme A thiolase), functions in peroxisomal beta-oxidation of fatty acids, deficiency is associated with rhizomelic chondrodysplasia punctata (RCDP)
SW:MDHC_HUMAN	MDH1	18	4	1.27	0.10	SW:MDHC_HUMAN P40925 homo sapiens (human). malate dehydrogenase, cytoplasmic (ec 1.1.1.37). 5/2000 [MASS=36295]/Cytosolic malate dehydrogenase, part of the malate-aspartate shuttle where it putatively catalyzes the reduction of oxaloacetate to malate
SW:ACON_HUMAN	ACO2	18	1	1.27	0.00	SW:ACON_HUMAN Q99798 homo sapiens (human). aconitate hydratase, mitochondrial precursor (ec 4.2.1.3) (citrate hydro-lyase) (aconitase). 5/2000 [MASS=85425]/Aconitase 2 mitochondrial (aconitate hydratase), catalyzes the conversion of citrate to cis-aconitate in the tricarboxylic acid cycle, may be involved in iron homeostasis; deficiency may be associated with lifelong exercise intolerence
SW:CPT1_HUMAN	CPT1A	18	1	1.30	0.00	SW:CPT1_HUMAN P50416 homo sapiens (human). carnitine o-palmitoyltransferase i, mitochondrial liver isoform (ec 2.3.1.21) (cpt i) (cpti-l). 7/1999 [MASS=88429]/Liver carnitine palmitoyltransferase I, enzyme of long-chain fatty acid beta-oxidation pathway; mutations in the corresponding gene are associated with carnitine palmitoyltransferase I deficiency

SW:D3D2_HUMAN	DCI	18	3	1.31	0.20	SW:D3D2_HUMAN P42126 homo sapiens (human). 3,2-trans-enoyl-coa isomerase, mitochondrial precursor (ec 5.3.3.8) (dodecenoyl-coa delta-isomerase). 7/1999 [MASS=32816]/Dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenzyme A isomerase), catalyzes the isomerization of 3-cis and 3-trans enoyl CoA esters to 2-trans enoyl CoA esters, functions in mitochondrial beta-oxidation of unsaturated fatty acids
PIR2:JC5938	Txnl	18	2	1.31	0.01	PIR2:JC5938 thioredoxin-like protein - human [MASS=32251]/Thioredoxin-like 32, a thioredoxin related protein that has thioredoxin-like reducing activity
SW:ECH1_HUMAN	ECH1	18	28	1.36	0.24	SW:ECH1_HUMAN Q13011 homo sapiens (human). delta3,5-delta2,4-dienoyl-coa isomerase precursor (ec 5.3.3.-). 7/1999 [MASS=35994]/Enoyl Coenzyme A hydratase 1 (peroxisomal), putative enzyme that may play a role in peroxisomal beta-oxidation
SW:KG3B_HUMAN	GSK3B	18	1	1.36	0.00	SW:KG3B_HUMAN P49841 homo sapiens (human). glycogen synthase kinase-3 beta (ec 2.7.1.37) (gsk-3 beta). 7/1999 [MASS=46768]/Glycogen synthase kinase-3 beta, a serine threonine protein kinase that phosphorylates several cytoplasmic and nuclear proteins, involved in embryonic development, and may hyperphosporylate tau (MAPT) in
SW:KCRU_HUMAN	CKMT1	18	6	1.45	0.16	SW:KCRU_HUMAN P12532 homo sapiens (human). creatine kinase, ubiquitous mitochondrial precursor (ec 2.7.3.2) (u-mtck) (mia-ck) (acidic-type mitochondrial creatine kinase). 7/1999 [MASS=47037]/Mitochondrial creatine kinase 1 (ubiquitous), mitochondrial isoform that has a probable role in the phosphocreatine shuttle, plays a role in energy pathways; inactivation is involved in anthracycline cardiotoxicity
SW:ACPM_HUMAN	NDUFAB1	18	3	1.46	0.23	SW:ACPM_HUMAN O14561 homo sapiens (human). acyl carrier protein, mitochondrial precursor (acp) (nadh-ubiquinone oxidoreductase 9.6 kda subunit) (ec 1.6.5.3) (ec 1.6.99.3) (ci-sdap). 5/2000 [MASS=14806]/NADH-ubiquinone oxidoreductase subunit of alpha-beta subcomplex 1 (8 kD), a probable acyl carrier component of the multiprotein complex that transports electrons from NADH to ubiquinone, present within the hydrophobic fraction of complex I
SW:OBRG_HUMAN	LEPR	18	1	1.46	0.00	SW:OBRG_HUMAN O15243 homo sapiens (human). leptin receptor gene-related protein (ob-r gene related protein) (ob-rgrp). 7/1999 [MASS=14254]/Leptin receptor, member of the gp130 (IL6ST) cytokine-receptor family, signals through the JAK/STAT cascade and functions in regulation of appetite, body fat, bone formation, and reproduction; mutations in the gene cause obesity and pituitary dysfunction
SW:CAOP_HUMAN	ACOX1 or ACOX	18	1	1.53	0.00	SW:CAOP_HUMAN Q15067 homo sapiens (human). acyl-coenzyme a oxidase, peroxisomal (ec 1.3.3.6) (palmitoyl-coa oxidase) (aox). 11/1997 [MASS=74502]/Peroxisomal acyl-coenzyme A oxidase, catalyzes the first step in very long chain fatty acid beta-oxidation, desaturates acyl-CoA to 2-trans-enoyl-CoA and produces hydrogen peroxide
SW:APE1_HUMAN	APEX	18	13	1.57	0.38	SW:APE1_HUMAN P27695 homo sapiens (human). dna-(apurinic or apyrimidinic site) lyase (ec 4.2.99.18) (ap endonuclease 1) (apex nuclease) (apen) (ref-1 protein). 12/1998 [MASS=35423]/Apurinic/apyrimidinic endonuclease 1, multifunctional DNA repair enzyme that coordinates the repair of abasic sites and repair synthesis, acts as a transcription regulator; mutations may correlate with inclusion body myositis and colorectal tumorigenesis
SW:DLDH_HUMAN	DLD	18	10	1.59	0.59	SW:DLDH_HUMAN P09622 homo sapiens (human). dihydrolipoamide dehydrogenase, mitochondrial precursor (ec 1.8.1.4). 5/2000 [MASS=54150]/Dihydrolipoamide dehydrogenase, E3 component of pyruvate dehydrogenase complex, also component of alpha-ketoglutarate dehydrogenase and branched-chain alpha-ketoacid dehydrogenase complexes and the glycine cleavage system
SW:CISY_HUMAN	CS	18	1	1.62	0.00	SW:CISY_HUMAN O75390 homo sapiens (human). citrate synthase, mitochondrial precursor (ec 4.1.3.7). 7/1999 [MASS=51706]/Citrate synthase, converts acetyl-CoA and oxaloacetate into citrate plus CoA in the tricarboxylic acid cycle
SW:ADRO_HUMAN	FDXR	18	1	1.82	0.00	SW:ADRO_HUMAN P22570 homo sapiens (human). nadph:adrenodoxin oxidoreductase precursor (ec 1.18.1.2) (adrenodoxin reductase) (ferredoxin-nadp(+) reductase). 7/1999 [MASS=53809]/Ferredoxin reductase, mitochondrial flavoprotein that mediates electron transport from NADPH to cytochrome P450scc
SW:ADT1_HUMAN	SLC25A4	18	2	1.84	0.94	SW:ADT1_HUMAN P12235 homo sapiens (human). adp,atp carrier protein, heart/skeletal muscle isoform t1 (adp/atp translocase 1) (adenine nucleotide translocator 1) (ant 1). 10/1994 [MASS=33064]/Solute carrier family 25 member 4, an ADP:ATP transporter that may act in mitochondrial genome stability, altered transport capacity due to autoimmune response leads to myocarditis and cardiomyopathy; mutation causes progressive external ophthalmoplegia
SW:NUAM_HUMAN	NDUFS1	18	1	1.87	0.00	SW:NUAM_HUMAN P28331 homo sapiens (human). nadh-ubiquinone oxidoreductase 75 kda subunit precursor (ec 1.6.5.3) (ec 1.6.99.3) (complex i-75kd) (ci-75kd). 7/1999 [MASS=79574]/NADH-dehydrogenase ubiquinone Fe-S protein 1 (75kD), a multiprotein complex that transports electrons from NADH to ubiquinone, present within the hydrophobic fraction of complex I; genetic variants are associated with mitochondrial complex I deficiency
SW:ECHB_HUMAN	HADHB	18	4	1.87	0.07	SW:ECHB_HUMAN P55084 homo sapiens (human). trifunctonal enzyme beta subunit, mitochondrial precursor (tp-beta) [includes: 3-ketoacyl-coa thiolase (ec 2.3.1.16) (acetyl-coa acyltransferase) (beta-ketothi [MASS=51294]/3-hydroxyacyl-CoA dehydrogenase, 3-ketoacyl-CoA thiolase trifunctional protein beta subunit, involved in fatty acid beta-oxidation; variants are associated with trifunctional protein deficiency, sudden infant death syndrome and liver failure
SW:LYAG_HUMAN	GAA	18	2	1.94	0.01	SW:LYAG_HUMAN P10253 homo sapiens (human). lysosomal alpha-glucosidase precursor (ec 3.2.1.20) (acid maltase). 5/2000 [MASS=105338]/Acid alpha-glucosidase, lysosomal alpha-glucosidase that hydrolyzes alpha(1->4) and alpha(1->6) linkages in glycogen during glycogen catabolism; heritable deficiency causes glycogenosis type II or Pompe disease
SW:COX1_HUMAN	MTCO1	18	1	1.97	0.00	SW:COX1_HUMAN P00395 homo sapiens (human). cytochrome c oxidase polypeptide i (ec 1.9.3.1). 5/2000 [MASS=57041]/Mitochondrial cytochrome c oxidase subunit I, a subunit of complex IV of the mitochondrial respiratory chain; mutations in the corresponding gene may be associated with mitochondrial diseases and acquired idiopathic sideroblastic anemia

SW:ECHA_HUMAN	HADHA	18	13	1.97	0.65	SW:ECHA_HUMAN P40939 homo sapiens (human). mitochondrial trifunctional enzyme alpha subunit precursor (tp-alpha) [includes: long-chain enoyl-coa hydratase (ec 4.2.1.17); long chain 3-hydroxyacyl-coa deh [MASS=82960]/Mitochondrial long-chain enoyl-CoA hydratase/3-hydroxyacyl-CoA dehydrogenase/3-ketoacyl-CoA thiolase alpha subunit, involved in fatty acid beta-oxidation, mutations are associated with trifuctional protein deficiency and Reye-like syndrome
SW:ETFB_HUMAN	ETFB	18	2	1.99	0.48	SW:ETFB_HUMAN P38117 homo sapiens (human). electron transfer flavoprotein beta-subunit (beta-etf). 5/2000 [MASS=27844]/Electron transfer flavoprotein beta subunit, shuttles electrons between primary flavoprotein dehydrogenases involved in mitochondrial fatty acid metabolism and ubiquinone oxidoreductase; genetic variants are associated with type II glutaric acidemia
PIR2:B53737	SLC25A3	18	21	2.02	0.42	PIR2:B53737 phosphate carrier protein precursor, mitochodrial, splice form B - human [MASS=39959]/Mitochondrial phosphate carrier (solute carrier family 25 member 3), catalyzes the transport of phosphate from the cytoplasm to the mitochondrial matrix for ATP synthesis during oxidative phosphorylation
SW:IDHP_HUMAN	IDH2	18	7	2.04	0.65	SW:IDHP_HUMAN P48735 homo sapiens (human). isocitrate dehydrogenase [nadp], mitochondrial precursor (ec 1.1.1.42) (oxalosuccinate decarboxylase) (idh) (nadp+-specific icdh) (idp) (icd-m). 2/1996 [MASS=50948]/Isocitrate dehydrogenase 2 (NADP+) mitochondrial, catalyzes the oxidative decarboxylation of isocitrate to form alpha-ketoglutarate
SW:CY1_HUMAN	CYC1	18	2	2.10	0.00	SW:CY1_HUMAN P08574 homo sapiens (human). cytochrome c1, heme protein precursor. 7/1999 [MASS=35390]/Cytochrome c1, a member of the cytochrome bc1 complex
SW:NUPM_HUMAN	NDUFA8	18	5	2.10	0.44	SW:NUPM_HUMAN P51970 homo sapiens (human). nadh-ubiquinone oxidoreductase 19 kda subunit (ec 1.6.5.3) (ec 1.6.99.3) (complex i-19kd) (ci-19kd) (complex i-pgiv) (ci-pgiv). 5/2000 [MASS=19974]/NADH dehydrogenase ubiquinone 1 alpha subcomplex 8 (19 kDa), a subunit of NADH-ubiquinone oxidoreductase (complex I), a multiprotein complex that transports electrons from NADH to ubiquinone
SW:KC2B_HUMAN	CSNK2B	18	2	2.11	0.18	SW:KC2B_HUMAN P13862 homo sapiens (human), mus musculus (mouse), rattus norvegicus (rat), bos taurus (bovine), sus scrofa (pig), oryctolagus cuniculus (rabbit), and gallus gallus (chicken). casein kinase [MASS=24942]/Casein kinase II beta subunit, regulatory subunit of casein kinase II (CK2), confers stability and specificity to CK2 catalytic subunits, may mediate formation of the tetrameric CK2 complex, and may be involved in heat stress response
SW:ATPG_HUMAN	ATP5C1	18	3	2.15	0.32	SW:ATPG_HUMAN P36542 homo sapiens (human). atp synthase gamma chain, mitochondrial precursor (ec 3.6.1.34). 5/2000 [MASS=32996]/ATP synthase H+ transporting mitochondrial F1 complex gamma 1, putative component of multisubunit enzyme that synthesizes ATP during oxidative phosphorylation, exists in tissue-specific alternative forms that are spliced in response to acidic conditions
SW:NUBM_HUMAN	NDUFV1	18	7	2.18	0.99	SW:NUBM_HUMAN P49821 homo sapiens (human). nadh-ubiquinone oxidoreductase 51 kda subunit precursor (ec 1.6.5.3) (ec 1.6.99.3) (complex i-51kd) (ci-51kd). 5/2000 [MASS=50956]/NADH dehydrogenase ubiquinone flavoprotein 1 (51 kDa), a subunit of NADH-ubiquinone oxidoreductase (Complex I); genetic variants are associated with mitochondrial complex I deficiency, leukodystrophy, and myoclonic epilepsy
SW:UCR1_HUMAN	UQCRC1	18	8	2.24	0.43	SW:UCR1_HUMAN P31930 homo sapiens (human). ubiquinol-cytochrome c reductase complex core protein i precursor (ec 1.10.2.2). 7/1999 [MASS=52619]/Ubiquinol-cytochrome c reductase core protein I, a subunit of the ubiquinol-cytochrome c oxidoreductase component of the mitochondrial respiratory chain, may function as an electron transporter in aerobic respiration and oxidative phosphorylation
SW:DHSB_HUMAN	SDHB	18	1	2.24	0.00	SW:DHSB_HUMAN P21912 homo sapiens (human). succinate dehydrogenase [ubiquinone] iron-sulfur protein, mitochondrial precursor (ec 1.3.5.1) (ip) (ip subunit of complex ii). 5/2000 [MASS=31629]/Succinate dehydrogenase complex iron sulfur subunit B, part of an enzyme complex that transports electrons from succinate to ubiquinone in the TCA cycle and aerobic respiratory chain, may be involved in familial pheochromocytoma
SW:NB8M_HUMAN	NDUFB7	18	2	2.27	0.65	SW:NB8M_HUMAN P17568 homo sapiens (human). nadh-ubiquinone oxidoreductase b18 subunit (ec 1.6.5.3) (ec 1.6.99.3) (complex i-b18) (ci-b18) (cell adhesion protein sqm1). 7/1998 [MASS=15648]/Subunit of the NADH-ubiquinone oxidoreductase (complex I), a multiprotein complex that transports electrons from NADH to ubiquinone, functions as a cell adhesion molecule with a role in metastasis, may have a role in drug transport
SW:MDHM_HUMAN	MDH2	18	27	2.29	1.04	SW:MDHM_HUMAN P40926 homo sapiens (human). malate dehydrogenase, mitochondrial precursor (ec 1.1.1.37). 5/2000 [MASS=35531]/Mitochondrial malate dehydrogenase, part of the malate-aspartate shuttle where it putatively catalyzes the oxidation of malate to oxaloacetate
SW:UCRH_HUMAN	UQCRH	18	3	2.36	0.26	SW:UCRH_HUMAN P07919 homo sapiens (human). ubiquinol-cytochrome c reductase complex 11 kda protein precursor (ec 1.10.2.2) (mitochondrial hinge protein) (cytochrome c1, nonheme 11 kda protein) (complex [MASS=10755]/Ubiquinol-cytochrome c reductase hinge protein, hinges cytochrome c with cytochrome c1 in the mitochondrial respiratory chain, may function to accelerate apoptosis by enhancing cytochrome c release from the mitochondria
SW:ETFA_HUMAN	ETFA	18	1	2.36	0.00	SW:ETFA_HUMAN P13804 homo sapiens (human). electron transfer flavoprotein alpha-subunit precursor (alpha-etf). 5/2000 [MASS=35080]/Electron transfer flavoprotein alpha subunit, shuttles electrons between flavoprotein dehydrogenases of mitochondrial fatty acid metabolism and ubiquinone oxidoreductase, deficiency associated with Type II glutaricaciduria
SW:ATPA_HUMAN	ATP5A1	18	8	2.38	0.42	SW:ATPA_HUMAN P25705 homo sapiens (human). atp synthase alpha chain, mitochondrial precursor (ec 3.6.1.34). 12/1998 [MASS=59751]/ATP synthase H+ transporting mitochondrial F1 complex alpha subunit isoform 1 cardiac muscle, part of the synthase enzymatic complex that catalyzes the synthesis of ATP during oxidative phosphorylation

SW:UCR2_HUMAN	UQCRC2	18	1	2.42	0.00	SW:UCR2_HUMAN P22695 homo sapiens (human). ubiquinol-cytochrome c reductase complex core protein 2 precursor (ec 1.10.2.2) (complex iii subunit ii). 7/1999 [MASS=48470]/Ubiquinol-cytochrome c reductase core protein II, a putative ubiquinol-cytochrome c reductase subunit of the mitochondrial cytochrome bc1 complex, likely to play a role in oxidative phosphorylation, may be involved in aerobic respiration
SW:THIL_HUMAN	ACAT1	18	2	2.44	0.44	SW:THIL_HUMAN P24752 homo sapiens (human). acetyl-coa acetyltransferase, mitochondrial precursor (ec 2.3.1.9) (acetoacetyl-coa thiolase) (t2). 7/1999 [MASS=45200]/Acetyl-Coenzyme A acetyltransferase 1 (mitochondrial acetoacetyl-coenzyme A thiolase); mutations in the corresponding gene are associated with 3-ketothiolase deficiency
SW:UCRI_HUMAN	UQCRFS1	18	4	2.45	0.39	SW:UCRI_HUMAN P47985 homo sapiens (human). ubiquinol-cytochrome c reductase iron-sulfur subunit, mitochondrial precursor (ec 1.10.2.2) (rieske iron-sulfur protein) (risp). 7/1999 [MASS=29652]/Ubiquinol-cytochrome c reductase Rieske iron-sulfur polypeptide 1, a subunit of cytochrome bc1 complex, which transfers electron from ubiquinol to cytochrome c, located in the mitochondrion; deficient mitochondrial uptake may cause mitochondrial myopathy
SW:PPCM_HUMAN	PCK2	18	6	2.45	1.09	SW:PPCM_HUMAN Q16822 homo sapiens (human). phosphoenolpyruvate carboxykinase, mitochondrial precursor [gtp] (ec 4.1.1.32) (phosphoenolpyruvate carboxylase) (pepck-m). 7/1999 [MASS=70637]/Phosphoenolpyruvate carboxykinase 2, catalyzes the formation of phosphoenolpyruvate by decarboxylation of oxaloacetate, rate-limiting step of gluconeogenesis
SW:DHSA_HUMAN	SDHA	18	5	2.48	0.32	SW:DHSA_HUMAN P31040 homo sapiens (human). succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial precursor (ec 1.3.5.1) (fp) (flavoprotein subunit of complex ii). 5/2000 [MASS=72692]/Succinate dehydrogenase complex subunit A (flavoprotein), transports electrons from succinate to ubiquinone in the TCA cycle and respiratory chain; gene mutation is associated with Leigh syndrome, which is a complex II respiratory chain deficiency
SW:ADT2_HUMAN	SLC25A5	18	8	2.53	1.17	SW:ADT2_HUMAN P05141 homo sapiens (human). adp,atp carrier protein, fibroblast isoform (adp/atp translocase 2) (adenine nucleotide translocator 2) (ant 2). 7/1999 [MASS=32895]/Solute carrier family 25 member 5 (adenine nucleotide translocator 2), may mediate the exchange of ADP and ATP between the cytosol and mitochondria, expression is altered in dilated cardiomyopathy
SW:ADT3_HUMAN	SLC25A6	18	1	2.57	0.00	SW:ADT3_HUMAN P12236 homo sapiens (human). adp,atp carrier protein, liver isoform t2 (adp/atp translocase 3) (adenine nucleotide translocator 3) (ant 3). 11/1995 [MASS=32866]/Solute carrier family 25 member 6 (adenine nucleotide translocator), member of the ADP/ATP translocase family
SW:ATPQ_HUMAN	ATP5H	18	3	2.67	0.53	SW:ATPQ_HUMAN O75947 homo sapiens (human). atp synthase d chain, mitochondrial (ec 3.6.1.34). 5/2000 [MASS=18360]/Protein with high similarity to subunit d of the mitochondrial H(+)-ATP synthase (rat Atp5jd), which is part of a multisubunit enzyme that catalyzes the synthesis of ATP during oxidative phosphorylation
SW:NIPM_HUMAN	NDUFS5	18	2	2.69	0.02	SW:NIPM_HUMAN O43920 homo sapiens (human). nadh-ubiquinone oxidoreductase 15 kda subunit (ec 1.6.5.3) (ec 1.6.99.3) (complex i-15 kda) (ci-15 kda). 7/1999 [MASS=12386]/NADH dehydrogenase Fe-S protein 5 (15kD) (NADH-coenzyme Q reductase), putative subunit of NADH-ubiquinone oxidoreductase (complex I), a multiprotein complex that transports electrons from NADH to ubiquinone in the mitochondrial respiratory chain
SW:COXG_HUMAN	COX6B	18	6	2.77	1.08	SW:COXG_HUMAN P14854 homo sapiens (human). cytochrome c oxidase polypeptide vib (ec 1.9.3.1) (aed). 11/1997 [MASS=10061]/Cytochrome c oxidase subunit VIb, a putative subunit of cytochrome C oxidase, which couples reduction of oxygen with proton translocation during oxidative phosphorylation
Lipid, Fat, and Sterol Metabolism						
SW:FDFT_HUMAN	FDFT1	19	1	0.22	0.00	SW:FDFT_HUMAN P37268 homo sapiens (human). farnesyl-diphosphate farnesyltransferase (ec 2.5.1.21) (squalene synthetase) (sqs) (ss) (fpp:fpp farnesyltransferase). 10/1996 [MASS=48115]/Squalene synthase (farnesyl-diphosphate farnesyltransferase 1), catalyzes the conversion of farnesyl diphosphate to squalene in cholesterol biosynthesis, may be a potential target for cholesterol lowering therapy
GPN:Y14436_1	PPAP2A	19	2	0.27	0.02	type-2 phosphatidic acid phosphatase alpha-1 /Phosphatidic acid phosphatase type 2a, catalyzes the dephosphorylation of various lipid phosphates, regulates the level of lipid phosphates which are involved in signal transduction
GP:D89053_1	FACL3	19	13	0.29	0.13	fatty-acid-Coenzyme A ligase, long-chain 3 /Fatty acid Coenzyme A ligase long chain 3, a putative long-chain fatty-acyl-CoA synthetase that may function in lipid synthesis and fatty acid degradation
SW:ACDV_HUMAN	ACADVL	19	1	0.32	0.00	SW:ACDV_HUMAN P49748 homo sapiens (human). acyl-coa dehydrogenase, very-long-chain specific, mitochondrial precursor (ec 1.3.99.-) (vlcad). 5/2000 [MASS=70390]/Very long chain acyl-coenzyme A dehydrogenase, oxidizes straight chain acyl-CoAs in the initial step of fatty acid beta-oxidation, severe deficiency results in infant cardiomyopathy with high mortality, mild deficiency results in hypoketotic hypoglycemia
SW:FAS_HUMAN	FASN	19	90	0.34	0.15	SW:FAS_HUMAN P49327 homo sapiens (human). fatty acid synthase (ec 2.3.1.85) [includes: ec 2.3.1.38; ec 2.3.1.39; ec 2.3.1.41; ec 1.1.1.100; ec 4.2.1.61; ec 1.3.1.10; ec 3.1.2.14]. 7/1999 [MASS=273102]/Fatty acid synthase, multifunctional enzyme that synthesizes fatty acids from dietary proteins and carbohydrates; increased expression is associated with tumor growth and development, expression may serve as a prognostic maker for breast cancer
SW:ERG7_HUMAN	LSS	19	1	0.37	0.00	SW:ERG7_HUMAN P48449 homo sapiens (human). lanosterol synthase (ec 5.4.99.7) (oxidosqualene--lanosterol cyclase) (2,3-epoxysqualene--lanosterol cyclase) (osc). 5/2000 [MASS=83309]/Lanosterol synthase, catalyzes the cyclization of (S)-2,3-oxidosqualene forming lanosterol in sterol biosynthesis
SW:COA1_HUMAN	ACACA	19	2	0.41	0.05	SW:COA1_HUMAN Q13085 homo sapiens (human). acetyl-coa carboxylase 1 (ec 6.4.1.2) (acc-alpha) [includes: biotin carboxylase (ec 6.3.4.14)]. 7/1999 [MASS=265040]/Acetyl-Coenzyme A carboxylase alpha, catalyzes the rate-limiting step in long-chain fatty acid biogenesis; deficiency leads to defects in fatty acid synthesis

