(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau

(43) International Publication Date
30 May 2003 (30.05.2003)

PCT

(10) International Publication Number
WO 2003/043580 A3

(51) International Patent Classification[7]: G01N 33/48, 33/50, G06F 19/00

(21) International Application Number: PCT/US2002/037146

(22) International Filing Date: 19 November 2002 (19.11.2002)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
60/331,701 19 November 2001 (19.11.2001) US

(71) Applicant *(for all designated States except US)*: **PROTEOLOGICS, INC.** [US/US]; 40 Ramland Road South, Suite 10, Orangeburg, NY 10962 (US).

(72) Inventors; and

(75) Inventors/Applicants *(for US only)*: **GREENER, Tsvika** [IL/IL]; Hahavazelet 9a, Ness-Ziona (IL). **LEVY, Avishai** [IL/IL]; Nordau 73, 75319 Rishon-Le-Zion (IL). **REISS, Yuval** [IL/IL]; Hahavazelet 11/6, Kiriat-Ono (IL). **BEN-AVRAHAM, Danny** [IL/IL]; Mahal 60, Tel-Aviv (IL). **ALROY, Iris** [IL/IL]; Hashirion Street 10, Apt. 17, 74065 Nes Ziona (IL).

(74) Agents: **VARMA, Anita** et al.; Ropes & Gray, One International Place, Boston, MA 02110-2624 (US).

(81) Designated States *(national)*: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW.

(84) Designated States *(regional)*: ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

Published:
— *with international search report*

(88) Date of publication of the international search report: 15 April 2004

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(54) Title: METHODS FOR IDENTIFYING AND VALIDATING POTENTIAL DRUG TARGETS

(57) Abstract: This application provides methods for identifying and validating potential drug targets. In one aspect, the application provides a systematic method of creating a database of related protein or nucleic acid sequences with annotations of the potential disease associations of the sequences; and a method for testing the potential disease associations by means of a biological assay and validating the disease association by either decreasing expression of the sequence of interest or increasing expression of the sequence of interest.

WO 2003/043580 A3

Methods for Identifying and Validating Potential Drug Targets

RELATED APPLICATIONS

This application claims the benefit of the filing date of U.S. Provisional Application No. 60/331,701, filed November 19, 2001, the specification of which is hereby incorporated by reference in its entirety.

BACKGROUND OF THE INVENTION

Potential drug target validation involves determining whether a DNA, RNA or protein molecule is implicated in a disease process and is therefore a suitable target for development of new therapeutic drugs. Drug discovery, the process by which bioactive compounds are identified and characterized, is a critical step in the development of new treatments for human diseases. The landscape of drug discovery has changed dramatically due to the genomics revolution. DNA and protein sequences are yielding a host of new drug targets and an enormous amount of associated information.

The task of deciphering which of these targets are implicated in diseases and should be used for subsequent drug development requires the development of not only systematic procedures but also high-throughput approaches for determining which targets are a part of disease relevant pathways are critical to the drug discovery process.

The levels of proteins are determined by the balance between their rates of synthesis and degradation. The ubiquitin-mediated proteolysis is the major pathway for the selective degradation of intracellular proteins. Consequently, selective ubiquitination of a variety of intracellular targets regulates essential cellular functions such as gene expression, cell cycle, signal transduction, biogenesis of ribosomes and DNA repair. Another major function of ubiquitin ligation is to regulate intracellular protein sorting. Whereas poly-ubiquitination targets proteins to proteasome-mediated degradation, attachment of a single ubiquitin molecule (mono-ubiquitination) to proteins regulates endocytosis of cell surface receptors and sorting into lysosomes. It was also demonstrated that ubiquitination controls sorting of proteins in the trans-golgi (TGN).

The linkage of ubiquitin to a substrate protein is generally carried out by three classes of accessory enzymes in a sequential reaction. Ubiquitin activating enzymes (E1) activate ubiquitin by forming a high energy thiol ester intermediate. Activation of the C-terminal Gly of ubiquitin by E1, is followed by the activity of a ubiquitin conjugating enzyme E2 which serves as a carrier of the activated thiol ester form of ubiquitin during the transfer of ubiquitin directly to the third enzyme, E3 ubiquitin protein ligase. E3 ubiquitin protein ligase is responsible for the final step in the conjugation process which results in the formation of an isopeptide bond between the activated Gly residue of ubiquitin, and an .alpha.-NH group of a Lys residue in the substrate or a previously conjugated ubiquitin moiety. See, e.g., Hochstrasser, M., Ubiquitin-Dependent Protein Degradation, Annu. Rev. Genet., 30:405 (1996).

E3 ubiquitin protein ligase, as the final player in the ubiquitination process, is responsible for target specificity of ubiquitin-dependent proteolysis. A number of E3 ubiquitin-protein ligases have previously been identified. See, e.g., D'Andrea, A. D., et al., Nature Genetics, 18:97 (1998); Gonen, H., et al., Isolation, Characterization, and Purification of a Novel Ubiquitin-Protein Ligase, E3-Targeting of Protein Substrates via Multiple and Distinct Recognition Signals and Conjugating Enzymes, J. Biol. Chem., 271:302 (1996). Accordingly, E3 enzymes are potential drug targets and this application provides a systematic method for identifying and validating potential E3 drug targets.

SUMMARY

In one aspect, the application provides a systematic method of creating a database of related protein or nucleic acid sequences with annotations of the potential disease associations of the sequences; and a method for testing the potential disease associations by means of a biological assay and validating the disease association by either decreasing expression of the sequence of interest or increasing expression of the sequence of interest.

In one aspect, the application provides a method of testing and validating potential drug targets. In one aspect the application provides a method of creating a comprehensive database of related protein and/or nucleic acid sequences; i.e., the

protein and nucleic acid sequences are included in the database based upon certain sequence information, structural and/or functional information. In one aspect, the application provides sequences that are sorted based upon sequence, structural, functional, and biological activity. The sequences may be further clustered based upon potential disease association; such as for example, the presence or absence of certain domains may be indicative of potential disease correlations of that protein or nucleic acid sequence. The database further comprises annotations indicating the relevant disease correlations.

The sequences so clustered may be tested for the potential associated disease correlations by means of biological assays. For example, if the associated disease is viral infection, a biological assay may be assaying for the release of virus like particles; if the disease is a proliferative disease the biological assay may be determining the rate of proliferation of the diseased cells. In another aspect, the associated disease may be a ubiquitin-mediated disorder and the assay may determine an aspect of protein degradation, protein trafficking, or cellular localization of proteins. In other embodiments, the assay may be determining any disease characteristic of the associated disease by means of the biological assay.

In another aspect, the application provides methods of validating the disease associations by decreasing the expression of the sequence of interest and determining the effect of such a decrease by means of a biological assay. In one embodiment, if the associated disease is a viral infection, the effect of decreasing expression of the sequence of interest on the release of the virus like particles is determined. Thus, if decreasing the expression of the sequence of interest results in a decrease in the release of the virus like particles the sequence may be a potential drug target for viral infection. Similarly, if decreasing the expression of the sequence of interest results in a decrease in the rate of proliferation of a diseased cell such as a tumor cell the sequence may be a potential drug target for proliferative disorders. Thus, if decreasing the expression alters any disease characteristic of the associated disease, the sequence may be a potential drug target for the associated disease.

In another embodiment, the application provides methods for validating the disease associations by increasing the expression of the sequence of interest. For

example, if the sequence of interest is a tumor suppressor increasing expression of the sequence may alter a disease characteristic of an associated disease. In other embodiments, the application provides additional drug targets such as the substrates of various enzymes such as the E3 proteins, wherein either increasing expression of the ligase or decreasing expression of its substrate may alter a disease characteristic of the associated disease. For example, the tumor suppressor von Hippel-Lindau is associated with certain E3-associated diseases; increasing expression of the von Hippel-Lindau gene or decreasing expression of its substrate would alter at least one disease characteristic of the E3 associated disease. Accordingly, in one aspect, the substrate may be a potential drug target for the E3-associated disease.

In one aspect, this invention provides a method of identifying a potential human E3 drug target comprising providing a database comprising human E3 nucleic acid or protein sequences. These sequences are sorted based on their structural and functional attributes providing an E3-associated disease specific database. The potential involvement of E3's in disease is assessed by the criteria which include the following:

1. An E3 that might interact with proteins whose modification by ubiquitin and/or abnormal degradation are the cause for a disease/pathological condition.

2. Potential E3's will be selected from E3's that contain specific structural domains and or motifs that are likely to interact with a specific domains/motifs on the interacting protein.

3. An E3, the cellular localization of which suggests possible interaction with an interacting protein.

4. Abnormal expression of an individual E3 that correlates with a disease/pathological condition.

5. Abnormal activity (due to a mutation or abnormal regulation) of an E3 that is associated with a disease or a pathological condition.

Once the E3 sequences are sorted based upon either their structural attributes or their E3 disease-associations, this invention provides assays for measuring a disease characteristic of said E3-associated disease; for example, such disease characteristics include determining the release of viral like particles from infected cells or cells transfected with plasmids containing a nucleic acid sequence encoding

for non infectious viral DNA (e.g. HIV-VLP, VP40 etc'), determining the differential expression of said E3s in a normal cells in comparison to a cell exhibiting at least one symptom of a E3-associated disease etc. Upon identifying a potential E3 target that is implicated in an E3-associated disease, the expression of said E3 is altered, i.e., either increased or decreased to determine whether the change in expression results in a change in the output of the assay.

In another aspect, this invention provides a database comprising human E3 nucleic acid or protein sequences and determining the differential expression of said human E3 in a cell exhibiting disease characteristics of an E3 associated disease and a corresponding normal cell. The expression of said E3 is then altered to determine the effect of decreased E3 expression on said cell exhibiting disease characteristics of an E3 associated disease, wherein a change in said disease characteristics is indicative that said human E3 is a potential drug target for said E3 associated disease.

Identification of potential E3 drug targets provides a means assaying for effective therapeutics.

BRIEF DESCRIPTION OF THE DRAWINGS

FIG. 1 is a flow-chart of a process for identifying human E3 proteins that may be involved in diseases or other biological processes of interest.

FIG. 2 is a flow-diagram illustrating creation of a database of human E3 proteins.

FIG. 3 provides an exemplary schematic representation of some of the E3-domains present in the E3 proteins.

Figure 4 shows results from a screen to identify E3 proteins that are drug targets for the treatment of HIV and related viruses. A Virus-Like Particle (VLP) Assay was used. The figure shows viral proteins in the cellular fraction (top panel) and in released VLPs (bottom panel). The VLP assay was performed with a wild-type viral p6 protein and a mutant p6 protein as positive and negative controls,

respectively. siRNA knockdowns of various mRNAs were tested for effects on VLP production. Knockdown of POSH resulted in complete or near-complete inhibition of VLP production.

Figure 5 shows a pulse-chase VLP experiment comparing the kinetics of VLP production in normal (WT) VLP assay conditions and in a POSH knockdown (POSH + WT). siRNA knockdown of POSH results in complete or near-complete inhibition of VLP production.

DETAILED DESCRIPTION

Definitions

As used herein, the following terms and phrases shall have the meanings set forth below. Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood to one of ordinary skill in the art to which this invention belongs.

The singular forms "a," "an," and "the" include plural reference unless the context clearly dictates otherwise.

The phrase "a corresponding normal cell of" or "normal cell corresponding to" or "normal counterpart cell of" a diseased cell refers to a normal cell of the same type as that of the diseased cell. For example, a corresponding normal cell of a B lymphoma cell is a B cell.

An "address" on an array, e.g., a microarray, refers to a location at which an element, e.g., an oligonucleotide, is attached to the solid surface of the array.

The term "antibody" as used herein is intended to include whole antibodies, e.g., of any isotype (IgG, IgA, IgM, IgE, etc), and includes fragments thereof which are also specifically reactive with a vertebrate, e.g., mammalian, protein. Antibodies can be fragmented using conventional techniques and the fragments screened for utility in the same manner as described above for whole antibodies. Thus, the term includes segments of proteolytically-cleaved or recombinantly-prepared portions of an antibody molecule that are capable of selectively reacting with a certain protein. Nonlimiting examples of such proteolytic and/or recombinant fragments include

Fab, F(ab')2, Fab', Fv, and single chain antibodies (scFv) containing a V[L] and/or V[H] domain joined by a peptide linker. The scFv's may be covalently or non-covalently linked to form antibodies having two or more binding sites. The subject invention includes polyclonal, monoclonal, or other purified preparations of antibodies and recombinant antibodies.

By "array" or "matrix" is meant an arrangement of addressable locations or "addresses" on a device. The locations can be arranged in two dimensional arrays, three dimensional arrays, or other matrix formats. The number of locations can range from several to at least hundreds of thousands. Most importantly, each location represents a totally independent reaction site. A "nucleic acid array" refers to an array containing nucleic acid probes, such as oligonucleotides or larger portions of genes. The nucleic acid on the array is preferably single stranded. Arrays wherein the probes are oligonucleotides are referred to as "oligonucleotide arrays" or "oligonucleotide chips." A "microarray," also referred to herein as a "biochip" or "biological chip" is an array of regions having a density of discrete regions of at least about 100/cm^2, and preferably at least about 1000/cm^2. The regions in a microarray have typical dimensions, e.g., diameters, in the range of between about 10-250 μm, and are separated from other regions in the array by about the same distance.

The term "associated disease" as used herein refers to a disease that is correlated to a certain nucleic acid or protein sequence because of the presence or absence of certain sequence information, structural or functional information, and/or biological activity of that nucleic acid or protein sequence.

The term "biological sample", as used herein, refers to a sample obtained from an organism or from components (e.g., cells) of an organism. The sample may be of any biological tissue or fluid. Frequently the sample will be a "clinical sample" which is a sample derived from a patient. Such samples include, but are not limited to, sputum, blood, blood cells (e.g., white cells), tissue or fine needle biopsy samples, urine, peritoneal fluid, and pleural fluid, or cells therefrom. Biological samples may also include sections of tissues such as frozen sections taken for histological purposes.

The term "biomarker" of a disease refers to a gene which is up- or down-regulated in a diseased cell of a subject having the disease relative to a counterpart normal cell, which gene is sufficiently specific to the diseased cell that it can be used, optionally with other genes, to identify or detect the disease. Generally, a biomarker is a gene that is characteristic of the disease.

A nucleotide sequence is "complementary" to another nucleotide sequence if each of the bases of the two sequences match, i.e., are capable of forming Watson-Crick base pairs. The term "complementary strand" is used herein interchangeably with the term "complement." The complement of a nucleic acid strand can be the complement of a coding strand or the complement of a non-coding strand.

The phrases "conserved residue" "or conservative amino acid substitution" refer to grouping of amino acids on the basis of certain common properties. A functional way to define common properties between individual amino acids is to analyze the normalized frequencies of amino acid changes between corresponding proteins of homologous organisms (Schulz, G. E. and R. H. Schirmer., Principles of Protein Structure, Springer-Verlag). According to such analyses, groups of amino acids may be defined where amino acids within a group exchange preferentially with each other, and therefore resemble each other most in their impact on the overall protein structure (Schulz, G. E. and R. H. Schirmer., Principles of Protein Structure, Springer-Verlag). Examples of amino acid groups defined in this manner include:

(i) a charged group, consisting of Glu and Asp, Lys, Arg and His,

(ii) a positively-charged group, consisting of Lys, Arg and His,

(iii) a negatively-charged group, consisting of Glu and Asp,

(iv) an aromatic group, consisting of Phe, Tyr and Trp,

(v) a nitrogen ring group, consisting of His and Trp,

(vi) a large aliphatic nonpolar group, consisting of Val, Leu and Ile,

(vii) a slightly-polar group, consisting of Met and Cys,

(viii) a small-residue group, consisting of Ser, Thr, Asp, Asn, Gly, Ala, Glu, Gln and Pro,

(ix) an aliphatic group consisting of Val, Leu, Ile, Met and Cys, and

(x) a small hydroxyl group consisting of Ser and Thr.

In addition to the groups presented above, each amino acid residue may form its own group, and the group formed by an individual amino acid may be referred to simply by the one and/or three letter abbreviation for that amino acid commonly used in the art.

The term "derivative" refers to the chemical modification of a polypeptide sequence, or a polynucleotide sequence. Chemical modifications of a polynucleotide sequence can include, for example, replacement of hydrogen by an alkyl, acyl, or amino group. A derivative polynucleotide encodes a polypeptide which retains at least one biological or immunological function of the natural molecule. A derivative polypeptide is one modified by glycosylation, pegylation, or any similar process that retains at least one biological or immunological function of the polypeptide from which it was derived.

"Differential gene expression pattern" between cell A and cell B refers to a pattern reflecting the differences in gene expression between cell A and cell B. A differential gene expression pattern can also be obtained between a cell at one time point and a cell at another time point, or between a cell incubated or contacted with a compound and a cell that was not incubated with or contacted with the compound.

The term "domain" as used herein refers to a region within a protein that comprises a particular structure or function different from that of other sections of the molecule.

A "HECT domain" or "HECT" is a protein also known as "HECTC" domain involved in E3 ubiquitin ligase activity. Certain HECT domains are 100 - 400 amino acids in length and comprise an amino acid sequence as set forth in the following consensus sequence (amino acid nomenclature is as set forth in Table 1): Pro Xaa3 Thr Cys Xaa2-4 Leu Xaa Leu Pro Xaa Tyr (SEQ ID NO: 1).

E3 as used herein refers to a nucleic acid or encoded protein that is involved with substrate recognition in ubiquitin-mediated proteolysis, in membrane trafficking and protein sorting. Ubiquitin-mediated proteolysis is the major pathway for the selective , controlled degradation of intracellular proteins in eukayotic cells. E3 proteins include one or more of the following exemplary domains and/or motifs: HECT, RING, F-BOX, U-BOX, PHD, etc.

"E3-associated Disease" refers to any disease wherein: (1) an E3 that interacts with interacting proteins whose modification by ubiquitin and/or abnormal degradation are the cause for a disease/pathological condition; (2) an E3 protein is implicated in interacting with a specific domains/motifs such as a domain of an interacting protein such as the late domain of a viral protein, thereby resulting in viral infectivity; (3) an E3, the cellular localization of which suggests possible interaction with an Interacting protein that may cause a disease or pathological condition; (4) differential expression of an E3 gene and or protein correlates with a disease/pathological condition: and (5) aberrant activity (due to a mutation or abnormal regulation) of an E3 that is associated with a disease or a pathological condition. Exemplary E-associated diseases include but are not limited to viral infections, preferably retroviral infections such as HIV, Ebola, CMV, etc., various cancers such as breast, lung, renal carcinoma, etc., cystic fibrosis, and certain diseases of the CNS such as autosomal recessive juvenile parkinsonism.

A "disease characteristic" as used herein refers any one or more of the following: any phenotype that is distinctive of a disease state or any artificial phenotype that is a proxy for a phenotype that is distinctive of a disease state, or that distinguishes a diseased cell from a normal cell.

"A diseased cell of an associated disease" refers to a cell present in subjects having an associated diseases D, which cell is a modified form of a normal cell and is not present in a subject not having disease D, or which cell is present in significantly higher or lower numbers in subjects having disease D relative to subjects not having disease D. For example, a diseased cell may be a cancerous cell.

"A diseased cell of an E3-associated disease" refers to a cell present in subjects having an E3-associated diseases D', which cell is a modified form of a normal cell and is not present in a subject not having disease D', or which cell is present in significantly higher or lower numbers in subjects having disease D' relative to subjects not having disease D'. For example, a diseased cell may be a cell infected with a virus or a cancerous cell.