SW:ACLY_HUMAN	ACLY	19	6	0.44	0.09	SW:ACLY_HUMAN P53396 homo sapiens (human). atp-citrate (pro-s-)-lyase (ec 4.1.3.8) (citrate cleavage enzyme). 10/1996 [MASS=121420]/ATP citrate lyase, catalyzes the formation of acetyl-CoA and oxaloacetate from citrate and CoA with the concomitant hydrolysis of ATP to ADP and phosphate, involved in cholesterol and fatty acid synthesis, nutritionally regulated
SW:LDLR_HUMAN	LDLR	19	3	0.55	0.04	SW:LDLR_HUMAN P01130 homo sapiens (human). low-density lipoprotein receptor precursor (ldl receptor). 5/2000 [MASS=95376]/Low density lipoprotein receptor, mediates uptake of low density lipoproteins, involved in lipid metabolism; gene variations are associated with familial hypercholesterolemia, hypertension, atherosclerosis, and coronary artery disease
SW:NSDL_HUMAN	NSDHL	19	6	0.58	0.16	SW:NSDL_HUMAN Q15738 homo sapiens (human). nad(p)-dependent steroid dehydrogenase-like protein (h105e3 protein). 5/2000 [MASS=41900]/NAD(P)H steroid dehydrogenase-like protein, a 3 beta-hydroxysteroid dehydrogenase that functions in cholesterol biosynthesis; mutations in the corresponding gene cause CHILD syndrome
SW:CP51_HUMAN	CYP51	19	3	0.71	0.04	SW:CP51_HUMAN Q16850 homo sapiens (human). cytochrome p450 51 (ec 1.14.14.1) (cypl1) (p450l1) (sterol 14-alpha demethylase) (lanosterol 14-alpha demethylase) (ldm) (p450-14dm). 5/2000 [MASS=56806]/Lanosterol 14-alpha-demethylase (sterol 14alpha-demethylase); cytochrome P450 enzyme involved in sterol biosynthesis
SW:LCFA_HUMAN	FACL1	19	14	0.81	0.13	SW:LCFA_HUMAN P41215 homo sapiens (human). long-chain-fatty-acid--coa ligase 1 (ec 6.2.1.3) (long-chain acyl-coa synthetase 1) (lacs 1) (palmitoyl-coa ligase). 10/1996 [MASS=78348]/Long chain fatty acid-Coenzyme A ligase (palmitoyl-CoA ligase), a member of the long chain acyl-CoA synthetase family required for lipid synthesis and fatty acid degradation
SW:LCB2_HUMAN	SPTLC2	19	1	0.82	0.00	SW:LCB2_HUMAN O15270 homo sapiens (human). serine palmitoyltransferase 2 (ec 2.3.1.50) (long chain base biosynthesis protein 2) (lcb 2) (serine-palmitoyl-coa transferase 2) (spt 2) (kiaa0526). 5/2000 [MASS=62924]/Serine palmitoyltransferase long chain base subunit 2, member of the aminolevulinate synthase superfamily, catalyzes the first step in ceramide formation, involved in epidermal cell response to UV exposure and in leukemia cell ectopside-induced apoptosis
SW:DRS1_HUMAN	PECI	19	9	0.83	0.22	SW:DRS1_HUMAN O75521 homo sapiens (human). dbi-related protein 1 (drs-1). 5/2000 [MASS=40151]/Peroxisomal D3,D2-enoyl-CoA isomerase, catalyzes the isomerization of 3-cis-octenoyl-CoA to 2-trans-octenoyl-CoAm, a step in the beta oxidation of fatty acids in peroxisomes
SWN:P23_HUMAN	p23	19	2	0.85	0.01	SWN:P23_HUMAN Q15185 homo sapiens (human). telomerase-binding protein p23 (hsp90 co-chaperone) (progesterone receptor complex p23). 8/2001 [MASS=18697]/Inactive progesterone receptor (23kD), cochaperone with prostaglandin E synthase activity that is a component of the unstimulated progesterone receptor complex and that enhances receptor complex formation through interactions with Hsp90 (HSPCA)
SW:KIME_HUMAN	MVK	19	1	0.91	0.00	SW:KIME_HUMAN Q03426 homo sapiens (human). mevalonate kinase (ec 2.7.1.36) (mk). 7/1999 [MASS=42451]/Mevalonate kinase (mevalonic aciduria), a peroxisomal enzyme involved in isoprenoid and cholesterol biosynthesis; mutations in the corresponding gene cause mevalonic aciduria, hyperimmunoglobulinemia D and periodic fever syndrome
GP:U66669_1	HIBCH	19	1	0.91	0.00	GP:U66669_1 Homo sapiens 3-hydroxyisobutyryl-coenzyme A hydrolase mRNA, complete cds. [MASS=42908]/Beta-hydroxyisobutyryl-coenzyme A hydrolase, enzyme that hydrolyzes 3-hydroxyisobutyryl CoA, an intermediate of valine catabolism
SW:ASAH_HUMAN	ASAH	19	1	0.99	0.00	SW:ASAH_HUMAN Q13510 homo sapiens (human). acid ceramidase precursor (ec 3.5.1.23) (acylsphingosine deacylase) (n-acylsphingosine amidohydrolase) (ac) (putative 32 kda heart protein) (php32). 5/2000 [MASS=44650]/N-acylsphingosine amidohydrolase (acid ceramidase), catalyzes hydrolysis of ceramide to sphingosine and free fatty acid, inhibits apoptosis, upregulated in prostate cancer, deficiency is associated with Farber disease
GP:AF126782_1	RETSDR1	19	8	1.06	0.21	GP:AF126782_1 Homo sapiens retinal short-chain dehydrogenase/reductase retSDR4 mRNA, complete cds. [MASS=32268]/Short-chain dehydrogenase-reductase 1, catalyzes the NADPH-dependent reduction of all-trans-retinal to retinol, may play a role in visual system phototransduction; the corresponding gene is deleted in many neuroblastoma cell lines with MYCN amplification
SW:OXYB_HUMAN	OSBP	19	3	1.08	0.26	SW:OXYB_HUMAN P22059 homo sapiens (human). oxysterol-binding protein. 11/1995 [MASS=89421]/Oxysterol binding protein, member of a family of intracellular lipid receptors, contains a pleckstrin domain and an oxysterol binding domain, binds oxysterols, may play a role in the regulation of cholesterol metabolism and oxysterol-induced cell death
SW:CPT2_HUMAN	CPT2	19	1	1.08	0.00	SW:CPT2_HUMAN P23786 homo sapiens (human). carnitine o-palmitoyltransferase ii, mitochondrial precursor (ec 2.3.1.21) (cpt ii). 5/2000 [MASS=73777]/Carnitine palmitoyltransferase II, a mitochondrial long-chain fatty acid oxidation enzyme; mutations are associated with a lipid metabolism disorder that includes recurrent myopathy with progressive rhabdomyolysis, muscle weakness and myoglobinuria
SW:FAAH_HUMAN	FAAH	19	3	1.10	0.22	SW:FAAH_HUMAN O00519 homo sapiens (human). fatty-acid amide hydrolase (ec 3.1.-.-) (oleamide hydrolase). 5/2000 [MASS=63038]/Fatty acid amide hydrolase, degrades neuromodulatory fatty acid amides, including anandamide, predicted to have a role in a wide variety of physiologic efffects such as voluntary movement, pain, sleep, and fertility, may have a role in Parkinson disease
SW:HBP_HUMAN	HDLBP	19	3	1.11	0.27	SW:HBP_HUMAN Q00341 homo sapiens (human). high density lipoprotein binding protein (hdl-binding protein). 12/1998 [MASS=141440]/High density lipoprotein binding protein, binds and inhibits cleavage of the 3' UTR of vitellogenin mRNA, binds and promotes nuclear export of tRNA, binds high density lipoproteins and may have roles in cholesterol metabolism and atherogenesis

SW:NPC1_HUMAN	NPC1	19	1	1.16	0.00	SW:NPC1_HUMAN O15118 homo sapiens (human). niemann-pick c1 protein precursor. 5/2000 [MASS=142149]/Niemann-Pick disease type C1, a lysosomal sterol transporter involved in cholesterol metabolism; mutation of the corresponding gene causes Niemann-Pick type C1 disease and mutation of mouse Npc1 causes a disease like Niemann-Pick type C1 disease
SW:PEBP_HUMAN	PBP	19	2	1.17	0.15	SW:PEBP_HUMAN P30086 homo sapiens (human). phosphatidylethanolamine-binding protein (pebp) (neuropolypeptide h3). 7/1999 [MASS=20926]/Phosphatidylethanolamine-binding protein, binds GTP, may regulate cAMP accumulation, enhance acetylcholine synthesis, and play a role in organizing phospholipids in the myelin sheath
SW:GLCM_HUMAN	GBA	19	2	1.21	0.09	SW:GLCM_HUMAN P04062 homo sapiens (human). glucosylceramidase precursor (ec 3.2.1.45) (beta-glucocerebrosidase) (acid beta-glucosidase) (d-glucosyl-n-acylsphingosine glucohydrolase) (alglucerase) (imigl [MASS=59697]/Acid beta glucosidase (beta-glucocerebrosidase), a lysosomal membrane protein that hydrolyzes glucosylceramide and glucosylsphingosine, may play a role in epidermal differentiation; mutations in the corresponding gene cause Gaucher's disease
SW:PI52_HUMAN	PIP5K2A	19	1	1.24	0.00	SW:PI52_HUMAN P48426 homo sapiens (human). phosphatidylinositol-4-phosphate 5-kinase type ii alpha (ec 2.7.1.68) (pip5kii-alpha) (1-phosphatidylinositol-4-phosphate kinase) (ptdins(4)p-5-kinase b isofor [MASS=46193]/Phosphatidylinositol-4-phosphate 5-kinase type II, alpha, a member of a family of kinases responsible for the synthesis of PtdIns(4,5)P2
GP:AF034544_1	DHCR7	19	6	1.25	0.30	GP:AF034544_1 Homo sapiens delta7-sterol reductase mRNA, complete cds; D7SR. [MASS=54516]/7-dehydrocholesterol reductase, catalyzes the reduction of the C7-C8 (delta 7) double bond of 7-dehydrocholesterol in the last step of cholesterol biosynthesis; mutations in the corresponding gene are associated with Smith-Lemli-Opitz
SW:THIK_HUMAN	ACAA1	19	15	1.26	0.25	SW:THIK_HUMAN P09110 homo sapiens (human). 3-ketoacyl-coa thiolase, peroxisomal precursor (ec 2.3.1.16) (beta-ketothiolase) (acetyl-coa acyltransferase) (peroxisomal 3-oxoacyl- coa thiolase). 7/1999 [MASS=44292]/Peroxisomal 3-oxoacyl-coenzyme A thiolase (peroxisomal 3-ketoacyl-Coenzyme A thiolase), functions in peroxisomal beta-oxidation of fatty acids, deficiency is associated with rhizomelic chondrodysplasia punctata (RCDP)
SW:CPT1_HUMAN	CPT1A	19	1	1.30	0.00	SW:CPT1_HUMAN P50416 homo sapiens (human). carnitine o-palmitoyltransferase i, mitochondrial liver isoform (ec 2.3.1.21) (cpt i) (cpti-l). 7/1999 [MASS=88429]/Liver carnitine palmitoyltransferase I, enzyme of long-chain fatty acid beta-oxidation pathway; mutations in the corresponding gene are associated with carnitine palmitoyltransferase I deficiency
SW:D3D2_HUMAN	DCI	19	3	1.31	0.20	SW:D3D2_HUMAN P42126 homo sapiens (human). 3,2-trans-enoyl-coa isomerase, mitochondrial precursor (ec 5.3.3.8) (dodecenoyl-coa delta-isomerase). 7/1999 [MASS=32816]/Dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenzyme A isomerase), catalyzes the isomerization of 3-cis and 3-trans enoyl CoA esters to 2-trans enoyl CoA esters, functions in mitochondrial beta-oxidation of unsaturated fatty acids
SW:SAP_HUMAN	PSAP	19	14	1.31	0.91	SW:SAP_HUMAN P07602 h proactivator polypeptide precursor [contains: saposin a (protein a); saposin b (sphingolipid activator protein 1) (sap-1) (dispersin) (sulfatide/gm1 activator); saposin c (co-beta- [MASS=58113]/Prosaposin, precursor of saposins A, B, C, and D which transport gangliosides and activate sphingolipid hydrolysis, stimulates neurite growth and inhibits apoptosis; variants are associated with metachromatic leukodystrophy and Gaucher disease
GP:AB037108_1	TPRA40	19	2	1.36	0.09	GP:AB037108_1 Homo sapiens mRNA for seven transmembrane domain orphan receptor, complete cds; seven transmembrane domain containing protein. [MASS=41090]/Protein with strong similarity to murine Tpra40, which is a seven transmembrane domain protein expressed in 3T3 adipocytes, and that has elevated expression in epididymal fat of genetically diabetic and obese mice
SW:ECH1_HUMAN	ECH1	19	28	1.36	0.24	SW:ECH1_HUMAN Q13011 homo sapiens (human). delta3,5-delta2,4-dienoyl-coa isomerase precursor (ec 5.3.3.-). 7/1999 [MASS=35994]/Enoyl Coenzyme A hydratase 1 (peroxisomal), putative enzyme that may play a role in peroxisomal beta-oxidation
SW:SAP3_HUMAN	GM2A	19	3	1.39	0.14	SW:SAP3_HUMAN P17900 homo sapiens (human). ganglioside gm2 activator precursor (cerebroside sulfate activator protein) (shingolipid activator protein 3) (sap-3). 7/1999 [MASS=20822]/GM2 ganglioside activator protein, binds glycolipids and is a cofactor for GM2 ganglioside hydrolysis by beta hexosaminidase A, activates phospholipase D, and inhibits platelet activating factor; mutation of the gene causes GM2-gangliosidosis variant AB
GP:AF035959_1	PPAP2C	19	1	1.42	0.00	GP:AF035959_1 Homo sapiens type-2 phosphatidic acid phosphatase-gamma (PAP2-g) mRNA, complete cds; phosphatidate phosphohydrolase; phospholipid phosphatase. [MASS=32574]/Phosphatidic acid phosphatase 2c, hydrolyzes phospholipids, may play a role in signal transduction
SW:OCRL_HUMAN	OCRL	19	2	1.42	1.00	SW:OCRL_HUMAN Q01968 homo sapiens (human). lowe's oculocerebrorenal syndrome protein. 7/1998 [MASS=111485]/Oculocerebrorenal syndrome of Lowe, phosphatidylinositol-4,5-bisphosphate 5-phosphatase, may play a role in intracellular protein trafficking; mutation of the corresponding gene causes Lowe oculocerebrorenal syndrome
GP:AB033078_1	SGPL1	19	2	1.44	0.06	GP:AB033078_1 Homo sapiens mRNA for KIAA1252 protein, partial cds; Start codon is not identified.. [MASS=64962]/Protein with strong similarity to sphingosine phosphate lyase 1 (mouse Sgpl1), which is a member of the carbon-carbon lyase subclass of aldehyde-lyases that catalyzes cleavage of sphingosine phosphate and is involved in proliferative signal transduction
SWN:CNE3_HUMAN	CPN3	19	28	1.47	0.27	SWN:CNE3_HUMAN O75131 homo sapiens (human). copine iii. 8/2001 [MASS=60131]/Copine III, a member of the copine family of phospholipid binding proteins, contains C2 and integrin A domains, may play a role in membrane trafficking, displays protein kinase activity, however, it does not contain a traditional kinase catalytic domain

SW:NLTP_HUMAN	SCP2	19	2	1.50	0.06	SW:NLTP_HUMAN P22307 homo sapiens (human). nonspecific lipid-transfer protein precursor (nsl-tp) (sterol carrier protein 2) (scp-2) (sterol carrier protein x) (scp-x) (scpx). 5/2000 [MASS=58994]/Sterol carrier protein 2, catalyzes the exchange of phospholipids between membranes, stimulates cholesterol metabolism and may regulate steroidogenesis; alternative form, SCPX, is a 3 oxoacyl CoA thiolase
SW:CAOP_HUMAN	ACOX1 or ACOX	19	1	1.53	0.00	SW:CAOP_HUMAN Q15067 homo sapiens (human). acyl-coenzyme a oxidase, peroxisomal (ec 1.3.3.6) (palmitoyl-coa oxidase) (aox). 11/1997 [MASS=74502]/Peroxisomal acyl-coenzyme A oxidase, catalyzes the first step in very long chain fatty acid beta-oxidation, desaturates acyl-CoA to 2-trans-enoyl-CoA and produces hydrogen peroxide
SW:PKBS_HUMAN	BZRP	19	2	1.57	0.04	SW:PKBS_HUMAN P30536 homo sapiens (human). peripheral-type benzodiazepine receptor (pbr) (pkbs) (mitochondrial benzodiazepine receptor). 6/1994 [MASS=18779]/Benzodiazepine receptor (peripheral), involved in steroid biosynthesis, cell proliferation, and may contribute to mitochondrial biogenesis and inhibit oxygen radical induced apoptosis; expression, nuclear location may correlate to breast tumor progression
SW:PXF_HUMAN	PXF	19	1	1.61	0.00	SW:PXF_HUMAN P40855 homo sapiens (human). peroxisomal farnesylated protein (33 kda housekeeping protein). 12/1998 [MASS=32807]/Peroxisomal farnesylated protein, peroxisomal protein that binds several peroxisomal membrane proteins (PMP), involved in early stages of PMP import and peroxisomal biogenesis; deficiency is associated with Zellweger syndrome complementation group J
SW:DHA4_HUMAN	ALDH3A2	19	2	1.62	0.67	SW:DHA4_HUMAN P51648 homo sapiens (human). fatty aldehyde dehydrogenase (ec 1.2.1.3) (aldehyde dehydrogenase, microsomal) (aldh class 3). 7/1999 [MASS=54848]/Aldehyde dehyrogenase 3 family member A2, catalyzes the oxidation of long chain fatty aldehydes and leukotrienes; mutation of the corresponding gene causes Sjogren Larsson syndrome, a disorder marked by mental retardation, spasticity, and ichthyosis
SW:HCD2_HUMAN	HADH2	19	4	1.67	0.12	SW:HCD2_HUMAN Q99714 homo sapiens (human). 3-hydroxyacyl-coa dehydrogenase type ii (ec 1.1.1.35) (endoplasmic reticulum-associated amyloid beta-peptide binding protein) (short- chain type dehydrogenase/ [MASS=26923]/Hydroxyacyl-Coenzyme A dehydrogenase (type II), catalyzes the oxidation of steroids and alcohols, binds amyloid-beta protein; overexpressed and mediates neurotoxicity of Alzheimer's disease, mutation in the corresponding gene causes hyperinsulinism
SW:DHB4_HUMAN	HSD17B4	19	12	1.74	0.52	SW:DHB4_HUMAN P51659 homo sapiens (human). estradiol 17 beta-dehydrogenase 4 (ec 1.1.1.62) (17-beta-hsd 4) (17-beta-hydroxysteroid dehydrogenase 4). 11/1997 [MASS=79686]/Type IV 17 beta-hydroxysteroid dehydrogenase, a peroxisomal multifunctional enzyme with estradiol 17 beta-dehydrogenase and D-3 hydroxyacyl CoA dehydratase activities, involved in steroid and bile acid metabolism
SW:AGAL_HUMAN	GLA	19	1	1.80	0.00	SW:BDH_HUMAN P06280 homo sapiens (human). alpha-galactosidase a precursor (ec 3.2.1.22) (melibiase) (alpha-d-galactoside galactohydrolase) (alpha-d-galactosidase a). 7/1998 [MASS=48767]/Alpha-galactosidase A (alpha-D-galactoside galactohydrolase), hydrolyzes glycosphingolipids to release alpha-D-galactosyl residues; mutation of the corresponding gene causes Fabry disease
SW:ADRO_HUMAN	FDXR	19	1	1.82	0.00	SW:ADRO_HUMAN P22570 homo sapiens (human). nadph:adrenodoxin oxidoreductase precursor (ec 1.18.1.2) (adrenodoxin reductase) (ferredoxin-nadp(+) reductase). 7/1999 [MASS=53809]/Ferredoxin reductase, mitochondrial flavoprotein that mediates electron transport from NADPH to cytochrome P450scc
SW:ECHB_HUMAN	HADHB	19	4	1.87	0.07	SW:ECHB_HUMAN P55084 homo sapiens (human). trifunctonal enzyme beta subunit, mitochondrial precursor (tp-beta) [includes: 3-ketoacyl-coa thiolase (ec 2.3.1.16) (acetyl-coa acyltransferase) (beta-ketothi [MASS=51294]/3-hydroxyacyl-CoA dehydrogenase, 3-ketoacyl-CoA thiolase trifunctional protein beta subunit, involved in fatty acid beta-oxidation; variants are associated with trifunctional protein deficiency, sudden infant death syndrome and liver failure
SW:CNBP_HUMAN	ZNF9	19	2	1.87	0.27	SW:CNBP_HUMAN P20694 homo sapiens (human), and rattus norvegicus (rat). cellular nucleic acid binding protein (cnbp). 11/1997 [MASS=19463]/Zinc-finger protein that binds to sterol regulatory element (SRE) and may function in sterol-mediated repression of genes encoding the low density lipoprotein receptor and enzymes of the cholesterol biosynthetic pathway
SW:MAOM_HUMAN	ME2	19	2	1.96	0.04	SW:MAOM_HUMAN P23368 homo sapiens (human). nad-dependent malic enzyme, mitochondrial precursor (ec 1.1.1.38) (nad-me). 5/2000 [MASS=65444]/Malic enzyme 2, a NAD(+)-dependent mitochondrial form of malic enzyme, catalyzes the oxidative decarboxylation of malate to form pyruvate
SW:ECHA_HUMAN	HADHA	19	13	1.97	0.65	SW:ECHA_HUMAN P40939 homo sapiens (human). mitochondrial trifunctional enzyme alpha subunit precursor (tp-alpha) [includes: long-chain enoyl-coa hydratase (ec 4.2.1.17); long chain 3-hydroxyacyl-coa deh [MASS=82960]/Mitochondrial long-chain enoyl-CoA hydratase/3-hydroxyacyl-CoA dehydrogenase/3-ketoacyl-CoA thiolase alpha subunit, involved in fatty acid beta-oxidation, mutations are associated with trifuctional protein deficiency and Reye-like syndrome
SW:ETFB_HUMAN	ETFB	19	2	1.99	0.48	SW:ETFB_HUMAN P38117 homo sapiens (human). electron transfer flavoprotein beta-subunit (beta-etf). 5/2000 [MASS=27844]/Electron transfer flavoprotein beta subunit, shuttles electrons between primary flavoprotein dehydrogenases involved in mitochondrial fatty acid metabolism and ubiquinone oxidoreductase; genetic variants are associated with type II glutaric acidemia
GP:AL023805_1	PLCB4	19	6	2.00	0.24	GP:AL023805_1 Human DNA sequence from clone RP4-811H13 on chromosome 20p12. Contains part of the PLCB4 gene for Phospholipase C beta 4, STSs, GSSs and a CpG island, complete sequence; combines with dJ1119D9.2.1 and .2 in Em:AL031652 to form isoforms 5 and 6; may a [MASS=61433]/1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase beta 4/Phospholipase C beta 4, member of a G protein-regulated family of phospholipases that hydrolyze phosphatidylinositol 4,5-bisphosphate to the second messengers inositol 1,4,5-trisphosphate and diacylglycerol