The term "drug target" refers to any gene or gene product (e.g. RNA or polypeptide) with implications in an associated disease or disorder. Examples

include various proteins such as enzymes, oncogenes and their polypeptide products, and cell cycle regulatory genes and their polypeptide products. In one aspect, the drug target may be an E3.

The term "expression profile," which is used interchangeably herein with "gene expression profile" and "finger print" of a cell refers to a set of values representing mRNA levels of 20 or more genes in a cell. An expression profile preferably comprises values representing expression levels of at least about 30 genes, preferably at least about 50, 100, 200 or more genes. Expression profiles preferably comprise an mRNA level of a gene which is expressed at similar levels in multiple cells and conditions, e.g., GAPDH. For example, an expression profile of a diseased cell of an E3-associated disease D' refers to a set of values representing mRNA levels of 20 or more genes in a diseased cell.

The term "heterozygote," as used herein, refers to an individual with different alleles at corresponding loci on homologous chromosomes. Accordingly, the term "heterozygous," as used herein, describes an individual or strain having different allelic genes at one or more paired loci on homologous chromosomes.

The term "homozygote," as used herein, refers to an individual with the same allele at corresponding loci on homologous chromosomes. Accordingly, the term "homozygous," as used herein, describes an individual or a strain having identical allelic genes at one or more paired loci on homologous chromosomes.

"Hybridization" refers to any process by which a strand of nucleic acid binds with a complementary strand through base pairing. Two single-stranded nucleic acids "hybridize" when they form a double-stranded duplex. The region of double-strandedness can include the full-length of one or both of the single-stranded nucleic acids, or all of one single stranded nucleic acid and a subsequence of the other single stranded nucleic acid, or the region of double-strandedness can include a subsequence of each nucleic acid. Hybridization also includes the formation of duplexes which contain certain mismatches, provided that the two strands are still forming a double stranded helix. "Stringent hybridization conditions" refers to hybridization conditions resulting in essentially specific hybridization.

The term "interact" as used herein is meant to include detectable relationships or association (e.g. biochemical interactions) between molecules, such as interaction between protein-protein, protein-nucleic acid, nucleic acid-nucleic acid, and protein-small molecule or nucleic acid-small molecule in nature.

The term "Interacting Protein" refers to protein capable of interacting, binding, and/or otherwise associating to a protein of interest, such as for example a human E3 protein. Examples of these proteins include for example the "Late domain" or "L domain", which is a small portion of a Gag protein that promotes efficient release of virion particles from the membrane of the host cell. L domains typically comprise one or more short motifs (L motifs). Exemplary sequences include: PTAPPEE, PTAPPEY, P(T/S)AP, PxxL, PPxY (eg. PPPY), YxxL (eg. YPDL), PxxP.

The term "isolated" as used herein with respect to nucleic acids, such as DNA or RNA, refers to molecules separated from other DNAs, or RNAs, respectively, that are present in the natural source of the macromolecule. The term isolated as used herein also refers to a nucleic acid or peptide that is substantially free of cellular material, viral material, or culture medium when produced by recombinant DNA techniques, or chemical precursors or other chemicals when chemically synthesized. Moreover, an "isolated nucleic acid" is meant to include nucleic acid fragments which are not naturally occurring as fragments and would not be found in the natural state. The term "isolated" is also used herein to refer to polypeptides which are isolated from other cellular proteins and is meant to encompass both purified and recombinant polypeptides.

As used herein, the terms "label" and "detectable label" refer to a molecule capable of detection, including, but not limited to, radioactive isotopes, fluorophores, chemiluminescent moieties, enzymes, enzyme substrates, enzyme cofactors, enzyme inhibitors, dyes, metal ions, ligands (e.g., biotin or haptens) and the like. The term "fluorescer" refers to a substance or a portion thereof which is capable of exhibiting fluorescence in the detectable range. Particular examples of labels which may be used under the invention include fluorescein, rhodamine, dansyl, umbelliferone, Texas red, luminol, NADPH, alpha - beta -galactosidase and horseradish peroxidase.

The "level of expression of a gene in a cell" refers to the level of mRNA, as well as pre-mRNA nascent transcript(s), transcript processing intermediates, mature mRNA(s) and degradation products, encoded by the gene in the cell.

The phrase "normalizing expression of a gene" in a diseased cell refers to a means for compensating for the altered expression of the gene in the diseased cell, so that it is essentially expressed at the same level as in the corresponding non diseased cell. For example, where the gene is over-expressed in the diseased cell, normalization of its expression in the diseased cell refers to treating the diseased cell in such a way that its expression becomes essentially the same as the expression in the counterpart normal cell. "Normalization" preferably brings the level of expression to within approximately a 50% difference in expression, more preferably to within approximately a 25%, and even more preferably 10% difference in expression. The required level of closeness in expression will depend on the particular gene, and can be determined as described herein.

The phrase "normalizing gene expression in a diseased cell" refers to a means for normalizing the expression of essentially all genes in the diseased cell.

As used herein, the term "nucleic acid" refers to polynucleotides such as deoxyribonucleic acid (DNA), and, where appropriate, ribonucleic acid (RNA). The term should also be understood to include, as equivalents, analogs of either RNA or DNA made from nucleotide analogs, and, as applicable to the embodiment being described, single (sense or antisense) and double-stranded polynucleotides. ESTs, chromosomes, cDNAs, mRNAs, and rRNAs are representative examples of molecules that may be referred to as nucleic acids.

The term "percent identical" refers to sequence identity between two amino acid sequences or between two nucleotide sequences. Identity can each be determined by comparing a position in each sequence which may be aligned for purposes of comparison. When an equivalent position in the compared sequences is occupied by the same base or amino acid, then the molecules are identical at that position; when the equivalent site occupied by the same or a similar amino acid residue (e.g., similar in steric and/or electronic nature), then the molecules can be referred to as homologous (similar) at that position. Expression as a percentage of

homology, similarity, or identity refers to a function of the number of identical or similar amino acids at positions shared by the compared sequences. Various alignment algorithms and/or programs may be used, including Hidden Markov Model (HMM), FASTA and BLAST. HMM, FASTA and BLAST are available through the National Center for Biotechnology Information, National Library of Medicine, National Institutes of Health, Bethesda, Md. and the European Bioinformatic Institute EBI. In one embodiment, the percent identity of two sequences can be determined by these GCG programs with a gap weight of 1, e.g., each amino acid gap is weighted as if it were a single amino acid or nucleotide mismatch between the two sequences. Other techniques for alignment are described in Methods in Enzymology, vol. 266: Computer Methods for Macromolecular Sequence Analysis (1996), ed. Doolittle, Academic Press, Inc., a division of Harcourt Brace & Co., San Diego, California, USA. Preferably, an alignment program that permits gaps in the sequence is utilized to align the sequences. The Smith-Waterman is one type of algorithm that permits gaps in sequence alignments. *See* Meth. Mol. Biol. 70: 173-187 (1997). Also, the GAP program using the Needleman and Wunsch alignment method can be utilized to align sequences. More techniques and algorithms including use of the HMM are describe in Sequence, Structure, and Databanks: A Practical Approach (2000), ed. Oxford University Press, Incorporated. In Bioinformatics: Databases and Systems (1999) ed. Kluwer Academic Publishers. An alternative search strategy uses MPSRCH software, which runs on a MASPAR computer. MPSRCH uses a Smith-Waterman algorithm to score sequences on a massively parallel computer. This approach improves ability to pick up distantly related matches, and is especially tolerant of small gaps and nucleotide sequence errors. Nucleic acid-encoded amino acid sequences can be used to search both protein and DNA databases. Databases with individual sequences are described in Methods in Enzymology, ed. Doolittle, *supra*. Databases include Genbank, EMBL, and DNA Database of Japan (DDBJ).

"Perfectly matched" in reference to a duplex means that the poly- or oligonucleotide strands making up the duplex form a double stranded structure with one other such that every nucleotide in each strand undergoes Watson-Crick basepairing with a nucleotide in the other strand. The term also comprehends the

pairing of nucleoside analogs, such as deoxyinosine, nucleosides with 2-aminopurine bases, and the like, that may be employed. A mismatch in a duplex between a target polynucleotide and an oligonucleotide or olynucleotide means that a pair of nucleotides in the duplex fails to undergo Watson-Crick bonding. In reference to a triplex, the term means that the triplex consists of a perfectly matched duplex and a third strand in which every nucleotide undergoes Hoogsteen or reverse Hoogsteen association with a basepair of the perfectly matched duplex.

As used herein, a nucleic acid or other molecule attached to an array, is referred to as a "probe" or "capture probe." When an array contains several probes corresponding to one gene, these probes are referred to as "gene-probe set." A gene-probe set can consist of, e.g., 2 to 10 probes, preferably from 2 to 5 probes and most preferably about 5 probes.

The "profile" of a cell's biological state refers to the levels of various constituents of a cell that are known to change in response to drug treatments and other perturbations of the cell's biological state. Constituents of a cell include levels of RNA, levels of protein abundances, or protein activity levels.

The term "protein" is used interchangeably herein with the terms "peptide" and "polypeptide."

An expression profile in one cell is "similar" to an expression profile in another cell when the level of expression of the genes in the two profiles are sufficiently similar that the similarity is indicative of a common characteristic, e.g., being one and the same type of cell. Accordingly, the expression profiles of a first cell and a second cell are similar when at least 75% of the genes that are expressed in the first cell are expressed in the second cell at a level that is within a factor of two relative to the first cell.

An "RCC1 domain" is a domain that interacts with small GTPases to promote loss of GDP and binding of GTP. Certain RCC1 domains are about 50-60 amino acids in length. Often RCC1 domains are found in a series of repeats. The first RCC1 domain was identified in a protein called "Regulator of Chromosome Condensation" (RCC1), which interacts with the small GTPase Ran. In the RCC1 protein, a series of seven tandem repeats of a domain of about 50 - 60 amino acids

fold to form a beta-propeller structure (Renault et al. *Nature* 1998 392:9-101). RCC1 domains are known to interact with other types of small GTPases including members of the Arf, Rab, Rac and Rho families.

The term "recombinant protein" refers to a protein of the present invention which is produced by recombinant DNA techniques, wherein generally DNA encoding the expressed protein is inserted into a suitable expression vector which is in turn used to transform a host cell to produce the heterologous protein. Moreover, the phrase "derived from", with respect to a recombinant gene encoding the recombinant protein is meant to include within the meaning of "recombinant protein" those proteins having an amino acid sequence of a native protein, or an amino acid sequence similar thereto which is generated by mutations including substitutions and deletions of a naturally occurring protein.

A "RING domain", "Ring Finger" or "RING" is a zinc-binding domain also known as "ZF-C2HC4" with a defined octet of cysteine and histidine residues. Certain RING domains comprise the consensus sequences as set forth below (amino acid nomenclature is as set forth in Table 1): Cys Xaa Xaa Cys Xaa_{10-20} Cys Xaa His Xaa_{2-5} Cys Xaa Xaa Cys Xaa_{13-50} Cys Xaa Xaa Cys (SEQ ID NO: 2) or Cys Xaa Xaa Cys Xaa_{10-20} Cys Xaa His Xaa_{2-5} His Xaa Xaa Cys Xaa_{13-50} Cys Xaa Xaa Cys (SEQ ID NO: 3). Preferred RING domains of the invention bind to various protein partners to form a complex that has ubiquitin ligase activity. RING domains preferably interact with at least one of the following protein types: F box proteins, E2 ubiquitin conjugating enzymes and cullins.

The term "RNA interference", "RNAi" or "siRNA" are all refers to any method by which expression of a gene or gene product is decreased by introducing into a target cell one or more double-stranded RNAs which are homologous to the gene of interest (particularly to the messenger RNA of the gene of interest).

As used herein, the term "transfection" means the introduction of a nucleic acid, e.g., via an expression vector, into a recipient cell by nucleic acid-mediated gene transfer.

"Transformation", as used herein, refers to a process in which a cell's genotype is changed as a result of the cellular uptake of exogenous DNA or RNA, and, for example, the transformed cell expresses a recombinant form of a

polypeptide or, in the case of anti-sense expression from the transferred gene, the expression of a naturally-occurring form of the polypeptide is disrupted.

As used herein, the term "transgene" means a nucleic acid sequence (encoding, e.g., one of the target nucleic acids, or an antisense transcript thereto) which has been introduced into a cell. A transgene could be partly or entirely heterologous, i.e., foreign, to the transgenic animal or cell into which it is introduced, or, is homologous to an endogenous gene of the transgenic animal or cell into which it is introduced, but which is designed to be inserted, or is inserted, into the animal's genome in such a way as to alter the genome of the cell into which it is inserted (e.g., it is inserted at a location which differs from that of the natural gene or its insertion results in a knockout). A transgene can also be present in a cell in the form of an episome. A transgene can include one or more transcriptional regulatory sequences and any other nucleic acid, such as introns, that may be necessary for optimal expression of a selected nucleic acid.

The term "treating" a disease in a subject or "treating" a subject having a disease refers to subjecting the subject to a pharmaceutical treatment, e.g., the administration of a drug, such that at least one symptom of the disease is decreased.

The term "Ubiquitin-mediated disorder" as used herein refers to a disorder resulting from an abnormal Ubiquitin-mediated cellular process such as for example ubiquitin-mediated degradation, protein trafficking, and or protein sorting.

The term "Unigene" or "unigene cluster" refers to an experimental system for automatically partitioning Genbank sequences into a non-redundant set of Unigene clusters. Each Unigene cluster contains sequences that represent a unique gene, as well as related information such as the tissue types in which the gene has been expressed and map location. In addition, to well characterized genes, EST sequences are also included in these clusters. Such clusters may be downloaded from ftp://ncbi.nlm.nih.gov/ repository/Unigene/.

The phrase "value representing the level of expression of a gene" refers to a raw number which reflects the mRNA level of a particular gene in a cell or biological sample, e.g., obtained from experiments for measuring RNA levels.

A "variant" of polypeptide X refers to a polypeptide having the amino acid sequence of peptide X in which is altered in one or more amino acid residues. The variant may have "conservative" changes, wherein a substituted amino acid has similar structural or chemical

properties (e.g., replacement of leucine with isoleucine). More rarely, a variant may have "nonconservative" changes (e.g., replacement of glycine with tryptophan). Analogous minor variations may also include amino acid deletions or insertions, or both. Guidance in determining which amino acid residues may be substituted, inserted, or deleted without abolishing biological or immunological activity may be found using computer programs well known in the art, for example, LASERGENE software (DNASTAR).

The term "variant," when used in the context of a polynucleotide sequence, may encompass a polynucleotide sequence related to that of gene X or the coding sequence thereof. This definition may also include, for example, "allelic," "splice," "species," or "polymorphic" variants. A splice variant may have significant identity to a reference molecule, but will generally have a greater or lesser number of polynucleotides due to alternate splicing of exons during mRNA processing. The corresponding polypeptide may possess additional functional domains or an absence of domains. Species variants are polynucleotide sequences that vary from one species to another. The resulting polypeptides generally will have significant amino acid identity relative to each other. A polymorphic variant is a variation in the polynucleotide sequence of a particular gene between individuals of a given species. Polymorphic variants also may encompass "single nucleotide polymorphisms" (SNPs) in which the polynucleotide sequence varies by one base. The presence of SNPs may be indicative of, for example, a certain population, a disease state, or a propensity for a disease state.

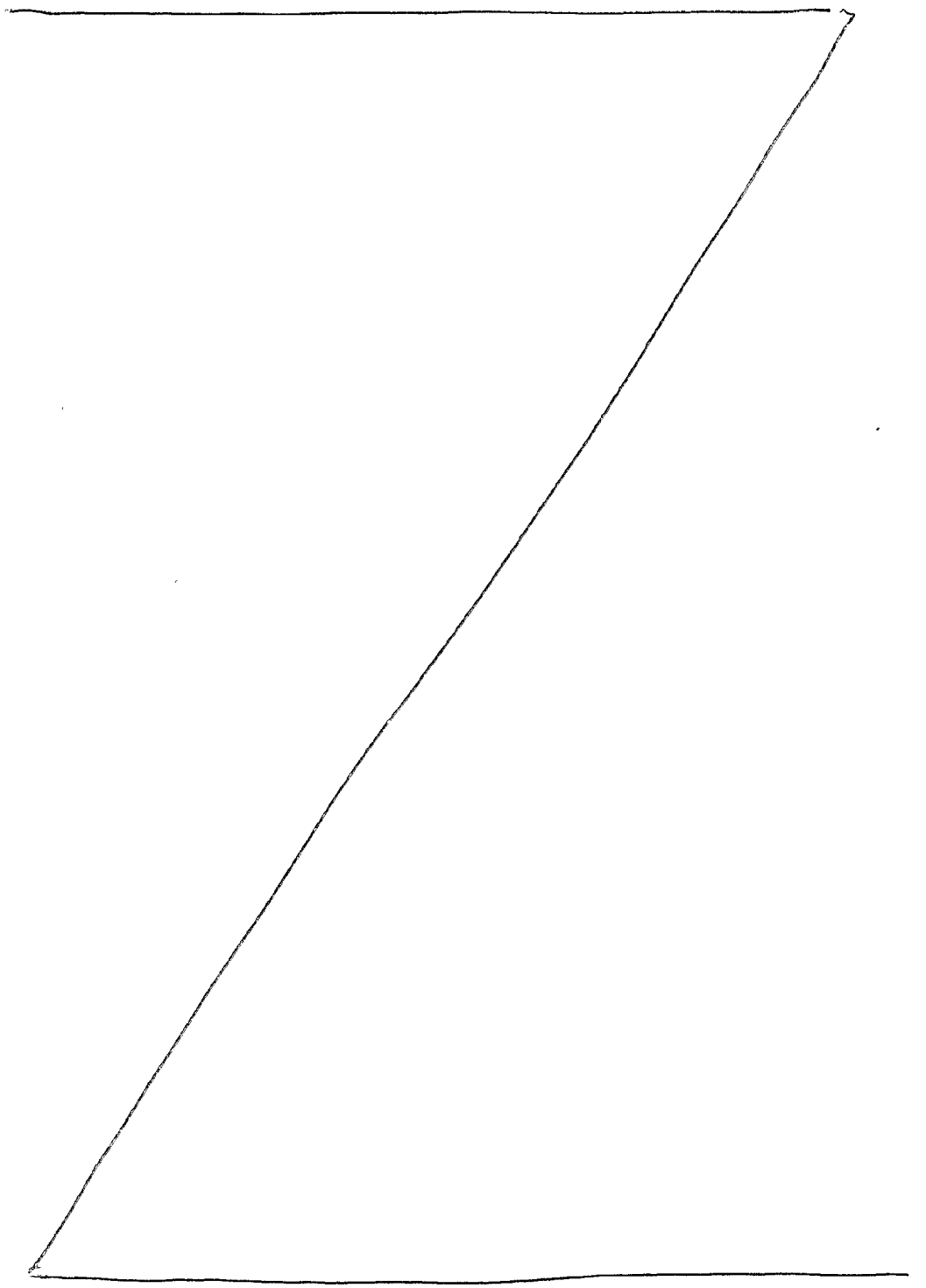
A "WW Domain" is a small functional domain found in a large number of proteins from a variety of species including humans, nematodes, and yeast. WW domains are approximately 30 to 40 amino acids in length. Certain WW domains may be defined by the following consensus sequence (Andre and Springael, 1994, Biochem. Biophys. Res. Comm. 205:1201-1205) (amino acid nomenclature is as set forth in Table 1): Trp Xaa_{6-9} Gly Xaa_{1-3} X4 X4 Xaa_{4-6} X1 X8 Trp Xaa_2 Pro (SEQ ID

NO: 4). In certain instances a WW domain will be flanked by stretches of amino acids rich in histidine or cysteine. In some cases, the amino acids in the center of WW domains are quite hydrophobic. Preferred WW domains bind to the L domains of retroviral Gag proteins. Particularly preferred WW domains bind to an amino acid sequence of ProProXaaTyr (SEQ ID NO: 5).

*Table 1: Abbreviations for classes of amino acids**

Symbol	**Category**	**Amino Acids Represented**
X1	Alcohol	Ser, Thr
X2	Aliphatic	Ile, Leu, Val
Xaa	Any	Ala, Cys, Asp, Glu, Phe, Gly, His, Ile, Lys, Leu, Met, Asn, Pro, Gln, Arg, Ser, Thr, Val, Trp, Tyr
X4	Aromatic	Phe, His, Trp, Tyr
X5	Charged	Asp, Glu, His, Lys, Arg
X6	Hydrophobic	Ala, Cys, Phe, Gly, His, Ile, Lys, Leu, Met, Thr, Val, Trp, Tyr
X7	Negative	Asp, Glu
X8	Polar	Cys, Asp, Glu, His, Lys, Asn, Gln, Arg, Ser, Thr
X9	Positive	His, Lys, Arg
X10	Small	Ala, Cys, Asp, Gly, Asn, Pro, Ser, Thr, Val
X11	Tiny	Ala, Gly, Ser
X12	Turnlike	Ala, Cys, Asp, Glu, Gly, His, Lys, Asn, Gln, Arg, Ser, Thr
X13	Asparagine-Aspartate	Asn, Asp

* Abbreviations as adopted from http://smart.embl-heidelberg.de/SMART_DATA/alignments/consensus/grouping.html.



Creating a Database In one aspect the application provides a method of creating a comprehensive database of related protein and/or nucleic acids; i.e., the protein and nucleic acid sequences are included in the database based upon certain sequence information, structural and/or functional information. In one aspect, the application provides sequences that are sorted based upon sequence, structural, functional, and biological activity. The sequences may be further clustered based upon potential disease association; such as for example, the presence or absence of certain domains may be indicative of potential disease correlations of that protein or nucleic acid sequence. The database further comprises annotations indicating the relevant disease correlations. In an illustrative example, the application provides method for creating an E3 database.

FIG. 1 illustrates a process 100 that identifies human E3 proteins and/or nucleic acid sequences that may be involved in diseases or other biological processes of interest. As shown, the process operates on data describing human protein or nucleic acid sequences. Such data may be downloaded 102 from a variety of sources such as the publicly available NCBI (National Center for Biotechnology Information) or Swiss Prot databases or from proprietary databases such as for examples the databases owned by Incyte Inc. or Celera Inc. Publicly available databases include for example, the NCBI database of human protein sequences on the World Wide Web at http://www.ncbi.nlm.nih.gov/Entrez/batch.html. and the EBI.

As shown, the process 100 may clean 104 the sequences to identify human protein sequences. For example, the process 100 may eliminate redundant sequence information. The process 100 may also eliminate sequence portions based on the polypeptide length. For instance, the process 100 may eliminate polypeptides less than some specified length of amino acids (e.g., 10 or 20) or between a range of lengths (e.g., 25-30).

The process 100 then identifies 106 which sequences correspond to human E3 protein sequences. For example, the process 100 may determine whether a particular sequence exhibits one or more domains associated with E3 proteins. A domain is a recurring sequence pattern or motif. Generally, these domains have a distinct evolutionary origin and function. In particular, the human E3 proteins can

include HECT, Ubox, RING, PHD, and/or fbox domains. Based on either the domains present or other characteristics, the process 100 can associate 108 a disease or other biological activity with the E3 proteins. The E3 proteins are identified as having at least a HECT, RING, Ubox, Fbox, ZN3 or PHD domain. In certain embodiments the E3 proteins are identified as having at least a HECT or RING domain.

FIG. 2 illustrates a sample implementation 200 of this process in greater detail. As shown, the implementation 200 includes a database 202 of sequence data. Again, the database 202 may be assembled or downloaded from a variety of sources such as the National Institute of Health's (NIH) human genome databases or the EBI human genome databases. Instead of, or in addition to, protein sequences, the database 202 may also include nucleotide and/or gene sequences associated with particular proteins. The database 202 may also include sequence annotations.

Sequence analysis software 204 can identify E3 characteristics 206 indicated by the sequences. Such characteristics 206 can include domains and motifs such as RING, HECT, Ubox, Fbox, PHD domains or the PTA/SP motif. For example, the software can search for consensus sequences of particular domains/motifs. The consensus sequences for some of these exemplary motifs are set forth in the definition section provided above.

The sequence analysis software 204 discussed above may include a number of different tools. For example, the CD-Search Service provided by NCBI. This service provides a useful method of identifying conserved domains that might be present in a protein sequence. The CDD (conserved domain database) contains domains derived from two collections, Smart and Pfam. In particular, Smart (Simple Modular Architecture Research Tool) is a web-based tool for studying such domains (http://SMART.embl-heidelberg.de). It includes more than 400 domain families found in signaling, extracellular, and chromatin-associated proteins. These domains are extensively annotated with respect to phyletic distributions, functional class, tertiary structures, and functionally important residues. Similarly, Pfam (http://pfam.wustl.edu) is a large collection of multiple sequence alignments and

hidden Markov models covering common protein domains. As of August 2001, Pfam contains alignments and models for 3071 protein families.

The sequence analysis software 204 may be independently developed. Alternatively, public software may be used. For example, the process may use the Reverse Position-Specific (RPS) Blast (Basic Local Alignment Search Tool) tool. In this algorithm, a query sequence is compared to a position-specific score matrix prepared from the underlying conserved domain alignment. Hits are displayed as a pair-wise alignment of the query sequence with a representative domain sequence, or as a multiple alignment.

The characteristics 206 may also include unigene clusters. Each human E3 protein is then compared to the downloaded clusters to determine the particular cluster that it belongs to. Once the E3 protein has been matched to a cluster we determine what other proteins belong to this cluster and introduce these into the E3 database.

As shown, analysis 204 of the sequence data 202 yields a comprehensive list of E3 proteins and other related proteins 210. Such information may be organized in a database 208 such as a relational database. The database 208 may also store characteristics 212 of the different proteins such as the presence or absence of domains such as WW, RCCI, C2, Cue, SH3, SH2, and even Ubox, fbox, RING, HECT and PHD themselves. Based on these characteristics 212, software can associate the protein 210 with a disorder, disease, or other biological activity. For example, the software may access a database 216 associating different protein characteristics 218 with different biological activities 220. Needless to say, the database 208 may be constantly updated to include either new proteins 210, or other associated characteristics 212 and biological activity 220.

As can be seen from this discussion, databases comprising related sequences may be created by sorting the protein and nucleic acid sequences based on structural, functional and biological activity. As such, the related sequences may be examined for particular domains or motifs and then further clustered based on potential correlations with various associated diseases.

Biological Assays

In one aspect, the application provides methods for determining or testing whether a particular sequence may be correlated to an associated disease. In one embodiment, this application provides a means for determining whether a particular gene or encoded protein, such as an E3 gene or the encoded human E3 protein, is involved in a disease or other biological process of interest. In one aspect, the application provides functional biological assays for correlating protein and nucleic acid sequences with associated diseases or pathological conditions.

The potential involvement of a protein such as a human E3 protein in a disease or biological process of interest may be assessed using a number of methods that are known to the skilled artisan. Some exemplary methods for assessing disease correlations or the involvement of proteins in a biological process of interest, include:

I. Interaction of the proteins such as the human E3 proteins with specific domains or motifs of an Interacting Protein. It is believed that in the course of normal activities the E3 proteins will be free in the cytoplasm or associated with an intracellular organelle, such as the nucleus, the Golgi network, etc. However, during a viral infection, it is possible that certain host proteins, such as certain E3 proteins may be recruited to the cell membrane to participate in viral maturation, including ubiquitination and membrane fusion. For example, the human E3 proteins containing a HECT domain, a RING domain, and a WW or SH3 domain interact with the viral proteins such as the gag protein. In one aspect, the WW domain of the E3 proteins interacts with the late domain of the gag protein having the consensus sequence PxxY. Therefore, E3 proteins having such domains may mediate the ubiquitination of gag to facilitate viral maturation, and as such may be potential drug targets for treating viral infections, such as retroviral infections.

In a further aspect the application provides diagnostic assays for determining whether a cell is infected with a virus and for characterizing the nature, progression and/or infectivity of the infection. As a result, the detection of a E3 protein associated with the plasma membrane fraction may be indicative of a viral infection. Additionally, the presence of E3 proteins at the plasma membrane may also suggest

that the infective virus is in the process of reproducing and is therefore actively engaged in infective or lytic activity (versus a lysogenic or otherwise dormant activity).

A number of assays may be useful in studying the potential interaction of human host proteins with viral interacting proteins. For example, such an assay could involve the detection of virus like particles from cells transfected with a virus or cells infected with a virus, such as a retrovirus.

Association of the proteins of the invention, such as the E3 proteins with the plasma membrane may be detected using a variety of techniques known in the art. For example, membrane preparations may be prepared by breaking open the cells (*via* sonication or detergent lysis) and then separating the membrane components from the cytosolic fraction *via* centrifugation. Segregation of proteins into the membrane fraction can be detected with antibodies specific for the protein of interest using western blot analysis or ELISA techniques. Plasma membranes may be separated from intracellular membranes on the basis of density using density gradient centrifugation. Alternatively, plasma membranes may be obtained by chemically or enzymatically modifying the surface of the cell and affinity purifying the plasma membrane by selectively binding the modifications. An exemplary modification includes non-specific biotinylation of proteins at the cell surface. Plasma membranes may also be selected for by affinity purifying for abundant plasma membrane proteins.

Transmembrane proteins, such as the E3 proteins containing an extracellular domain can be detected using FACS analysis. For FACS analysis, whole cells are incubated with a fluorescently labeled antibody (e.g., an FITC-labelled antibody) capable of recognizing the extracellular domain of the protein of interest. The level of fluorescent staining of the cells may then be determined by FACS analyses (see e.g., Weiss and Stobo, (1984) J. Exp. Med., 160:1284-1299). Such proteins are expected to reside on intracellular membranes in uninfected cells and the plasma membrane in infected cells. FACS analysis would fail to detect an extracellular domain unless the protein is present at the plasma membrane.

Localization of the proteins of interest, such as for example the E3 proteins of the invention may also be determined using histochemical techniques. For

example, cells may be fixed and stained with a fluorescently labeled antibody specific for the protein of interest. The stained cells may then be examined under the microscope to determine the subcellular localization of the antibody bound proteins.

II. Potential drug target proteins may also be identified on the basis of an interaction with an interacting protein that may be modified by ubiquitin or may undergo abnormal degradation in disease cells, in comparison with normal cells. For example, it is expected that a number of diseases are related to abnormal protein folding and/or protein aggregate formation. In these cases, the abnormally processed protein may be identified, and a drug target such as an E3s drug target may be identified on the basis of an interaction therewith. Interactions may be identified bioinformatically, using, for example, proteome interaction databases that are generated in a variety of ways (high throughput immunoprecipitations, high throughput two-hybrid analysis, etc.). Various databases include information culled from the literature relating to protein function, and such information may also be used to identify drug target E3s that interact with an abnormally processed protein. Interactions may also be determined de novo, using techniques such as those mentioned above. Once a potential drug target such as an E3 is identified, a number of assays may be used for testing its biological effects.

In one example, the abnormally ubiquitinated, degraded or aggregated protein is monitored for ubiquitination, degradation or aggregation in response to a manipulation in activity of the candidate drug target. For example, ubiquitination has been implicated in the turnover of the tumor supressor protein, p53, and other cell cycle regulators such as cyclin A and cyclin B, the kinase c-mos, and various transcription factors such as c-jun, c-fos, and I.kappa B/NF kappa.B. Altering the half-lives of these cellular proteins is expected to have great therapeutic potential, particularly in the areas of autoimmune disease, inflammation, cancer, as well as other proliferative disorders. Rolfe, M., et al., The Ubiquitin-Mediated Proteolytic Pathway as a Therapeutic Area, J. Mol. Med., 75:5 (1997). Many assays described herein and, in view of this application, known to one of skill in the art may be used to test the biological effects of the potential drug target such as the E3s.

III. Potential drug target proteins such as the E3 proteins may be selected on the basis of cellular localization. In a variety of disease states, a cellular dysfunction can be traced to one or more cellular compartments. A protein such as an E3 that localizes to that compartment may be implicated in the disease, particularly where a dysfunctional protein appears to interact with the ubiquitination system. For example, Cystic Fibrosis is an inherited disorder that is linked to reduced surface expression of the Cystic Fibrosis Transduction Regulator (CFTR). Nearly 70% of the affected patients are homozygous for the CFTR $^{\Delta F508}$ mutation. Mutant CFTR is rapidly degraded in the endoplasmic reticulum (ER) via the ubiquitin proteolytic system resulting in reduced surface expression. It is known that modulation of ER-associated protein degradation triggers the Unfolded Protein Response (UPR) which results in the production of a number of proteins that mediate protein folding. The combination of decreased ubiquitination and increased protein folding are expected cause a greater proportion of proteins to successfully mature (Travers et al. (2000) Cell 101:249-258). Accordingly, human E3 proteins that are either known as being localized to the ER or that are integral membrane E3 proteins may mediate the degradation of the mutant CFTR and as such may be potential drug targets for treating cystic fibrosis.

Protein localization such as localization of the E3 may be determined or predicted by bioinformatic analysis, e.g. through examination of protein localization signals present in the amino acid sequences of the E3s present in a database. Exemplary localization signals include signal peptides (indicating that the protein is routed into the ER-mediated secretion pathway), retention sequences, indicating retention at one or more positions in the secretory pathway, such as the ER, a part of the Golgi, etc., nuclear localization signals, membrane domains, lipid modification sequences, etc. In view of this specification, one of skill in the art will be able to identify numerous types of sequence information that are indicative of protein localization. In another variant, localization may be determined directly by expression of E3s in a cell line, preferably a mammalian cell line. The protein may be expressed as a native protein, wherein localization would typically be determined by immunofluorescence micorscopy. Alternatively, the protein may be expressed

with a detectable tag, such as a fluorescent protein (e.g. GFP, BFP, RFP, etc.), and the localization may be determined by direct immunofluorescence microscopy. Localization may also be determined by cellular fractionation followed by high-throughput protein identification, such as by coupled two-dimensional electrophoresis and mass spectroscopy. This would permit rapid identification of proteins present in various cellular compartments.

Having identified one or more drug target E3 proteins, a number of different assays are available to test the role of the E3 in the disease state. For example, in numerous diseases, a membrane protein is not properly processed and partitioned to the plasma membrane. Accordingly, E3 function may be manipulated (see below) and the level of membrane protein arriving at the membrane measured. Increased delivery of protein to the membrane in response to manipulation of E3 function indicates that the E3 is a valid target for disease therapeutics. As noted above, CFTR maturation is perturbed in cystic fibrosis. In one example, E3s are validated by manipulating the subject E3 and determining the level of mutant CFTR $^{\Delta F508}$ accumulated at the plasma membrane. Likewise, 98% of the erythropoietin receptor fails to mature and is degraded in the secretory pathway. An increased yield of erythropoietin receptor may mimic the effects of erythropoietin itself, which is clinically important stimulator of hematopoiesis. Accordingly, an E3 may be validated by assessing the effect of increasing or decreasing its activity on the amount of erythropoietin at the cell surface.

In further examples, a variety of E3 enzymes may interact with viral proteins that affect the degradation of host proteins passing through the ER. Many viruses co-opt the ER-associated protein degradation pathway to destabilize host proteins that are unfavorable to viral infection. For example, human cytomegalovirus (HCMV) evades the immune system in part by causing the destruction of MHC class I heavy chains. Two HCMV proteins, US11 and US2 cause rapid retrograde transport of the MHC class I heavy chains from the ER to the cytosol, where they are degraded by the proteasome. This process is ubiquitin-dependent. In addition, the HIV virus targets the host CD4 protein for destruction through an ER-associated, ubiquitin-dependent protein degradation pathway. Destruction of CD4 is important because CD4 in the ER associates with and inhibits the maturation of the HIV

glycoprotein gp160. Therefore, E3s may be validated, for example, by assessing effects on the processing or localization of MHC class I heavy chains (or other MHC class I complexes) or CD4.

IV. Potential drug targets may also be identified by the differential expression of certain nucleic acids or proteins in disease cells in comparison to normal cells.

In one aspect, differential expression of a protein in a normal cell in comparison with diseased cells, such as a cell manifesting an associated disease, is indicative that the differentially expressed gene may be involved in the associated disease or other biological process. For example, differential expression of an E3 protein in a tumor tissue in comparison with normal tissue may be indicative that the E3 may be involved in tumorigenesis.

In one embodiment, the invention is based on the gene expression profile of cells from an E-3associated disease. Diseased cells may have genes that are expressed at higher levels (i.e., which are up-regulated) and/or genes that are expressed at lower levels (i.e., which are down-regulated) relative to normal cells that do not have any symptoms of the E3-assocaited disease. In particular, certain E3 genes may be up-regulated by at least about 1 fold, preferably 2 fold, more preferably 5 fold, in the diseased cell as compared to the normal cell. Alternatively, certain E3 genes may be down-regulated by at least about 1 fold, preferably 2 fold, more preferably 5 fold in the diseased cells relative to the corresponding normal cells.

Preferred methods comprise determining the level of expression of one or more E3 genes in diseased cells in comparison to the corresponding normal cells. Methods for determining the expression of tens, hundreds or thousands of genes, in diseased cells relative to the corresponding normal cells include, for e.g., using microarray technology. The expression levels of the E3 genes are then compared to the expression levels of the same E3 genes one or more other cell, e.g., a normal cell.

Comparison of the expression levels can be performed visually. In a preferred embodiment, the comparison is performed by a computer.

In another embodiment, values representing expression levels of genes characteristic of an E3 associated disease are entered into a computer system, comprising one or more databases with reference expression levels obtained from more than one cell. For example, the computer comprises expression data of diseased and normal cells. Instructions are provided to the computer, and the computer is capable of comparing the data entered with the data in the computer to determine whether the data entered is more similar to that of a normal cell or of a diseased cell.

In one embodiment, the invention provides a method for determining the level of expression of one or more E3 genes which are up- or down-regulated in a particular E3-associated diseased cell and comparing these levels of expression with the levels of expression of the E3 genes in a diseased cell from a subject known to have the disease, such that a similar level of expression of the genes is indicative that the E3 gene may be implicated in the disease.

Comparison of the expression levels of one or more E3 genes involved with an E3-associated disease with reference expression levels, e.g., expression levels in diseased cells of or in normal counterpart cells, is preferably conducted using computer systems. In one embodiment, expression levels are obtained in two cells and these two sets of expression levels are introduced into a computer system for comparison. In a preferred embodiment, one set of expression levels is entered into a computer system for comparison with values that are already present in the computer system, or in computer-readable form that is then entered into the computer system.

In one embodiment, the invention provides a system that comprises a means for receiving gene expression data for one or a plurality of genes; a means for comparing the gene expression data from each of said one or plurality of genes to a common reference frame; and a means for presenting the results of the comparison. This system may further comprise a means for clustering the data.