SW:GST3_HUMAN	MGST3	19	2	2.31	0.83	SW:GST3_HUMAN O14880 homo sapiens (human). microsomal glutathione s-transferase 3 (ec 2.5.1.18) (microsomal gst-3) (microsomal gst-iii). 5/2000 [MASS=16516]/Microsomal glutathione S-transferase 3, a microsomal membrane protein that has glutathione-dependent transferase and peroxidase activities, member of a family that includes 5-lipoxygenase activating protein (ALOX5AP) and leukotriene-C4 synthase (LTC4S)
SW:ETFA_HUMAN	ETFA	19	1	2.36	0.00	SW:ETFA_HUMAN P13804 homo sapiens (human). electron transfer flavoprotein alpha-subunit precursor (alpha-etf). 5/2000 [MASS=35080]/Electron transfer flavoprotein alpha subunit, shuttles electrons between flavoprotein dehydrogenases of mitochondrial fatty acid metabolism and ubiquinone oxidoreductase, deficiency associated with Type II glutaricaciduria
SW:MAZ_HUMAN	MAZ	19	1	2.37	0.00	SW:MAZ_HUMAN P56270 homo sapiens (human). myc-associated zinc finger protein (mazi) (purine-binding transcription factor) (pur-1) (zf87) (zif87). 7/1999 [MASS=48608]/MYC-associated zinc finger protein (purine-binding transcription factor), functions both as a positive and a negative regulator of gene expression and may also have roles in initiating and terminating transcription
SW:THIL_HUMAN	ACAT1	19	2	2.44	0.44	SW:THIL_HUMAN P24752 homo sapiens (human). acetyl-coa acetyltransferase, mitochondrial precursor (ec 2.3.1.9) (acetoacetyl-coa thiolase) (t2). 7/1999 [MASS=45200]/Acetyl-Coenzyme A acetyltransferase 1 (mitochondrial acetoacetyl-coenzyme A thiolase); mutations in the corresponding gene are associated with 3-ketothiolase deficiency
GP:AF161397_1	HPCL2	19	2	2.53	0.16	GP:AF161397_1 Homo sapiens HSPC279 mRNA, partial cds. [MASS=64199]/Homo sapiens mRNA for 2-hydroxyphytanoyl-CoA lyase; thiamine pyrophosphate dependent enzyme/2-Hydroxyphytanoyl-CoA lyase (peroxisomal 2-hydroxyphytanoyl-CoA lyase), catalyzes the thiamine pyrophosphate-dependent cleavage of C-C bonds during alpha-oxidation of 3-methyl-branched fatty acids to form formyl-CoA and 2-methyl-branched fatty aldehyde
SW:TPP1_HUMAN	CLN2	19	1	2.62	0.00	SW:TPP1_HUMAN O14773 homo sapiens (human). tripeptidyl-peptidase i precursor (ec 3.4.14.9) (tpp-i) (tripeptidyl aminopeptidase) (lysosomal pepstatin insensitive protease) (lpic). 5/2000 [MASS=61229]/Tripeptidyl peptidase I (ceroid-lipofuscinosis neuronal 2), a lysosomal serine-type peptidase required for degradation of ATP synthase subunit c (ATP5G1 and ATP5G2); mutations in the corresponding gene cause late infantile neuronal ceroid lipofuscinosis
GP:AF002668_1	DEGS	19	1	3.29	0.00	GP:AF002668_1 Homo sapiens putative fatty acid desaturase MLD mRNA, complete cds; putative fatty acid desaturase. [MASS=37866]/Degenerative spermatocyte homolog (Drosophila), member of the membrane fatty acid desaturase family, regulates the biosynthesis of the epidermal growth factor receptor (EGFR)
SW:PA2M_HUMAN	PLA2G2A	19	3	3.94	1.93	SW:PA2M_HUMAN P14555 homo sapiens (human). phospholipase a2, membrane associated precursor (ec 3.1.1.4) (phosphatidylcholine 2-acylhydrolase) (group ii phospholipase a2) (non-pancreatic secretory phosph [MASS=16083]/Group IIA phospholipase A2, a secreted member of the phospholipase A2 family that hydrolyzes the phospholipid sn-2 ester bond, plays roles in phospholipid metabolism, host defense, and inflammation; gene loss reported in a sporadic colorectal tumor
GP:AJ002744_1	GALNT7	19	1	4.00	0.00	GP:AJ002744_1 Homo sapiens mRNA for UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase 7. [MASS=75402]/UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 7, enzyme that functions in O-glycosylation and is specific for partially glycosylated substrates
Nucleotide Metabolism						
SW:IMA1_HUMAN	KPNA1	25	1	0.33	0.00	SW:IMA1_HUMAN P52294 homo sapiens (human). importin alpha-1 subunit (karyopherin alpha-1 subunit) (srp1-beta) (rag cohort protein 2) (nucleoprotein interactor 1) (npi-1). 12/1998 [MASS=60307]/Karyopherin alpha (importin alpha), a subunit of the nuclear localization sequence (NLS) receptor complex that binds to and mediates the nuclear import of RAG1 and STAT1
SW:ACLY_HUMAN	ACLY	25	6	0.44	0.09	SW:ACLY_HUMAN P53396 homo sapiens (human). atp-citrate (pro-s-)-lyase (ec 4.1.3.8) (citrate cleavage enzyme). 10/1996 [MASS=121420]/ATP citrate lyase, catalyzes the formation of acetyl-CoA and oxaloacetate from citrate and CoA with the concomitant hydrolysis of ATP to ADP and phosphate, involved in cholesterol and fatty acid synthesis, nutritionally regulated
GP:AB007851_1	PRPSAP2	25	4	0.51	0.10	GP:AB007851_1 Homo sapiens mRNA for 41-kDa phosphoribosylpyrophosphate synthetase-associated protein, complete cds. [MASS=40926]/Phosphoribosyl pyrophosphate synthetase-associated protein 2, a component of phosphoribosylpyrophosphate (PRPP) synthetase that is related to the other components of PRPP synthetase (PRPS1, PRPS2 and PRPSAP1)
GP:AB011173_1	KIAA0601	25	1	0.59	0.00	GP:AB011173_1 Homo sapiens mRNA for KIAA0601 protein, partial cds. [MASS=96760]/KIAA0601 protein, a riboflavin-binding protein, member of a FAD dependent enzyme superfamily, component of the HDAC1 histone deacetylase complex, may be involved in gene silencing via covalent chromatin modification
SW:HS71_HUMAN	HSPA1A	25	6	0.62	0.14	SW:HS71_HUMAN P08107 homo sapiens (human). heat shock 70 kda protein 1 (hsp70.1) (hsp70-1/hsp70-2). 5/2000 [MASS=70052]/Heat shock 70 kDa protein 1A, a member of the HSP70 chaperone family involved in protein folding, translocation, and complex assembly, blocks AU-rich mRNA decay by nuclear sequestering of AU-rich binding protein, may contribute to celiac disease
SW:PUR8_HUMAN	ADSL	25	2	0.80	0.00	SW:PUR8_HUMAN P30566 homo sapiens (human). adenylosuccinate lyase (ec 4.3.2.2) (adenylosuccinase) (asl) (asase). 5/2000 [MASS=54889]/Adenylosuccinate lyase, catalyzes two steps in adenosine monophosphate biosynthesis; deficiency is associated with psychomotor retardation, epilepsy, and autism
SW:AMD2_HUMAN	AMPD2	25	1	0.81	0.00	SW:AMD2_HUMAN Q01433 homo sapiens (human). amp deaminase 2 (ec 3.5.4.6) (amp deaminase isoform l). 11/1997 [MASS=88198]/Adenosine monophosphate deaminase 2 (isoform L), catalyzes the deamination of adenosine monophosphate to form inosine monophosphate in purine nucleotide metabolism

PIR2:S71460	PRPS1	25	2	0.82	0.12	PIR2:S71460 ribose-phosphate pyrophosphokinase (EC 2.7.6.1) 39K regulatory chain - human [MASS=39480]/Phosphoribosyl pyrophosphate (PRPP) synthetase 1, generates PRPP, which is required for de novo purine and pyrimdine biosynthesis; mutations causing superactivity are associated with gout and neurological impairment
SW:SYA_HUMAN	AARS	25	1	0.83	0.00	SW:SYA_HUMAN P49588 homo sapiens (human). alanyl-trna synthetase (ec 6.1.1.7) (alanine--trna ligase) (alars). 7/1998 [MASS=106801]/Alanyl-tRNA synthetase, aminoacylates its cognate tRNA with alanine for protein biosynthesis, acts as an autoantigen in patients with polymyositis
SWN:ENT1_HUMAN	ENT1	25	1	0.83	0.00	SWN:ENT1_HUMAN Q99808 homo sapiens (human). equilibrative nucleoside transporter 1 (equilibrative nitrobenzylmercaptopurine riboside-sensitive nucleoside transporter) (equilibrative nbmpr-sensitive nucle [MASS=50088]/Solute carrier family 29 member 1 (equilibrative nucleoside transporter 1), functions in the transport of physiologic nucleosides and chemotherapeutic nucleoside analog drugs, inhibited by nitrobenzylthioinosine, dipyridamole, and dilazep
SW:CST1_HUMAN	CSTF1	25	1	0.93	0.00	SW:CST1_HUMAN Q05048 homo sapiens (human). cleavage stimulation factor, 50 kda subunit (cstf 50 kda subunit) (cf-1 50 kda subunit). 7/1998 [MASS=48358]/Cleavage stimulation factor subunit 1, the 50 kDa subunit of the cleavage stimulation factor complex required for pre-mRNA polyadenylation and 3'-end cleavage, interacts with BARD1 and the C-terminal domain of the RNA polymerase II large subunit
SW:SYQ_HUMAN	QARS	25	2	0.94	0.20	SW:SYQ_HUMAN P47897 homo sapiens (human). glutaminyl-trna synthetase (ec 6.1.1.18) (glutamine--trna ligase) (glnrs). 5/2000 [MASS=87799]/Glutaminyl-tRNA synthetase, aminoacylates cognate tRNAs with glutamine for protein biosynthesis, also suppresses FAS (TNFRSF6)-mediated apoptosis by inhibiting ASK1 (MAP3K5) kinase activity, contains N-terminal appended and C-terminal catalytic domains
SW:IMD2_HUMAN	IMPDH2	25	8	0.95	0.32	SW:IMD2_HUMAN P12268 homo sapiens (human). inosine-5'-monophosphate dehydrogenase 2 (ec 1.1.1.205) (imp dehydrogenase 2) (impdh-ii) (impd 2). 5/2000 [MASS=55805]/Inosine monophosphate dehydrogenase type 2, catalyzes the oxidation of inosine monophosphate to xanthosine monophosphate in GTP biosynthesis, required for T cell activation, a target for immunosuppressive and anticancer chemotherapy
SW:PUR6_HUMAN	PAICS	25	7	0.99	0.09	SW:PUR6_HUMAN P22234 homo sapiens (human). multifunctional protein ade2 [includes: phosphoribosylaminoimidazole-succinocarboxamide synthase (ec 6.3.2.6) (saicar synthetase); phosphoribosylaminoimidazol [MASS=47079]/SAICAR (phosphoribosylaminoimidazole-succinocarboxamide) synthetase and AIR (phosphoribosylaminoimidazole) carboxylase, a bifunctional protein required for de novo purine biosynthesis
SW:RINI_HUMAN	RNH	25	1	1.01	0.00	SW:RINI_HUMAN P13489 homo sapiens (human). placental ribonuclease inhibitor (ribonuclease/angiogenin inhibitor) (rai) (ri). 12/1998 [MASS=49842]/Ribonuclease and angiogenin inhibitor, tightly binds and inhibits alkaline and neutral ribonucleases and angiogenin, functions in mRNA degradation and inhibition of HT-29 human colon adenocarcinoma cell binding to angiogenin (ANG)
GP:AF132941_1	LOC51068	25	1	1.02	0.00	GP:AF132941_1 Homo sapiens CGI-07 protein mRNA, complete cds. [MASS=57585]/Protein with moderate similarity to S. cerevisiae Nmd3p, which is a protein involved in the nuclear export of 60S ribosomal subunits
PIR2:A57017	ABCE1	25	5	1.03	0.03	PIR2:A57017 RNase L inhibitor - human [MASS=67559]/Ribonuclease L inhibitor, inhibits the nuclease activity and 2-5A binding ability of RNase L, may be induced by HIV-1 to inhibit the 2-5A/RNase L pathway, can inhibit the antiviral activity of interferon when overexpressed
SW:NPM_HUMAN	NPM1	25	3	1.11	0.14	SW:NPM_HUMAN P06748 homo sapiens (human). nucleophosmin (npm) (nucleolar phosphoprotein b23) (numatrin) (nucleolar protein no38). 5/2000 [MASS=32575]/Nucleophosmin (numatrin), a nucleic acid-binding phosphoprotein involved in apoptosis, abundant in tumor cells; gene fusion with anaplastic lymphoma kinase (ALK) is detected in non-Hodgkin's lymphoma and fusion with MLF1 is seen in acute myeloid leukemia
SW:NDK6_HUMAN	NME2	25	1	1.22	0.00	SW:NDK6_HUMAN O60361 homo sapiens (human). putative nucleoside diphosphate kinase (ec 2.7.4.6) (ndk) (ndp kinase). 12/1998 [MASS=15529]/Nucleoside diphosphate kinase B, a transcription factor and endodeoxyribonuclease that binds to the Myc promoter, may function in DNA repair, may suppress metastasis in some tumors, displays reduced expression in breast carcinoma cells
SW:PAB1_HUMAN	PABPC1	25	13	1.22	0.44	SW:PAB1_HUMAN P11940 homo sapiens (human). polyadenylate-binding protein 1 (poly(a) binding protein 1) (pabp 1). 7/1998 [MASS=70671]/Poly(A)-binding protein cytoplasmic 1, binds to poly(A) tails of mRNA and plays roles in regulating mRNA stability and translation, also implicated in mRNA transport from the nucleus to the cytoplasm
SWN:SYFB_HUMAN	FRSB	25	4	1.25	0.44	SWN:SYFB_HUMAN Q9nsd9 homo sapiens (human). phenylalanyl-trna synthetase beta chain (ec 6.1.1.20) (phenylalanine--trna ligase beta chain) (phers) (protein hspc173). 8/2001 [MASS=66130]/Phenylalanyl-tRNA synthetase beta-subunit, regulatory subunit that forms heterodimers with the catalytic alpha subunit (FARSL), involved in protein synthesis, may play a role in tumorigenic events
SW:ROF_HUMAN	HNRPF	25	3	1.37	0.10	SW:ROF_HUMAN P52597 homo sapiens (human). heterogeneous nuclear ribonucleoprotein f (hnrnp f). 11/1997 [MASS=45672]/Heterogeneous nuclear ribonucleoprotein F, an RNA binding protein which contains quasi-RRMs (RNA recognition motifs) and plays a role in pre-mRNA splicing
PIR2:T13159	E1B-AP5	25	3	1.38	0.41	PIR2:T13159 E1B-55kDa-associated protein - human [MASS=95810]/E1B-55kDa-associated protein 5, a heterogeneous nuclear ribonucleoprotein involved in nucleocytoplasmic transport of adenovirus and cellular mRNAs, binds adenovirus early 1B (E1B-55 kD) protein and may regulate viral oncogenic transformation
PIR2:T02673	HNRPR	25	3	1.43	0.18	no_description_avail/Heterogeneous nuclear ribonucleoprotein R, a putative pre-mRNA processing protein that contains three RNA recognition domains and an RGG domain, interacts with survival motor neuron protein and is an autoantigen in autoimmune disease

GP:U85625_1	RNASE6PL	25	3	1.44	0.04	GP:U85625_1 Homo sapiens ribonuclease 6 precursor, mRNA, complete cds. [MASS=29481]/Ribonuclease 6 precursor, a putative ribonuclease that plays a role in the negative regulation of proliferation, may be involved in senescence, may be a class II tumor suppressor, downregulated in ovarian cancer and in ovarian cancer cell lines
GP:AF037448_1	NSAP1	25	4	1.45	0.22	GP:AF037448_1 Homo sapiens RRM RNA binding protein Gry-rbp (GRY-RBP) mRNA, complete cds; RRM RNA binding protein; Glycine, arginine and tyrosine-rich at C-terminus. [MASS=69633]/NS1 associated protein 1, component of the ApoB mRNA editosome involved in apolipoprotein B (APOB) mRNA editing, may bind RNA, may play a role in the regulation of mRNA splicing or transport from the nucleus
SW:PYR1_HUMAN	CAD	25	6	1.47	0.46	SW:PYR1_HUMAN P27708 homo sapiens (human). cad protein [includes: glutamine-dependent carbamoyl-phosphate synthase (ec 6.3.5.5); aspartate carbamoyltransferase (ec 2.1.3.2); dihydroorotase (ec 3.5.2.3)] [MASS=242917]/Carbamoylphosphate synthetase 2-aspartate transcarbamylase-dihydroorotase, a trifunctional enzyme that catalyzes the first three steps of pyrimidine biosynthesis
SW:ROK_HUMAN	HNRPK	25	6	1.51	0.30	SW:ROK_HUMAN Q07244 homo sapiens (human), and rattus norvegicus (rat). heterogeneous nuclear ribonucleoprotein k (hnrnp k) (dc-stretch binding protein) (csbp) (transformation upregulated nuclear protein [MASS=50976]/Heterogeneous nuclear ribonucleoprotein K, a transcription factor which binds to poly(C) of RNA and DNA and is involved in RNA processing, gene transcription and translational controls, may induce apoptosis and play a role in viral infection
SW:SMD3_HUMAN	SNRPD3	25	1	1.55	0.00	SW:SMD3_HUMAN P43331 homo sapiens (human). small nuclear ribonucleoprotein sm d3 (snrnp core protein d3) (sm-d3). 10/1996 [MASS=13916]/Small nuclear ribonucleoprotein D3, part of a multimeric complex involved in biogenesis of snRNPs and mRNA splicing, interacts with the spinal muscular atrophy disease protein (SMN); autoantigen for antibodies associated with systemic lupus erythematosus
SW:PSS1_HUMAN	PAPSS1	25	1	1.56	0.00	SW:PSS1_HUMAN P48651 homo sapiens (human). phosphatidylserine synthase i (serine-exchange enzyme i) (ec 2.7.8.-) (kiaa0024). 11/1997 [MASS=55528]/3'-phosphoadenosine 5'-phosphosulfate synthase 1, bifunctional polypeptide with ATP sulfurylase and adenosine 5'-phosphosulfate kinase activites, required for the synthesis of the sulfonate donor 3'-phosphoadenosine 5'-phosphosulfate
SW:ROA0_HUMAN	HNRPA0	25	2	1.64	0.40	SW:ROA0_HUMAN Q13151 homo sapiens (human). heterogeneous nuclear ribonucleoprotein a0 (hnrnp a0). 5/2000 [MASS=30841]/Heterogeneous nuclear ribonucleoprotein A0, has triplet repeats, two consensus sequence-type RNA-binding domains, and a glycine-rich auxiliary domain, found in low abundance hnRNP complexes
SW:ROH1_HUMAN	HNRPH1	25	4	1.66	0.22	SW:ROH1_HUMAN P31943 homo sapiens (human). heterogeneous nuclear ribonucleoprotein h (hnrnp h). 11/1997 [MASS=49229]/Heterogeneous nuclear ribonucleoprotein H1, a pre-mRNA splicing factor that is a component of a complex that mediates post-transcriptional processing of primary transcripts
SW:DDX1_HUMAN	DDX1	25	6	1.67	0.10	SW:DDX1_HUMAN Q92499 homo sapiens (human). dead box protein 1 (dead box protein-retinoblastoma) (dbp-rb). 5/2000 [MASS=82432]/DEAD box protein 1, a member of the DEAD-H box ATP-dependent RNA helicase protein family, plays a role in the processing of pre-mRNAs, may interact with CSTF2; corresponding gene is coamplified with MYC in some neuroblastoma and retinoblastoma cell lines
PIR2:JW0079	HNRPDL	25	1	1.72	0.00	PIR2:JW0079 heterogeneous nuclear ribonucleoprotein homolog JKTBP [imported] - human [MASS=33589]/Heterogeneous nuclear ribonucleoprotein D-like, an RNA- and DNA-binding protein that may play a role in mRNA biogenesis
GP:AC003972_1	RENT1	25	1	1.74	0.00	GP:AC003972_1 Homo sapiens DNA from chromosome 19, cosmid R33485 containing pNORF1, complete sequence; human type 1 RNA helicase; DPS similarity to (U59323) type 1 RNA helicase pNORF1 [Homo sapiens]; Score. [MASS=123036]/regulator of nonsense transcripts 1 (nonsense mrna reducing factor 1) (norf1) (up-frameshift suppressor 1 homolog). 10/2001 [MASS=124345]
SW:RUXF_HUMAN	SNRPF	25	1	1.76	0.00	SW:RUXF_HUMAN Q15356 homo sapiens (human). small nuclear ribonucleoprotein f (snrnp-f) (sm protein f). 7/1999 [MASS=9725]/Sm protein F, a spliceosomal snRNA-associated Sm core protein that is involved in the biogenesis of the snRNPs; a target of autoantibodies in patients with the autoimmune disease systemic lupus erythematosus
GP:AF177344_1	FLJ10581	25	1	1.89	0.00	GP:AF177344_1 Homo sapiens clone HC90 unknown mRNA. [MASS=30998]/ weakly similar to a methyltransferase/Member of the RNA methyltransferase family, which catalyze 2'-O-methylation of ribose groups in R
PIR2:T09073	SFRS2IP	25	1	1.89	0.00	PIR2:T09073 splicing factor Sip1 - human [MASS=128875]/Splicing factor arginine serine rich 2 interacting protein, a SR domain family protein that interacts with the RNA polymerase II C-terminal domain and several splicing factors, is essential in mRNA splicing and possibly spliceosome A-complex formation
PIR2:I55595	RNPC2	25	1	1.92	0.00	PIR2:I55595 splicing factor - human [MASS=58657]/Splicing factor CC1.3, a novel nuclear protein and putative member of the SR family of alternative splicing factors; target of autoantibodies from a patient with hepatocellular carcinoma
PIR2:S78046	RNASE6	25	3	1.94	0.00	PIR2:S78046 ribonuclease 6 (EC 3.1.27.-) precursor - human [MASS=21941]/Ribonuclease k6, a ribonuclease of the ribonuclease A superfamily, possibly functions in host defense
SW:DRN2_HUMAN	DNASE2	25	3	2.01	0.42	SW:DRN2_HUMAN O00115 homo sapiens (human). deoxyribonuclease ii precursor (ec 3.1.22.1) (dnase ii) (acid dnase) (lysosomal dnase ii) (r31240_2). 7/1999 [MASS=39581]/Deoxyribonuclease II lysosomal, an acid-activated DNA nicking enzyme, may participate in DNA fragmentation during apoptosis, induces apoptotic chromosome condensation when transfected into cell lines
SW:SMD2_HUMAN	SNRPD2	25	2	2.02	0.82	SW:SMD2_HUMAN P43330 homo sapiens (human). small nuclear ribonucleoprotein sm d2 (snrnp core protein d2) (sm-d2). 10/1996 [MASS=13527]/Small nuclear ribonucleoprotein D2 polypeptide, one of seven common core snRNP proteins involved in snRNP biogenesis and pre-mRNA splicing, autoantigen for anti-Sm antibodies produced by individuals with systemic lupus erythematosus

SW:U2AF_HUMAN	U2AF65	25	1	2.05	0.00	SW:U2AF_HUMAN P26368 homo sapiens (human). splicing factor u2af 65 kda subunit (u2 auxiliary factor 65 kda subunit) (u2 snrnp auxiliary factor large subunit). 12/1998 [MASS=53501]/U2 small nuclear ribonucleoprotein auxiliary factor (65 kDa), a component of U2 small nucleoprotein auxiliary factor, which is necessary for mRNA splicing, binds to pre-mRNA
GP:D21163_1	U5-116KD	25	1	2.11	0.00	GP:D21163_1 Human mRNA for KIAA0031 gene, complete cds; similar to human elongation factor 2 mRNA (HSEF2).. [MASS=109436]/U5 snRNP-specific protein 116 kD, a spliceosome component with GTPAse activity, plays a role in mRNA splicing and processing
SW:RU17_HUMAN	SNRP70	25	3	2.11	0.26	SW:RU17_HUMAN P08621 homo sapiens (human). u1 small nuclear ribonucleoprotein 70 kda (u1 snrnp 70 kda) (snrp70). 11/1995 [MASS=70081]/U1 small nuclear 70 kDa ribonucleoprotein, involved in pre mRNA splicing, acts as an autoantigen in systemic lupus erythematosus and mixed connective tissue disease
PIR2:A54601	HNRPD	25	9	2.17	0.65	PIR2:A54601 RNA-binding protein AUF1 - human [MASS=31200]/Heterogeneous nuclear ribonucleoprotein D (AU-rich element RNA-binding protein 1 37kD), an RNA and DNA-binding protein which binds to AU-rich elements in the 3' untranslated regions of mRNAs and mediates their degradation
SW:NHPX_HUMAN	NHP2L1	25	2	2.21	0.20	SW:NHPX_HUMAN P55769 homo sapiens (human). nhp2/rs6 family protein yel026w homolog (high mobility group-like nuclear protein 2 homolog) (otk27). 5/2000 [MASS=14174]/Non-histone chromosome protein 2 (S. cerevisiae)-like 1, a member of a family of RNP-associated proteins, a component of the spliceosome and rRNA processing machinery, recognizes a shared stem-internal loop-stem structure in its RNA targets
SW:DDX5_HUMAN	DDX5	25	1	2.27	0.00	SW:DDX5_HUMAN P17844 homo sapiens (human). probable rna-dependent helicase p68 (dead-box protein p68) (dead box protein 5). 7/1998 [MASS=69148]/DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 5 (RNA helicase 68kD), a ATP-dependent RNA helicase that has ATP-independent RNA renaturation activity and catalyses branch migration, binds estrogen receptor alpha and function as a transcriptional coactivator
SW:U2AG_HUMAN	U2AF35	25	2	2.34	0.02	SW:U2AG_HUMAN Q01081 homo sapiens (human). splicing factor u2af 35 kda subunit (u2 auxiliary factor 35 kda subunit) (u2 snrnp auxiliary factor small subunit). 12/1998 [MASS=27872]/U2(RNU2) small nuclear RNA auxiliary factor 1, functions as a pre-mRNA splicing protein, involved in the functional recognition of the 3' splice site AG dinucleotide, interacts with ZNF265 protein involved in alternative splicing
SW:ROU_HUMAN	HNRPU	25	29	2.48	0.62	SW:ROU_HUMAN Q00839 homo sapiens (human). heterogenous nuclear ribonucleoprotein u (hnrnp u) (scaffold attachment factor a) (saf-a). 5/2000 [MASS=90479]/Heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A), binds RNA, binds EP300 in a complex that binds scaffold-matrix attachment regions of TOP1, involved in chromatin structure, apoptosis, and perhaps RNA processing and transcription
SW:ROA1_HUMAN	HNRPA1	25	11	2.48	0.85	SW:ROA1_HUMAN P09651 homo sapiens (human). heterogeneous nuclear ribonucleoprotein a1 (helix-destabilizing protein) (single-strand binding protein) (hnrnp core protein a1). 11/1997 [MASS=38715]/Heterogeneous nuclear ribonucleoprotein A1, an RNA-binding protein involved in mRNA splicing and translational control, undergoes nucleocytoplasmic shuttling possibly for mRNA export and telomerase recruitment; an autoantigen in autoimmune disorders
SW:DD17_HUMAN	DDX17	25	1	2.58	0.00	SW:DD17_HUMAN Q92841 homo sapiens (human). probable rna-dependent helicase p72 (dead-box protein p72) (dead box protein 17). 5/2000 [MASS=72371]/DEAD H box protein 17, a member of the DEAD box family of RNA-dependent ATPases and ATP-dependent RNA helicases, a component of an estrogen receptor alpha (ESR) transcriptional coactivator complex
SW:Y017_HUMAN	SF3B3	25	7	2.63	0.59	SW:Y017_HUMAN Q15393 homo sapiens (human). hypothetical protein kiaa0017. 5/2000 [MASS=44606]/ Homo sapiens mRNA for SAP 130 spliceosomal protein/Splicing factor 3b subunit 3, a component of the U2 snRNP-associated protein complex SF3b that plays a role in spliceosome assembly, interacts with STAGA and TFTC complexes implicated in DNA repair, chromatin modification, and transcription
SW:NR54_HUMAN	NONO	25	2	3.38	1.09	SW:NR54_HUMAN Q15233 homo sapiens (human). 54 kda nuclear rna-binding protein (p54(nrb)) (p54nrb) (55 kda nuclear protein) (nmt55). 5/2000 [MASS=54232]/Non-POU-domain-containing octamer-binding nuclear protein, binds DNA and RNA, and implicated in transcription and pre-mRNA splicing; a fusion partner with TFE3 in papillary renal cell carcinoma
SW:SFR7_HUMAN	SFRS7	25	2	3.66	0.49	SW:SFR7_HUMAN Q16629 homo sapiens (human). splicing factor, arginine/serine-rich 7 (splicing factor 9g8). 5/2000 [MASS=27367]/Splicing factor arginine serine rich 7, a splicing factor of the SR protein family containing an RNA binding domain (RBD) and a serine/arginine (SR) domain that is implicated in alternative pre-mRNA splicing
Protein Synthesis						
SW:RS12_HUMAN	RPS12	35	2	0.40	0.09	SW:RS12_HUMAN P25398 homo sapiens (human). 40s ribosomal protein s12. 5/2000 [MASS=14395]/Ribosomal protein S12, a component of the small 40S ribosomal subunit; overexpressed in colorectal cancer
PIR2:JC4775	DNAJC3	35	2	0.51	0.27	PIR2:JC4775 p58k protein - human [MASS=57580]/The 58,000-dalton cellular inhibitor of the interferon-induced double-stranded RNA-activated protein kinase (PKR) is a member of the tetratricopeptide repeat family of proteins/DnaJ (Hsp40) homolog subfamily C member 3 (protein kinase inhibitor p58), a member of the tetratricopeptide repeat family of proteins that may act as a cochaperone that inhibits the activity of double-stranded RNA-dependent protein kinase (PRKR)
SW:SYTC_HUMAN	TARS	35	4	0.51	0.06	SW:SYTC_HUMAN P26639 homo sapiens (human). threonyl-trna synthetase, cytoplasmic (ec 6.1.1.3) (threonine--trna ligase) (thrrs). 6/1994 [MASS=82124]/Threonyl-tRNA synthetase, a class II aminoacyl tRNA synthetase which aminoacylates its cognate tRNAs with threonine for protein synthesis, autoantigen in several autoimmune disorders

SW:IF2P_HUMAN	IF2	35	2	0.65	0.02	SW:IF2P_HUMAN O60841 homo sapiens (human). translation initiation factor if-2. 5/2000 [MASS=138755]/Translation initiation factor, member of the Tu elongation factor family, has moderate similarity to yeast YAL035W translation initiation factor 2 (eIF2)
SW:RL7A_HUMAN	RPL7A	35	1	0.67	0.00	SW:RL7A_HUMAN P11518 homo sapiens (human), and rattus norvegicus (rat). 60s ribosomal protein l7a (surfeit locus protein 3) (pla-x polypeptide). 7/1999 [MASS=29864]/Ribosomal protein L7a (surfeit-3), a putative component of the 60S ribosomal subunit, likely to be involved in protein biosynthesis and in colorectal carcinogenesis; trk-2h fusion oncogene in breast cancer cells comprises a fragment of RPL7A fused to TRK
SW:SYG_HUMAN	GARS	35	1	0.69	0.00	SW:SYG_HUMAN P41250 homo sapiens (human). glycyl-trna synthetase (ec 6.1.1.14) (glycine--trna ligase) (glyrs). 10/1996 [MASS=77531]/Glycyl-tRNA synthetase; functions in protein biosynthesis, aminoacylates its cognate tRNAs with phenylalanine/Glycyl-tRNA synthetase, a class II aminoacyl-tRNA synthetase that catalyzes aminoacylation of its cognate tRNA with glycine for protein biosynthesis; an autoantigen in dermatomyositis
SW:IF32_HUMAN	TRIP1	35	3	0.72	0.09	SW:IF32_HUMAN Q13347 homo sapiens (human). eukaryotic translation initiation factor 3 subunit 2 (eif-3 beta) (eif3 p36) (tgf-beta receptor interacting protein 1) (trip-1). 5/2000 [MASS=36502]/Eukaryotic translation initiation factor 3 subunit 2, an eIF3 subunit with a predicted role in translation initiation, binds transforming growth factor beta receptor II (TGFBR2) and acts as a modulator of TGFBR2 signaling pathways
SW:RS4_HUMAN	RPS4X	35	3	0.73	0.14	SW:RS4_HUMAN P12750 homo sapiens (human), rattus norvegicus (rat), mus musculus (mouse), mesocricetus auratus (golden hamster), and felis silvestris catus (cat). 40s ribosomal protein s4, x isoform (sin [MASS=29467]/Ribosomal protein S4 X-linked, a component of the small 40S ribosomal subunit with roles in translation, cell cycle, and cell proliferation; gene is X-linked but escapes X inactivation, and may therefore contribute to haploinsufficency in Turner syndrome
SW:SYD_HUMAN	DARS	35	4	0.77	0.15	SW:SYD_HUMAN P14868 homo sapiens (human). aspartyl-trna synthetase (ec 6.1.1.12) (aspartate--trna ligase) (asprs). 11/1997 [MASS=57192]/Aspartyl-tRNA synthetase, a class II aminoacyl tRNA synthetase that aminoacylates its cognate tRNA with aspartate for protein biosynthesis, associates with a multisynthetase complex, N-terminus may aid interaction with elongation factor 1 alpha
SW:EF11_HUMAN	EEF1A1	35	11	0.78	0.11	SW:EF11_HUMAN P04720 homo sapiens (human), and oryctolagus cuniculus (rabbit). elongation factor 1-alpha 1 (ef-1-alpha-1) (elongation factor tu) (ef- tu). 12/1998 [MASS=50141]/Eukaryotic translation elongation factor 1 alpha 1, involved in cytoskeletal rearrangment, has putative roles in translational elongation and senescence and GTP binding; possibly involved in diabetes, Felty syndrome, and HIV life cycle
SW:SYA_HUMAN	AARS	35	1	0.83	0.00	SW:SYA_HUMAN P49588 homo sapiens (human). alanyl-trna synthetase (ec 6.1.1.7) (alanine--trna ligase) (alars). 7/1998 [MASS=106801]/Alanyl-tRNA synthetase, aminoacylates its cognate tRNA with alanine for protein biosynthesis, acts as an autoantigen in patients with polymyositis
SW:SYR_HUMAN	RARS	35	7	0.84	0.08	SW:SYR_HUMAN P54136 homo sapiens (human). arginyl-trna synthetase (ec 6.1.1.19) (arginine--trna ligase) (argrs). 5/2000 [MASS=74977]/Arginyl-tRNA synthetase, aminoacylates its cognate tRNAs with arginine for protein biosynthesis
SW:SYM_HUMAN	MARS	35	9	0.87	0.18	SW:SYM_HUMAN P56192 homo sapiens (human). methionyl-trna synthetase (ec 6.1.1.10) (methionine--trna ligase) (metrs). 12/1998 [MASS=101129]/Methionine-tRNA synthetase, putative tRNA synthetase that is predicted to aminoacylate its cognate tRNAs with methionine for protein biosynthesis, required for rRNA synthesis in the nucleolus
SW:RL8_HUMAN	RPL8	35	4	0.88	0.57	SW:RL8_HUMAN P25120 homo sapiens (human), rattus norvegicus (rat), and mus musculus (mouse). 60s ribosomal protein l8. 5/2000 [MASS=28025]/Ribosomal protein L8, putative component of the large 60S ribosomal subunit
PIR2:B55053	SCYE1	35	9	0.88	0.07	PIR2:B55053 endothelial monocyte-activating protein II precursor - human [MASS=34254]/Endothelial monocyte activating polypeptide II, a proinflammatory cytokine that interacts with ATP synthase and inhibits endothelial cell growth, released during apoptosis, may sensitize tumors to killing by tumor necrosis factor alpha (TNF)
SW:SYEP_HUMAN	EPRS	35	23	0.92	0.84	SW:SYEP_HUMAN P07814 homo sapiens (human). multifunctional aminoacyl-trna synthetase [includes: glutamyl-trna synthetase (ec 6.1.1.17) (glutamate--trna ligase); prolyl-trna synthetase (ec 6.1.1.15) (pro [MASS=163026]/Glutamyl-prolyl-tRNA synthetase, a bifunctional enzyme with two functionally separable domains, one that aminoacylates prolyl-tRNA with proline and another that is believed to aminoacylate glutamyl-tRNA with glutamate for protein biosynthesis
SWN:E2BD_HUMAN	DKFZP586J0119	35	2	0.94	0.19	SWN:E2BD_HUMAN Q9ui10 homo sapiens (human). translation initiation factor eif-2b delta subunit (eif-2b gdp-gtp exchange factor). 8/2001 [MASS=57599]/Protein with strong similarity to eukaryotic translation initiation factor 2B delta subunit (rat Eif2b), which is a guanine nucleotide-exchange factor subunit of eIF-2B that mediates inhibition of eIF-2B, member of the initiation factor 2 subunit family
SW:SYQ_HUMAN	QARS	35	2	0.94	0.20	SW:SYQ_HUMAN P47897 homo sapiens (human). glutaminyl-trna synthetase (ec 6.1.1.18) (glutamine--trna ligase) (glnrs). 5/2000 [MASS=87799]/Glutaminyl-tRNA synthetase, aminoacylates cognate tRNAs with glutamine for protein biosynthesis, also suppresses FAS (TNFRSF6)-mediated apoptosis by inhibiting ASK1 (MAP3K5) kinase activity, contains N-terminal appended and C-terminal catalytic domains
SW:SYV_HUMAN	VARS2	35	4	0.95	0.14	SW:SYV_HUMAN P26640 homo sapiens (human). valyl-trna synthetase (ec 6.1.1.9) (valine--trna ligase) (valrs). 2/1996 [MASS=140377]/Valyl-tRNA synthetase 2, a putative class I tRNA sythetase, predicted to function in aminoacylation of valyl tRNAs for protein biosynthesis
SW:IF5A_HUMAN	EIF5A	35	4	0.96	0.06	SW:IF5A_HUMAN P10159 homo sapiens (human). initiation factor 5a (eif-5a) (eif-4d) (rev binding factor). 5/2000 [MASS=16701]/Eukaryotic initiation factor 5A, a translation initiation factor, also an HIV-1 transactivator protein Rev cofactor that exports viral mRNA from the nucleus

SW:RM03_HUMAN	MRPL3	35	1	0.96	0.00	SW:RM03_HUMAN P09001 homo sapiens (human). mitochondrial 60s ribosomal protein l3. 8/1992 [MASS=38633]/Mitochondrial ribosomal protein L3, a likely component of the large mitochondrial 60S ribosomal subunit, may be involved in mRNA binding to the ribosome, can interact with the 3' UTR of hepatitis C; elevated levels are associated with hepatocarcinoma
SWN:SU12_HUMAN	GC20	35	4	0.98	0.06	SWN:SU12_HUMAN Q9unq9 homo sapiens (human). protein translation factor sui1 homolog a121. 8/2001 [MASS=12745]/Translation factor sui1 homolog, a translation initiation factor, plays a role in initiating translation, may modulate translation initiation during periods of cell stress such as UV-induced and endoplasmic reticulum stress
SW:RL32_HUMAN	RPL32	35	7	1.00	0.12	SW:RL32_HUMAN P02433 homo sapiens (human), mus musculus (mouse), and rattus norvegicus (rat). 60s ribosomal protein l32. 6/1994 [MASS=15729]/Ribosomal protein L32, an RNA-binding structural component of the large 60S ribosomal subunit that is likely to play a role in protein biosynthesis
GP:AF112214_1	RPL13	35	1	1.01	0.00	GP:AF112214_1 Homo sapiens ribosomal protein L13 mRNA, complete cds; RPL13. [MASS=19917]/Ribosomal protein L13, putative component of the 60S ribosomal subunit, expressed at higher levels in benign breast lesions than in carcinomas
SW:SYK_HUMAN	KARS	35	7	1.01	0.18	SW:SYK_HUMAN Q15046 homo sapiens (human). lysyl-trna synthetase (ec 6.1.1.6) (lysine--trna ligase) (lysrs) (kiaa0070). 7/1998 [MASS=68034]/Lysyl-tRNA synthetase, a class II aminoacyl tRNA synthetase, aminoacylates its cognate tRNAs with lysine for protein biosynthesis, packaged into HIV virions, exists as cytoplasmic and mitochondrial alternative forms
GP:AB037819_1	RRBP1	35	7	1.02	0.13	GP:AB037819_1 Homo sapiens mRNA for KIAA1398 protein, partial cds; Start codon is not identified.. [MASS=170212]/Ribosome binding protein 1, a putative ribosome receptor, may play a role in protein biosynthesis, appears to be involved in cardiac development, may play a role in cardiac remodeling in heart failure
GP:AF132941_1	LOC51068	35	1	1.02	0.00	GP:AF132941_1 Homo sapiens CGI-07 protein mRNA, complete cds. [MASS=57585]/Protein with moderate similarity to S. cerevisiae Nmd3p, which is a protein involved in the nuclear export of 60S ribosomal subunits
SW:EF1G_HUMAN	EEF1G	35	7	1.05	0.15	SW:EF1G_HUMAN P26641 homo sapiens (human). elongation factor 1-gamma (ef-1-gamma). 5/2000 [MASS=50119]/Eukaryotic elongation factor 1 gamma, a likely translation elongation factor 1 (EF-1) complex component that binds cytoplasmic cysteinyl-tRNA synthetase and possibly EF-1 beta; overexpression in gastric carcinoma correlates with vascular permeation
SW:RS8_HUMAN	RPS8	35	9	1.07	0.56	SW:RS8_HUMAN P09058 homo sapiens (human), rattus norvegicus (rat), and mus musculus (mouse). 40s ribosomal protein s8. 2/1996 [MASS=24074]/Ribosomal protein S8, component of the small 40S ribosomal subunit
SW:IF4G_HUMAN	EIF4G1	35	2	1.08	0.39	SW:IF4G_HUMAN Q04637 homo sapiens (human). eukaryotic translation initiation factor 4 gamma (eif-4-gamma) (eif- 4g) (eif4g) (p220). 7/1999 [MASS=153361]/Eukaryotic translation initiation factor 4 gamma 1, gamma subunit of eIF4, functions in translation initiation, binds RNA and forms a bridge between the mRNA cap and polyA tail, cleaved during apoptosis and poliovirus infection
SW:EF2_HUMAN	EEF2	35	39	1.09	0.20	SW:EF2_HUMAN P13639 homo sapiens (human). elongation factor 2 (ef-2). 12/1998 [MASS=95338]/Translation elongation factor 2, member of the superfamily of GTP hydrolases, binds ribosomes, catalyzes the translocation step of peptide elongation in protein biosynthesis, target of ADP-ribosylation by diphteria toxin and Pseudomonas exotoxin
SW:SYI_HUMAN	IARS	35	9	1.10	0.16	SW:SYI_HUMAN P41252 homo sapiens (human). isoleucyl-trna synthetase, cytoplasmic (ec 6.1.1.5) (isoleucine--trna ligase) (ilers) (irs). 7/1999 [MASS=144959]/Isoleucine-tRNA synthetase, a class I aminoacyl tRNA synthetase, aminoacylates isoleucyl-tRNA with isoleucine for protein biosynthesis, acts as an autoantigen in some autoimmune diseases
GP:AF132939_1	LOC51067	35	1	1.11	0.00	GP:AF132939_1 Homo sapiens CGI-04 protein mRNA, complete cds. [MASS=53063]/Member of the class I tryptophanyl and tyrosyl (W and Y) tRNA synthetase family, has low similarity to tyrosyl-tRNA synthetase mitochondrial (S. cerevisiae Msy1p), which is involved in tyrosyl-tRNA aminoacylation
SW:IF38_HUMAN	EIF3S8	35	5	1.11	0.32	SW:IF38_HUMAN Q99613 homo sapiens (human). eukaryotic translation initiation factor 3 subunit 8 (eif3 p110). 5/2000 [MASS=105344]/Translation initiation factor 3 subunit 8, 110 kDa eIF3 subunit that recruits translation initiation factor 1 (human SUI1) to 40S ribosomes, interacts with viral internal ribosome entry sites, and may be involved in seminoma development
SW:RL3_HUMAN	RPL3	35	2	1.11	0.01	SW:RL3_HUMAN P39023 homo sapiens (human). 60s ribosomal protein l3 (hiv-1 tar rna binding protein b) (tarbp-b). 5/2000 [MASS=45978]/Ribosomal protein L3, component of the large 60S ribosomal subunit; overexpressed in rapidly dividing cells
SW:E2BE_HUMAN	EIF2B5	35	1	1.12	0.00	SW:E2BE_HUMAN Q13144 homo sapiens (human). translation initiation factor eif-2b epsilon subunit (eif-2b gdp-gtp exchange factor) (fragment). 7/1999 [MASS=72237]/Translation initiation factor 2B subunit 5 (epsilon, 82kD), putative guanyl-nucleotide exchange factor component of the translation initiation factor 2B complex, predicted to mediate the exchange of GDP bound to translation initiation factor eIF2 for GTP
SW:RL9_HUMAN	RPL9	35	8	1.12	0.30	SW:RL9_HUMAN P32969 homo sapiens (human). 60s ribosomal protein l9. 5/2000 [MASS=21863]/Ribosomal protein L9, putative component of the large 60S ribosomal subunit
SW:RS5_HUMAN	RPS5	35	19	1.12	0.89	SW:RS5_HUMAN P46782 homo sapiens (human). 40s ribosomal protein s5. 5/2000 [MASS=22777]/Ribosomal protein S5, a component of the 40S ribosomal subunit; gene expression is altered in colorectal carcinoma cells
SW:RS25_HUMAN	RPS25	35	4	1.13	0.24	SW:RS25_HUMAN P25111 homo sapiens (human), and rattus norvegicus (rat). 40s ribosomal protein s25. 10/1993 [MASS=13742]/Ribosomal protein S25, a putative RNA-binding component of the small 40S ribosomal subunit that may play a role in protein biosynthesis

SW:IF2A_HUMAN	EIF2S1	35	1	1.16	0.00	SW:IF2A_HUMAN P05198 homo sapiens (human). eukaryotic translation initiation factor 2 alpha subunit (eif-2- alpha). 7/1999 [MASS=35981]/Eukaryotic translation initiation factor 2 subunit 1 (alpha subunit of eIF2), a translation initiation factor, involved in translational regulation, inhibited by phosphorylation
SW:RS29_HUMAN	RPS29	35	1	1.17	0.00	SW:RS29_HUMAN P30054 homo sapiens (human), mus musculus (mouse), rattus norvegicus (rat), and bos taurus (bovine). 40s ribosomal protein s29. 5/2000 [MASS=6546]Ribosomal protein S29, a component of the small 40S ribosomal subunit, contains a zinc finger-like motif, enhances activity of the tumor suppressor Krev-1 (RAP1A)
SW:RS14_HUMAN	RPS14	35	3	1.20	0.12	SW:RS14_HUMAN P06366 homo sapiens (human), and cricetulus griseus (chinese hamster). 40s ribosomal protein s14. 8/1992 [MASS=16273]/Ribosomal protein S14, a putative component of the small 40S ribosomal subunit, may play a role in protein biosynthesis, may bind RNA, upregulated in prostate carcinoma cell lines
SW:EF12_HUMAN	EEF1A2	35	6	1.22	0.11	SW:EF12_HUMAN Q05639 homo sapiens (human). elongation factor 1-alpha 2 (ef-1-alpha-2) (statin s1). 12/1998 [MASS=50470]/Eukaryotic translation elongation factor 1 alpha 2, a putative translation elongation factor, upregulated in an estrogen receptor-expressing breast carcinoma cell line; mutation in mouse Eef1a2 causes the multiple-defect wasted phenotype
SW:PAB1_HUMAN	PABPC1	35	13	1.22	0.44	SW:PAB1_HUMAN P11940 homo sapiens (human). polyadenylate-binding protein 1 (poly(a) binding protein 1) (pabp 1). 7/1998 [MASS=70671]/Poly(A)-binding protein cytoplasmic 1, binds to poly(A) tails of mRNA and plays roles in regulating mRNA stability and translation, also implicated in mRNA transport from the nucleus to the cytoplasm
SW:IF2G_HUMAN	EIF2S3	35	22	1.23	0.22	SW:IF2G_HUMAN P41091 homo sapiens (human). eukaryotic translation initiation factor 2 gamma subunit (eif-2- gamma). 5/2000 [MASS=50978]/Eukaryotic initiation factor 2G, gamma subunit of the heterotrimeric GTP binding protein involved in recruitment of Met-tRNAi to the 40S ribosomal subunit, activity is regulated by herpes simplex virus type 1 gamma 34.5 and by the cellular GADD34 proteins
SW:IF37_HUMAN	EIF3S7	35	6	1.23	0.32	SW:IF37_HUMAN O15371 homo sapiens (human). eukaryotic translation initiation factor 3 subunit 7 (eif-3 zeta) (eif3 p66). 5/2000 [MASS=63973]/Eukaryotic translation initiation factor 3 subunit 7, mRNA-binding subunit of the tranlation initiation factor 3 complex, which mediates dissociation of 80S ribosomes and stabilizes initiator Met-tRNAi binding to 40S subunits
SW:RL4_HUMAN	RPL4	35	17	1.23	0.33	SW:RL4_HUMAN P36578 homo sapiens (human). 60s ribosomal protein l4 (l1). 12/1998 [MASS=47759]/Ribosomal protein L4, a putative component of the large 60S ribosomal subunit, may bind RNA
SW:RS17_HUMAN	RPS17	35	6	1.23	0.24	SW:RS17_HUMAN P08708 homo sapiens (human). 40s ribosomal protein s17. 8/1992 [MASS=15419]/Ribosomal protein S17, component of the small 40S ribosomal subunit
SW:RS3A_HUMAN	RPS3A	35	13	1.23	0.20	SW:RS3A_HUMAN P49241 homo sapiens (human), and felis silvestris catus (cat). 40s ribosomal protein s3a. 5/2000 [MASS=29814]/Ribosomal protein S3A (v fos transformation effector), component of the 40S ribosomal subunit, may play roles in apoptosis, cell growth and protein biosynthesis
GP:AF257077_1	EIF2B3	35	2	1.24	0.11	GP:AF257077_1 Homo sapiens eukaryotic translation initiation factor EIF2B subunit 3 (EIF2B3) mRNA, complete cds; eukaryotic translation initiation factor EIF2Bgamma; guanine nucleotide exchange factor. [MASS=50240]/Eukaryotic translation initiation factor 2B gamma subunit, has a putative role in the initiation of protein synthesis; acts as a cofactor for hepatitis C virus IRES-mediated translation
SWN:SYFB_HUMAN	FRSB	35	4	1.25	0.44	SWN:SYFB_HUMAN Q9nsd9 homo sapiens (human). phenylalanyl-trna synthetase beta chain (ec 6.1.1.20) (phenylalanine--trna ligase beta chain) (phers) (protein hspc173). 8/2001 [MASS=66130]/Phenylalanyl-tRNA synthetase beta-subunit, regulatory subunit that forms heterodimers with the catalytic alpha subunit (FARSL), involved in protein synthesis, may play a role in tumorigenic events
SW:SR09_HUMAN	SRP9	35	7	1.25	0.29	SW:SR09_HUMAN P49458 homo sapiens (human). signal recognition particle 9 kda protein (srp9). 12/1998 [MASS=9981]/Signal recognition particle 9 kDa, a subunit of the signal recognition particle that forms the Alu RNA-binding protein and binds to Alu RNA with SRP14, involved in translocation of newly synthesized proteins across the membrane of the rough ER
SW:RL23_HUMAN	RPL23	35	10	1.30	0.27	SW:RL23_HUMAN P23131 homo sapiens (human), rattus norvegicus (rat), and sus scrofa (pig). 60s ribosomal protein l23 (l17). 7/1999 [MASS=14865]/Ribosomal protein L23, a putative large ribosomal subunit component that is likely to play a role in protein biosynthesis
SW:RS21_HUMAN	RPS21	35	3	1.30	0.29	SW:RS21_HUMAN P35265 homo sapiens (human), and sus scrofa (pig). 40s ribosomal protein s21. 5/2000 [MASS=9111]/Ribosomal protein S21, component of the small 40S ribosomal subunit
SW:ERF1_HUMAN	ETF1	35	1	1.32	0.00	SW:ERF1_HUMAN P46055 homo sapiens (human), mesocricetus auratus (golden hamster), and oryctolagus cuniculus (rabbit). eukaryotic peptide chain release factor subunit 1 (erf1) (tb3-1) (c11 protein). 5/20 [MASS=49031]/ Eukaryotic translation termination factor 1, an RNA binding translation release factor involved in translation termination, expression is increased in H. pylori infected gastric cancer cells; may be candidate gene for certain malignant myeloid diseases
SW:RL5_HUMAN	RPL5	35	7	1.32	0.51	SW:RL5_HUMAN P46777 homo sapiens (human). 60s ribosomal protein l5. 7/1999 [MASS=34317]/Ribosomal protein L5, a putative component of the 60S ribosomal subunit, binds 5S rRNA, undergoes nuclear export, may play a role in rev-mediated HIV-1 RNA nucleocytoplasmic transport; expression is altered in colorectal cancer and astrocytomas
GPN:AF293383_1	ABCF1	35	1	1.33	0.00	ATP-binding cassette subfamily F member 1, a member of the ATP-binding cassette family that does not contain a transmembrane domain and may play a role in translation
SW:RS11_HUMAN	RPS11	35	8	1.33	0.07	SW:RS11_HUMAN P04643 homo sapiens (human), rattus norvegicus (rat), and mus musculus (mouse). 40s ribosomal protein s11. 5/2000 [MASS=18431]/Ribosomal protein S11, putative component of the small 40S ribosomal subunit
SW:RLA0_HUMAN	RPLP0	35	14	1.35	0.20	SW:RLA0_HUMAN P05388 homo sapiens (human). 60s acidic ribosomal protein p0 (l10e). 5/2000 [MASS=34274]/Ribosomal protein P0, acidic phosphoprotein component of the large 60S ribosomal subunit; shows increased expression in hepatocellular and colon carcinomas