In one embodiment, the invention provides a computer readable form of the E3 gene expression profile data of the invention, or of values corresponding to the level of expression of at least one E3 gene implicated in an E3-associated disease in a diseased cell. The values can be mRNA expression levels obtained from experiments, e.g., microarray analysis. The values can also be mRNA levels normalized relative to a reference gene whose expression is constant in numerous cells under numerous conditions, e.g., GAPDH. In other embodiments, the values in the computer are ratios of, or differences between, normalized or non-normalized mRNA levels in different samples.

The gene expression profile data can be in the form of a table, such as an Excel table. The data can be alone, or it can be part of a larger database, e.g., comprising other expression profiles. For example, the expression profile data of the invention can be part of a public database. The computer readable form can be in a computer. In another embodiment, the invention provides a computer displaying the gene expression profile data.

In one embodiment, the invention provides a method for determining the similarity between the level of expression of one or more E3 genes characteristic of an E3 associated disease in a first cell, e.g., a cell of a subject, and that in a second cell, comprising obtaining the level of expression of one or more genes characteristic of E3 associated disease in a first cell and entering these values into a computer comprising a database including records comprising values corresponding to levels of expression of one or more genes characteristic of said E3 associated disease in a second cell, and processor instructions, e.g., a user interface, capable of receiving a selection of one or more values for comparison purposes with data that is stored in the computer. The computer may further comprise a means for converting the comparison data into a diagram or chart or other type of output.

In another embodiment, the invention provides a computer program for analyzing gene expression data comprising (i) a computer code that receives as input gene expression data for a plurality of genes and (ii) a computer code that compares said gene expression data from each of said plurality of genes to a common reference frame.

The invention also provides a machine-readable or computer-readable medium including program instructions for performing the following steps: (i) comparing a plurality of values corresponding to expression levels of one or more genes characteristic of an E3-associated disease D in a query cell with a database including records comprising reference expression or expression profile data of one or more reference cells and an annotation of the type of cell; and (ii) indicating to which cell the query cell is most similar based on similarities of expression profiles. The reference cells can be cells from subjects at different stages of the E3-associated disease.

The relative abundance of an mRNA in two biological samples can be scored as a perturbation and its magnitude determined (i.e., the abundance is different in the two sources of mRNA tested), or as not perturbed (i.e., the relative abundance is the same). In various embodiments, a difference between the two sources of RNA of at least a factor of about 25% (RNA from one source is 25% more abundant in one source than the other source), more usually about 50%, even more often by a factor of about 2 (twice as abundant), 3 (three times as abundant) or 5 (five times as abundant) is scored as a perturbation. Perturbations can be used by a computer for calculating and expression comparisons.

Preferably, in addition to identifying a perturbation as positive or negative, it is advantageous to determine the magnitude of the perturbation. This can be carried out, as noted above, by calculating the ratio of the emission of the two fluorophores used for differential labeling, or by analogous methods that will be readily apparent to those of skill in the art.

In operation, the means for receiving gene expression data, the means for comparing the gene expression data, the means for presenting, the means for normalizing, and the means for clustering within the context of the systems of the present invention can involve a programmed computer with the respective functionalities described herein, implemented in hardware or hardware and software; a logic circuit or other component of a programmed computer that performs the operations specifically identified herein, dictated by a computer program; or a computer memory encoded with executable instructions representing a computer

program that can cause a computer to function in the particular fashion described herein.

Those skilled in the art will understand that the systems and methods described herein may be supported by and executed on any suitable platform, including commercially available hardware systems, such as IBM-compatible personal computers executing a variety of the UNIX operating systems, such as Linux or BSD, or any suitable operating system such as MS-DOS or Microsoft Windows. In one embodiment, the data processor may be a MIPS R10000, based mullet-processor Silicon-Graphic Challenge server, running IRIX 6.2. Alternatively and optionally, the systems and methods described herein may be realized as embedded programmable data processing systems that implement the processes of the invention. For example, the data processing system can comprise a single board computer system that has been integrated into a piece of laboratory equipment for performing the data analysis described above. The single board computer (SBC) system can be any suitable SBC, including the SBCs sold by the Micro/Sys Company, which include microprocessors, data memory and program memory, as well as expandable bus configurations and an on-board operating system.

Optionally, the data processing systems may comprise an Intel Pentium®-based processor or AMD processor or their equals of adequate clock rate and with adequate main memory, as known to those skilled in the art. Optional external components may include a mass storage system, which can be one or more hard disks (which are typically packaged together with the processor and memory), tape drives, CDROMS devices, storage area networks, or other devices. Other external components include a user interface device, which can be a monitor, together with an input device, which can be a "mouse", or other graphic input devices, and/or a keyboard. A printing device can also be attached to the computer.

Typically, the computer system is also linked to a network link, which can be part of an Ethernet link to other local computer systems, remote computer systems, or wide area communication networks, such as the Internet. This network link allows the computer system to share data and processing tasks with other computer systems. The network can be, for example, an NFS network with a Postgres SQL relational database engine and a web server, such as the Apache web server engine.

However, the server may be any suitable server process including any HTTP server process including the Apache server. Suitable servers are known in the art and are described in Jamsa, *Internet Programming*, Jamsa Press (1995), the teachings of which are herein incorporated by reference. Accordingly, it shall be understood that in certain embodiments, the systems and methods described herein may be implemented as web-based systems and services that allow for network access, and remote access. To this end, the server may communicate with clients stations. Each of the client stations can be a conventional personal computer system, such as a PC compatible computer system that is equipped with a client process that can operate as a browser, such as the Netscape Navigator browser process, the Microsoft Explorer browser process, or any other conventional or proprietary browser process that allows the client station to download computer files, such as web pages, from the server.

In certain embodiments the systems and methods described herein are realized as software systems that comprise one or more software components that can load into memory during operation. These software components collectively cause the computer system to function according to the methods of this invention. In such embodiments, the systems may be implemented as a C language computer program, or a computer program written in any high level language including C++, Fortran, Java or BASIC. Additionally, in an embodiment where SBCs are employed, the systems and methods may be realized as a computer program written in microcode or written in a high level language and compiled down to microcode that can be executed on the platform employed. The development of such systems is known to those of skill in the art, and such techniques are set forth in Digital Signal Processing Applications with the TMS320 Family, Volumes I, II, and III, Texas Instruments (1990). Additionally, general techniques for high level programming are known, and set forth in, for example, Stephen G. Kochan, *Programming in C*, Hayden Publishing (1983).

Additionally, in certain embodiments, these software components may be programmed in mathematical software packages which allow symbolic entry of equations and high-level specification of processing, including algorithms to be used, thereby freeing a user of the need to procedurally program individual

equations or algorithms. Such packages include Matlab from Mathworks (Natick, Mass.), Mathematica from Wolfram Research (Champaign, Ill.), or S-Plus from Math Soft (Cambridge, Mass.). Accordingly, a software component represents the analytic methods of this invention as programmed in a procedural language or symbolic package. In a preferred embodiment, the computer system also contains a database comprising values representing levels of expression of one or more genes characteristic of am E3 associated disease. The database may contain one or more expression profiles of genes characteristic of the E3 associated disease in different cells.

The database employed may be any suitable database system, including the commercially available Microsoft Access database, Postgre SQL database system, MySQL database systems, and optionally can be a local or distributed database system. The design and development of suitable database systems are described in McGovern et al., *A Guide To Sybase and SQL Server*, Addison-Wesley (1993). The database can be supported by any suitable persistent data memory, such as a hard disk drive, RAID system, tape drive system, floppy diskette, or any other suitable system. The system 200 depicted in Figure 2 depicts several separate databases devices. However, it will be understood by those of ordinary skill in the art that in other embodiments the database device can be integrated into a single system.

In an exemplary implementation, to practice the methods of the present invention, a user first loads expression profile data into the computer system. These data can be directly entered by the user from a monitor and keyboard, or from other computer systems linked by a network connection, or on removable storage media such as a CD-ROM or floppy disk or through the network. Next the user causes execution of expression profile analysis software which performs the steps of comparing and, e.g., clustering co-varying genes into groups of genes.

In an exemplary implementation, to practice the methods of the present invention, a user first loads expression profile data into the computer system. These data can be directly entered by the user from a monitor and keyboard, or from other computer systems linked by a network connection, or on removable storage media such as a CD-ROM or floppy disk or through the network. Next the user causes

execution of expression profile analysis software which performs the steps of comparing and, e.g., clustering co-varying genes into groups of genes.

In another exemplary implementation, expression profiles are compared using a method described in U.S. Patent No. 6,203,987. A user first loads expression profile data into the computer system. Geneset profile definitions are loaded into the memory from the storage media or from a remote computer, preferably from a dynamic geneset database system, through the network. Next the user causes execution of projection software which performs the steps of converting expression profile to projected expression profiles. The projected expression profiles are then displayed.

In yet another exemplary implementation, a user first leads a projected profile into the memory. The user then causes the loading of a reference profile into the memory. Next, the user causes the execution of comparison software which performs the steps of objectively comparing the profiles.

Once again, having identified one or more drug target proteins that are differentially expressed in disease cells, a number of different assays are available to test the role of the drug target protein in the disease state.

For instance, if a E3 protein is identified as being over-expressed in a particular tumor-type, the skilled artisan can readily test for the role of the E3 by conducting a number of assays, for example one could use techniques such as antisense constructs, RNAi constructs, DNA enzymes etc. to decrease the expression of the E3 in a tumor cell line to determine whether inhibition of the E3 results in decreased proliferation. In other embodiments the activity of the E# may be decreased by using techniques such as dominant negative mutants, small molecules, antibodies etc. Other techniques include proliferation assays such as determining thymidine incorporation.

V. Aberrant activity of certain human drug target proteins may also be associated with a disease state or pathological condition.

For example, the association of the E3 proteins with certain disease or disorders provides a disease specific database containing human E3 proteins that may be implicated in the disease or disorder.

Validating Potential Drug Targets

In another aspect, this application provides methods for validating the selected proteins, such as the E3 proteins as viable drug targets. In one embodiment, the methods provide for decreasing the expression of the potential drug targets and determining the effects of the reduction of such expression. The expression of the drug targets may be reduced by a number of methods that are known in the art, such as the use of antisense methods, dominant negative mutants, DNA enzymes, RNAi, ribozymes, to name but a few of such methods.

In another embodiment, the methods provide for increasing the expression of the potential drug targets and determining the effects of the increase of such expression.

One aspect of the invention relates to the use of the isolated "antisense" nucleic acids to inhibit expression, e.g., by inhibiting transcription and/or translation. of the potential drug target. The antisense nucleic acids may bind to the potential drug target by conventional base pair complementarity, or, for example, in the case of binding to DNA duplexes, through specific interactions in the major groove of the double helix. In general, these methods refer to the range of techniques generally employed in the art, and include any methods that rely on specific binding to oligonucleotide sequences.

An antisense construct of the present invention can be delivered, for example, as an expression plasmid which, when transcribed in the cell, produces RNA which is complementary to at least a unique portion of the cellular mRNA which encodes the potential drug target. Alternatively, the antisense construct is an oligonucleotide probe, which is generated ex vivo and which, when introduced into the cell causes inhibition of expression by hybridizing with the mRNA and/or genomic sequences of the potential drug target. Such oligonucleotide probes are preferably modified oligonucleotides, which are resistant to endogenous nucleases,

e.g., exonucleases and/or endonucleases, and are therefore stable in vivo. Exemplary nucleic acid molecules for use as antisense oligonucleotides are phosphoramidate, phosphothioate and methylphosphonate analogs of DNA (see also U.S. Patents 5,176,996; 5,264,564; and 5,256,775). Additionally, general approaches to constructing oligomers useful in antisense therapy have been reviewed, for example, by Van der Krol et al. (1988) BioTechniques 6:958-976; and Stein et al. (1988) Cancer Res 48:2659- 2668.

With respect to antisense DNA, oligodeoxyribonucleotides derived from the translation initiation site, e.g., between the -10 and +10 regions of the potential drug target, are preferred. Antisense approaches involve the design of oligonucleotides (either DNA or RNA) that are complementary to mRNA encoding the potential drug target. The antisense oligonucleotides will bind to the mRNA transcripts and prevent translation. Absolute complementarity, although preferred, is not required. In the case of double-stranded antisense nucleic acids, a single strand of the duplex DNA may thus be tested, or triplex formation may be assayed. The ability to hybridize will depend on both the degree of complementarity and the length of the antisense nucleic acid. Generally, the longer the hybridizing nucleic acid, the more base mismatches with an RNA it may contain and still form a stable duplex (or triplex, as the case may be). One skilled in the art can ascertain a tolerable degree of mismatch by use of standard procedures to determine the melting point of the hybridized complex.

Oligonucleotides that are complementary to the 5' end of the mRNA, e.g., the 5' untranslated sequence up to and including the AUG initiation codon, should work most efficiently at inhibiting translation. However, sequences complementary to the 3' untranslated sequences of mRNAs have recently been shown to be effective at inhibiting translation of mRNAs as well. (Wagner, R. 1994. Nature 372:333). Therefore, oligonucleotides complementary to either the 5' or 3' untranslated, non-coding regions of a gene could be used in an antisense approach to inhibit translation of that mRNA. Oligonucleotides complementary to the 5' untranslated region of the mRNA should include the complement of the AUG start codon. Antisense oligonucleotides complementary to mRNA coding regions are less efficient inhibitors of translation but could also be used in accordance with the invention.

Whether designed to hybridize to the 5', 3' or coding region of mRNA, antisense nucleic acids should be at least six nucleotides in length, and are preferably less that about 100 and more preferably less than about 50, 25, 17 or 10 nucleotides in length.

Regardless of the choice of target sequence, it is preferred that in vitro studies are first performed to quantitate the ability of the antisense oligonucleotide to quantitate the ability of the antisense oligonucleotide to inhibit gene expression. It is preferred that these studies utilize controls that distinguish between antisense gene inhibition and nonspecific biological effects of oligonucleotides. It is also preferred that these studies compare levels of the target RNA or protein with that of an internal control RNA or protein. Additionally, it is envisioned that results obtained using the antisense oligonucleotide are compared with those obtained using a control oligonucleotide. It is preferred that the control oligonucleotide is of approximately the same length as the test oligonucleotide and that the nucleotide sequence of the oligonucleotide differs from the antisense sequence no more than is necessary to prevent specific hybridization to the target sequence.

The oligonucleotides can be DNA or RNA or chimeric mixtures or derivatives or modified versions thereof, single-stranded or double-stranded. The oligonucleotide can be modified at the base moiety, sugar moiety, or phosphate backbone, for example, to improve stability of the molecule, hybridization, etc. The oligonucleotide may include other appended groups such as peptides (e.g., for targeting host cell receptors), or agents facilitating transport across the cell membrane (see, e.g., Letsinger et al., 1989, Proc. Natl. Acad. Sci. U.S.A. 86:6553-6556; Lemaitre et al., 1987, Proc. Natl. Acad. Sci. 84:648-652; PCT Publication No. W088/09810, published December 15, 1988) or the blood- brain barrier (see, e.g., PCT Publication No. W089/10134, published April 25, 1988), hybridization-triggered cleavage agents. (See, e.g., Krol et al., 1988, BioTechniques 6:958- 976) or intercalating agents. (See, e.g., Zon, 1988, Pharm. Res. 5:539-549). To this end, the oligonucleotide may be conjugated to another molecule, e.g., a peptide, hybridization triggered cross-linking agent, transport agent, hybridization-triggered cleavage agent, etc.

The antisense oligonucleotide may comprise at least one modified base moiety which is selected from the group including but not limited to 5-fluorouracil, 5- bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xantine, 4-acetylcytosine, 5- (carboxyhydroxytiethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5- carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6- isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6- isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5- oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3- N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine.

The antisense oligonucleotide may also comprise at least one modified sugar moiety selected from the group including but not limited to arabinose, 2-fluoroarabinose, xylulose, and hexose.

The antisense oligonucleotide can also contain a neutral peptide-like backbone. Such molecules are termed peptide nucleic acid (PNA)-oligomers and are described, e.g., in Perry-O'Keefe et al. (1996) Proc. Natl. Acad. Sci. U.S.A. 93:14670 and in Eglom et al. (1993) Nature 365:566. One advantage of PNA oligomers is their capability to bind to complementary DNA essentially independently from the ionic strength of the medium due to the neutral backbone of the DNA. In yet another embodiment, the antisense oligonucleotide comprises at least one modified phosphate backbone selected from the group consisting of a phosphorothioate, a phosphorodithioate, a phosphoramidothioate, a phosphoramidate, a phosphordiamidate, a methylphosphonate, an alkyl phosphotriester, and a formacetal or analog thereof.

In yet a further embodiment, the antisense oligonucleotide is an -anomeric oligonucleotide. An -anomeric oligonucleotide forms specific double-stranded

hybrids with complementary RNA in which, contrary to the usual -units, the strands run parallel to each other (Gautier et al., 1987, Nucl. Acids Res. 15:6625-6641). The oligonucleotide is a 2'-0-methylribonucleotide (Inoue et al., 1987, Nucl. Acids Res. 15:6131-6148), or a chimeric RNA-DNA analogue (Inoue et al., 1987, FEBS Lett. 215:327-330).

Oligonucleotides of the invention may be synthesized by standard methods known in the art, e.g., by use of an automated DNA synthesizer (such as are commercially available from Biosearch, Applied Biosystems, etc.). As examples, phosphorothioate oligonucleotides may be synthesized by the method of Stein et al. (1988, Nucl. Acids Res. 16:3209), methylphosphonate olgonucleotides can be prepared by use of controlled pore glass polymer supports (Sarin et al., 1988, Proc. Natl. Acad. Sci. U.S.A. 85:7448-7451), etc.

While antisense nucleotides complementary to the coding region of an mRNA sequence can be used, those complementary to the transcribed untranslated region and to the region

In certain instances, it may be difficult to achieve intracellular concentrations of the antisense sufficient to suppress translation on endogenous mRNAs. Therefore a preferred approach utilizes a recombinant DNA construct in which the antisense oligonucleotide is placed under the control of a strong pol III or pol II promoter. The use of such a construct to transfect target cells will result in the transcription of sufficient amounts of single stranded RNAs that will form complementary base pairs with the endogenous potential drug target transcripts and thereby prevent translation. For example, a vector can be introduced such that it is taken up by a cell and directs the transcription of an antisense RNA. Such a vector can remain episomal or become chromosomally integrated, as long as it can be transcribed to produce the desired antisense RNA. Such vectors can be constructed by recombinant DNA technology methods standard in the art. Vectors can be plasmid, viral, or others known in the art, used for replication and expression in mammalian cells. Expression of the sequence encoding the antisense RNA can be by any promoter known in the art to act in mammalian, preferably human cells. Such promoters can be inducible or constitutive. Such promoters include but are not limited to: the SV40 early promoter region (Bernoist and Chambon, 1981, Nature 290:304-310),

the promoter contained in the 3' long terminal repeat of Rous sarcoma virus (Yamamoto et al., 1980, Cell 22:787-797), the herpes thymidine kinase promoter (Wagner et al., 1981, Proc. Natl. Acad. Sci. U.S.A. 78:1441-1445), the regulatory sequences of the metallothionein gene (Brinster et al, 1982, Nature 296:39-42), etc. Any type of plasmid, cosmid, YAC or viral vector can be used to prepare the recombinant DNA construct, which can be introduced directly into the tissue site.