SW:R27A_HUMAN	RPS27A	35	3	1.38	0.38	SW:R27A_HUMAN P14798 homo sapiens (human), and cavia porcellus (guinea pig). 40s ribosomal protein s27a. 5/2000 [MASS=9418]/Ribosomal protein S27a, component of the small ribosomal subunit, consists of ubiquitin at the N-terminus and ribosomal protein S27a at the C-terminus; overexpressed in colon and renal cancers
SW:R10A_HUMAN	RPL10A	35	1	1.38	0.00	SW:R10A_HUMAN P53025 homo sapiens (human). 60s ribosomal protein l10a (csa-19). 10/1996 [MASS=24859]/Ribosomal protein L10a, a component of the large 60S ribosomal subunit; expression in the thymus is downregulated by cyclosporin-A
SW:EFTU_HUMAN	TUFM	35	8	1.41	0.11	SW:EFTU_HUMAN P49411 homo sapiens (human). elongation factor tu, mitochondrial precursor (p43). 12/1998 [MASS=49542]/Tu translation elongation factor (mitochondrial), a putative translation elongation factor, may be involved in protein biosynthesis, upregulated in some tumors
SW:SYN_HUMAN	NARS	35	4	1.42	0.19	SW:SYN_HUMAN O43776 homo sapiens (human). asparaginyl-trna synthetase, cytoplasmic (ec 6.1.1.22) (asparagine-- trna ligase) (asnrs). 5/2000 [MASS=62943]/Asparaginyl-tRNA synthetase, a class II aminoacyl tRNA synthetase, aminoacylates its cognate tRNAs with asparagine for protein biosynthesis, acts as an autoantigen in patients with inflammatory myopathy in interstitial lung disease
SW:IF39_HUMAN	EIF3S9	35	5	1.44	0.20	SW:IF39_HUMAN P55884 homo sapiens (human). eukaryotic translation initiation factor 3 subunit 9 (eif-3 eta) (eif3 p116) (eif3 p110). 5/2000 [MASS=92492]/Eukaryotic translation initiation factor 3 subunit (EIF3 subunit eta), the 116 kDa subunit of the EIF3 complex that plays a role in protein synthesis initiation
SW:RL2A_HUMAN	RPL27A	35	7	1.44	0.56	SW:RL2A_HUMAN P46776 homo sapiens (human). 60s ribosomal protein l27a. 5/2000 [MASS=16430]/Ribosomal protein L27a, component of the large 60S ribosomal subunit; gene is abnormally expressed in colorectal carcinomas
SW:RSP4_HUMAN	LAMR1	35	7	1.44	0.05	SW:RSP4_HUMAN P08865 homo sapiens (human). 40s ribosomal protein sa (p40) (34/67 kda laminin receptor) (colon carcinoma laminin-binding protein) (nem/1chd4). 5/2000 [MASS=32854]/Laminin receptor 1, a ribosomal protein of the small 40S ribosomal subunit, plays a role in cancer cell and basement membrane glycoprotein laminin interactions during tumor invasion and metastasis, expression correlates with cancer cell aggressiveness
SW:RL18_HUMAN	RPL18	35	5	1.49	0.46	SW:RL18_HUMAN Q07020 homo sapiens (human). 60s ribosomal protein l18. 5/2000 [MASS=21503]/Ribosomal protein L18, a component of the large 60S ribosomal subunit, a negative regulator of double-stranded RNA-activated protein kinase (PKR) which is involved in control of protein synthesis initiation; gene expression increases in colon cancer
SW:RL3L_HUMAN	RPL3L	35	11	1.51	0.24	SW:RL3L_HUMAN Q92901 homo sapiens (human). 60s ribosomal protein l3-like. 11/1997 [MASS=46165]/Ribosomal protein L3-like, a putative RNA-binding ribosome structural protein that plays a role in protein biosynthesis
SW:RS6_HUMAN	RPS6	35	5	1.52	0.13	SW:RS6_HUMAN P10660 homo sapiens (human), rattus norvegicus (rat), and mus musculus (mouse). 40s ribosomal protein s6 (phosphoprotein np33). 7/1998 [MASS=28681]/Ribosomal protein S6, structural component of the cytosolic small (40S) ribosomal subunit, functions in RNA binding and protein biosynthesis
SW:IF34_HUMAN	EIF3S4	35	1	1.53	0.00	SW:IF34_HUMAN O75821 homo sapiens (human). eukaryotic translation initiation factor 3 subunit 4 (eif-3 delta) (eif3 p44) (eif-3 rna-binding subunit) (eif3 p42). 5/2000 [MASS=35696]/Eukaryotic translation initiation factor 3 subunit 4 (delta 44kD), a component of the eIF-3 translation initiation complex which plays a role in formation of the 40S initiator complex containing methionyl-tRNA and 40S subunit, binds RNA
SW:RL10_HUMAN	RPL10	35	14	1.53	1.04	SW:RL10_HUMAN P27635 homo sapiens (human). 60s ribosomal protein l10 (qm protein) (tumor suppressor qm) (laminin receptor homolog). 5/2000 [MASS=24446]/Ribosomal protein L10, a component of the 60S ribosomal subunit; may be involved in the maintenance of the nontumorigenic phenotype in Wilms' microcell hybrid cells
SW:RL12_HUMAN	RPL12	35	35	1.62	0.58	SW:RL12_HUMAN P30050 homo sapiens (human). 60s ribosomal protein l12. 7/1998 [MASS=17819]/Ribosomal protein L12, a likely RNA-binding structural component of the large 60S ribosomal subunit that plays a role in protein biosynthesis; autoantibodies to ribosomal protein L12 are associated with systemic lupus erythematosus
SW:RL14_HUMAN	RPL14	35	23	1.63	0.47	SW:RL14_HUMAN P50914 homo sapiens (human). 60s ribosomal protein l14 (cag-isl 7). 12/1998 [MASS=23158]/Ribosomal protein L14, a putative component of the large 60S ribosomal subunit; transcripts can contain either fixed or variable numbers of CAG triplet repeats depending on cell type
SW:RL17_HUMAN	RPL17	35	4	1.63	0.06	SW:RL17_HUMAN P18621 homo sapiens (human). 60s ribosomal protein l17 (l23). 5/2000 [MASS=21397]/Ribosomal protein L17, an RNA-binding structural component of the large 60S ribosomal subunit that plays a role in protein biosynthesis
SW:DDX1_HUMAN	DDX1	35	6	1.67	0.10	SW:DDX1_HUMAN Q92499 homo sapiens (human). dead box protein 1 (dead box protein-retinoblastoma) (dbp-rb). 5/2000 [MASS=82432]/DEAD box protein 1, a member of the DEAD-H box ATP-dependent RNA helicase protein family, plays a role in the processing of pre-mRNAs, may interact with CSTF2; corresponding gene is coamplified with MYC in some neuroblastoma and retinoblastoma cell lines
SW:R37A_HUMAN	RPL37A	35	2	1.69	0.23	SW:R37A_HUMAN P12751 homo sapiens (human), rattus norvegicus (rat), and mus musculus (mouse). 60s ribosomal protein l37a. 2/1996 [MASS=10144]/Ribosomal protein L37a, component of the large 60S ribosomal subunit
SW:IF2B_HUMAN	EIF2S2	35	2	1.70	0.48	SW:IF2B_HUMAN P20042 homo sapiens (human). eukaryotic translation initiation factor 2 beta subunit (eif-2-beta). 7/1999 [MASS=38400]/Eukaryotic translation initiation factor 2 subunit 2, the beta subunit of eIF2, a translation initiation factor, involved in the initiation of protein synthesis, binds GDP
SW:RL44_HUMAN	RPL44	35	4	1.80	0.47	SW:RL44_HUMAN P09896 homo sapiens (human), rattus norvegicus (rat), mus musculus (mouse), and sus scrofa (pig). 60s ribosomal protein l44 (l36a). 7/1998 [MASS=12310]/Ribosomal protein L44, a component of the 60S ribosomal subunit; has very strong similarity to Rpl36a, which may be part of the peptidyl transferase center
SW:RL40_HUMAN	UBA52	35	3	2.00	0.50	SW:RL40_HUMAN P14793 homo sapiens (human), rattus norvegicus (rat), and gallus gallus (chicken). 60s ribosomal protein l40 (cep52). 11/1997 [MASS=6181]/Ubiquitin A-52 residue ribosomal protein fusion product 1, protein consisting of ubiquitin at the N-terminus and ribosomal protein L40 at the C-terminus; the corresponding gene is upregulated in colon cancer but not in gastric cancer

SW:RL24_HUMAN	RPL24	35	6	2.02	0.10	SW:RL24_HUMAN P38663 homo sapiens (human), rattus norvegicus (rat), and bos taurus (bovine). 60s ribosomal protein l24 (l30). 5/2000 [MASS=17779]/Ribosomal protein L24, a putative component of the 60S ribosomal subunit
SW:DDX6_HUMAN	DDX6	35	3	2.06	0.72	SW:DDX6_HUMAN P26196 homo sapiens (human). probable atp-dependent rna helicase p54 (oncogene rck) (dead box protein 6). 7/1998 [MASS=54418]/DEAD box protein 6, a member of the DEAD/H box ATP-dependent RNA helicase protein family, may be involved in cell proliferation, upregulated in colorectal adenocarcinoma and colonic adenoma; gene is translocated in a diffuse large B-cell lymphoma
SW:RS16_HUMAN	RPS16	35	8	2.18	0.76	SW:RS16_HUMAN P17008 homo sapiens (human), and rattus norvegicus (rat). 40s ribosomal protein s16. 7/1999 [MASS=16314]/Ribosomal protein S16, putative component of the small 40S ribosomal subunit
SW:RS20_HUMAN	RPS20	35	1	2.42	0.00	SW:RS20_HUMAN P17075 homo sapiens (human), and rattus norvegicus (rat). 40s ribosomal protein s20. 5/2000 [MASS=13373]/Ribosomal protein S20, a putative component of the small 40S ribosomal subunit, may play a role in apoptosis
SW:RS2_HUMAN	RPS2	35	7	2.46	1.54	SW:RS2_HUMAN P15880 homo sapiens (human). 40s ribosomal protein s2 (s4) (llrep3 protein). 10/1996 [MASS=31324]/Ribosomal protein S2, a putative component of the small 40S ribosomal subunit, may bind RNA, upregulated in squamous cell carcinoma and in breast and colon tumors
SW:IF4E_HUMAN	EIF4E	35	1	2.94	0.00	SW:IF4E_HUMAN P06730 homo sapiens (human). eukaryotic translation initiation factor 4e (eif-4e) (eif4e) (mrna cap-binding protein) (eif-4f 25 kda subunit). 5/2000 [MASS=25097]/Eukaryotic translation initiation factor 4E, a subunit of eIF4F, a mRNA cap-binding protein involved in translation initiation, a target of insulin dependent signaling pathway, expression is upregulated in breast carcinomas
RNA Processing/Modifications						
SW:SYTC_HUMAN	TARS	37	4	0.51	0.06	SW:SYTC_HUMAN P26639 homo sapiens (human). threonyl-trna synthetase, cytoplasmic (ec 6.1.1.3) (threonine--trna ligase) (thrrs). 6/1994 [MASS=82124]/Threonyl-tRNA synthetase, a class II aminoacyl tRNA synthetase which aminoacylates its cognate tRNAs with threonine for protein synthesis, autoantigen in several autoimmune disorders
SW:SYG_HUMAN	GARS	37	1	0.69	0.00	SW:SYG_HUMAN P41250 homo sapiens (human). glycyl-trna synthetase (ec 6.1.1.14) (glycine--trna ligase) (glyrs). 10/1996 [MASS=77531]/Glycyl-tRNA synthetase; functions in protein biosynthesis, aminoacylates its cognate tRNAs with phenylalanine/Glycyl-tRNA synthetase, a class II aminoacyl-tRNA synthetase that catalyzes aminoacylation of its cognate tRNA with glycine for protein biosynthesis; an autoantigen in dermatomyositis
SW:SYD_HUMAN	DARS	37	4	0.77	0.15	SW:SYD_HUMAN P14868 homo sapiens (human). aspartyl-trna synthetase (ec 6.1.1.12) (aspartate--trna ligase) (asprs). 11/1997 [MASS=57192]/Aspartyl-tRNA synthetase, a class II aminoacyl tRNA synthetase that aminoacylates its cognate tRNA with aspartate for protein biosynthesis, associates with a multisynthetase complex, N-terminus may aid interaction with elongation factor 1 alpha
SW:SYA_HUMAN	AARS	37	1	0.83	0.00	SW:SYA_HUMAN P49588 homo sapiens (human). alanyl-trna synthetase (ec 6.1.1.7) (alanine--trna ligase) (alars). 7/1998 [MASS=106801]/Alanyl-tRNA synthetase, aminoacylates its cognate tRNA with alanine for protein biosynthesis, acts as an autoantigen in patients with polymyositis
SW:SYR_HUMAN	RARS	37	7	0.84	0.08	SW:SYR_HUMAN P54136 homo sapiens (human). arginyl-trna synthetase (ec 6.1.1.19) (arginine--trna ligase) (argrs). 5/2000 [MASS=74977]/Arginyl-tRNA synthetase, aminoacylates its cognate tRNAs with arginine for protein biosynthesis
SW:SYM_HUMAN	MARS	37	9	0.87	0.18	SW:SYM_HUMAN P56192 homo sapiens (human). methionyl-trna synthetase (ec 6.1.1.10) (methionine--trna ligase) (metrs). 12/1998 [MASS=101129]/Methionine-tRNA synthetase, putative tRNA synthetase that is predicted to aminoacylate its cognate tRNAs with methionine for protein biosynthesis, required for rRNA synthesis in the nucleolus
SW:SYEP_HUMAN	EPRS	37	23	0.92	0.84	SW:SYEP_HUMAN P07814 homo sapiens (human). multifunctional aminoacyl-trna synthetase [includes: glutamyl-trna synthetase (ec 6.1.1.17) (glutamate--trna ligase); prolyl-trna synthetase (ec 6.1.1.15) (pro [MASS=163026]/Glutamyl-prolyl-tRNA synthetase, a bifunctional enzyme with two functionally separable domains, one that aminoacylates prolyl-tRNA with proline and another that is believed to aminoacylate glutamyl-tRNA with glutamate for protein biosynthesis
SW:CST1_HUMAN	CSTF1	37	1	0.93	0.00	SW:CST1_HUMAN Q05048 homo sapiens (human). cleavage stimulation factor, 50 kda subunit (cstf 50 kda subunit) (cf-1 50 kda subunit). 7/1998 [MASS=48358]/Cleavage stimulation factor subunit 1, the 50 kDa subunit of the cleavage stimulation factor complex required for pre-mRNA polyadenylation and 3'-end cleavage, interacts with BARD1 and the C-terminal domain of the RNA polymerase II large subunit
SW:SYQ_HUMAN	QARS	37	2	0.94	0.20	SW:SYQ_HUMAN P47897 homo sapiens (human). glutaminyl-trna synthetase (ec 6.1.1.18) (glutamine--trna ligase) (glnrs). 5/2000 [MASS=87799]/Glutaminyl-tRNA synthetase, aminoacylates cognate tRNAs with glutamine for protein biosynthesis, also suppresses FAS (TNFRSF6)-mediated apoptosis by inhibiting ASK1 (MAP3K5) kinase activity, contains N-terminal appended and C-terminal catalytic domains
SW:SYV_HUMAN	VARS2	37	4	0.95	0.14	SW:SYV_HUMAN P26640 homo sapiens (human). valyl-trna synthetase (ec 6.1.1.9) (valine--trna ligase) (valrs). 2/1996 [MASS=140377]/Valyl-tRNA synthetase 2, a putative class I tRNA sythetase, predicted to function in aminoacylation of valyl tRNAs for protein biosynthesis
SW:SYK_HUMAN	KARS	37	7	1.01	0.18	SW:SYK_HUMAN Q15046 homo sapiens (human). lysyl-trna synthetase (ec 6.1.1.6) (lysine--trna ligase) (lysrs) (kiaa0070). 7/1998 [MASS=68034]/Lysyl-tRNA synthetase, a class II aminoacyl tRNA synthetase, aminoacylates its cognate tRNAs with lysine for protein biosynthesis, packaged into HIV virions, exists as cytoplasmic and mitochondrial alternative forms
SW:SYI_HUMAN	IARS	37	9	1.10	0.16	SW:SYI_HUMAN P41252 homo sapiens (human). isoleucyl-trna synthetase, cytoplasmic (ec 6.1.1.5) (isoleucine--trna ligase) (ilers) (irs). 7/1999 [MASS=144959]/Isoleucine-tRNA synthetase, a class I aminoacyl tRNA synthetase, aminoacylates isoleucyl-tRNA with isoleucine for protein biosynthesis, acts as an autoantigen in some autoimmune diseases

SW:NPM_HUMAN	NPM1	37	3	1.11	0.14	SW:NPM_HUMAN P06748 homo sapiens (human). nucleophosmin (npm) (nucleolar phosphoprotein b23) (numatrin) (nucleolar protein no38). 5/2000 [MASS=32575]/Nucleophosmin (numatrin), a nucleic acid-binding phosphoprotein involved in apoptosis, abundant in tumor cells; gene fusion with anaplastic lymphoma kinase (ALK) is detected in non-Hodgkin's lymphoma and fusion with MLF1 is seen in acute myeloid leukemia
SW:PCB1_HUMAN	PCBP1	37	20	1.23	0.19	SW:PCB1_HUMAN Q15365 homo sapiens (human). poly(rc)-binding protein 1 (hnrnp-e1) (nucleic acid binding protein sub2.3) (alpha-cp1). 5/2000 [MASS=37526]/Poly(rC)-binding protein 1, contains KH RNA-binding domains, binds poly(rC) RNA, acts as a translational repressor and plays a role in mRNA stability
SWN:SYFB_HUMAN	FRSB	37	4	1.25	0.44	SWN:SYFB_HUMAN Q9nsd9 homo sapiens (human). phenylalanyl-trna synthetase beta chain (ec 6.1.1.20) (phenylalanine--trna ligase beta chain) (phers) (protein hspc173). 8/2001 [MASS=66130]/Phenylalanyl-tRNA synthetase beta-subunit, regulatory subunit that forms heterodimers with the catalytic alpha subunit (FARSL), involved in protein synthesis, may play a role in tumorigenic events
GP:AB020880_1	SART3	37	5	1.37	0.17	GP:AB020880_1 Homo sapiens mRNA for squamous cell carcinoma antigen SART-3, complete cds; squamous cell carcinoma antigen recognized by T cells. [MASS=109935]/Squamous cell carcinoma antigen recognized by T-cells 3, a snRNA binding protein that functions in spliceosome reassembly, acts as a tumor antigen recognized by cytotoxic T lymphocytes, may be a target for immunotherapy in a number of cancers
SW:ROF_HUMAN	HNRPF	37	3	1.37	0.10	SW:ROF_HUMAN P52597 homo sapiens (human). heterogeneous nuclear ribonucleoprotein f (hnrnp f). 11/1997 [MASS=45672]/Heterogeneous nuclear ribonucleoprotein F, an RNA binding protein which contains quasi-RRMs (RNA recognition motifs) and plays a role in pre-mRNA splicing
PIR2:T13159	E1B-AP5	37	3	1.38	0.41	PIR2:T13159 E1B-55kDa-associated protein - human [MASS=95810]/E1B-55kDa-associated protein 5, a heterogeneous nuclear ribonucleoprotein involved in nucleocytoplasmic transport of adenovirus and cellular mRNAs, binds adenovirus early 1B (E1B-55 kD) protein and may regulate viral oncogenic transformation
SW:SYN_HUMAN	NARS	37	4	1.42	0.19	SW:SYN_HUMAN O43776 homo sapiens (human). asparaginyl-trna synthetase, cytoplasmic (ec 6.1.1.22) (asparagine-- trna ligase) (asnrs). 5/2000 [MASS=62943]/Asparaginyl-tRNA synthetase, a class II aminoacyl tRNA synthetase, aminoacylates its cognate tRNAs with asparagine for protein biosynthesis, acts as an autoantigen in patients with inflammatory myopathy in interstitial lung disease
PIR2:T02673	HNRPR	37	3	1.43	0.18	no_description_avail/Heterogeneous nuclear ribonucleoprotein R, a putative pre-mRNA processing protein that contains three RNA recognition domains and an RGG domain, interacts with survival motor neuron protein and is an autoantigen in autoimmune disease
GP:AF037448_1	NSAP1	37	4	1.45	0.22	GP:AF037448_1 Homo sapiens RRM RNA binding protein Gry-rbp (GRY-RBP) mRNA, complete cds; RRM RNA binding protein; Glycine, arginine and tyrosine-rich at C-terminus. [MASS=69633]/NS1 associated protein 1, component of the ApoB mRNA editosome involved in apolipoprotein B (APOB) mRNA editing, may bind RNA, may play a role in the regulation of mRNA splicing or transport from the nucleus
SW:ROK_HUMAN	HNRPK	37	6	1.51	0.30	SW:ROK_HUMAN Q07244 homo sapiens (human), and rattus norvegicus (rat). heterogeneous nuclear ribonucleoprotein k (hnrnp k) (dc-stretch binding protein) (csbp) (transformation upregulated nuclear protein [MASS=50976]/Heterogeneous nuclear ribonucleoprotein K, a transcription factor which binds to poly(C) of RNA and DNA and is involved in RNA processing, gene transcription and translational controls, may induce apoptosis and play a role in viral infection
SW:FBRL_HUMAN	FBL	37	1	1.53	0.00	SW:FBRL_HUMAN P22087 homo sapiens (human). fibrillarin (34 kda nucleolar scleroderma antigen). 7/1999 [MASS=33818]/Fibrillarin, a nucleolar RNA-binding protein that is involved in ribosomal RNA processing; recognized by antisera from patients with scleroderma autoimmune disease, systemic sclerosis, and other connective tissue diseases
SW:SMD3_HUMAN	SNRPD3	37	1	1.55	0.00	SW:SMD3_HUMAN P43331 homo sapiens (human). small nuclear ribonucleoprotein sm d3 (snrnp core protein d3) (sm-d3). 10/1996 [MASS=13916]/Small nuclear ribonucleoprotein D3, part of a multimeric complex involved in biogenesis of snRNPs and mRNA splicing, interacts with the spinal muscular atrophy disease protein (SMN); autoantigen for antibodies associated with systemic lupus erythematosus
SW:ROA0_HUMAN	HNRPA0	37	2	1.64	0.40	SW:ROA0_HUMAN Q13151 homo sapiens (human). heterogeneous nuclear ribonucleoprotein a0 (hnrnp a0). 5/2000 [MASS=30841]/Heterogeneous nuclear ribonucleoprotein A0, has triplet repeats, two consensus sequence-type RNA-binding domains, and a glycine-rich auxiliary domain, found in low abundance hnRNP complexes
SW:ROH1_HUMAN	HNRPH1	37	4	1.66	0.22	SW:ROH1_HUMAN P31943 homo sapiens (human). heterogeneous nuclear ribonucleoprotein h (hnrnp h). 11/1997 [MASS=49229]/Heterogeneous nuclear ribonucleoprotein H1, a pre-mRNA splicing factor that is a component of a complex that mediates post-transcriptional processing of primary transcripts
SW:DDX1_HUMAN	DDX1	37	6	1.67	0.10	SW:DDX1_HUMAN Q92499 homo sapiens (human). dead box protein 1 (dead box protein-retinoblastoma) (dbp-rb). 5/2000 [MASS=82432]/DEAD box protein 1, a member of the DEAD-H box ATP-dependent RNA helicase protein family, plays a role in the processing of pre-mRNAs, may interact with CSTF2; corresponding gene is coamplified with MYC in some neuroblastoma and retinoblastoma cell lines
PIR2:JW0079	HNRPDL	37	1	1.72	0.00	PIR2:JW0079 heterogeneous nuclear ribonucleoprotein homolog JKTBP [imported] - human [MASS=33589]/Heterogeneous nuclear ribonucleoprotein D-like, an RNA- and DNA-binding protein that may play a role in mRNA biogenesis
SW:PCB2_HUMAN	PCBP2	37	10	1.73	0.20	SW:PCB2_HUMAN Q15366 homo sapiens (human). poly(rc)-binding protein 2 (hnrnp-e2). 5/2000 [MASS=38580]/Poly(rC)-binding protein 2, poly(rC) and poly(U)-binding protein, involved in the translational regulation of poliovirus, papillomavirus, and hepatitis C virus transcripts

GP:AC003972_1	RENT1	37	1	1.74	0.00	GP:AC003972_1 Homo sapiens DNA from chromosome 19, cosmid R33485 containing pNORF1, complete sequence; human type 1 RNA helicase; DPS similarity to (U59323) type 1 RNA helicase pNORF1 [Homo sapiens]; Score. [MASS=123036]/regulator of nonsense transcripts 1 (nonsense mrna reducing factor 1) (norf1) (up-frameshift suppressor 1 homolog). 10/2001 [MASS=124345]
SW:RUXF_HUMAN	SNRPF	37	1	1.76	0.00	SW:RUXF_HUMAN Q15356 homo sapiens (human). small nuclear ribonucleoprotein f (snrnp-f) (sm protein f). 7/1999 [MASS=9725]/Sm protein F, a spliceosomal snRNA-associated Sm core protein that is involved in the biogenesis of the snRNPs; a target of autoantibodies in patients with the autoimmune disease systemic lupus erythematosus
GP:AF177344_1	FLJ10581	37	1	1.89	0.00	GP:AF177344_1 Homo sapiens clone HC90 unknown mRNA. [MASS=30998]/ weakly similar to a methyltransferase/Member of the RNA methyltransferase family, which catalyze 2'-O-methylation of ribose groups in R
PIR2:I55595	RNPC2	37	1	1.92	0.00	PIR2:I55595 splicing factor - human [MASS=58657]/Splicing factor CC1.3, a novel nuclear protein and putative member of the SR family of alternative splicing factors; target of autoantibodies from a patient with hepatocellular carcinoma
SW:ROA3_HUMAN	FBRNP	37	2	1.93	0.06	SW:ROA3_HUMAN P51991 homo sapiens (human). heterogeneous nuclear ribonucleoprotein a3 (hnrnp a3) (fbrnp) (d10s102). 7/1999 [MASS=39686]/Protein with similarity to heterogeneous ribonucleoproteins, contains RRM (RNA recognition motif) domains
SW:SMD2_HUMAN	SNRPD2	37	2	2.02	0.82	SW:SMD2_HUMAN P43330 homo sapiens (human). small nuclear ribonucleoprotein sm d2 (snrnp core protein d2) (sm-d2). 10/1996 [MASS=13527]/Small nuclear ribonucleoprotein D2 polypeptide, one of seven common core snRNP proteins involved in snRNP biogenesis and pre-mRNA splicing, autoantigen for anti-Sm antibodies produced by individuals with systemic lupus erythematosus
SW:U2AF_HUMAN	U2AF65	37	1	2.05	0.00	SW:U2AF_HUMAN P26368 homo sapiens (human). splicing factor u2af 65 kda subunit (u2 auxiliary factor 65 kda subunit) (u2 snrnp auxiliary factor large subunit). 12/1998 [MASS=53501]/U2 small nuclear ribonucleoprotein auxiliary factor (65 kDa), a component of U2 small nucleoprotein auxiliary factor, which is necessary for mRNA splicing, binds to pre-mRNA
GP:D21163_1	U5-116KD	37	1	2.11	0.00	GP:D21163_1 Human mRNA for KIAA0031 gene, complete cds; similar to human elongation factor 2 mRNA (HSEF2).. [MASS=109436]/U5 snRNP-specific protein 116 kD, a spliceosome component with GTPAse activity, plays a role in mRNA splicing and processing
SW:RU17_HUMAN	SNRP70	37	3	2.11	0.26	SW:RU17_HUMAN P08621 homo sapiens (human). u1 small nuclear ribonucleoprotein 70 kda (u1 snrnp 70 kda) (snrp70). 11/1995 [MASS=70081]/U1 small nuclear 70 kDa ribonucleoprotein, involved in pre mRNA splicing, acts as an autoantigen in systemic lupus erythematosus and mixed connective tissue disease
PIR2:A54601	HNRPD	37	9	2.17	0.65	PIR2:A54601 RNA-binding protein AUF1 - human [MASS=31200]/Heterogeneous nuclear ribonucleoprotein D (AU-rich element RNA-binding protein 1 37kD), an RNA and DNA-binding protein which binds to AU-rich elements in the 3' untranslated regions of mRNAs and mediates their degradation
SW:NHPX_HUMAN	NHP2L1	37	2	2.21	0.20	SW:NHPX_HUMAN P55769 homo sapiens (human). nhp2/rs6 family protein yel026w homolog (high mobility group-like nuclear protein 2 homolog) (otk27). 5/2000 [MASS=14174]/Non-histone chromosome protein 2 (S. cerevisiae)-like 1, a member of a family of RNP-associated proteins, a component of the spliceosome and rRNA processing machinery, recognizes a shared stem-internal loop-stem structure in its RNA targets
SW:DDX5_HUMAN	DDX5	37	1	2.27	0.00	SW:DDX5_HUMAN P17844 homo sapiens (human). probable rna-dependent helicase p68 (dead-box protein p68) (dead box protein 5). 7/1998 [MASS=69148]/DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 5 (RNA helicase 68kD), a ATP-dependent RNA helicase that has ATP-independent RNA renaturation activity and catalyses branch migration, binds estrogen receptor alpha and function as a transcriptional coactivator
SW:U2AG_HUMAN	U2AF35	37	2	2.34	0.02	SW:U2AG_HUMAN Q01081 homo sapiens (human). splicing factor u2af 35 kda subunit (u2 auxiliary factor 35 kda subunit) (u2 snrnp auxiliary factor small subunit). 12/1998 [MASS=27872]/U2(RNU2) small nuclear RNA auxiliary factor 1, functions as a pre-mRNA splicing protein, involved in the functional recognition of the 3' splice site AG dinucleotide, interacts with ZNF265 protein involved in alternative splicing
SW:ROU_HUMAN	HNRPU	37	29	2.48	0.62	SW:ROU_HUMAN Q00839 homo sapiens (human). heterogenous nuclear ribonucleoprotein u (hnrnp u) (scaffold attachment factor a) (saf-a). 5/2000 [MASS=90479]/Heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A), binds RNA, binds EP300 in a complex that binds scaffold-matrix attachment regions of TOP1, involved in chromatin structure, apoptosis, and perhaps RNA processing and transcription
SW:ROA1_HUMAN	HNRPA1	37	11	2.48	0.85	SW:ROA1_HUMAN P09651 homo sapiens (human). heterogeneous nuclear ribonucleoprotein a1 (helix-destabilizing protein) (single-strand binding protein) (hnrnp core protein a1). 11/1997 [MASS=38715]/Heterogeneous nuclear ribonucleoprotein A1, an RNA-binding protein involved in mRNA splicing and translational control, undergoes nucleocytoplasmic shuttling possibly for mRNA export and telomerase recruitment; an autoantigen in autoimmune disorders
SW:DD17_HUMAN	DDX17	37	1	2.58	0.00	SW:DD17_HUMAN Q92841 homo sapiens (human). probable rna-dependent helicase p72 (dead-box protein p72) (dead box protein 17). 5/2000 [MASS=72371]/DEAD H box protein 17, a member of the DEAD box family of RNA-dependent ATPases and ATP-dependent RNA helicases, a component of an estrogen receptor alpha (ESR) transcriptional coactivator complex
SW:Y017_HUMAN	SF3B3	37	7	2.63	0.59	SW:Y017_HUMAN Q15393 homo sapiens (human). hypothetical protein kiaa0017. 5/2000 [MASS=44606]/ Homo sapiens mRNA for SAP 130 spliceosomal protein/Splicing factor 3b subunit 3, a component of the U2 snRNP-associated protein complex SF3b that plays a role in spliceosome assembly, interacts with STAGA and TFTC complexes implicated in DNA repair, chromatin modification, and transcription

SW:NR54_HUMAN	NONO	37	2	3.38	1.09	SW:NR54_HUMAN Q15233 homo sapiens (human). 54 kda nuclear rna-binding protein (p54(nrb)) (p54nrb) (55 kda nuclear protein) (nmt55). 5/2000 [MASS=54232]/Non-POU-domain-containing octamer-binding nuclear protein, binds DNA and RNA, and implicated in transcription and pre-mRNA splicing; a fusion partner with TFE3 in papillary renal cell carcinoma
SW:SFR7_HUMAN	SFRS7	37	2	3.66	0.49	SW:SFR7_HUMAN Q16629 homo sapiens (human). splicing factor, arginine/serine-rich 7 (splicing factor 9g8). 5/2000 [MASS=27367]/Splicing factor arginine serine rich 7, a splicing factor of the SR protein family containing an RNA binding domain (RBD) and a serine/arginine (SR) domain that is implicated in alternative pre-mRNA splicing
RNA Splicing						
GP:AF037448_1	NSAP1	38	4	1.45	0.22	GP:AF037448_1 Homo sapiens RRM RNA binding protein Gry-rbp (GRY-RBP) mRNA, complete cds; RRM RNA binding protein; Glycine, arginine and tyrosine-rich at C-terminus. [MASS=69633]/NS1 associated protein 1, component of the ApoB mRNA editosome involved in apolipoprotein B (APOB) mRNA editing, may bind RNA, may play a role in the regulation of mRNA splicing or transport from the nucleus
SW:SMD3_HUMAN	SNRPD3	38	1	1.55	0.00	SW:SMD3_HUMAN P43331 homo sapiens (human). small nuclear ribonucleoprotein sm d3 (snrnp core protein d3) (sm-d3). 10/1996 [MASS=13916]/Small nuclear ribonucleoprotein D3, part of a multimeric complex involved in biogenesis of snRNPs and mRNA splicing, interacts with the spinal muscular atrophy disease protein (SMN); autoantigen for antibodies associated with systemic lupus erythematosus
SW:RUXF_HUMAN	SNRPF	38	1	1.76	0.00	SW:RUXF_HUMAN Q15356 homo sapiens (human). small nuclear ribonucleoprotein f (snrnp-f) (sm protein f). 7/1999 [MASS=9725]/Sm protein F, a spliceosomal snRNA-associated Sm core protein that is involved in the biogenesis of the snRNPs; a target of autoantibodies in patients with the autoimmune disease systemic lupus erythematosus
PIR2:T09073	SFRS2IP	38	1	1.89	0.00	PIR2:T09073 splicing factor Sip1 - human [MASS=128875]/Splicing factor arginine serine rich 2 interacting protein, a SR domain family protein that interacts with the RNA polymerase II C-terminal domain and several splicing factors, is essential in mRNA splicing and possibly spliceosome A-complex formation
PIR2:I55595	RNPC2	38	1	1.92	0.00	PIR2:I55595 splicing factor - human [MASS=58657]/Splicing factor CC1.3, a novel nuclear protein and putative member of the SR family of alternative splicing factors; target of autoantibodies from a patient with hepatocellular carcinoma
SW:SMD2_HUMAN	SNRPD2	38	2	2.02	0.82	SW:SMD2_HUMAN P43330 homo sapiens (human). small nuclear ribonucleoprotein sm d2 (snrnp core protein d2) (sm-d2). 10/1996 [MASS=13527]/Small nuclear ribonucleoprotein D2 polypeptide, one of seven common core snRNP proteins involved in snRNP biogenesis and pre-mRNA splicing, autoantigen for anti-Sm antibodies produced by individuals with systemic lupus erythematosus
SW:U2AF_HUMAN	U2AF65	38	1	2.05	0.00	SW:U2AF_HUMAN P26368 homo sapiens (human). splicing factor u2af 65 kda subunit (u2 auxiliary factor 65 kda subunit) (u2 snrnp auxiliary factor large subunit). 12/1998 [MASS=53501]/U2 small nuclear ribonucleoprotein auxiliary factor (65 kDa), a component of U2 small nucleoprotein auxiliary factor, which is necessary for mRNA splicing, binds to pre-mRNA
GP:D21163_1	U5-116KD	38	1	2.11	0.00	GP:D21163_1 Human mRNA for KIAA0031 gene, complete cds; similar to human elongation factor 2 mRNA (HSEF2).. [MASS=109436]/U5 snRNP-specific protein 116 kD, a spliceosome component with GTPase activity, plays a role in mRNA splicing and processing
SW:RU17_HUMAN	SNRP70	38	3	2.11	0.26	SW:RU17_HUMAN P08621 homo sapiens (human). u1 small nuclear ribonucleoprotein 70 kda (u1 snrnp 70 kda) (snrp70). 11/1995 [MASS=70081]/U1 small nuclear 70 kDa ribonucleoprotein, involved in pre mRNA splicing, acts as an autoantigen in systemic lupus erythematosus and mixed connective tissue disease
SW:U2AG_HUMAN	U2AF35	38	2	2.34	0.02	SW:U2AG_HUMAN Q01081 homo sapiens (human). splicing factor u2af 35 kda subunit (u2 auxiliary factor 35 kda subunit) (u2 snrnp auxiliary factor small subunit). 12/1998 [MASS=27872]/U2(RNU2) small nuclear RNA auxiliary factor 1, functions as a pre-mRNA splicing protein, involved in the functional recognition of the 3' splice site AG dinucleotide, interacts with ZNF265 protein involved in alternative splicing
SW:ROA1_HUMAN	HNRPA1	38	11	2.48	0.85	SW:ROA1_HUMAN P09651 homo sapiens (human). heterogeneous nuclear ribonucleoprotein a1 (helix-destabilizing protein) (single-strand binding protein) (hnrnp core protein a1). 11/1997 [MASS=38715]/Heterogeneous nuclear ribonucleoprotein A1, an RNA-binding protein involved in mRNA splicing and translational control, undergoes nucleocytoplasmic shuttling possibly for mRNA export and telomerase recruitment; an autoantigen in autoimmune disorders
SW:Y017_HUMAN	SF3B3	38	7	2.63	0.59	SW:Y017_HUMAN Q15393 homo sapiens (human). hypothetical protein kiaa0017. 5/2000 [MASS=44606]/ Homo sapiens mRNA for SAP 130 spliceosomal protein/Splicing factor 3b subunit 3, a component of the U2 snRNP-associated protein complex SF3b that plays a role in spliceosome assembly, interacts with STAGA and TFTC complexes implicated in DNA repair, chromatin modification, and transcription
SW:NR54_HUMAN	NONO	38	2	3.38	1.09	SW:NR54_HUMAN Q15233 homo sapiens (human). 54 kda nuclear rna-binding protein (p54(nrb)) (p54nrb) (55 kda nuclear protein) (nmt55). 5/2000 [MASS=54232]/Non-POU-domain-containing octamer-binding nuclear protein, binds DNA and RNA, and implicated in transcription and pre-mRNA splicing; a fusion partner with TFE3 in papillary renal cell carcinoma
SW:SFR7_HUMAN	SFRS7	38	2	3.66	0.49	SW:SFR7_HUMAN Q16629 homo sapiens (human). splicing factor, arginine/serine-rich 7 (splicing factor 9g8). 5/2000 [MASS=27367]/Splicing factor arginine serine rich 7, a splicing factor of the SR protein family containing an RNA binding domain (RBD) and a serine/arginine (SR) domain that is implicated in alternative pre-mRNA splicing
Vesicular Transport						

SW:SNAG_HUMAN	NAPG	43	2	0.43	0.31	SW:SNAG_HUMAN Q99747 homo sapiens (human). gamma-soluble nsf attachment protein (snap-gamma). 7/1999 [MASS=34746]/N-ethylmaleimide-sensitive factor (NSF) attachment protein gamma, member of a family of proteins involved in membrane fusion during exocytosis, may have roles in platelet exocytosis and in the attachment of mitochondria to the cytoskeleton
GP:AB018298_1	SEC24D	43	1	0.47	0.00	sec24-related protein D (human)/Protein with high similarity to SEC24 (S. cerevisiae) related gene family member C (human SEC24C), which is a putative COPII vesicle coat protein that forms a complex with Sec23Ap (human SEC23) and functions in ER-Golgi transport
SW:RB3B_HUMAN	RAB3B	43	2	0.50	0.00	SW:RB3B_HUMAN P20337 homo sapiens (human). ras-related protein rab-3b. 10/1994 [MASS=24760]/Ras-related GTP-binding protein 3b, a GTP-binding protein and GTPase that is involved in exocytosis
SW:ADG_HUMAN	ADTG	43	4	0.51	0.13	SW:ADG_HUMAN O43747 homo sapiens (human). gamma-adaptin (golgi adaptor ha1/ap1 adaptin gamma subunit) (clathrin assembly protein complex 1 gamma large chain). 7/1999 [MASS=91592]/Adaptor-related protein complex 1 gamma 1 subunit, promotes the formation of clathrin coated vesicles and pits for intracellular transport; deletion of the corresponding gene occurs in Wilm's tumor, prostate adenocarcinomas, and hepatocellular carcinomas
SW:LDLR_HUMAN	LDLR	43	3	0.55	0.04	SW:LDLR_HUMAN P01130 homo sapiens (human). low-density lipoprotein receptor precursor (ldl receptor). 5/2000 [MASS=95376]/Low density lipoprotein receptor, mediates uptake of low density lipoproteins, involved in lipid metabolism; gene variations are associated with familial hypercholesterolemia, hypertension, atherosclerosis, and coronary artery disease
SW:RB4A_HUMAN	RAB4A	43	1	0.56	0.00	SW:RB4A_HUMAN P20338 homo sapiens (human). ras-related protein rab-4a. 10/1996 [MASS=23902]/GTP-binding protein, a member of the rab family of proteins, involved in early endosome trafficking and receptor recycling
PIR2:A53016	MYO5A	43	1	0.58	0.00	PIR2:A53016 myosin heavy chain VA - human (fragment) [MASS=96052]/Class V myosin (Myoxin), a member of the myosin family of proteins, a motor protein that may be involved in vesicle transport and epidermal differentiation; mutation of the corresponding genge is associated with Griscelli syndrome
SW:EGFR_HUMAN	EGFR	43	2	0.62	0.00	SW:EGFR_HUMAN P00533 homo sapiens (human). epidermal growth factor receptor precursor (ec 2.7.1.112). 12/1998 [MASS=134277]/Epidermal growth factor receptor, a receptor protein tyrosine kinase that binds epidermal growth factor (EGF) and transforming growth factor alpha (TGFA), involved in cell proliferation and differentiation, implicated in tumor invasion and metastasis
SW:STB3_HUMAN	STXBP3	43	6	0.66	0.15	SW:STB3_HUMAN O00186 homo sapiens (human). syntaxin binding protein 3 (unc-18 homolog 3) (unc-18c) (unc-18-3). 5/2000 [MASS=67574]/Syntaxin binding protein 3, binds syntaxin 4 (STX4), predicted to be involved in vesicle transport and docking and in neurotransmitter release
SW:CLH2_HUMAN	CLTCL1	43	10	0.66	0.15	SW:CLH2_HUMAN P53675 homo sapiens (human). clathrin heavy chain 2 (clh-22). 5/2000 [MASS=187030]/Clathrin heavy polypeptide-like 1, may play roles in vesicle budding and in cytoskeleton-dependent trans-Golgi network membrane sorting; gene is among those deleted in velocardiofacial and DiGeorge syndromes, and is a fusion partner with ALK in lymphoma
SW:S23B_HUMAN	SEC23B	43	1	0.69	0.00	SW:S23B_HUMAN Q15437 homo sapiens (human). protein transport protein sec23 homolog isoform b. 11/1997 [MASS=86470]/Member of the SEC23 family of vesicle trafficking proteins
GP:AF038535_1	SYT7	43	1	0.70	0.00	GP:AF038535_1 Homo sapiens synaptotagmin VII mRNA, partial cds; similar to rat synaptotagmin VII. [MASS=47195]/Very strongly similar to synaptotagmin 7 (Rn.10193); may be a phospholipid-binding calcium sensor protein
SW:KINH_HUMAN	KIF5B	43	2	0.73	0.05	SW:KINH_HUMAN P33176 homo sapiens (human). kinesin heavy chain (ubiquitous kinesin heavy chain) (ukhc). 7/1999 [MASS=109685]/Kinesin family member 5B (kinesin heavy chain), a microtubule-associated motor protein that may function in intracellular organelle transport and may play a role in susceptibility and resistance
SW:RB35_HUMAN	RAB35	43	1	0.73	0.00	SW:RB35_HUMAN Q15286 homo sapiens (human). ras-related protein rab-35 (rab-1c) (gtp-binding protein ray). 5/2000 [MASS=23025]/Ras-related GTP-binding protein 35, member of the Rab family of GTP-binding proteins, may function in vesicular transport
GPN:AB047846_1	LOC51137	43	7	0.74	0.24	SW:COPG_HUMAN Q9y678 homo sapiens (human). coatomer gamma subunit (gamma-coat protein) (gamma-cop). 10/2001 [MASS=97718]/Coatomer protein complex subunit gamma 1, a subunit of the coat of COP I-coated vesicles, predicted to be involved in retrograde Golgi to endoplasmic reticulum transport, contains two clathrin-associated adaptin N-terminal domains
SW:SN23_HUMAN	SNAP23	43	2	0.74	0.06	SW:SN23_HUMAN O00161 homo sapiens (human). synaptosomal associated protein 23 (snap-23) (vesicle-membrane fusion protein snap-23). 5/2000 [MASS=23354]/Synaptosomal-associated protein 23, a member of the SNARE family of proteins that regulate membrane fusion during exocytosis, a t-SNARE that binds to syntaxins and is involved in docking and fusion of transport vesicles during exocytosis
SW:RB3D_HUMAN	RAB3D	43	1	0.74	0.00	SW:RB3D_HUMAN O95716 homo sapiens (human). ras-related protein rab-3d. 5/2000 [MASS=24267]/Ras-related GTP-binding protein 3d, putative small monomeric GTP-binding protein and GTPase that plays a role in regulated secretion
SW:RAB2_HUMAN	RAB2	43	5	0.77	0.05	SW:RAB2_HUMAN P08886 homo sapiens (human), and canis familiaris (dog). ras-related protein rab-2. 10/1994 [MASS=23546]/Ras-related GTP-binding protein 2, a GTPase which plays a role in vesicle transport from the ER to the Golgi complex; overexpression in nonmalignant peripheral blood lymphocytes is associated with Searzy syndrome
SW:GBAK_HUMAN	GNAI3	43	4	0.77	0.10	SW:GBAK_HUMAN P08754 homo sapiens (human). guanine nucleotide-binding protein g(k), alpha subunit (g(i) alpha-3). 11/1997 [MASS=40401]/G protein alpha i3 subunit, a component of pertussis toxin sensitive heterotrimeric G protein complexes, transduces signals from G protein-coupled receptors to intracellular effectors, inhibits forskolin-stimulated cAMP production

GP:AF091079_1	YKT6	43	1	0.78	0.00	GP:AF091079_1 Homo sapiens clone 560 SNARE protein Ykt6 mRNA, partial cds. [MASS=21607]/Homolog of S. cerevisiae Ykt6p, which is a v-SNARE required for ER to Golgi transport, likely involved in trafficking proteins from the ER to the Golgi
SW:CLH1_HUMAN	CLTC	43	49	0.78	0.44	SW:CLH1_HUMAN Q00610 homo sapiens (human). clathrin heavy chain 1 (clh-17) (kiaa0034). 5/2000 [MASS=191615]/Clathrin heavy polypetide c, involved in endocytosis, may bind to endocytic proteins through an LLDLD consensus sequence, interacts with huntingtin interacting protein 1 (HIP1), amino terminus folds into a seven-bladed beta-propeller
GP:AJ131245_1	SEC24B	43	1	0.81	0.00	GP:AJ131245_1 Homo sapiens mRNA for Sec24 protein (Sec24B isoform). [MASS=137789]/SEC24 related gene family member B, a member of the SEC24 family of vesicle trafficking proteins, interacts with SEC23A, predicted to be localized to COPII-coated vesicles and to be involved in the export of proteins from the endoplasmic reticulum
SW:DYN2_HUMAN	DNM2	43	1	0.81	0.00	SW:DYN2_HUMAN P50570 homo sapiens (human). dynamin 2. 10/1996 [MASS=98018]/Dynamin II, member of a family of 100-kD guanosine triphosphatases, regulates budding of endocytic vesicles at the plasma membrane and may function in the formation of transport vesicles at the trans-Golgi
GP:D31886_1	RAB3GAP	43	3	0.83	0.11	GP:D31886_1 Human mRNA for KIAA0066 gene, partial cds. [MASS=110524]/RAB3 GTPase-activating protein, GTPase-activating protein specific for lipid-modified members of the Rab3 subfamily, may influence calcium-dependent exocytosis of synaptic vesicles
SW:CALX_HUMAN	CANX	43	4	0.84	0.04	SW:CALX_HUMAN P27824 homo sapiens (human). calnexin precursor (major histocompatibility complex class i antigen-binding protein p88) (p90) (ip90). 11/1995 [MASS=67568]/Calnexin, a calcium and lectin binding protein that functions as a chaperone in the endoplasmic reticulum, involved in protein folding and secretion, mediates retention of misfolded proteins in the endoplasmic reticulum
SW:ER53_HUMAN	LMAN1	43	2	0.84	0.00	SW:ER53_HUMAN P49257 homo sapiens (human). ergic-53 protein precursor (er-golgi intermediate compartment 53 kda protein) (gp58) (mr60) (lectin, mannose-binding 1). 7/1998 [MASS=57563]/Mannose-binding lectin 1, involved in the traffic of glycoproteins between endoplasmic reticulum and the Golgi apparatus; mutations of the corresponding gene is associated with combined factor V and VIII coagulation deficiency
GP:U45976_1	PICALM	43	1	0.85	0.00	GP:U45976_1 Human clathrin assembly protein lymphoid myeloid leukemia (CALM) mRNA, complete cds. [MASS=70695]/Phosphatidylinositol binding clathrin assembly protein, binds to clathrin heavy chain (CLTC) and plays a role in coated pit internalization; rearrangements in the corresponding gene are associated with acute lymphoblastic and acute myeloid leukemias
SW:ADB_HUMAN	AP2B1	43	5	0.86	0.14	SW:ADB_HUMAN P21851 homo sapiens (human), rattus norvegicus (rat), and bos taurus (bovine). beta-adaptin (plasma membrane adaptor ha2/ap2 adaptin beta subunit) (clathrin assembly protein complex 2 beta [MASS=104553]/Adaptor-related protein complex 2 beta 1 subunit, a large subunit of the AP2 adaptor complex, involved in clathrin coat assembly at the plasma membrane; may bind to the transmembrane envelope protein of HIV-1 and HTLV retroviruses
SW:MPRI_HUMAN	IGF2R	43	76	0.86	0.21	SW:MPRI_HUMAN P11717 homo sapiens (human). cation-independent mannose-6-phosphate receptor precursor (ci man-6-p receptor) (ci-mpr) (insulin-like growth factor ii receptor) (300 kda mannose 6-phosphate [MASS=274309]/Insulin-like growth factor II receptor, functions in transport of mannose 6-phosphate-containing lysosomal enzymes and IGF-II maturation and clearance, mediates granzyme B-induced apoptosis, putative tumor suppressor
GP:AF044670_1	VAP33	43	2	0.88	0.24	GP:AF044670_1 Homo sapiens 33 kDa Vamp-associated protein (VAP33) mRNA, complete cds; VAP-33. [MASS=27318]/Vesicle-associated membrane protein (VAMP)-associated protein A, binds v-SNAREs, t-SNAREs, VAPB, and VAMP, predicted to be involved in vesicle transport and fusion
GP:AF128536_1	PACSIN2	43	4	0.89	0.45	GP:AF128536_1 Homo sapiens cytoplasmic phosphoprotein PACSIN2 mRNA, complete cds; related to PACSIN1; contains CDC15 N-terminal domain, 3 EH domain-binding NPF motifs, and a C-terminal SH3 domain. [MASS=55905]/Protein kinase C and casein kinase substrate in neurons 2, member of the PACSIN family of cytoplasmic adapter proteins, may function to organize the actin cytoskeleton and regulate vesicular traffic
GP:AF004563_1	STXBP1	43	4	0.89	0.26	GP:AF004563_1 Homo sapiens hUNC18b alternatively-spliced mRNA, complete cds; alternatively-spliced; similar to rat n-Sec1. [MASS=68736]/Syntaxin-binding protein 1, binds syntaxins, may be involved in synaptic vesicle exocytosis
SW:G25B_HUMAN	CDC42	43	13	0.90	0.13	SW:G25B_HUMAN P21181 homo sapiens (human), mus musculus (mouse), and bos taurus (bovine). g25k gtp-binding protein, brain isoform (gp) (cdc42 homolog). 12/1998 [MASS=21311]/Cell division cycle 42 (GTP binding protein 25kD), Rho GTPase involved in actin cytoskeleton organization, cell migration, cell cycle progression and apoptosis, downregulated in fibroblasts and macrophages from patients with Tangiers disease
SW:143T_HUMAN	YWHAQ	43	3	0.91	0.05	SW:143T_HUMAN P27348 homo sapiens (human). 14-3-3 protein tau (14-3-3 protein theta) (14-3-3 protein t-cell) (hs1 protein). 11/1997 [MASS=27764]/14-3-3 theta (14-3-3 tau in T-cells), may modulate T-cell signaling and cytokine expression through interaction with and inhibition of protein kinase C and phosphatidylinositol 3-kinase, may promote cell survival during amyotrophic lateral sclerosis (ALS)
SW:ACTZ_HUMAN	ACTR1A	43	7	0.92	0.04	SW:ACTZ_HUMAN P42024 homo sapiens (human), mus musculus (mouse), and canis familiaris (dog). alpha-centractin (centractin) (centrosome-associated actin homolog) (actin-rpv) (arp1). 7/1999 [MASS=42614]/Actin-related protein 1, a component of the dynactin complex involved in transport along microtubules, associates with centrophilin NUMA1 at nuclear envelope breakdown, expression is significantly reduced in Down syndrome fetal brain