Alternatively, the potential drug target gene expression can be reduced by targeting deoxyribonucleotide sequences complementary to the regulatory region of the gene (i.e., the promoter and/or enhancers) to form triple helical structures that prevent transcription of the gene in target cells in the body. (See generally, Helene, C. 1991, Anticancer Drug Des., 6(6):569-84; Helene, C., et al., 1992, Ann. N.Y. Acad. Sci., 660:27-36; and Maher, L.J., 1992, Bioassays 14(12):807-15).

Nucleic acid molecules to be used in triple helix formation for the inhibition of transcription are preferably single stranded and composed of deoxyribonucleotides. The base composition of these oligonucleotides should promote triple helix formation via Hoogsteen base pairing rules, which generally require sizable stretches of either purines or pyrimidines to be present on one strand of a duplex. Nucleotide sequences may be pyrimidine-based, which will result in TAT and CGC triplets across the three associated strands of the resulting triple helix. The pyrimidine-rich molecules provide base complementarity to a purine-rich region of a single strand of the duplex in a parallel orientation to that strand. In addition, nucleic acid molecules may be chosen that are purine- rich, for example, containing a stretch of G residues. These molecules will form a triple helix with a DNA duplex that is rich in GC pairs, in which the majority of the purine residues are located on a single strand of the targeted duplex, resulting in CGC triplets across the three strands in the triplex.

Alternatively, the potential sequences that can be targeted for triple helix formation may be increased by creating a so called "switchback" nucleic acid molecule. Switchback molecules are synthesized in an alternating 5'-3', 3'-5' manner, such that they base pair with first one strand of a duplex and then the other,

eliminating the necessity for a sizable stretch of either purines or pyrimidines to be present on one strand of a duplex.

Antisense RNA and DNA, ribozyme, and triple helix molecules of the invention may be prepared by any method known in the art for the synthesis of DNA and RNA molecules. These include techniques for chemically synthesizing oligodeoxyribonucleotides and oligoribonucleotides well known in the art such as for example solid phase phosphoramidite chemical synthesis. Alternatively, RNA molecules may be generated by in vitro and in vivo transcription of DNA sequences encoding the antisense RNA molecule. Such DNA sequences may be incorporated into a wide variety of vectors which incorporate suitable RNA polymerase promoters such as the T7 or SP6 polymerase promoters. Alternatively, antisense cDNA constructs that synthesize antisense RNA constitutively or inducibly, depending on the promoter used, can be introduced stably into cell lines.

Preferred embodiments of the invention make use of materials and methods for effecting repression of one or more target genes by means of RNA interference (RNAi). RNAi is a process of sequence-specific post-transcriptional gene repression which can occur in eukaryotic cells. In general, this process involves degradation of an mRNA of a particular sequence induced by double-stranded RNA (dsRNA) that is homologous to that sequence. For example, the expression of a long dsRNA corresponding to the sequence of a particular single-stranded mRNA (ss mRNA) will labilize that message, thereby "interfering" with expression of the corresponding gene. Accordingly, any selected gene may be repressed by introducing a dsRNA which corresponds to all or a substantial part of the mRNA for that gene. It appears that when a long dsRNA is expressed, it is initially processed by a ribonuclease III into shorter dsRNA oligonucleotides of as few as 21 to 22 base pairs in length. Furthermore, Accordingly, RNAi may be effected by introduction or expression of relatively short homologous dsRNAs. Indeed the use of relatively short homologous dsRNAs may have certain advantages as discussed below.

Mammalian cells have at least two pathways that are affected by double-stranded RNA (dsRNA). In the RNAi (sequence-specific) pathway, the initiating dsRNA is first broken into short interfering (si) RNAs, as described above. The

siRNAs have sense and antisense strands of about 21 nucleotides that form approximately 19 nucleotide si RNAs with overhangs of two nucleotides at each 3' end. Short interfering RNAs are thought to provide the sequence information that allows a specific messenger RNA to be targeted for degradation. In contrast, the nonspecific pathway is triggered by dsRNA of any sequence, as long as it is at least about 30 base pairs in length. The nonspecific effects occur because dsRNA activates two enzymes: PKR, which in its active form phosphorylates the translation initiation factor eIF2 to shut down all protein synthesis, and 2', 5' oligoadenylate synthetase (2', 5'-AS), which synthesizes a molecule that activates Rnase L, a nonspecific enzyme that targets all mRNAs. The nonspecific pathway may represents a host response to stress or viral infection, and, in general, the effects of the nonspecific pathway are preferably minimized under preferred methods of the present invention. Significantly, longer dsRNAs appear to be required to induce the nonspecific pathway and, accordingly, dsRNAs shorter than about 30 bases pairs are preferred to effect gene repression by RNAi (see Hunter et al. (1975) J Biol Chem 250: 409-17; Manche et al. (1992) Mol Cell Biol 12: 5239-48; Minks et al. (1979) J Biol Chem 254: 10180-3; and Elbashir et al. (2001) Nature 411: 494-8).

RNAi has been shown to be effective in reducing or eliminating the expression of a target gene in a number of different organisms including *Caenorhabditiis elegans* (see e.g. Fire et al. (1998) Nature 391: 806-11), mouse eggs and embryos (Wianny et al. (2000) Nature Cell Biol 2: 70-5; Svoboda et al. (2000) Development 127: 4147-56), and cultured RAT-1 fibroblasts (Bahramina et al. (1999) Mol Cell Biol 19: 274-83), and appears to be an anciently evolved pathway available in eukaryotic plants and animals (Sharp (2001) Genes Dev. 15: 485-90). RNAi has proven to be an effective means of decreasing gene expression in a variety of cell types including HeLa cells, NIH/3T3 cells, COS cells, 293 cells and BHK-21 cells, and typically decreases expression of a gene to lower levels than that achieved using antisense techniques and, indeed, frequently eliminates expression entirely (see Bass (2001) Nature 411: 428-9). In mammalian cells, siRNAs are effective at concentrations that are several orders of magnitude below the concentrations typically used in antisense experiments (Elbashir et al. (2001) Nature 411: 494-8).

The double stranded oligonucleotides used to effect RNAi are preferably less than 30 base pairs in length and, more preferably, comprise about 25, 24, 23, 22, 21, 20, 19, 18 or 17 base pairs of ribonucleic acid. Optionally the dsRNA oligonucleotides of the invention may include 3' overhang ends. Exemplary 2-nucleotide 3' overhangs may be composed of ribonucleotide residues of any type and may even be composed of 2'-deoxythymidine resides, which lowers the cost of RNA synthesis and may enhance nuclease resistance of siRNAs in the cell culture medium and within transfected cells (see Elbashi et al. (2001) Nature 411: 494-8). Longer dsRNAs of 50, 75, 100 or even 500 base pairs or more may also be utilized in certain embodiments of the invention. Exemplary concentrations of dsRNAs for effecting RNAi are about 0.05 nM, 0.1 nM, 0.5 nM, 1.0 nM, 1.5 nM, 25 nM or 100 nM, although other concentrations may be utilized depending upon the nature of the cells treated, the gene target and other factors readily discernable the skilled artisan. Exemplary dsRNAs may be synthesized chemically or produced in vitro or in vivo using appropriate expression vectors. Exemplary synthetic RNAs include 21 nucleotide RNAs chemically synthesized using methods known in the art (e.g. Expedite RNA phophoramidites and thymidine phosphoramidite (Proligo, Germany). Synthetic oligonucleotides are preferably deprotected and gel-purified using methods known in the art (see e.g. Elbashir et al. (2001) Genes Dev. 15: 188-200). Longer RNAs may be transcribed from promoters, such as T7 RNA polymerase promoters, known in the art. A single RNA target, placed in both possible orientations downstream of an in vitro promoter, will transcribe both strands of the target to create a dsRNA oligonucleotide of the desired target sequence.

The specific sequence utilized in design of the oligonucleotides may be any contiguous sequence of nucleotides contained within the expressed gene message of the target. Programs and algorithms, known in the art, may be used to select appropriate target sequences. In addition, optimal sequences may be selected utilized programs designed to predict the secondary structure of a specified single stranded nucleic acid sequence and allow selection of those sequences likely to occur in exposed single stranded regions of a folded mRNA. Methods and compositions for designing appropriate oligonucleotides may be found, for example,

in U.S. Patent Nos. 6,251,588, the contents of which are incorporated herein by reference. Messenger RNA (mRNA) is generally thought of as a linear molecule which contains the information for directing protein synthesis within the sequence of ribonucleotides, however studies have revealed a number of secondary and tertiary structures exist in most mRNAs. Secondary structure elements in RNA are formed largely by Watson-Crick type interactions between different regions of the same RNA molecule. Important secondary structural elements include intramolecular double stranded regions, hairpin loops, bulges in duplex RNA and internal loops. Tertiary structural elements are formed when secondary structural elements come in contact with each other or with single stranded regions to produce a more complex three dimensional structure. A number of researchers have measured the binding energies of a large number of RNA duplex structures and have derived a set of rules which can be used to predict the secondary structure of RNA (see e.g. Jaeger et al. (1989) Proc. Natl. Acad. Sci. USA 86:7706 (1989); and Turner et al. (1988) Annu. Rev. Biophys. Biophys. Chem. 17:167) . The rules are useful in identification of RNA structural elements and, in particular, for identifying single stranded RNA regions which may represent preferred segments of the mRNA to target for silencing RNAi, ribozyme or antisense technologies. Accordingly, preferred segments of the mRNA target can be identified for design of the RNAi mediating dsRNA oligonucleotides as well as for design of appropriate ribozyme and hammerheadribozyme compositions of the invention.

The dsRNA oligonucleotides may be introduced into the cell by transfection with an heterologous target gene using carrier compositions such as liposomes, which are known in the art- e.g. Lipofectamine 2000 (Life Technologies) as described by the manufacturer for adherent cell lines. Transfection of dsRNA oligonucleotides for targeting endogenous genes may be carried out using Oligofectamine (Life Technologies). Transfection efficiency may be checked using fluorescence microscopy for mammalian cell lines after co-transfection of hGFP-encoding pAD3 (Kehlenback et al. (1998) J Cell Biol 141: 863-74). The effectiveness of the RNAi may be assessed by any of a number of assays following introduction of the dsRNAs. These include Western blot analysis using antibodies which recognize the targeted gene product following sufficient time for turnover of

the endogenous pool after new protein synthesis is repressed, and Northern blot analysis to determine the level of existing target mRNA.

Further compositions, methods and applications of RNAi technology are provided in U.S. Patent Application Nos. 6,278,039, 5,723,750 and 5,244,805, which are incorporated herein by reference.

Ribozyme molecules designed to catalytically cleave the potential drug target mRNA transcripts can also be used to prevent translation of mRNA(See, e.g., PCT International Publication WO90/11364, published October 4, 1990; Sarver et al., 1990, Science 247:1222-1225 and U.S. Patent No. 5,093,246). While ribozymes that cleave mRNA at site specific recognition sequences can be used to destroy particular mRNAs, the use of hammerhead ribozymes is preferred. Hammerhead ribozymes cleave mRNAs at locations dictated by flanking regions that form complementary base pairs with the target mRNA. The sole requirement is that the target mRNA have the following sequence of two bases: 5'-UG-3'. The construction and production of hammerhead ribozymes is well known in the art and is described more fully in Haseloff and Gerlach, 1988, Nature, 334:585-591.

The ribozymes of the present invention also include RNA endoribonucleases (hereinafter "Cech-type ribozymes") such as the one which occurs naturally in Tetrahymena thermophila (known as the IVS, or L-19 IVS RNA) and which has been extensively described by Thomas Cech and collaborators (Zaug, et al., 1984, Science, 224:574-578; Zaug and Cech, 1986, Science, 231:470-475; Zaug, et al., 1986, Nature, 324:429-433; published International patent application No. WO88/04300 by University Patents Inc.; Been and Cech, 1986, Cell, 47:207-216). The Cech-type ribozymes have an eight base pair active site which, hybridizes to a target RNA sequence whereafter cleavage of the target RNA takes place. The invention encompasses those Cech-type ribozymes which target eight base-pair active site sequences.

As in the antisense approach, the ribozymes can be composed of modified oligonucleotides (e.g., for improved stability, targeting, etc.) and should be delivered to cells expressing the potential drug target. A preferred method of delivery

involves using a DNA construct "encoding" the ribozyme under the control of a strong constitutive pol III or pol II promoter, so that transfected cells will produce sufficient quantities of the ribozyme to destroy targeted messages and inhibit translation. Because ribozymes unlike antisense molecules, are catalytic, a lower intracellular concentration is required for efficiency.

A further aspect of the invention relates to the use of DNA enzymes to decrease expression of the potential drug targets. DNA enzymes incorporate some of the mechanistic features of both antisense and ribozyme technologies. DNA enzymes are designed so that they recognize a particular target nucleic acid sequence, much like an antisense oligonucleotide, however much like a ribozyme they are catalytic and specifically cleave the target nucleic acid.

There are currently two basic types of DNA enzymes, and both of these were identified by Santoro and Joyce (see, for example, US Patent No. 6110462). The 10-23 DNA enzyme (shown schematically in Figure 1) comprises a loop structure which connect two arms. The two arms provide specificity by recognizing the particular target nucleic acid sequence while the loop structure provides catalytic function under physiological conditions.

Briefly, to design an ideal DNA enzyme that specifically recognizes and cleaves a target nucleic acid, one of skill in the art must first identify the unique target sequence. This can be done using the same approach as outlined for antisense oligonucleotides. Preferably, the unique or substantially sequence is a G/C rich of approximately 18 to 22 nucleotides. High G/C content helps insure a stronger interaction between the DNA enzyme and the target sequence.

When synthesizing the DNA enzyme, the specific antisense recognition sequence that will target the enzyme to the message is divided so that it comprises the two arms of the DNA enzyme, and the DNA enzyme loop is placed between the two specific arms.

Methods of making and administering DNA enzymes can be found, for example, in US 6110462. Similarly, methods of delivery DNA ribozymes in vitro or in vivo include methods of delivery RNA ribozyme, as outlined in detail above. Additionally, one of skill in the art will recognize that, like antisense

oligonucleotide, DNA enzymes can be optionally modified to improve stability and improve resistance to degradation.

The present invention is further illustrated by the following examples which should not be construed as limiting in any way. The contents of all cited references including literature references, issued patents, published or non published patent applications as cited throughout this application are hereby expressly incorporated by reference. The practice of the present invention will employ, unless otherwise indicated, conventional techniques of cell biology, cell culture, molecular biology, transgenic biology, microbiology, recombinant DNA, and immunology, which are within the skill of the art. Such techniques are explained fully in the literature. (See, for example, *Molecular Cloning A Laboratory Manual, 2nd Ed.*, ed. by Sambrook, Fritsch and Maniatis (Cold Spring Harbor Laboratory Press: 1989); *DNA Cloning*, Volumes I and II (D. N. Glover ed., 1985); Oligonucleotide Synthesis (M. J. Gait ed., 1984); Mullis et al. U.S. Patent No: 4,683,195; *Nucleic Acid Hybridization* (B. D. Hames & S. J. Higgins eds. 1984); *Transcription And Translation* (B. D. Hames & S. J. Higgins eds. 1984); (R. I. Freshney, Alan R. Liss, Inc., 1987); *Immobilized Cells And Enzymes* (IRL Press, 1986); B. Perbal, *A Practical Guide To Molecular Cloning* (1984); the treatise, *Methods In Enzymology* (Academic Press, Inc., N.Y.); *Gene Transfer Vectors For Mammalian Cells* (J. H. Miller and M. P. Calos eds., 1987, Cold Spring Harbor Laboratory); , Vols. 154 and 155 (Wu et al. eds.), *Immunochemical Methods In Cell And Molecular Biology* (Mayer and Walker, eds., Academic Press, London, 1987); *Handbook Of Experimental Immunology*, Volumes I-IV (D. M. Weir and C. C. Blackwell, eds., 1986) (Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1986).

Examples

Examples

Example 1: Method of creating the database

The following procedure illustrates one embodiment of creating a database.

1. NCBI protein database is downloaded from NCBI ftp site: ftp.ncbi.nlm.nih.gov

2. Retrieve hum nr: Retrieve all the human sequence in an automatic way from the following url: http://www.ncbi.nlm.nih.gov/Entrez/batch.html. In the HTML form one can specify that all the protein sequences, from *Homo Sapiens* are to be retrieved.

3. Whether the protein is a human protein is determined by downloading the full nr file from ncbi ftp site, in a fasta format. All the sequences that have the pattern [*Homo Sapiens*] at the end of the description sentence (i.e. from the first line) are parsed out.

4. Clean sequences: These sequences are then cleaned. Two scripts are run in order to clean the Human nr fasta file. The first script eliminates all the redundant sequences, and leaves all the unique sequences. The second script removes all the short sequences (less then 30 aa).

5. Run RPS-Blast: RPS-Blast is run locally against the CDD database (which contains the Pfam, SMART and LOAD domains). In addition we look for domains in the prosite database. We also look for different features in the sequences: Transmembrane regions (alom2, tmap), signal peptide and other internal domains/features.

6. Find E3 proteins: this search is done automatically. We look for all the proteins that have one or more of the following domains (Hect, Ring, Ubox, Fbox, PHD). These five domains appear in the different databases (pfam, smart and prosite) in different names. In our search we look for these domains in all the different names, in all the databases.

7. Unigene clusters data: We download the clusters (Hs.data file) from the following url: ftp://ncbi.nlm.nih.gov/repository/UniGene/.

❽ E3 Vs. Unigene: We look at each E3 protein from the E3 table; to see in which Unigene Cluster it belongs.

❾ We check which other proteins are in the E3 clusters, which are not E3 proteins, and introduce them in the E3 database.

In addition, multiple sequence alignment may be performed between all the cluster members against the relative genomic piece. In this way we can see the alternative transcripts of the gene.

In particular, RPS-Blast may be run at least twice. In the first run, an E value of 0.01 may be used, and then all the domains may be run against the human nr. In the second run, an E value of 10 may be used , and only the E3 domains (hect, ring, ubox, fbox, phd) are run against the human nr. In this manner the database will have a lower number of false positives, but have a higher sensitivity to the E3 domains.

Further, the E3 database can integrate links to articles, links to patents, annotations of the proteins and other biological information that may be available for the particular protein.

Examples of E3 polypeptides and nucleic acids that may be incorporated into one or more databases are presented in Table 2, appended at the end of the text. Applicants incorporate by reference herein the nucleic acid and amino acid sequences corresponding to the accession numbers provided in Table 2.

Example 2: Domains and/or Motifs of Interest

A. Protein domains that may play a role in virus biogenesis, maturation and release

E3 - domain of E3 ubiquitin-protein ligase

RING -

SMART SM0184; RING = RNF, E3 ubiquitin-protein ligase activity is intrinsic to the RING domain of c-Cbl and is likely to be a general function of this domain; Various RING fingers exhibit binding activity towards E2's, i.e., the ubiquitin-conjugating enzymes (UBC's).

HECTc -

SMART SM0119; Pfam PF00632; HECTc = HECT, E3 ubiquitin-protein ligases. Can bind to E2 enzymes. The name HECT comes from 'Homologous to the E6-

AP Carboxyl Terminus'. Proteins containing this domain at the C-terminus include ubiquitin-protein ligase activity, which regulates ubiquitination of CDC25. Ubiquitin-protein ligase accepts ubiquitin from an E2 ubiquitin-conjugating enzyme in the form of a thioester, and then directly transfers the ubiquitin to targeted substrates. A cysteine residue is required for ubiquitin-thiolester formation. Human thyroid receptor interacting protein 12, which also contains this domain, is a component of an ATP-dependent multi-subunit protein that interacts with the ligand binding domain of the thyroid hormone receptor. It could be an E3 ubiquitin-protein ligase. Human ubiquitin-protein ligase E3A interacts with the E6 protein of the cancer-associated human papillomavirus types 16 and 18. The E6/E6-AP complex binds to and targets the P53 tumor-suppressor protein for ubiquitin-mediated proteolysis.

F-BOX -

SMART SM0256; Pfam PF00646; F-BOX = FBOX = F-box = Fbox. The F-box domain was first described as a sequence domain found in cyclin-F that interacts with the protein SKP1. This domain is present in numerous proteins and serves as a link between a target protein and a ubiquitin-conjugating enzyme. The SCF complex (e.g., Skp1-Cullin-F-box) plays a similar role as an E3 ligase in the ubiquitin protein degradation pathway.

U-BOX –

SMART SM0504. The U-box domain is a modified RING finger domain that is without the full complement of Zn2+-binding ligands. It is found in pre-mRNA splicing factor, several hypothetical proteins, and ubiquitin fusion degradation protein 2, where it may be involved in E2-dependent ubiquitination.

PHD -

SMART SM0249. The PHD domain is a C4HC3 zinc-finger-like motif found in nuclear proteins that are thought to be involved in chromatin-mediated transcriptional regulation. The PHD finger motif is reminiscent of, but distinct from the C3HC4 type RING finger. Like the RING finger and the LIM domain, the PHD finger is expected to bind two zinc ions.

B. Protein domains that may play a role in virus biogenesis, maturation and release in combination with E3 ubiquitin-protein ligase

RCC1 - domain that interacts with small GTPases such ARF1 that activates AP1 to polymerize Clathrin

Pfam PF00415; The regulator of chromosome condensation (RCC1) [MEDLINE: 93242659] is a eukaryotic protein which binds to chromatin and interacts with ran, a nuclear GTP-binding protein IPR002041, to promote the loss of bound GDP and the uptake of fresh GTP, thus acting as a guanine-nucleotide dissociation stimulator (GDS). The interaction of RCC1 with ran probably plays an important role in the regulation of gene expression. RCC1, known as PRP20 or SRM1 in yeast, pim1 in fission yeast and BJ1 in Drosophila, is a protein that contains seven tandem repeats of a domain of about 50 to 60 amino acids. As shown in the following schematic representation, the repeats make up the major part of the length of the protein. Outside the repeat region, there is just a small N-terminal domain of about 40 to 50 residues and, in the Drosophila protein only, a C-terminal domain of about 130 residues.

WW - domain that interacts with *PxxPP* seq. on *gag* L-domain of HIV

SMART SM0456; Pfam PF00397; Also known as the WWP or rsp5 domain. Binds proline-rich polypeptides. The WW domain (also known as rsp5 or WWP) is a short conserved region in a number of unrelated proteins, among them dystrophin, responsible for Duchenne muscular dystrophy. This short domain may be repeated up to four times in some proteins. The WW domain binds to proteins with particular proline-domains, [AP]-P-P-[AP]-Y, and having four conserved aromatic positions that are generally Trp. The name WW or WWP derives from the presence of these Trp as well as that of a conserved Pro. It is frequently associated with other domains typical for proteins in signal transduction processes. A large variety of proteins containing the WW domain are known. These include; dystrophin, a multidomain cytoskeletal protein; utrophin, a dystrophin-like protein of unknown function; vertebrate YAP protein, substrate of an unknown serine kinase; mouse NEDD-4, involved in the embryonic development and differentiation of the central nervous

system; yeast RSP5, similar to NEDD-4 in its molecular organization; rat FE65, a transcription-factor activator expressed preferentially in liver; tobacco DB10 protein and others.

C2 - domain that interacts with phospholipids, inositol polyphosphates, and intracellular proteins

SMART SM0239; Pfam PF00168; Ca2+-binding domain present in phospholipases, protein kinases C, and synaptotamins (among others). Some do not appear to contain Ca2+-binding sites. Particular C2s appear to bind phospholipids, inositol polyphosphates, and intracellular proteins. Unusual occurrence in perforin. Synaptotagmin and PLC C2s are permuted in sequence with respect to N- and C-terminal beta strands. SMART detects C2 domains using one or both of two profiles.

Interpro abstract (IPR000008): Some isozymes of protein kinase C (PKC) is located between the two copies of the C1 domain (that bind phorbol esters and diacylglycerol) and the protein kinase catalytic domain. Regions with significant homology to the C2-domain have been found in many proteins. The C2 domain is thought to be involved in calcium-dependent phospholipid binding. Since domains related to the C2 domain are also found in proteins that do not bind calcium, other putative functions for the C2 domain like e.g. binding to inositol-1,3,4,5-tetraphosphate have been suggested. The 3D structure of the C2 domain of synaptotagmin has been reported the domain forms an eight-stranded beta sandwich constructed around a conserved 4-stranded domain, designated a C2 key. Calcium binds in a cup-shaped depression formed by the N- and C-terminal loops of the C2-key domain.

CUE - domain that recruits E2 to ER membrane proximity

SMART SM0546; Pfam PF02845; Domain that may be involved in binding ubiquitin-conjugating enzymes (UBCs). CUE domains also occur in two proteins of the IL-1 signal transduction pathway, tollip and TAB2.

SH3 & SH2 -

SMART SM0252; Pfam PF00017; Src homology 2 domains bind phosphotyrosine-containing polypeptides via 2 surface pockets. Specificity is provided via interaction

with residues that are distinct from the phosphotyrosine. Only a single occurrence of a SH2 domain has been found in S. cerevisiae. The Src homology 2 (SH2) domain is a protein domain of about 100 amino-acid residues first identified as a conserved sequence region between the oncoproteins Src and Fps. Similar sequences were later found in many other intracellular signal-transducing proteins. SH2 domains function as regulatory modules of intracellular signalling cascades by interacting with high affinity to phosphotyrosine-containing target peptides in a sequence-specific and strictly phosphorylation-dependent manner. They are found in a wide variety of protein contexts e.g., in association with catalytic domains of phospholipase Cy (PLCy) and the nonreceptor protein tyrosine kinases; within structural proteins such as fodrin and tensin; and in a group of small adaptor molecules, i.e Crk and Nck. In many cases, when an SH2 domain is present so too is an SH3 domain, suggesting that their functions are inter-related. The domains are frequently found as repeats in a single protein sequence. The structure of the SH2 domain belongs to the alpha+beta class, its overall shape forming a compact flattened hemisphere. The core structural elements comprise a central hydrophobic anti-parallel beta-sheet, flanked by 2 short alpha-helices. In the v-src oncogene product SH2 domain, the loop between strands 2 and 3 provides many of the binding interactions with the phosphate group of its phosphopeptide ligand, and is hence designated the phosphate binding loop.

The SH3 domain (SMART SM0326) shares 3D similarity with the WW domain, and may bind to PxxPP sequence of the viral gag protein. Src homology 3 (SH3) domains bind to target proteins through sequences containing proline and hydrophobic amino acids. Pro-containing polypeptides may bind to SH3 domains in 2 different binding orientations. The SH3 domain has a characteristic fold which consists of five or six beta-strands arranged as two tightly packed anti-parallel beta sheets. The linker regions may contain short helices.

Protein domain information may be obtained from any of the following websites: SMART (http://smart.embl-heidelberg.de/), Pfam (http://smart.embl-heidelberg.de/), InterPro (http://www.ebi.ac.uk/interpro/scan.html).

Example 3: Methods for screening the biological activity of the E3 proteins and validating the role of E3's as potential drug targets

A functional biological assay for a disease or a pathological condition is developed in each instance. RNA interference (RNAi) technology or dominant negative forms of candidate E3s or any of the other techniques that are used in the art to inhibit expression of relevant target proteins may be used. The ability of these method to remedy the abnormality that causes a disease/pathological condition validates the role of the specific E3 and its relevance as a potential drug target.

Identification of an E3 involved in the ubiquitin-mediated viral release

Experimental evidence supports a model wherein the release of viral like particles (VLP) from infected cells is dependent on ubiquitination of a viral protein such as gag. Ubiquitintaion of gag indicates that a human E3 protein is involved. The gag proteins, such as the late domain, are known to interact with the HECT domain and a WW or SH3 domain of the E3 proteins. Therefore, human E3 proteins that may have wither a HECT or a WW or SH3domain may mediate the ubiquitination of gag to facilitate viral release.

The detection and/or measurement of the release of VLP from cells infected with retroviral infections provide a convenient biological assay.

The inhibition of VLP release by decreasing the expression of the potential drug target validates the potential drug target.

Identification of an E3 involved in the ubiquitin-mediated degradation of an Interacting Protein

A ubiquitin-protein ligase that mediates the ubiquitination of CFTR is identified. Cystic fibrosis (CF) is an inherited disorder is caused by the malfunction or reduced surface expression of the Cystic Fibrosis Transduction Regulator (CFTR). Approximately 70% of the affected individuals are homozygous to the $CFTR^{\Delta F508}$ mutation. Mutant CFTR is rapidly degraded in the endoplasmic reticulum (ER) via the ubiquitin proteolytic system resulting in inhibition of surface expression. An ER-associated E3 is likely to mediate the ubiquitination of CFTR. Accordingly, preferred E3 candidates are those localized to the ER or those that

have the CUE domain. Cell surface expression of $CFTR^{\Delta F508}$ is used as the functional biological assay. Finally, the target is validated by detecting increased surface expression of $CFTR^{\Delta F508}$ in cells co-expressing a dominant negative form of a candidate E3 or transfected with a specific RNAi derived from a candidate E3.

Example 4: Identification and validation of POSH as a drug target for antiviral agents

An example of the systems disclosed herein was used to successfully identify a drug target for antiviral agents, and especially agents that are effective against HIV and related viruses.

A database of greater than 500 E3 proteins was assembled. The database contained many of the proteins presented in Table 2. A subset of proteins was selected based on various characteristics, such as the presence of RING and SH3 domains or HECT and RCC domains. The proteins of this subset are shown in Table 3. Proteins of the subset were tested for their effects on the lifecycle of HIV using the Virus-Like Particle (VLP) assay system. A knockdown for each protein was created by contacting the assay cells with an siRNA construct specific for an mRNA sequence corresponding to each of the proteins of Table 3. Results for POSH and proteins 1 – 6 are shown in Figure 5. Decrease in POSH production by siRNA led to a complete or near-complete disruption of VLP production. A few of the other E3s tested gave partial effects on VLP production, and most E3s had no effect. Tsg101 is used as a positive control.

Table 3: E3 subset selected for VLP Assays

Gene	Accession
1. CEB1	AB027289
2. HERC1	U50078
3. HERC2	AF071172
4. HERC3	D25215

5. ITCH	AF095745
6. KIAA1301	AB037722
7. KIAA1593	AB046813
8. Nedd4	D42055
9. NeddL1	AB048365
10. Need4L	AB007899
11. PAM	AF07558
12. POSH	protlog1
13. SMURF1	AC004893
14. SMURF2	NM_022739
15. WWP1	AL136739
16. WWP2	U96114

Figure 6 shows a pulse-chase VLP assay confirming that a decrease in POSH function leads to a complete or near-complete inhibition of VLP production. Accordingly, systems disclosed herein are effective for rapidly generating drug targets.

Detailed protocols for performing VLP assays and siRNA knockdown experiments are as follows.

Steady-state VLP assay:

1. Objective:

Use RNAi to inhibit POSH gene expression and compare the efficiency of viral budding and GAG expression and processing in treated and untreated cells.

2. Study Plan:

HeLa SS-6 cells are transfected with mRNA-specific RNAi in order to knockdown the target proteins. Since maximal reduction of target protein by RNAi is achieved after 48 hours, cells are transfected twice – first to reduce target mRNAs, and subsequently to express the viral Gag protein. The second transfection is performed with pNLenv (plasmid that encodes HIV) and with low amounts of RNAi to maintain the knockdown of target protein during the time of gag expression and

budding of VLPs. Reduction in mRNA levels due to RNAi effect is verified by RT-PCR amplification of target mRNA.

3. Methods, Materials, Solutions

a. Methods

i. Transfections according to manufacturer's protocol and as described in procedure.

ii. Protein determined by Bradford assay.

iii. SDS-PAGE in Hoeffer miniVE electrophoresis system. Transfer in Bio-Rad mini-protean II wet transfer system. Blots visualized using Typhoon system, and ImageQuant software (ABbiotech)

b. Materials

Material	Manufacturer	Catalog #	Batch #
Lipofectamine 2000 (LF2000)	Life Technologies	11668-019	1112496
OptiMEM	Life Technologies	31985-047	3063119
RNAi Lamin A/C	Self	13	
RNAi TSG101 688	Self	65	
RNAi Posh 524	Self	81	
plenvl1 PTAP	Self	148	
plenvl1 ATAP	Self	149	
Anti-p24 polyclonal antibody	Seramun		A-0236/5-10-01
Anti-Rabbit Cy5 conjugated antibody	Jackson	144-175-115	48715
10% acrylamide Tris-Glycine SDS-PAGE gel	Life Technologies	NP0321	1081371
Nitrocellulose membrane	Schleicher & Schuell	401353	BA-83
NuPAGE 20X transfer buffer	Life Technologies	NP0006-1	224365
0.45μm filter	Schleicher & Schuell	10462100	CS1018-1

c. Solutions

Lysis Buffer	Compound	Concentration
	Tris-HCl pH 7.6	50mM

	$MgCl_2$	15mM
	NaCl	150mM
	Glycerol	10%
	EDTA	1mM
	EGTA	1mM
	ASB-14 (add immediately before use)	1%
6X Sample Buffer	Tris-HCl, pH=6.8	1M
	Glycerol	30%
	SDS	10%
	DTT	9.3%
	Bromophenol Blue	0.012%
TBS-T	Tris pH=7.6	20mM
	NaCl	137mM
	Tween-20	0.1%

4. Procedure

a. Schedule

Day				
1	2	3	4	5
Plate cells	Transfection I (RNAi only)	Passage cells (1:3)	Transfection II (RNAi and pNlenv) (12:00, PM)	Extract RNA for RT-PCR (post transfection)
			Extract RNA for RT-PCR (pre-transfection)	Harvest VLPs and cells

b. Day 1

Plate HeLa SS-6 cells in 6-well plates (35mm wells) at concentration of 5 X105 cells/well.

c. Day 2

2 hours before transfection replace growth medium with 2 ml growth medium without antibiotics.

Transfection I:

Reaction	RNAi name	TAGDA#	Reactions	RNAi [nM]	RNAi [20µM] µl	A OPtiMEM (µl)	B LF2000 mix (µl)
1	Lamin A/C	13	2	50	12.5	500	500

2	Lamin A/C	13	1	50	6.25	250	250
3	TSG101 688	65	2	20	5	500	500
5	Posh 524	81	2	50	12.5	500	500

Transfections:

Prepare LF2000 mix : 250µl OptiMEM + 5 µl LF2000 for each reaction. Mix by inversion, 5 times. Incubate 5 minutes at room temperature.

Prepare RNA dilution in OptiMEM (Table 1, column A). Add LF2000 mix dropwise to diluted RNA (Table 1, column B). Mix by gentle vortex. Incubate at room temperature 25 minutes, covered with aluminum foil.

Add 500µl transfection mixture to cells dropwise and mix by rocking side to side.

Incubate overnight.

d. Day 3

Split 1:3 after 24 hours. (Plate 4 wells for each reaction, except reaction 2 which is plated into 3 wells.)

e. Day 4

2 hours pre-transfection replace medium with DMEM growth medium without antibiotics.

Transfection II

					A	B	C	D
RNAi name	TAGDA#	Plasmid	Reactions	Plasmid (µg/µl)	Plasmid for 2.4 µg (µl)	RNAi [20µM] for 10nM (µl)	OPtiMEM (µl)	LF2000 mix (µl)
Lamin A/C	13	PTAP	3		3.4	3.75	750	750
Lamin A/C	13	ATAP	3		2.5	3.75	750	750
TSG101 688	65	PTAP	3		3.4	3.75	750	750
Posh 524	81	PTAP	3		3.4	3.75	750	750

Prepare LF2000 mix: 250µl OptiMEM + 5 µl LF2000 for each reaction. Mix by inversion, 5 times. Incubate 5 minutes at room temperature.

Prepare RNA+DNA diluted in OptiMEM (Transfection II, A+B+C)

Add LF2000 mix (Transfection II, D) to diluted RNA+DNA dropwise, mix by gentle vortex, and incubate 1h while protected from light with aluminum foil.

Add LF2000 and DNA+RNA to cells, 500µl/well, mix by gentle rocking and incubate overnight.

f. Day 5

Collect samples for VLP assay (approximately 24 hours post-transfection) by the following procedure (cells from one well from each sample is taken for RNA assay, by RT-PCR).

g. Cell Extracts

i. Pellet floating cells by centrifugation (5min, 3000rpm at 40°C), save supernatant (continue with supernatant immediately to step h), scrape remaining cells in the medium which remains in the well, add to the corresponding floating cell pellet and centrifuge for 5 minutes, 1800rpm at 40°C.

ii. Wash cell pellet twice with ice-cold PBS.

iii. Resuspend cell pellet in 100µl lysis buffer and incubate 20 minutes on ice.

iv. Centrifuge at 14,000rpm for 15min. Transfer supernatant to a clean tube. This is the cell extract.

v. Prepare 10µl of cell extract samples for SDS-PAGE by adding SDS-PAGE sample buffer to 1X, and boiling for 10 minutes. Remove an aliquot of the remaining sample for protein determination to verify total initial starting material. Save remaining cell extract at -80 °C.

h. Purification of VLPs from cell media

i. Filter the supernatant from step g through a 0.45m filter.

ii. Centrifuge supernatant at 14,000rpm at 40C for at least 2h.

iii. Aspirate supernatant carefully.

iv. Re-suspend VLP pellet in hot (100°C warmed for 10 min at least) 1X sample buffer.

v. Boil samples for 10 minutes, 100°C.

i. Western Blot analysis

i. Run all samples from stages A and B on Tris-Glycine SDS-PAGE 10% (120V for 1.5h.).

ii. Transfer samples to nitrocellulose membrane (65V for 1.5h.).

iii. Stain membrane with ponceau S solution.

iv. Block with 10% low fat milk in TBS-T for 1h.

v. Incubate with anti p24 rabbit 1:500 in TBS-T o/n.

vi. Wash 3 times with TBS-T for 7min each wash.

vii. Incubate with secondary antibody anti rabbit cy5 1:500 for 30min.

viii. Wash five times for 10min in TBS-T

ix. View in Typhoon gel imaging system (Molecular Dynamics/APBiotech) for fluorescence signal.