SWN:STX8_HUMAN	STX8	43	1	0.93	0.00	SWN:STX8_HUMAN Q9unk0 homo sapiens (human). syntaxin 8. 8/2001 [MASS=26907]/Syntaxin 8, member of the soluble NSF attachment protein receptor (SNARE) family, plays a role in endosome trafficking, may mediate vesicle docking and fusion, may regulate CFTR -mediated chloride currents
GP:AC005545_2	AP3D1	43	2	0.93	0.18	GP:AC005545_2 Homo sapiens chromosome 19, cosmid R26634, complete sequence; vesicle coat component, similar to alpha and gamma adaptins. [MASS=121170]/Adaptor-related protein complex 3 delta 1 subunit, a component of the AP-3 complex, involved in intracellular vesicle transport
SW:S23A_HUMAN	SEC23A	43	5	0.94	0.18	SW:S23A_HUMAN Q15436 homo sapiens (human). protein transport protein sec23 homolog isoform a. 11/1997 [MASS=86147]/Sec23 homolog A, a putative intracellular transporter that plays a role in protein trafficking, interacts with SEC24B and SEC24C
SW:ADB1_HUMAN	AP1B1	43	20	0.99	0.27	SW:ADB1_HUMAN Q10567 homo sapiens (human). beta-adaptin 1 (plasma membrane adaptor ha2/ap2 adaptin beta subunit) (clathrin assembly protein complex 2 beta large chain) (ap105a). 7/1999 [MASS=104607]/Adaptor-related protein complex 1 beta 1, likely participates in clathrin-coated vesicle endocytosis and intracellular receptor transport; loss is associated with meningioma tumors
SW:TERA_HUMAN	VCP	43	41	0.99	0.20	SW:TERA_HUMAN P55072 homo sapiens (human). transitional endoplasmic reticulum atpase (ter atpase) (15s mg(2+)-atpase p97 subunit) (valosin containing protein) (vcp) [contains: valosin]. 7/1999 [MASS=89322]/Valosin-containing protein, a putative clathrin-binding ATPase involved in cell cycle control, ubiquitin-dependent protein degradation, and JAK-STAT signaling, may be involved in DNA repair via BRCA1, may be involved in receptor-mediated endocytosis
GP:AC006942_1	ADTAA	43	5	1.00	0.28	GP:AC006942_1 Homo sapiens chromosome 19, cosmid R31181, complete sequence CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-A LARGE CHAIN); Non- consensussplice junction found at position 18996. [MASS=90046]/Adaptor-related protein complex 2 alpha 1 subunit, component of the clathrin adaptor complex, involved in vesicle transport
GP:AF020797_1	HSMU1B	43	1	1.03	0.00	GP:AF020797_1 Homo sapiens AP-mu chain family member mu1B (HSMU1B) mRNA, complete cds. [MASS=48108]/Adaptor-related protein complex 1 mu 2 subunit, involved in protein sorting
SW:MPRD_HUMAN	M6PR	43	1	1.03	0.00	SW:MPRD_HUMAN P20645 homo sapiens (human). cation-dependent mannose-6-phosphate receptor precursor (cd man-6-p receptor) (cd-mpr) (46 kda mannose 6-phosphate receptor) (mpr 46). 5/2000 [MASS=30993]/Cation-dependent mannose-6-phosphate receptor, involved in intracellular sorting and transport of acid hydrolases, transports lysosomal enzymes
GP:AC006378_1	BET1	43	1	1.04	0.00	GP:AC006378_1 Homo sapiens BAC clone RP11-455I9 from 7q21.2-q22, complete sequence; match to AAB62941.1 (PID:2253426); H_NH0455I09.1. [MASS=13289]/S. cerevisiae Bet1 homolog, may be involved in ER to Golgi transport
PIR2:I53171	H-SP1	43	1	1.06	0.00	PIR2:I53171 pantophysin - human [MASS=28565]/Synaptophysin-like protein (pantophysin), a protein that has similarity to the synaptic vesicle protein synaptophysin (SYP), may play a role in vesicle transport
GP:AF260566_1	HGS	43	1	1.06	0.00	GP:AF260566_1 Homo sapiens hepatocyte growth factor-regulated tyrosine kinase substrate HRS isoform 2 (HRS) mRNA, complete cds. [MASS=76362]/Hepatocyte growth factor regulated tyrosine kinase substrate, zinc-finger protein with ATPase activity, tyrosine phosphorylated upon growth factor stimulation, involved in endosome trafficking and mediates FOS transcription via cytokine signaling
SW:COPB_HUMAN	COPB	43	1	1.07	0.00	SW:COPB_HUMAN P53618 homo sapiens (human). coatomer beta subunit (beta-coat protein) (beta-cop) (fragment). 11/1997 [MASS=33444]/Coatomer protein beta, component of non-clathrin-coated vesicles essential for membrane trafficking, binds to HIV-1 Nef protein
SWN:SNX3_HUMAN	SNX3	43	1	1.07	0.00	SWN:SNX3_HUMAN O60493 homo sapiens (human). sorting nexin 3 (sdp3 protein). 8/2001 [MASS=18762]/Sorting nexin 3, involved in intracellular protein trafficking
SW:ARF6_HUMAN	ARF6	43	2	1.07	0.05	SW:ARF6_HUMAN P26438 homo sapiens (human), mus musculus (mouse), and rattus norvegicus (rat). adp-ribosylation factor 6. 12/1998 [MASS=19951]/ADP-ribosylation factor 6, GTP-binding protein that stimulates cholera toxin activity and is involved in endocytosis, exocytosis, membrane trafficking, and possibly regulation of glucose transport
GP:AF151858_1	LOC50999	43	2	1.09	0.01	GP:AF151858_1 Homo sapiens CGI-100 protein mRNA, complete cds. [MASS=26005]/Protein with high similarity to T1-ST2 receptor binding protein (human IL1RL1LG), which binds to the T1/ST2 receptor (human IL1RL1), member of the emp24 family, which are involved in protein transport from endoplasmic reticulum to Golgi
GP:AF032922_1	UNC-18C	43	2	1.09	0.03	GP:AF032922_1 Homo sapiens syntaxin 4 binding protein UNC-18c (UNC-18c) mRNA, complete cds. [MASS=67764]/Syntaxin binding protein 3, binds syntaxin 4 (STX4), predicted to be involved in vesicle transport and docking and in neurotransmitter release
SW:STB2_HUMAN	STXBP2	43	4	1.09	0.34	SW:STB2_HUMAN Q15833 homo sapiens (human). syntaxin binding protein 2 (unc-18 homolog 2) (unc-18b). 5/2000 [MASS=66439]/Syntaxin-binding protein 2, a member of the Sec1 family of proteins involved in synaptic transmission and secretion, may be involved in intracellular vesicular transport
SW:AP50_HUMAN	AP2M1	43	3	1.10	0.08	SW:AP50_HUMAN P20172 homo sapiens clathrin coat assembly protein ap50 (clathrin coat associated protein ap50) (plasma membrane adaptor ap-2 50 kda protein) (ha2 50 kda subunit) (clathrin assembly protei [MASS=49655]/Medium chain subunit of the clathrin associated protein complex AP2, involved in vesicle transport, endocytosis, and required for V-ATPase complex activity
SW:NSF_HUMAN	NSF	43	6	1.12	0.16	SW:NSF_HUMAN P46459 homo sapiens (human). vesicular-fusion protein nsf (n-ethylmaleimide-sensitive fusion protein) (nem-sensitive fusion protein). 12/1998 [MASS=82654]/N-ethylmaleimide-sensitive factor, an ATPase involved in membrane fusion during exocytosis
GPN:AB047847_1	COPG2	43	5	1.14	0.06	no_description_avail/Coatomer protein complex subunit gamma 2, putative intracellular transporter that may be involved in non-selective vesicle transport

SW:COPP_HUMAN	COPB2	43	5	1.15	0.22	SW:COPP_HUMAN P35606 homo sapiens (human). coatomer beta' subunit (beta'-coat protein) (beta'-cop) (p102). 12/1998 [MASS=102356]/Coatomer protein (COP) complex subunit beta 2 (COP beta prime), part of a Golgi coatomer complex that comprises the coat of non-clathrin coated vesicles, likely to play a role in exocytosis
SW:RAB7_HUMAN	RAB7	43	1	1.16	0.00	SW:RAB7_HUMAN P51149 homo sapiens (human). ras-related protein rab-7. 7/1998 [MASS=23490]/Ras-related GTP-binding protein 7, a member of the rab family of proteins that is involved in vesicle transport, membrane fusion, and vacuole formation; implicated in Chediak Higashi Syndrome
GP:AB019435_1	P125	43	3	1.17	0.10	GP:AB019435_1 Homo sapiens mRNA for putative phospholipase, complete cds; putative. [MASS=111076]/Sec23-interacting protein p125, a proline rich protein containing a phospholipase motif, binds to the COPII vesicle coat protein Sec23p (mouse Sec23a), may play a role in protein transport between the endoplasmic reticulum and Golgi
GP:U85946_1	SEC10L1	43	5	1.33	0.11	GP:U85946_1 Homo sapiens brain secretory protein hSec10p (HSEC10) mRNA, complete cds; similar to S. cerevisiae Sec10p. [MASS=81853]/SEC10 (S. cerevisiae)-like 1, a component of the exocyst complex, involved in the synthesis and delivery of secretory proteins in epithelial cells, involved in the development of epithelial cysts and tubules
GPN:AF191298_1	VPS35	43	7	1.35	0.49	Homo sapiens, vacuolar protein sorting 35/Maternal-embryonic 3, may be a component of the sorting machinery required for vesicle to Golgi retrieval
PIR2:S33377	CKAP4	43	5	1.35	0.22	PIR2:S33377 P63 protein - human [MASS=65793]/Cytoskeleton-associated protein 4, type II membrane protein of the endoplasmic reticulum, binds to microtubules and links them to the endoplasmic reticulum, promotes tubulin polymerization and endoplasmic reticulum reorganization
SW:TM21_HUMAN	TMP21	43	3	1.37	0.60	SW:TM21_HUMAN P49755 homo sapiens (human). transmembrane protein tmp21 precursor (s31iii125) (s31i125). 12/1998 [MASS=24976]/Transmembrane protein Mr 21,000, involved in biosynthetic protein transport from the ER to Golgi, regulates Rac-GTP levels through interaction with beta 2-chimaerin (CHN2); corresponding gene is located in the AD3 region mutated in Alzheimer's Disease
SWN:CNE3_HUMAN	CPN3	43	28	1.47	0.27	SWN:CNE3_HUMAN O75131 homo sapiens (human). copine iii. 8/2001 [MASS=60131]/Copine III, a member of the copine family of phospholipid binding proteins, contains C2 and integrin A domains, may play a role in membrane trafficking, displays protein kinase activity, however, it does not contain a traditional kinase catalytic domain
SW:RB13_HUMAN	RAB13	43	1	1.49	0.00	SW:RB13_HUMAN P51153 homo sapiens (human). ras-related protein rab-13. 12/1998 [MASS=22774]/Ras-related GTP-binding protein 13, a putative RAB small monomeric GTPase that is likely to play a role in intracellular protein trafficking and cell adhesion
SW:GDIB_HUMAN	GDI2	43	2	1.70	0.01	SW:GDIB_HUMAN P50395 homo sapiens (human). rab gdp dissociation inhibitor beta (rab gdi beta) (gdi-2). 7/1998 [MASS=50664]/Guanosine diphosphate dissociation inhibitor 2, one of a family proteins that regulate GDP/GTP cycle and are involved in intracellular vesicular trafficking, associates with RAB1B, RAB5 and RAB6 and may play a role in their intracellular targeting
PIR2:I53799	KTN1	43	2	1.73	0.08	PIR2:I53799 CG1 protein - human [MASS=149611]/human kinectin/Kinectin, functions as a receptor for the microtubule-motor protein kinesin and plays a role in intracellular movement of organelles; mutations in the corresponding gene are associated with childhood papillary thyroid carcinoma
PIR2:A55575	ANK3	43	9	1.85	0.18	PIR2:A55575 ankyrin 3, long splice form - human [MASS=480403]/Ankyrin 3 (ankyrin G), may link integral membrane proteins to the cytoskeleton, may play a role in localizing sodium channels to the axonal initial segment and nodes of Ranvier, may play a role in vesicle transport
SW:COPA_HUMAN	COPA	43	15	1.95	3.01	SW:COPA_HUMAN P53621 homo sapiens (human). coatomer alpha subunit (alpha-coat protein) (alpha-cop) (hepcop) (hep-cop) [contains: xenin (xenopsin-related peptide); proxenin]. 5/2000 [MASS=138332]/ Coatomer protein complex subunit alpha, involved in transport between the endoplasmic reticulum and the Golgi apparatus, binds to RNA, N-terminal 25 amino acids may be cleaved to release the peptide xenin, which stimulates pancreatic secretion

Panel 10, pgs. 270-274

Metabolic Pathways	AccessID	Gene	Cellular Process	Gravy Index	XPRESS Count	d0:d8 ratio	d0:d8 StdDev	Description
TCA Cycle								
Pyruvate dehydrogenase complex	SW:ODPB_HUMAN	PDHB	5, 18		1	1.05	0.00	SW:ODPB_HUMAN P11177 homo sapiens (human). pyruvate dehydrogenase e1 component beta subunit, mitochondrial precursor (ec 1.2.4.1) (pdhe1-b). 7/1999 [MASS=39219]/E1 beta subunit of pyruvate dehydrogenase complex, oxidatively decarboxylates pyruvate to acetyl-CoA
	SW:ODPA_HUMAN	PDHA1	5		3	1.17	0.41	SW:ODPA_HUMAN P08559 homo sapiens (human). pyruvate dehydrogenase e1 component alpha subunit, somatic form, mitochondrial precursor (ec 1.2.4.1) (pdhe1-a type i). 7/1999 [MASS=43296]/E1 alpha subunit of pyruvate dehydrogenase complex, somatic form, oxidatively decarboxylates pyruvate to acetyl-CoA; mutation of the corresponding gene causes the majority of pyruvate dehydrogenase deficiencies
	SW:ODPX_HUMAN	PDX1	5		3	1.24	0.16	SW:ODPX_HUMAN O00330 homo sapiens (human). pyruvate dehydrogenase protein x component, mitochondrial precursor (dihydrolipoamide dehydrogenase-binding protein of pyruvate dehydrogenase complex) (e3-bind [MASS=54138]/Dihydrolipoamide dehydrogenase-binding protein (protein X), lipoyl-containing component of the pyruvate dehydrogenase complex, anchors the dihydrolipoamide dehydrogenase (E3) to the dihydrolipoamide transacetylase (E2) core, deficiency causes disease
	SW:DLDH_HUMAN	DLD	5, 18		10	1.59	0.59	SW:DLDH_HUMAN P09622 homo sapiens (human). dihydrolipoamide dehydrogenase, mitochondrial precursor (ec 1.8.1.4). 5/2000 [MASS=54150]/Dihydrolipoamide dehydrogenase, E3 component of pyruvate dehydrogenase complex, also component of alpha-ketoglutarate dehydrogenase and branched-chain alpha-ketoacid dehydrogenase complexes and the glycine cleavage system
Citrate Synthase	SW:CISY_HUMAN	CS	5, 18		1	1.62	0.00	SW:CISY_HUMAN O75390 homo sapiens (human). citrate synthase, mitochondrial precursor (ec 4.1.3.7). 7/1999 [MASS=51706]/Citrate synthase, converts acetyl-CoA and oxaloacetate into citrate plus CoA in the tricarboxylic acid cycle
Aconitase	SW:ACON_HUMAN	ACO2	5, 18		1	1.27	0.00	SW:ACON_HUMAN Q99798 homo sapiens (human). aconitate hydratase, mitochondrial precursor (ec 4.2.1.3) (citrate hydro-lyase) (aconitase). 5/2000 [MASS=85425]/Aconitase 2 mitochondrial (aconitate hydratase), catalyzes the conversion of citrate to cis-aconitate in the tricarboxylic acid cycle, may be involved in iron homeostasis; deficiency may be associated with lifelong exercise intolerence
Isocitrate dehydrogenase	SW:IDHP_HUMAN	IDH2	5, 18	-0.391	7	2.04	0.65	SW:IDHP_HUMAN P48735 homo sapiens (human). isocitrate dehydrogenase [nadp], mitochondrial precursor (ec 1.1.1.42) (oxalosuccinate decarboxylase) (idh) (nadp+-specific icdh) (idp) (icd-m). 2/1996 [MASS=50948]/Isocitrate dehydrogenase 2 (NADP+) mitochondrial, catalyzes the oxidative decarboxylation of isocitrate to form alpha-ketoglutarate
a-ketoglutarate dehydrogenase	SW:ODO1_HUMAN	OGDH	5, 18		9	0.94	0.18	SW:ODO1_HUMAN Q02218 homo sapiens (human). 2-oxoglutarate dehydrogenase e1 component, mitochondrial precursor (ec 1.2.4.2) (alpha-ketoglutarate dehydrogenase). 7/1999 [MASS=113475]/2-Oxoglutarate dehydrogenase (alpha-ketoglutarate dehydrogenase), E1 component of the complex that converts alpha-ketoglutarate to succinyl coenzyme A in the Krebs cycle; deficiency has been observed in Alzheimer and Parkinson disease
Succinyl CoA synthase	NI							
Succinate dehydrogenase	SW:DHSB_HUMAN	SDHB	5, 18	-0.410	1	2.24	0.00	SW:DHSB_HUMAN P21912 homo sapiens (human). succinate dehydrogenase [ubiquinone] iron-sulfur protein, mitochondrial precursor (ec 1.3.5.1) (ip) (ip subunit of complex ii). 5/2000 [MASS=31629]/Succinate dehydrogenase complex iron sulfur subunit B, part of an enzyme complex that transports electrons from succinate to ubiquinone in the TCA cycle and aerobic respiratory chain, may be involved in familial pheochromocytoma
	SW:DHSA_HUMAN	SDHA	5, 18	-0.270	5	2.48	0.32	SW:DHSA_HUMAN P31040 homo sapiens (human). succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial precursor (ec 1.3.5.1) (fp) (flavoprotein subunit of complex ii). 5/2000 [MASS=72692]/Succinate dehydrogenase complex subunit A (flavoprotein), transports electrons from succinate to ubiquinone in the TCA cycle and respiratory chain; gene mutation is associated with Leigh syndrome, which is a complex II respiratory chain deficiency
Malate dehydrogenase	SW:MDHM_HUMAN	MDH2	18	0.151	27	2.29	1.04	SW:MDHM_HUMAN P40926 homo sapiens (human). malate dehydrogenase, mitochondrial precursor (ec 1.1.1.37). 5/2000 [MASS=35531]/Mitochondrial malate dehydrogenase, part of the malate-aspartate shuttle where it putatively catalyzes the oxidation of malate to oxaloacetate
Glycerol 3-phosphate shuttle								
Mitochondrial glycerol 3-phosphate	SW:GPDM_HUMAN	GPD2	5	-0.211	1	3.30	0.00	SW:GPDM_HUMAN P43304 homo sapiens (human). glycerol-3-phosphate dehydrogenase, mitochondrial precursor (ec 1.1.99.5) (gpd-m) (gpdh-m). 5/2000 [MASS=80815]/Mitochondrial glycerol-3-phosphate dehydrogenase, component of the glycerol phosphate shuttle; mutation of the calcium binding domain in the corresponding gene has been found in a patient with type A diabetes
Malate-aspartate shuttle								
Cytosolic malate dehydrogenase	SW:MDHC_HUMAN	MDH1	18		4	1.27	0.10	SW:MDHC_HUMAN P40925 homo sapiens (human). malate dehydrogenase, cytoplasmic (ec 1.1.1.37). 5/2000 [MASS=36295]/Cytosolic malate dehydrogenase, part of the malate-aspartate shuttle where it putatively catalyzes the reduction of oxaloacetate to malate
Mitochondrial malate dehydrogenase	SW:MDHM_HUMAN	MDH2	18	0.151	27	2.29	1.04	SW:MDHM_HUMAN P40926 homo sapiens (human). malate dehydrogenase, mitochondrial precursor (ec 1.1.1.37). 5/2000 [MASS=35531]/Mitochondrial malate dehydrogenase, part of the malate-aspartate shuttle where it putatively catalyzes the oxidation of malate to oxaloacetate
Mitochondrial Fatty Acid beta-oxidation								
Liproprotein Lipase	NI							
Fatty acid Coenzyme A Ligase	SW:LCFA_HUMAN	FACL1	19		14	0.81	0.13	SW:LCFA_HUMAN P41215 homo sapiens (human). long-chain-fatty-acid--coa ligase 1 (ec 6.2.1.3) (long-chain acyl-coa synthetase 1) (lacs 1) (palmitoyl-coa ligase). 10/1996 [MASS=78348]/Long chain fatty acid-Coenzyme A ligase (palmitoyl-CoA ligase), a member of the long chain acyl-CoA synthetase family required for lipid synthesis and fatty acid degradation
Carnitine acyltransferase	SW:CPT1_HUMAN	CPT1A	18, 19		1	1.30	0.00	SW:CPT1_HUMAN P50416 homo sapiens (human). carnitine o-palmitoyltransferase i, mitochondrial liver isoform (ec 2.3.1.21) (cpt i) (cpti-l). 7/1999 [MASS=88429]/Liver carnitine palmitoyltransferase I, enzyme of long-chain fatty acid beta-oxidation pathway; mutations in the corresponding gene are associated with carnitine palmitoyltransferase I deficiency