Exemplary RT-PCR primers for POSH

	Name	Position	Sequence
Sense primer	POSH=271	271	5' CTTGCCTTGCCAGCATAC 3' (SEQ ID NO:12)
Anti-sense primer	POSH=926c	926C	5' CTGCCAGCATTCCTTCAG 3' (SEQ ID NO:13)

siRNA duplexes:

siRNA No: 153

siRNA Name: POSH-230

Position in mRNA 426-446

Target sequence: 5' AACAGAGGCCTTGGAAACCTG 3' SEQ ID NO: 14

siRNA sense strand: 5' dTdTCAGAGGCCUUGGAAACCUG 3' SEQ ID NO: 15

siRNA anti-sense strand: 5'dTdTCAGGUUUCCAAGGCCUCUG 3' SEQ ID NO: 16

siRNA No: 155

siRNA Name: POSH-442

Position in mRNA 638-658

Target sequence: 5' AAAGAGCCTGGAGACCTTAAA 3' SEQ ID NO: 17

siRNA sense strand: 5' ddTdTAGAGCCUGGAGACCUUAAA 3' SEQ ID NO: 18

siRNA anti-sense strand: 5' ddTdTUUUAAGGUCUCCAGGCUCU 3' SEQ ID NO: 19

siRNA No: 157

siRNA Name: POSH-U111

Position in mRNA 2973-2993

Target sequence: 5' AAGGATTGGTATGTGACTCTG 3' SEQ ID NO: 20

siRNA sense strand: 5' dTdTGGAUUGGUAUGUGACUCUG 3' SEQ ID NO: 21

siRNA anti-sense strand: 5' dTdTCAGAGUCACAUACCAAUCC 3' SEQ ID NO: 22

siRNA No: 159

siRNA Name: POSH-U410

Position in mRNA 3272-3292

Target sequence: 5' AAGCTGGATTATCTCCTGTTG 3' SEQ ID NO: 23

siRNA sense strand: 5' ddTdTGCUGGAUUAUCUCCUGUUG 3' SEQ ID NO: 24

siRNA anti-sense strand: 5' ddTdTCAACAGGAGAUAAUCCAGC 3' SEQ ID NO: 25

Protocol for Assessing POSH siRNA effects on the kinetics of VLP release

A1. Transfections

1. One day before transfection plate cells at a concentration of $5x10^6$ cell/well in 15cm plates.
2. Two hours before transfection, replace cell media to 20ml complete DMEM without antibiotics.
3. DNA dilution: for each transfection dilute 62.5µl RNAi in 2.5ml OptiMEM according to the table below. RNAi stock is 20µM (recommended concentration: 50nM, dilution in total medium amount 1:400).
4. LF 2000 dilution: for each transfection dilute 50µl lipofectamine 2000 reagent in 2.5ml OptiMEM.
5. Incubate diluted RNAi and LF 2000 for 5 minutes at RT.
6. Mix the diluted RNAi with diluted LF2000 and incubated for 20-25 minutes at RT.
7. Add the mixure to the cells (drop wise) and incubate for 24 hours at 37°C in CO_2 incubator.
8. One day after RNAi transfection split cells (in complete MEM medium to 2 15cm plate and 1 well in a 6 wells plate)
9. One day after cells split perform HIV transfection according to SP 30-012-01.
10. 6 hours after HIV transfection replace medium to complete MEM medium.

* Perform RT-PCR for POSH to assess degree of knockdown.

A2. Total RNA purification.

1. One day after transfection, wash cells twice with sterile PBS.
2. Scrape cells in 2.3ml/200µl (for 15cm plate/1 well of a 6 wells plate) Tri reagent (with sterile scrapers) and freeze in -70°C.

Treatment	Chase time (hours)	Fraction	Labeling
Control=WT	1	Cells	A1
		VLP	A1 V
	2	Cells	A2
		VLP	A2 V
	3	Cells	A3
		VLP	A3 V
	4	Cells	A4
		VLP	A4 V
	5	Cells	A5
		VLP	A5 V
Posh+WT	1	Cells	B1
		VLP	B1 V
	2	Cells	B2
		VLP	B2 V
	3	Cells	B3
		VLP	B3 V
	4	Cells	B4
		VLP	B4 V
	5	Cells	B5
		VLP	B5 V

B. Labeling

1. Take out starvation medium, thaw and place at 37^0C.
2. Scrape cells in growth medium and transfer gently into 15 ml conical tube.
3. Centrifuge to pellet cells at 1800rpm for 5 minutes at room temperature.

4. Aspirate supernatant and let tube stand for 10 sec. Remove the rest of the supernatant with a 200µl pipetman.

5. Gently add 10ml warm starvation medium and resuspend carefully with a 10ml pipette, up and down, just turning may not resolve the cell pellet).

6. Transfer cells to 10cm tube and place in the incubator for 60 minutes. Set an Eppendorf thermo mixer to 37^0C.

7. Centrifuge to pellet cells at 1800rpm for 5 minutes at room temperature.

8. Aspirate supernatant and let tube stand for 10 sec. Remove the rest of the supernatant with a 200 µl pipetman.

9. Cut a 200µl tip from the end and resuspend cells (~ 1.5 10^7 cells in 150 µl RPIM without Met, but try not to go over 250 µl if you have more cells) gently in 150 µl starvation medium. Transfer cells to an Eppendorf tube and place in the thermo mixer. Wait 10 sec and transfer the rest of the cells from the 10 ml tube to the Eppendorf tube, if necessary add another 50 µl to splash the rest of the cells out (all specimens should have the same volume of labeling reaction!).

10. Pulse: Add 50 µl of ^{35}S-methionine (specific activity 14.2 µCi/µl), tightly cup tubes and place in thermo mixer. Set the mixing speed to the lowest possible (700 rpm) and incubate for 25 minutes.

11. Stop the pulse by adding 1ml ice-cold chase/stop medium. Shake tube very gently three times and pellet cells at 6000rpm for 6 sec.

12. Remove supernatant with a 1ml tip. Add gently 1ml ice-cold chase/stop medium to the pelleted cells and invert gently to resuspend.

13. Chase: Transfer all tubes to the thermo mixer and incubate for the required chase time (**830**:1,2,3,4 and 5 hours; **828**: 3 hours only). At the end of total chase time, place tubes on ice, add 1ml ice-cold chase/stop and pellet cells for 1 minute at 14,000 rpm. Remove supernatant and transfer supernatant to a second eppendorf tube. The cell pellet freeze at -80^0C, until all tubes are ready.

14. Centrifuge supernatants for 2 hours at 14,000rpm, 4°C. Remove the supernatant very gently, leave 20 µl in the tube (labeled as V) and freeze at -80°C until the end of the time course.

*** All steps are done on ice with ice-cold buffers

15. When the time course is over, remove all tubes form –80°C. Lyse VLP pellet (from step 14) and cell pellet (step 13) by adding 500 µl of lysis buffer (see solutions), resuspend well by pipeting up and down three times. Incubate on ice for 15 minutes, and spin in an eppendorf centrifuge for 15 minutes at 4°C, 14,000 rpm. Remove supernatant to a fresh tube, discard pellet.

16. Perform IP with anti-p24 sheep for all samples.

C. Immunoprecipitation

1. Preclearing: add to all samples 15µl ImmunoPure PlusG (Pierce). Rotate for 1 hour at 4°C in a cycler, spin 5 min at 4°C, and transfer to a new tube for IP.
2. Add to all samples 20µl of p24-protein G conjugated beads and incubate 4 hours in a cycler at 4°C.
3. Post immunoprecipitations, transfer all immunoprecipitations to a fresh tube.
4. Wash beads once with high salt buffer, once with medium salt buffer and once with low salt buffer. After each spin don't remove all solution, but leave 50 µl solution on the beads. After the last spin remove supernatant carefully with a loading tip and leave ~10 µl solution.
5. Add to each tube 20 µl 2x SDS sample buffer. Heat to 70°C for 10 minutes.
6. Samples were separated on 10% SDS-PAGE.
7. Fix gel in 25% ethanol and 10% acetic acid for 15 minutes.
8. Pour off the fixation solution and soak gels in Amplify solution (NAMP 100 Amersham) for 15 minutes.
9. Dry gels on warm plate (60-80 °C) under vacuum.

10. Expose gels to screen for 2 hours and scan.

Example 5: Identification of drug targets for anti-neoplastic agents

A database of greater than 500 E3 proteins is assembled. The database contains many of the proteins presented in Table 2. A subset of proteins is selected based on various characteristics, such as the presence of certain domains. The expression of genes encoding the proteins is assessed in cancerous and non-cancerous tissues to identify genes of the database that are overexpressed or underexpressed in cancerous tissues. Examples of cancerous and non-cancerous tissues to be tested include: lung, laryngopharynx, pancreas, liver, rectum, colon, stomach, breast, cervix, uterus, ovary, testes, prostate and skin.

Genes that are identified as overexpressed in cancer are subjected to siRNA knockdown in a cancerous cell line, such as HeLa cells. If the knockdown decreases proliferation of the cancerous cell line, the gene and the encoded protein are targets for developing anti-neoplastic agents.

POSH is overexpressed in certain cancerous tissues, and POSH siRNA decreases proliferation of HeLa cells.

INCORPORATION BY REFERENCE

All of the patents and publications cited herein are hereby incorporated by reference.

EQUIVALENTS

Those skilled in the art will recognize, or be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments of the invention described herein. Such equivalents are intended to be encompassed by the following claims.

Reset

TABLE 2.

Hs.1004
Gene: BRPF1 Sequence count: 105

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	6630865	AAF19605.1	-	1214	putative 8-hydroxyguanine DNAglycosylase [Homo sapiens]
☐	15295343	XP_054520.1	-	1214	similar to bromodomain and PHDfinger containing, 1 (H. sapiens) [Homo sapiens]
☐	190352	AAB02119.1	M91585	1214	Br140
☐	4757866	NP_004625.1	NM_004634	1214	bromodomain-containing proteinperegrin bromodomain-containing protein, 140kD [Homo sapiens]

Hs.10101
Gene: FLJ12875 Sequence count: 197

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	15297553	XP_015234.2	-	352	hypothetical protein FLJ12875[Homo sapiens]
☐	10434615	BAB14317.1	AK022937	352	unnamed protein product [Homosapiens]
☐	14603284	AAH10101.1	BC010101	352	AAH10101 hypothetical proteinFLJ12875 [Homo sapiens]
☐	15559301	AAH14010.1	BC014010	352	AAH14010 hypothetical proteinFLJ12875 [Homo sapiens]
☐	13375705	NP_078820.1	NM_024544	352	hypothetical protein FLJ12875[Homo sapiens]

Hs.102652
Gene: ASH1 Sequence count: 190

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	7739725	AAF68983.1	AF257305	2969	AF257305_1 ASH1 [Homo sapiens]
☐	8922081	NP_060959.1	NM_018489	2969	hypothetical protein ASH1 [Homosapiens]

Hs.102737
Gene: GP Sequence count: 363

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	14733373	XP_003972.2	-	264	goliath protein [Homo sapiens]
☐	16877726	AAH17100.1	-	276	AAH17100 likely ortholog of mouseg1-related zinc finger protein [Homo sapiens]
☐	7677054	AAF67007.1	AF155650	276	AF155650_1 goliath protein [Homosapiens]
☐	10092651	NP_060904.1	NM_018434	276	goliath protein likely orthologof mouse g1-related zinc finger protein [Homo sapiens]

Hs.1042
Gene: SSA1 Sequence count: 62

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	665918	AAB87094.1	-	475	52 kda component of SS-A/Roautoantigen [Homo sapiens]
☐	747927	AAA79867.1	-	475	RO52 gene product
☐	14994115	AAK76432.1	-	475	AF391283_1 SSA1 [Homo sapiens]
☐	14790039	AAH10861.1	BC010861	475	AAH10861 Unknown (protein forMGC:9233) [Homo sapiens]
☐	337485	AAA36581.1	M34551	475	52-kD Ro/SSA ribonucleoprotein
☐	338490	AAA36651.1	M62800	475	52-kD SS-A/Ro autoantigen
☐	15208660	NP_003132.2	NM_003141	475	52kD Ro/SSA autoantigen Sjogrensyndrome antigen A1 Sicca syndrome antigen A tripartite motifprotein TRIM21 [Homo sapiens]

Hs.105280
Gene: GP Sequence count: 83

Select	GI	Protein Acc.	DNA Acc.	Length	Description

☐	15530305	AAH13948.1	BC013948	237	AAH13948 Similar to RIKEN cDNA1700045I19 gene [Homo sapiens]

Hs.10590
Gene: ZNF313 Sequence count: 500

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	5304869	CAB46028.1	-	228	dJ963K23.2 (novel protein) [Homosapiens]
☐	8489813	AAF75763.1	AF265215	228	AF265215_1 DJ963K23.2 [Homo sapiens]
☐	15489174	AAH13695.1	BC013695	228	AAH13695 zinc finger protein 313[Homo sapiens]
☐	8923898	NP_061153.1	NM_018683	228	zinc finger protein 313 DJ963K23.2[Homo sapiens]

Hs.106826
Gene: BHC80 Sequence count: 167

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	7582284	AAF64262.1	-	328	AF208848_1 BM-006 [Homo sapiens]
☐	16041692	AAH15714.1	-	680	AAH15714 Similar to KIAA1696 protein[Homo sapiens]
☐	19923462	NP_057705.2	-	634	BRAF35/HDAC2 complex [Homosapiens]
☐	20135652	AAM09095.1	-	634	BRAF35/HDAC2 complex 80 kDa protein[Homo sapiens]
☐	12697937	BAB21787.1	AB051483	635	KIAA1696 protein [Homo sapiens]
☐	10435111	BAB14492.1	AK023258	634	unnamed protein product [Homosapiens]

Hs.107153
Gene: ING1L Sequence count: 91

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	4115555	BAA36419.1	AB012853	280	ING1Lp [Homo sapiens]

☐	9992838	AAG11395.1	AF053537	280	AF053537_1 p33 [Homo sapiens]
☐	12053588	CAC20567.1	AJ006851	280	p32 protein [Homo sapiens]
☐	4504695	NP_001555.1	NM_001564	280	inhibitor of growth 1-like [Homosapiens]

Hs.108106
Gene: UHRF1 Sequence count: 118

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	6815251	AAF28469.1	AF129507	793	AF129507_1 transcription factor ICBP90[Homo sapiens]
☐	14190527	AAK55744.1	AF274048	793	AF274048_1 nuclear zinc fingerprotein Np95 [Homo sapiens]
☐	10438137	BAB15177.1	AK025578	189	unnamed protein product [Homosapiens]
☐	16507204	NP_037414.2	NM_013282	793	ubiquitin-like, containing PHD andRING finger domains, 1 transcription factor ICBP90 [Homo sapiens]

Hs.108183
Gene: ING4 Sequence count: 193

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	17456536	XP_006980.2	-	245	candidate tumor suppressor p33ING1 homolog [Homo sapiens]
☐	18873723	AAL79773.1	-	249	AF156552_1 p29ING4 [Homo sapiens]
☐	12002020	AAG43153.1	AF063594	262	AE063594_1 brain my036 protein [Homosapiens]
☐	5730480	AAD48585.1	AF110645	249	candidate tumor suppressor p33 ING1homolog [Homo sapiens]
☐	14043612	AAH07781.1	BC007781	249	AAH07781 Unknown (protein forMGC:12557) [Homo sapiens]
☐	15278375	AAH13038.1	BC013038	221	AAH13038 Similar to RIKEN cDNA1700027H23 gene [Homo

					sapiens]
☐	7705861	NP_057246.1	NM_016162	249	p29ING4 [Homo sapiens]

Hs.10915
Gene: MGC11279 Sequence count: 127

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	10178315	CAC08401.1	-	296	bA18I14.4 (novel protein) [Homosapiens]
☐	12804119	AAH02912.1	BC002912	296	AAH02912 Unknown (protein forMGC:11279) [Homo sapiens]
☐	13236573	NP_077302.1	NM_024326	296	hypothetical protein MGC11279[Homo sapiens]

Hs.110457
Gene: WHSC1 Sequence count: 470

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	19913346	NP_055734.1	-	802	Wolf-Hirschhorn syndrome candidate1 protein, isoform 2 IL-5 promoter REII-region-binding proteintrithorax/ash1-related protein 5 multiple myeloma SET domain protein[Homo sapiens]
☐	19913348	NP_579877.1	-	1365	Wolf-Hirschhorn syndrome candidate1 protein, isoform 1 IL-5 promoter REII-region-binding proteintrithorax/ash1-related protein 5 multiple myeloma SET domain protein[Homo sapiens]
☐	19913350	NP_579878.1	-	1365	Wolf-Hirschhorn syndrome candidate1 protein, isoform 1 IL-5 promoter REII-region-binding proteintrithorax/ash1-related protein 5 multiple myeloma SET domain protein[Homo sapiens]
☐	19913358	NP_579890.1	-	1365	Wolf-Hirschhorn syndrome candidate1 protein, isoform 1 IL-5 promoter REII-region-binding proteintrithorax/ash1-related protein 5 multiple myeloma SET domain protein[Homo sapiens]

	19913361	NP_579891.1	-	584	Wolf-Hirschhorn syndrome candidate1 protein, isoform 5 IL-5 promoter REII-region-binding proteintrithorax/ash1-related protein 5 multiple myeloma SET domain protein[Homo sapiens]
	5689517	BAA83042.1	AB029013	713	KIAA1090 protein [Homo sapiens]
	3249713	AAC24150.1	AF071593	1365	MMSET type II [Homo sapiens]
	4378019	AAD19343.1	AF083386	1365	putative WHSC1 protein [Homo sapiens]
	4521954	AAD21770.1	AF083387	1365	putative WHSC1 protein [Homo sapiens]
	4521955	AAD21771.1	AF083388	1365	putative WHSC1 protein [Homo sapiens]
	12642795	AAK00344.1	AF330040	584	AF330040_1 IL-5 promoterREII-region-binding protein [Homo sapiens]
	5123789	CAB45386.1	AJ007042	1365	TRX5 protein [Homo sapiens]
	6594683	*NP_015627.1*	*NM_007331*	*629*	*Wolf-Hirschhorn syndrome candidate1 protein, isoform 4 IL-5 promoter REII-region-binding proteintrithorax/ash1-related protein 5 multiple myeloma SET domain protein[Homo sapiens]*
	3249715	*AAC24151.1*	*AF071594*	*647*	*MMSET type I [Homo sapiens]*
	4378022	*AAD19346.1*	*AF083391*	*629*	*putative WHSC1 protein [Homo sapiens]*
	4378021	*AAD19345.1*	*AF083390*	*647*	*putative WHSC1 protein [Homo sapiens]*
	4378020	*AAD19344.1*	*AF083389*	*647*	*putative WHSC1 protein [Homo sapiens]*

Hs.11050
Gene: FBXO9 Sequence count: 328

Select	GI	Protein Acc.	DNA Acc.	Length	Description

☐	5360123	AAD42880.1	AF155114	434	AF155114_1 NY-REN-57 antigen [Homosapiens]
☐	6164737	AAF04518.1	AF174597	327	AF174597_1 F-box protein Fbx9 [Homosapiens]
☐	6103647	AAF03704.1	AF176704	447	F-box protein FBX9 [Homo sapiens]
☐	6808184	CAB70786.1	AL137520	547	hypothetical protein [Homo sapiens]
☐	12653729	AAH00650.1	BC000650	327	AAH00650 Similar to F-box onlyprotein 9 [Homo sapiens]
☐	6912546	NP_036479.1	NM_012347	447	F-box only protein 9, isoform 1F-box protein Fbx9 [Homo sapiens]
☐	15812201	NP_258441.1	NM_033480	437	F-box only protein 9 F-boxprotein Fbx9 [Homo sapiens]
☐	15812203	NP_258442.1	NM_033481	327	F-box only protein 9 F-boxprotein Fbx9 [Homo sapiens]

Hs.110953
Gene: - Sequence count: 0

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	6599192	CAB63768.1	-	392	hypothetical protein [Homo sapiens]

Hs.11123
Gene: DKFZP564G092 Sequence count: 107

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	9884661	CAC04175.1	-	103	bA57G10.5 (A novel protein, similarto KIAA0032) [Homo sapiens]
☐	10047261	BAB13419.1	AB046813	953	KIAA1593 protein [Homo sapiens]
☐	5419849	CAB46371.1	AL096715	110	hypothetical protein [Homo sapiens]
☐	7661612	NP_056416.1	NM_015601	110	DKFZP564G092 protein [Homo sapiens]