	SW:CPT2_HUMAN	CPT2	18, 19, 42		1	1.08	0.00	SW:CPT2_HUMAN P23786 homo sapiens (human). carnitine o-palmitoyltransferase ii, mitochondrial precursor (ec 2.3.1.21) (cpt ii). 5/2000 [MASS=73777]/Carnitine palmitoyltransferase II, a mitochondrial long-chain fatty acid oxidation enzyme; mutations are associated with a lipid metabolism disorder that includes recurrent myopathy with progressive rhabdomyolysis, muscle weakness and myoglobinuria
Acyl CoA dehydrogenase	SW:ACDV_HUMAN	ACADVL	18, 19	-0.065	1	0.32	0.00	SW:ACDV_HUMAN P49748 homo sapiens (human). acyl-coa dehydrogenase, very-long-chain specific, mitochondrial precursor (ec 1.3.99.-) (vlcad). 5/2000 [MASS=70390]/Very long chain acyl-coenzyme A dehydrogenase, oxidizes straight chain acyl-CoAs in the initial step of fatty acid beta-oxidation, severe deficiency results in infant cardiomyopathy with high mortality, mild deficiency results in hypoketotic hypoglycemia
Enoyl CoA hydratase	SW:D3D2_HUMAN	DCI	18, 19		3	1.31	0.20	SW:D3D2_HUMAN P42126 homo sapiens (human). 3,2-trans-enoyl-coa isomerase, mitochondrial precursor (ec 5.3.3.8) (dodecenoyl-coa delta-isomerase). 7/1999 [MASS=32816]/Dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenzyme A isomerase), catalyzes the isomerization of 3-cis and 3-trans enoyl CoA esters to 2-trans enoyl CoA esters, functions in mitochondrial beta-oxidation of unsaturated fatty acids
3-hydroxyacyl-CoA dehydrogenase	SW:HCD2_HUMAN	HADH2	19	0.233	4	1.67	0.12	SW:HCD2_HUMAN Q99714 homo sapiens (human). 3-hydroxyacyl-coa dehydrogenase type ii (ec 1.1.1.35) (endoplasmic reticulum-associated amyloid beta-peptide binding protein) (short- chain type dehydrogenase/ [MASS=26923]/Hydroxyacyl-Coenzyme A dehydrogenase (type II), catalyzes the oxidation of steroids and alcohols, binds amyloid-beta protein; overexpressed and mediates neurotoxicity of Alzheimer's disease, mutation in the corresponding gene causes hyperinsulinism
b-ketothiolase	SW:ECHB_HUMAN	HADHB	18, 19, 42	-0.072	4	1.87	0.07	SW:ECHB_HUMAN P55084 homo sapiens (human). trifunctonal enzyme beta subunit, mitochondrial precursor (tp-beta) [includes: 3-ketoacyl-coa thiolase (ec 2.3.1.16) (acetyl-coa acyltransferase) (beta-ketothi [MASS=51294]/3-hydroxyacyl-CoA dehydrogenase, 3-ketoacyl-CoA thiolase trifunctional protein beta subunit, involved in fatty acid beta-oxidation; variants are associated with trifunctional protein deficiency, sudden infant death syndrome and liver failure
	SW:ECHA_HUMAN	HADHA	18, 19, 42	-0.083	13	1.97	0.65	SW:ECHA_HUMAN P40939 homo sapiens (human). mitochondrial trifunctional enzyme alpha subunit precursor (tp-alpha) [includes: long-chain enoyl-coa hydratase (ec 4.2.1.17); long chain 3-hydroxyacyl-coa deh [MASS=82960]/Mitochondrial long-chain enoyl-CoA hydratase/3-hydroxyacyl-CoA dehydrogenase/3-ketoacyl-CoA thiolase alpha subunit, involved in fatty acid beta-oxidation, mutations are associated with trifuctional protein deficiency and Reye-like syndrome
Peroxisomal Fatty Acid beta-oxidation								
Acyl-CoA synthetase	NI							
Phytanoyl-CoA hydroxylase	NI							
2-hydroxyphytanoyl-CoA lyase	GP:AF161397_1	HPCL2	19	-0.059	2	2.53	0.16	GP:AF161397_1 Homo sapiens HSPC279 mRNA, partial cds. [MASS=64199]/Homo sapiens mRNA for 2-hydroxyphytanoyl-CoA lyase; thiamine pyrophosphate dependent enzyme/2-Hydroxyphytanoyl-CoA lyase (peroxisomal 2-hydroxyphytanoyl-CoA lyase), catalyzes the thiamine pyrophosphate-dependent cleavage of C-C bonds during alpha-oxidation of 3-methyl-branched fatty acids to form formyl-CoA and 2-methyl-branched fatty aldehyde
Aldehyde dehydrogenase	SW:DHA4_HUMAN	ALDH3A2	16, 19		2	1.62	0.67	SW:DHA4_HUMAN P51648 homo sapiens (human). fatty aldehyde dehydrogenase (ec 1.2.1.3) (aldehyde dehydrogenase, microsomal) (aldh class 3). 7/1999 [MASS=54848]/Aldehyde dehyrogenase 3 family member A2, catalyzes the oxidation of long chain fatty aldehydes and leukotrienes; mutation of the corresponding gene causes Sjogren Larsson syndrome, a disorder marked by mental retardation, spasticity, and ichthyosis
alpha-methyl-CoA racemase	NI							
branched chain acyl-CoA oxidase	SW:CAOP_HUMAN	ACOX	18, 19		1	1.53	0.00	SW:CAOP_HUMAN Q15067 homo sapiens (human). acyl-coenzyme a oxidase, peroxisomal (ec 1.3.3.6) (palmitoyl-coa oxidase) (aox). 11/1997 [MASS=74502]/Peroxisomal acyl-coenzyme A oxidase, catalyzes the first step in very long chain fatty acid beta-oxidation, desaturates acyl-CoA to 2-trans-enoyl-CoA and produces hydrogen peroxide
2-enoyl-CoA hydratase	NI							
3-hydroxyacyl-CoA dehydrogenase	NI							
3-ketoacyl-CoA thiolase	SW:THIK_HUMAN	ACAA1	18, 19		15	1.26	0.25	SW:THIK_HUMAN P09110 homo sapiens (human). 3-ketoacyl-coa thiolase, peroxisomal precursor (ec 2.3.1.16) (beta-ketothiolase) (acetyl-coa acyltransferase) (peroxisomal 3-oxoacyl- coa thiolase). 7/1999 [MASS=44292]/Peroxisomal 3-oxoacyl-coenzyme A thiolase (peroxisomal 3-ketoacyl-Coenzyme A thiolase), functions in peroxisomal beta-oxidation of fatty acids, deficiency is associated with rhizomelic chondrodysplasia punctata (RCDP)
Gluconeogenesis								
Pyruvate carboxylase	NI							
Phosphoenolpyruvate carboxykinase	SW:PPCM_HUMAN	PCK2	5, 18	-0.266	6	2.45	1.09	SW:PPCM_HUMAN Q16822 homo sapiens (human). phosphoenolpyruvate carboxykinase, mitochondrial precursor [gtp] (ec 4.1.1.32) (phosphoenolpyruvate carboxylase) (pepck-m). 7/1999 [MASS=70637]/Phosphoenolpyruvate carboxykinase 2, catalyzes the formation of phosphoenolpyruvate by decarboxylation of oxaloacetate, rate-limiting step of gluconeogenesis
Fructose 1, 6-bisphosphatase	NI							
Glucose 6-phosphatase	NI							
Glycolysis								
Hexokinase	SW:HXK1_HUMAN	HK1	5, 18		5	1.07	0.11	SW:HXK1_HUMAN P19367 homo sapiens (human). hexokinase, type i (ec 2.7.1.1) (hk i) (brain form hexokinase). 12/1998 [MASS=102503]/Hexokinase Type I (ATP:D-hexose 6-phosphotransferase), catalyzes ATP-dependent conversion of glucose to glucose 6 phosphate in glycolysis, deficiency may lead to non-spherocytic hemolytic anemia
Phosphoglucose isomerase	SW:G6PI_HUMAN	GPI	5		2	0.85	0.01	SW:G6PI_HUMAN P06744 homo sapiens (human). glucose-6-phosphate isomerase (gpi) (ec 5.3.1.9) (phosphoglucose isomerase) (pgi) (phosphohexose isomerase) (phi) (neuroleukin) (nlk). 5/2000 [MASS=63189]/Glucose phosphate isomerase, plays a role in glycolysis and gluconeogenesis, tumor-secreted form (neuroleukin) acts as an autocrine factor to stimulate motility, invasion and metastasis of cancer cells; deficiency is associated with hemolytic anemia
Phosphofructokinase	SW:K6PL_HUMAN	PFKL	5, 18		8	0.97	0.17	SW:K6PL_HUMAN P17858 homo sapiens (human). 6-phosphofructokinase, liver type (ec 2.7.1.11) (phosphofructokinase 1) (phosphohexokinase) (phosphofructo-1-kinase isozyme b). 10/1996 [MASS=85148]/Liver phosphofructokinase, catalyses the phosphorylation of fructose-6-phosphate to fructose-1,6-bisphosphate in glycolysis, deficiency is linked to glycogenosis type VII while overexpression may lead to the cognitive diabilites of Down's syndrome
	SW:K6PP_HUMAN	PFKP	5	-0.146	1	2.96	0.00	SW:K6PP_HUMAN Q01813 homo sapiens (human). 6-phosphofructokinase, type c (ec 2.7.1.11) (phosphofructokinase 1) (phosphohexokinase) (phosphofructo-1-kinase isozyme c) (6-phosphofructokinase, platelet typ [MASS=85596]/Platelet-type phosphofructokinase, rate-limiting enzyme of glycolysis that catalyzes the formation of fructose 1,6-bisphosphate from fructose 6-phosphate and ATP; expression may be elevated upon malignant transformation

Aldolase	SW:ALFA_HUMAN	ALDOA	5		4	0.71	0.25	SW:ALFA_HUMAN P04075 homo sapiens (human). fructose-bisphosphate aldolase a (ec 4.1.2.13) (muscle-type aldolase). 5/2000 [MASS=39289]/Aldolase A (fructose-bisphosphate aldolase); reversibly cleaves FBP into DHAP and GAP in glycolysis
Triose phosphate isomerase	SW:TPIS_HUMAN	TPI1	5, 16, 18		9	1.00	0.18	SW:TPIS_HUMAN P00938 homo sapiens (human), and pan troglodytes (chimpanzee). triosephosphate isomerase (ec 5.3.1.1) (tim). 7/1998 [MASS=26538]/Triosephosphate isomerase 1, catalyzes the reversible interconversion of glyceraldehyde 3-phosphate and dihydroxyacetone phosphate in glycolysis; variant forms cause hemolytic anemia and neurodegeneration; variant form is an antigen on melanoma cells
Glyceraldehyde 3-phosphate dehydrogenoase	SW:G3P2_HUMAN	GAPD	5, 14, 18		2	0.85	0.01	SW:G3P2_HUMAN P04406 homo sapiens (human). glyceraldehyde 3-phosphate dehydrogenase, liver (ec 1.2.1.12). 7/1999 [MASS=35922]/Glyceraldehyde-3-phosphate dehydrogenase, catalyzes reversible oxidation and phosphorylation of glyceraldehyde-3-phosphate to 1,3-diphosphoglycerate in glycolysis, involved in apoptosis, may play a role in neurodegeneration in diseases like Alzheimer's
Phosphoglycerate kinase	SW:PGK1_HUMAN	PGK1	5, 18		16	0.93	0.18	SW:PGK1_HUMAN P00558 homo sapiens (human). phosphoglycerate kinase 1 (ec 2.7.2.3) (primer recognition protein 2) (prp 2). 7/1999 [MASS=44597]/Phosphoglycerate kinase 1, catalyzes conversion of 1,3-diphosphoglycerate to 3-phosphoglycerate in glycolysis, forming one molecule of ATP; PGK1 gene transcription is induced by hypoxia and mutation is associated with non-spherocytic hemolytic anemia
Phosphoglyceromutase	NI							
Enolase	SW:ENOB_HUMAN	ENO3	5, 18		4	0.86	0.13	SW:ENOB_HUMAN P13929 homo sapiens (human). beta enolase (ec 4.2.1.11) (2-phospho-d-glycerate hydro-lyase) (skeletal muscle enolase) (mse). 7/1998 [MASS=46856]/Enolase 3 (muscle-specific enolase, beta enolase), a putative enolase which catalyzes the conversion of 2-phospho-D-glycerate to phosphoenolpyruvate in muscle glycolysis, deficiency is associated with exercise intolerance and myalgias
	SW:ENOA_HUMAN	ENO1	5, 18, 29		3	1.01	0.08	SW:ENOA_HUMAN P06733 homo sapiens (human). alpha enolase (ec 4.2.1.11) (2-phospho-d-glycerate hydro-lyase) (non-neural enolase) (nne) (phosphopyruvate hydratase). 7/1998 [MASS=47038]/Enolase 1 (alpha enolase), converts 2-phospho-D-glycerate to phosphoenolpyruvate in glycolysis, an autoantigen in multiple autoimmune diseases, shorter alternative form c-myc promoter binding protein (MPB1) is a transcriptional repressor
Pyruvate kinase	SW:KPY1_HUMAN	PKM2	5, 18		19	1.09	0.24	SW:KPY1_HUMAN P14618 homo sapiens (human). pyruvate kinase, m1 isozyme (ec 2.7.1.40) (pyruvate kinase muscle isozyme) (cytosolic thyroid hormone-binding protein) (cthbp) (thbp1). 12/1998 [MASS=57747]/Pyruvate kinase muscle (pyruvate kinase 3), glycolytic enzyme that converts phosphoenolpyruvate to pyruvate with phosphorylation of ADP to ATP, exists as M1 and M2 alternative forms, may have roles in viral transformation and cell differentiation
Glycogen Catabolism								
Phosphorylase kinase	SW:KPB1_HUMAN	PHKA1	5, 18		3	1.00	0.09	SW:KPB1_HUMAN P46020 homo sapiens (human). phosphorylase b kinase alpha regulatory chain, skeletal muscle isoform (phosphorylase kinase alpha m subunit). 2/1996 [MASS=137338]/Phosphorylase kinase regulatory subunit alpha-1 (muscle), which phosphorylates and thereby activates muscle-specific glycogen phosphorylase (PYGM); mutations in the corresponding gene are associated with muscle glycogenosis, a glycogen storage disease
Glycogen phosphorylase	SW:PHS2_HUMAN	PYGM	5, 18	-0.371	1	0.36	0.00	SW:PHS2_HUMAN P11217 homo sapiens (human). glycogen phosphorylase, muscle form (ec 2.4.1.1) (myophosphorylase). 5/2000 [MASS=97092]/Muscle glycogen phosphorylase, participates in glycogen catabolism; mutation of corresponding gene is associated with McArdle disease
	SW:PHS3_HUMAN	PYGB	5, 18	-0.334	10	0.48	0.06	SW:PHS3_HUMAN P11216 homo sapiens (human). glycogen phosphorylase, brain form (ec 2.4.1.1). 10/1996 [MASS=96683]/Brain glycogen phosphorylase, catalyzes the rate-limiting step in glycogen catabolism, activated by AMP and phosphorylation, may play a role in intestinal development; associated with gastric carcinomas displaying a differentiated intestinal phenotype
Glycogen transferase	SW:GLYG_HUMAN	GYG	5, 18	-0.158	6	0.51	0.11	SW:GLYG_HUMAN P46976 homo sapiens (human). glycogenin-1 (ec 2.4.1.186). 7/1999 [MASS=37347]Glycogenin (glycogenin glucosyltransferase), autocatalytic and self-glucosylating enzyme that primes de novo glycogen synthesis
Alpha-1, 6-glucosidase	SW:GDE_HUMAN	AGL	5, 18		18	0.92	0.22	SW:GDE_HUMAN P35573 homo sapiens (human). glycogen debranching enzyme (glycogen debrancher) [includes: 4-alpha-glucanotransferase (ec 2.4.1.25) (oligo-1,4-1,4-glucantransferase); amylo-1,6-glucosidase [MASS=172497]/Glycogen debranching enzyme, (amylo-1,6-glucosidase 4-alpha-glucanotransferase), catalyzes glycantransferase and glucosidase activities required for glycogen degradation; mutations and dysregulation are associated with type III glycogen storage diseases
Fatty Acid Synthesis								
ATP citrate lyase	SW:ACLY_HUMAN	ACLY	5, 19, 25	-0.093	6	0.44	0.09	SW:ACLY_HUMAN P53396 homo sapiens (human). atp-citrate (pro-s-)-lyase (ec 4.1.3.8) (citrate cleavage enzyme). 10/1996 [MASS=121420]/ATP citrate lyase, catalyzes the formation of acetyl-CoA and oxaloacetate from citrate and CoA with the concomitant hydrolysis of ATP to ADP and phosphate, involved in cholesterol and fatty acid synthesis, nutritionally regulated
Acetyl CoA carboxylase	SW:COA1_HUMAN	ACACA	19	-0.242	2	0.41	0.05	SW:COA1_HUMAN Q13085 homo sapiens (human). acetyl-coa carboxylase 1 (ec 6.4.1.2) (acc-alpha) [includes: biotin carboxylase (ec 6.3.4.14)]. 7/1999 [MASS=265040]/Acetyl-Coenzyme A carboxylase alpha, catalyzes the rate-limiting step in long-chain fatty acid biogenesis; deficiency leads to defects in fatty acid synthesis
Fatty acid synthase	SW:FAS_HUMAN	FASN	19	-0.095	90	0.34	0.15	SW:FAS_HUMAN P49327 homo sapiens (human). fatty acid synthase (ec 2.3.1.85) [includes: ec 2.3.1.38; ec 2.3.1.39; ec 2.3.1.41; ec 1.1.1.100; ec 4.2.1.61; ec 1.3.1.10; ec 3.1.2.14]. 7/1999 [MASS=273102]/Fatty acid synthase, multifunctional enzyme that synthesizes fatty acids from dietary proteins and carbohydrates; increased expression is associated with tumor growth and development, expression may serve as a prognostic maker for breast cancer
Cholesterol Synthesis								
Hydroxymethyl glutraryl CoA synthase	NI							
Hydroxymethyl glutraryl CoA reductase	NI							
Melavonate Kinase	NI							
Phosphomelavonate kinase	NI							
Diphosphomelavonate decarboxylase	NI							
Isopentenyldiphosphate isomerase	NI							
Dimethylally-trans-transferase	NI							
Geranyl-trans-transferase	NI							
Farnesyl-PP farnesyl transferase	SW:FDFT_HUMAN	FDFT1	19	-0.224	1	0.22	0.00	SW:FDFT_HUMAN P37268 homo sapiens (human). farnesyl-diphosphate farnesyltransferase (ec 2.5.1.21) (squalene synthetase) (sqs) (ss) (fpp:fpp farnesyltransferase). 10/1996 [MASS=48115]/Squalene synthase (farnesyl-diphosphate farnesyltransferase 1), catalyzes the conversion of farnesyl diphosphate to squalene in cholesterol biosynthesis, may be a potential target for cholesterol lowering therapy
Squalene Monooxygenase	NI							

Lanosterol synthase	SW:ERG7_HUMAN	LSS	19	-0.319	1	0.37	0.00	SW:ERG7_HUMAN P48449 homo sapiens (human). lanosterol synthase (ec 5.4.99.7) (oxidosqualene--lanosterol cyclase) (2,3-epoxysqualene--lanosterol cyclase) (osc). 5/2000 [MASS=83309]/Lanosterol synthase, catalyzes the cyclization of (S)-2,3-oxidosqualene forming lanosterol in sterol biosynthesis
Oxidative Phosphorylation								
Complex I								
NDUFB7	SW:NB8M_HUMAN	NDUFB7	6, 18	-0.990	2	2.27	0.65	SW:NB8M_HUMAN P17568 homo sapiens (human). nadh-ubiquinone oxidoreductase b18 subunit (ec 1.6.5.3) (ec 1.6.99.3) (complex i-b18) (ci-b18) (cell adhesion protein sqm1). 7/1998 [MASS=15648]/Subunit of the NADH-ubiquinone oxidoreductase (complex I), a multiprotein complex that transports electrons from NADH to ubiquinone, functions as a cell adhesion molecule with a role in metastasis, may have a role in drug transport
NDUFA8	SW:NUPM_HUMAN	NDUFA8	18	-0.780	5	2.10	0.44	SW:NUPM_HUMAN P51970 homo sapiens (human). nadh-ubiquinone oxidoreductase 19 kda subunit (ec 1.6.5.3) (ec 1.6.99.3) (complex i-19kd) (ci-19kd) (complex i-pgiv) (ci-pgiv). 5/2000 [MASS=19974]/NADH dehydrogenase ubiquinone 1 alpha subcomplex 8 (19 kDa), a subunit of NADH-ubiquinone oxidoreductase (complex I), a multiprotein complex that transports electrons from NADH to ubiquinone
NDUFV1	SW:NUBM_HUMAN	NDUFV1	18	-0.260	7	2.18	0.99	SW:NUBM_HUMAN P49821 homo sapiens (human). nadh-ubiquinone oxidoreductase 51 kda subunit precursor (ec 1.6.5.3) (ec 1.6.99.3) (complex i-51kd) (ci-51kd). 5/2000 [MASS=50956]/NADH dehydrogenase ubiquinone flavoprotein 1 (51 kDa), a subunit of NADH-ubiquinone oxidoreductase (Complex I); genetic variants are associated with mitochondrial complex I deficiency, leukodystrophy, and myoclonic epilepsy
NDUFS5	SW:NIPM_HUMAN	NDUFS5	18	-0.941	2	2.69	0.02	SW:NIPM_HUMAN O43920 homo sapiens (human). nadh-ubiquinone oxidoreductase 15 kda subunit (ec 1.6.5.3) (ec 1.6.99.3) (complex i-15 kda) (ci-15 kda). 7/1999 [MASS=12386]/NADH dehydrogenase Fe-S protein 5 (15kD) (NADH-coenzyme Q reductase), putative subunit of NADH-ubiquinone oxidoreductase (complex I), a multiprotein complex that transports electrons from NADH to ubiquinone in the mitochondrial respiratory chain
NDUFAB1	SW:ACPM_HUMAN	NDUFAB1	18		3	1.46	0.23	SW:ACPM_HUMAN O14561 homo sapiens (human). acyl carrier protein, mitochondrial precursor (acp) (nadh-ubiquinone oxidoreductase 9.6 kda subunit) (ec 1.6.5.3) (ec 1.6.99.3) (ci-sdap). 5/2000 [MASS=14806]/NADH-ubiquinone oxidoreductase subunit of alpha-beta subcomplex 1 (8 kD), a probable acyl carrier component of the multiprotein complex that transports electrons from NADH to ubiquinone, present within the hydrophobic fraction of complex I
NDUFS1	SW:NUAM_HUMAN	NDUFS1	18	-0.107	1	1.87	0.00	SW:NUAM_HUMAN P28331 homo sapiens (human). nadh-ubiquinone oxidoreductase 75 kda subunit precursor (ec 1.6.5.3) (ec 1.6.99.3) (complex i-75kd) (ci-75kd). 7/1999 [MASS=79574]/NADH-dehydrogenase ubiquinone Fe-S protein 1 (75kD), a multiprotein complex that transports electrons from NADH to ubiquinone, present within the hydrophobic fraction of complex I; genetic variants are associated with mitochondrial complex I deficiency
Complex II								
SDHA	SW:DHSA_HUMAN	SDHA	5, 18	-0.270	5	2.48	0.32	SW:DHSA_HUMAN P31040 homo sapiens (human). succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial precursor (ec 1.3.5.1) (fp) (flavoprotein subunit of complex ii). 5/2000 [MASS=72692]/Succinate dehydrogenase complex subunit A (flavoprotein), transports electrons from succinate to ubiquinone in the TCA cycle and respiratory chain; gene mutation is associated with Leigh syndrome, which is a complex II respiratory chain deficiency
SDHB	SW:DHSB_HUMAN	SDHB	5, 18	-0.410	1	2.24	0.00	SW:DHSB_HUMAN P21912 homo sapiens (human). succinate dehydrogenase [ubiquinone] iron-sulfur protein, mitochondrial precursor (ec 1.3.5.1) (ip) (ip subunit of complex ii). 5/2000 [MASS=31629]/Succinate dehydrogenase complex iron sulfur subunit B, part of an enzyme complex that transports electrons from succinate to ubiquinone in the TCA cycle and aerobic respiratory chain, may be involved in familial pheochromocytoma
Complex III								
UQCRC2	SW:UCR2_HUMAN	UQCRC2	18	-0.077	1	2.42	0.00	SW:UCR2_HUMAN P22695 homo sapiens (human). ubiquinol-cytochrome c reductase complex core protein 2 precursor (ec 1.10.2.2) (complex iii subunit ii). 7/1999 [MASS=48470]/Ubiquinol-cytochrome c reductase core protein II, a putative ubiquinol-cytochrome c reductase subunit of the mitochondrial cytochrome bc1 complex, likely to play a role in oxidative phosphorylation, may be involved in aerobic respiration
CYC1	SW:CY1_HUMAN	CYC1	18	-0.130	2	2.10	0.00	SW:CY1_HUMAN P08574 homo sapiens (human). cytochrome c1, heme protein precursor. 7/1999 [MASS=35390]/Cytochrome c1, a member of the cytochrome bc1 complex
UQCRH	SW:UCRH_HUMAN	UQCRH	18	-1.141	3	2.36	0.26	SW:UCRH_HUMAN P07919 homo sapiens (human). ubiquinol-cytochrome c reductase complex 11 kda protein precursor (ec 1.10.2.2) (mitochondrial hinge protein) (cytochrome c1, nonheme 11 kda protein) (complex [MASS=10755]/Ubiquinol-cytochrome c reductase hinge protein, hinges cytochrome c with cytochrome c1 in the mitochondrial respiratory chain, may function to accelerate apoptosis by enhancing cytochrome c release from the mitochondria
UQCRFS1	SW:UCRI_HUMAN	UQCRC1	18	-0.135	8	2.24	0.43	SW:UCR1_HUMAN P31930 homo sapiens (human). ubiquinol-cytochrome c reductase complex core protein i precursor (ec 1.10.2.2). 7/1999 [MASS=52619]/Ubiquinol-cytochrome c reductase core protein I, a subunit of the ubiquinol-cytochrome c oxidoreductase component of the mitochondrial respiratory chain, may function as an electron transporter in aerobic respiration and oxidative phosphorylation
Complex IV								
MTCO1	SW:COX1_HUMAN	MTCO1	18	0.682	1	1.97	0.00	SW:COX1_HUMAN P00395 homo sapiens (human). cytochrome c oxidase polypeptide i (ec 1.9.3.1). 5/2000 [MASS=57041]/Mitochondrial cytochrome c oxidase subunit I, a subunit of complex IV of the mitochondrial respiratory chain; mutations in the corresponding gene may be associated with mitochondrial diseases and acquired idiopathic sideroblastic anemia
COX6B	SW:COXG_HUMAN	COX6B	18	-1.021	6	2.77	1.08	SW:COXG_HUMAN P14854 homo sapiens (human). cytochrome c oxidase polypeptide vib (ec 1.9.3.1) (aed). 11/1997 [MASS=10061]/Cytochrome c oxidase subunit VIb, a putative subunit of cytochrome C oxidase, which couples reduction of oxygen with proton translocation during oxidative phosphorylation
COX17	SW:COXS_HUMAN	COX17	18, 42		1	1.18	0.00	SW:COXS_HUMAN Q14061 homo sapiens (human). cytochrome c oxidase copper chaperone. 7/1999 [MASS=6784]/Cytochrome c oxidase assembly protein 17, a putative copper binding protein, may function to transport copper to mitochondria for assembly into cytochrome oxidase complex; mutation does not appear to be a common cause of COX deficiency disorders
Complex V								

ATP6D	SW:VATX_HUMAN	ATP6D	42		2	0.89	0.03	SW:VATX_HUMAN Q02547 homo sapiens (human). vacuolar atp synthase subunit ac39 (ec 3.6.1.34) (v-atpase ac39 subunit) (32 kda accessory protein) (p39). 11/1997 [MASS=31704]/Vacuolar H+-ATPase proton pump (subunit D), an accessory subunit in the peripheral catalytic V1 complex, may be involved in coupling ATP hydrolysis (V1 complex) and proton transport (V0 complex)
ATP5C1	SW:ATPG_HUMAN	ATP5C1	18, 42	-0.180	3	2.15	0.32	SW:ATPG_HUMAN P36542 homo sapiens (human). atp synthase gamma chain, mitochondrial precursor (ec 3.6.1.34). 5/2000 [MASS=32996]/ATP synthase H+ transporting mitochondrial F1 complex gamma 1, putative component of multisubunit enzyme that synthesizes ATP during oxidative phosphorylation, exists in tissue-specific alternative forms that are spliced in response to acidic conditions
ATP5A1	SW:ATPA_HUMAN	ATP5A1	18, 42	-0.067	8	2.38	0.42	SW:ATPA_HUMAN P25705 homo sapiens (human). atp synthase alpha chain, mitochondrial precursor (ec 3.6.1.34). 12/1998 [MASS=59751]/ATP synthase H+ transporting mitochondrial F1 complex alpha subunit isoform 1 cardiac muscle, part of the synthase enzymatic complex that catalyzes the synthesis of ATP during oxidative phosphorylation
ATP5H	SW:ATPQ_HUMAN	ATP5H	18	-0.569	3	2.67	0.53	SW:ATPQ_HUMAN O75947 homo sapiens (human). atp synthase d chain, mitochondrial (ec 3.6.1.34). 5/2000 [MASS=18360]/Protein with high similarity to subunit d of the mitochondrial H(+)-ATP synthase (rat Atp5jd), which is part of a multisubunit enzyme that catalyzes the synthesis of ATP during oxidative phosphorylation
NI = Not Identified								