Hs.11156
Gene: LOC51255 Sequence count: 257

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	7106866	AAF36158.1	-	153	AF151072_1 HSPC238 [Homo sapiens]
☐	12803913	AAH02803.1	BC002803	153	AAH02803 hypothetical protein [Homosapiens]
☐	7706039	NP_057578.1	NM_016494	153	hypothetical protein LOC51255 [Homosapiens]

Hs.112227
Gene: - Sequence count: 0

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	9837125	AAG00432.1	-	1048	AF255303_1 membrane-associated nucleicacid binding protein [Homo sapiens]

Hs.117414
Gene: KIAA1320 Sequence count: 56

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	14759464	XP_045095.1	-	562	KIAA1320 protein [Homo sapiens]
☐	7243021	BAA92558.1	AB037741	567	KIAA1320 protein [Homo sapiens]

Hs.118174
Gene: TTC3 Sequence count: 575

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	1304132	BAA11769.1	D83077	2025	TPRD [Homo sapiens]
☐	2662364	BAA23666.1	D83327	1941	DCRR1 [Homo sapiens]
☐	1632762	BAA12301.1	D84294	2025	TPRDI [Homo sapiens]
☐	1632764	BAA12302.1	D84295	1792	possible protein TPRDII [Homosapiens]

☐	1632766	BAA12303.1	D84296	1715	TPRDIII [Homo sapiens]
☐	10835037	NP_003307.1	NM_003316	1792	tetratricopeptide repeat domain 3tetratricopeptide repeat protein 3 (TPR repeat protein D) [Homosapiens]

Hs.119120
Gene: SMURF1 Sequence count: 153

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	3694664	AAC62434.1	-	712	similar to NEDD-4 (KIA0093) similarto P46934 (PID:g1171682) [Homo sapiens]
☐	10047327	BAB13451.1	AB046845	859	KIAA1625 protein [Homo sapiens]
☐	6446606	AAF08298.2	AF199364	722	E3 ubiquitin ligase SMURF1 [Homosapiens]

Hs.119960
Gene: DKFZP727G051 Sequence count: 190

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	14739106	XP_045308.1	-	371	DKFZP727G051 protein [Homosapiens]
☐	5911951	CAB55950.1	AL117477	473	hypothetical protein [Homo sapiens]

Hs.12017
Gene: NEDD4L Sequence count: 228

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	2662159	BAA23711.1	AB007899	995	KIAA0439 [Homo sapiens]
☐	12003318	AAG43524.1	AF210730	854	AF210730_1 NEDD4La [Homo sapiens]
☐	6808077	CAB70754.1	AL137469	820	hypothetical protein [Homo sapiens]
☐	12653675	AAH00621.1	BC000621	858	AAH00621 Unknown (protein forIMAGE:3346045) [Homo sapiens]

☐	14719404	NP_056092.1	NM_015277	854	ubiquitin-protein ligaseNEDD4-like potential epithelial sodium channel regulator neuralprecursor cell expressed, developmentally down-regulated gene 4-likehomolog of yeast ubiquitin-protein ligase Rsp5 [Homo sapiens]

Hs.121429
Gene: TRIM36 Sequence count: 46

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	8648883	CAB94831.1	AJ272269	728	zinc-binding protein [Homo sapiens]
☐	8924238	NP_061170.1	NM_018700	728	tripartite motif protein 36zinc-binding protein Rbcc728 [Homo sapiens]

☐

Hs.121748
Gene: TRIM17 Sequence count: 21

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	5114351	AAD40286.1	AF156271	477	RING finger protein terf [Homosapiens]
☐	7705825	NP_057186.1	NM_016102	477	tripartite motif-containing 17testis RING finger protein RING finger protein terf ring fingerprotein 16 [Homo sapiens]

Hs.12256
Gene: MID2_ Sequence count: 40

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	6358719	AAF07341.1	AF196481	685	AF196481_1 RING finger protein FXY2[Homo sapiens]
☐	6912504	NP_036348.1	NM_012216	715	midline 2, isoform 1 tripartitemotif protein 1 midin 2 [Homo sapiens]
	16445409	NP_438112.1	NM_052817	685	midline 2, isoform 2 tripartitemotif protein 1 midin 2

					[Homo sapiens]
	5912440	CAB56154.1	Y18880	715	midline 2 protein [Homo sapiens]

Hs.12271
Gene: - Sequence count: 0

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	6164727	AAF04513.1	-	283	AF174592_1 F-box protein Fbl6 [Homosapiens]

Hs.122764
Gene: BRAP Sequence count: 108

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	3252872	AAC24200.1	AF035620	600	BRCA1-associated protein 2 [Homosapiens]
	10800417	NP_006759.2	NM_006768	592	BRCA1 associated protein [Homosapiens]
	2665906	*AAB88538.1*	*AF035950*	*237*	*putative DDB p127-associated protein[Homo sapiens]*

Hs.12372
Gene: TRIM2 Sequence count: 220

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	14723164	XP_018435.2	-	744	tripartite motif protein TRIM2[Homo sapiens]
	3043558	BAA25443.1	AB011089	792	KIAA0517 protein [Homo sapiens]
	12407367	AAG53472.1	AF220018	744	AF220018_1 tripartite motif proteinTRIM2 [Homo sapiens]
	15029681	AAH11052.1	BC011052	744	AAH11052 tripartite motif protein 2[Homo sapiens]
	13446227	NP_056086.1	NM_015271	744	tripartite motif protein TRIM2KIAA0517 protein tripartite motif protein 2 [Homo sapiens]
	13477123	*AAH05016.1*	*BC005016*	*324*	*AAH05016 Unknown (protein forIMAGE:3636175) [Homo*

					sapiens]
	5817175	*CAB53687.1*	*AL110234*	*230*	*hypothetical protein [Homo sapiens]*

Hs.12376
Gene: - Sequence count: 0

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	6433936	CAB60727.1	-	759	aczonin [Homo sapiens]

Hs.124024
Gene: DTX1 Sequence count: 72

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	16163343	XP_051773.2	-	620	deltex homolog 1 [Homo sapiens]
	2981175	AAC06246.1	AF053700	620	deltex [Homo sapiens]
	13543301	AAH05816.1	BC005816	228	AAH05816 Similar to deltex(Drosophila) homolog 1 [Homo sapiens]
	4758202	NP_004407.1	NM_004416	620	deltex homolog 1 deltex(Drosophila) homolog 1 hDx-1 [Homo sapiens]

Hs.124186
Gene: RNF2 Sequence count: 63

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	11423783	XP_001741.1	-	336	ring finger protein 2 [Homosapiens]
	4769008	AAD29717.1	AF141327	336	AF141327_1 ring finger protein BAP-1[Homo sapiens]
	15214887	AAH12583.1	BC012583	336	AAH12583 Similar to ring fingerprotein 2 [Homo sapiens]
	6005747	NP_009143.1	NM_007212	336	ring finger protein 2 [Homosapiens]
	1785643	CAA71596.1	Y10571	336	dinG [Homo sapiens]

Hs.12439
Gene: FLJ20188 Sequence count: 126

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	16306784	AAH01586.1	-	326	AAH01586 hypothetical proteinFLJ20188 [Homo sapiens]
☐	7020121	BAA91002.1	AK000195	326	unnamed protein product [Homosapiens]
☐	8923179	NP_060173.1	NM_017703	326	hypothetical protein FLJ20188 [Homosapiens]
☐	*10440008*	*BAB15622.1*	*AK027004*	*273*	*unnamed protein product [Homosapiens]*

Hs.124835
Gene: FLJ20225 Sequence count: 39

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	7020180	BAA91024.1	AK000232	227	unnamed protein product [Homosapiens]
☐	9506663	NP_061935.1	NM_019062	227	hypothetical protein FLJ20225 [Homosapiens]

Hs.12504
Gene: DKFZp761D081 Sequence count: 175

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	7018493	CAB75669.1	AL157474	137	hypothetical protein [Homo sapiens]
☐	14714485	AAH10369.1	BC010369	137	AAH10369 likely ortholog of mouseArkadia [Homo sapiens]
☐	8922165	NP_060080.1	NM_017610	137	hypothetical protein DKFZp761D081[Homo sapiens]

Hs.125300
Gene: TRIM34 Sequence count: 39

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	18087807	NP_067629.2	-	488	tripartite motif protein 34,isoform 1 ring finger protein 21, interferon-responsiveinterferon-responsive finger protein 1 [Homo sapiens]

☐	18641345	NP_569074.1	-	270	tripartite motif protein 34,isoform 3 ring finger protein 21, interferon-responsiveinterferon-responsive finger protein 1 [Homo sapiens]
☐	11022688	BAB17049.1	AB039902	488	interferon-responsive fingerprotein 1 middle form [Homo sapiens]
☐	11022690	BAB17050.1	AB039903	842	interferon-responsive fingerprotein 1 long form [Homo sapiens]
☐	11022692	BAB17051.1	AB039904	270	interferon-responsive fingerprotein 1 short form [Homo sapiens]
☐	12407455	AAG53516.1	AF220143	488	AF220143_1 tripartite motif proteinTRIM34 alpha [Homo sapiens]
☐	14042869	BAB55424.1	AK027876	488	unnamed protein product [Homosapiens]
☐	*12407457*	*AAG53517.1*	*AF220144*	*243*	*AF220144_1 tripartite motif proteinTRIM34 epsilon [Homo sapiens]*
☐	*13093781*	*CAC29498.1*	*AL583914*	*410*	*hypothetical protein [Homo sapiens]*

Hs.127392
Gene: - Sequence count: 0

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	18418643	AAL68979.1	-	240	AF189286_1 p28 ING5 [Homo sapiens]
☐	18644730	NP_115705.2	-	240	p28 ING5 [Homo sapiens]

Hs.127799
Gene: BIRC3 Sequence count: 168

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	3978244	AAC83232.1	AF070674	604	inhibitor of apoptosis protein-1[Homo sapiens]
☐	1160975	AAC41943.1	L49432	604	TNFR2-TRAF signalling complex protein
	4502139	NP_001156.1	NM_001165	604	baculoviral IAP repeat-

☐					containingprotein 3 cIAP2 hiap-1 apoptosis inhibitor 2 TNFR2-TRAF signallingcomplex protein [Homo sapiens]
☐	1145291	AAC50507.1	U37546	604	MIHC
☐	1184316	AAC50371.1	U45878	604	inhibitor of apoptosis protein 1

Hs.127808
Gene: BIRC3 Sequence count: 42

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	6599277	CAB63756.1	AL133632	180	hypothetical protein [Homo sapiens]

Hs.127950
Gene: BRD1 Sequence count: 88

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	4200325	CAB11574.1	-	1058	dJ522J7.2 (bromodomain-containing 1(similar to peregrin, BR140)) [Homo sapiens]
☐	6979019	AAF34320.1	AF005067	1058	AF005067_1 BRL [Homo sapiens]
☐	11321642	NP_055392.1	NM_014577	1058	bromodomain containing protein 1BR140-like gene [Homo sapiens]
☐	*5262603*	*CAB45742.1*	*AL080149*	*715*	*hypothetical protein [Homo sapiens]*

Hs.1287
Gene: TRIM26 Sequence count: 204

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	15277237	BAB63330.1	-	539	Widely expressed acid zinc finger[Homo sapiens]
☐	4508005	NP_003440.1	NM_003449	539	tripartite motif-containing 26acid finger protein zinc finger protein 173 [Homo sapiens]
☐	563127	AAA93131.1	U09825	539	acid finger protein

Hs.129829
Gene: AIRE Sequence count: 8

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	2696619	BAA23990.1	-	545	AIRE-1 [Homo sapiens]
☐	2696620	BAA23991.1	-	348	AIRE-2 [Homo sapiens]
☐	2696621	BAA23992.1	-	254	AIRE-3 [Homo sapiens]
☐	3392940	CAA08759.1	-	515	AIRE [Homo sapiens]
☐	2696615	BAA23988.1	AB006682	545	AIRE-1 [Homo sapiens]
☐	2696617	BAA23989.1	AB006683	348	AIRE-2 [Homo sapiens]
☐	2696623	BAA23993.1	AB006685	254	AIRE-3 [Homo sapiens]
☐	4557291	NP_000374.1	NM_000383	545	autoimmune regulator AIRE isoform1 AIRE protein autoimmune regulator (autoimmune polyendocrinopathycandidiasis ectodermal dystrophy) autoimmune regulator (APECEDprotein) [Homo sapiens]
☐	4557293	NP_000649.1	NM_000658	348	autoimmune regulator AIRE isoform2 AIRE protein autoimmune regulator (autoimmune polyendocrinopathycandidiasis ectodermal dystrophy) autoimmune regulator (APECEDprotein) [Homo sapiens]
☐	4557295	NP_000650.1	NM_000659	254	autoimmune regulator AIRE isoform3 AIRE protein autoimmune regulator (autoimmune polyendocrinopathycandidiasis ectodermal dystrophy) autoimmune regulator (APECEDprotein) [Homo

					sapiens]
	2665371	CAB10790.1	Z97990	545	AIRE protein [Homo sapiens]

Hs.130541
Gene: KIAA1542 Sequence count: 113

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	7959351	BAA96066.1	AB040975	1654	KIAA1542 protein [Homo sapiens]
	13436320	*AAH04950.1*	*BC004950*	*322*	*AAH04950 Unknown (protein forIMAGE:3619689) [Homo sapiens]*

Hs.131731
Gene: FLJ11099 Sequence count: 76

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	7023550	BAA92002.1	AK001961	152	unnamed protein product [Homosapiens]
	10434923	BAB14423.1	AK023139	327	unnamed protein product [Homosapiens]
	8922863	NP_060790.1	NM_018320	152	hypothetical protein FLJ11099 [Homosapiens]

Hs.131859
Gene: FBXO11 Sequence count: 12

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	6164741	AAF04520.1	-	197	AF174599_1 F-box protein Fbx11 [Homosapiens]
	6573266	AAF17611.1	AF176706	192	F-box protein FBX11 [Homo sapiens]

Hs.132753
Gene: FBXO2 Sequence count: 122

Select	GI	Protein Acc.	DNA Acc.	Length	Description

☐	19263634	AAH25233.1	-	296	F-box only protein 2 [Homo sapiens]
☐	6164731	AAF04515.1	AF174594	257	AF174594_1 F-box protein Fbx2 [Homosapiens]
☐	6018317	AAF01822.1	AF187318	295	AF187318_1 F-box protein Fbx2 [Homosapiens]
☐	15812198	NP_036300.2	NM_012168	296	F-box only protein 2 F-boxprotein 2 [Homo sapiens]

Hs.13495
Gene: REQ Sequence count: 273

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	15928853	AAH14889.1	-	391	AAH14889 requiem, apoptosis responsezinc finger gene [Homo sapiens]
☐	2529705	AAB81203.1	AF001433	391	requiem neuroD4 ubi-d4 [Homosapiens]
☐	5454004	NP_006259.1	NM_006268	391	requiem apoptosis response zincfinger protein ubi-d4 [Homo sapiens]
☐	2121234	AAB58307.1	U94585	391	requiem homolog [Homo sapiens]

Hs.135890
Gene: PF1 Sequence count: 84

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	14278861	AAK38349.1	AY030283	704	PHD zinc finger transcription factor[Homo sapiens]
☐	12804495	AAH01657.1	BC001657	487	AAH01657 Unknown (protein forIMAGE:3356959) [Homo sapiens]
☐	*7959313*	*BAA96047.1*	*AB040956*	*687*	*KIAA1523 protein [Homo sapiens]*
☐	*10436636*	*BAB14875.1*	*AK024290*	*590*	*unnamed protein product [Homosapiens]*

Hs.13755
Gene: FBXW2 Sequence count: 102

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	6164612	AAF04465.1	-	422	AF129531_1 F-box protein Fbw2 [Homosapiens]
☐	6467890	AAF13226.1	AF176698	422	F-box protein FBW2 [Homo sapiens]
☐	10433896	BAB14051.1	AK022484	454	unnamed protein product [Homosapiens]
☐	6912360	NP_036296.1	NM_012164	422	F-box and WD-40 domain protein 2F-box protein Fbw2 [Homo sapiens]

Hs.137732
Gene: TRIM35 Sequence count: 65

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	14743792	XP_027437.1	-	306	tripartite motif-containing 35[Homo sapiens]
☐	5689533	BAA83050.1	AB029021	504	KIAA1098 protein [Homo sapiens]

Hs.138617
Gene: TRIP12 Sequence count: 320

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	460711	BAA05837.1	D28476	1992	KIAA0045 [Homo sapiens]
☐	703100	AAC41731.1	L40383	174	thyroid receptor interactor
☐	10863903	NP_004229.1	NM_004238	1992	thyroid hormone receptorinteractor 12 thyroid receptor interacting protein 12 [Homo sapiens]

Hs.14084
Gene: RNF7 Sequence count: 191

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	4588034	AAD25962.1	-	113	AF092878_1 zinc RING finger proteinSAG [Homo sapiens]
	4809218	AAD30147.1	-	113	AF142060_1 RING finger protein

					[Homosapiens]
	5917674	AAD55984.1	-	113	AF164679_1 ring finger protein CKBBP1[Homo sapiens]
	13543636	AAH05966.1	-	113	AAH05966 ring finger protein 7 [Homosapiens]
	14250389	AAH08627.1	-	113	AAH08627 ring finger protein 7 [Homosapiens]

Hs.142653
Gene: RFP Sequence count: 334

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	5851985	CAB55434.1	-	249	dJ25J6.4 (ret finger protein) [Homosapiens]
	12275874	AAG50172.1	AF230393	513	AF230393_1 tripartite motif proteinTRIM27 alpha [Homo sapiens]
	12275876	AAG50173.1	AF230394	358	AF230394_1 tripartite motif proteinTRIM27 beta [Homo sapiens]
	15488901	AAH13580.1	BC013580	513	AAH13580 ret finger protein [Homosapiens]
	337372	AAA36564.1	J03407	513	rfp transforming protein
	5730009	NP_006501.1	NM_006510	513	ret finger protein isoform alphatripartite motif protein TRIM27 [Homo sapiens]
	15011933	NP_112212.1	NM_030950	358	ret finger protein, isoform betatripartite motif protein TRIM27 [Homo sapiens]

Hs.142684
Gene: DKFZP667O116 Sequence count: 78

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	13543372	AAH05847.1	BC005847	857	AAH05847 Unknown (protein forIMAGE:2907142) [Homo sapiens]

	12224978	*CAC21676.1*	*AL512757*	*184*	*hypothetical protein [Homo sapiens]*

Hs.143198
Gene: ING3 Sequence count: 139

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	3041855	AAC12956.1	-	408	similar to tumor suppressor p33ING1similar to AF044076 (PID:g2829208) [Homo sapiens]
	10039541	AAG12172.1	AF074968	418	AF074968_1 p47ING3 protein [Homosapiens]
	7019962	BAA90942.1	AK000096	418	unnamed protein product [Homosapiens]
	10863863	AAG23285.1	AY007790	418	p47 [Homo sapiens]
	9506659	NP_061944.1	NM_019071	418	inhibitor of growth family, member3 hypothetical protein similar to tumor suppressor p33ING1 [Homosapiens]
	15131675	*CAC48260.1*	*AL603623*	*378*	*hypothetical protein [Homo sapiens]*
	14602533	*AAH09777.1*	*BC009777*	*92*	*AAH09777 Unknown (protein forMGC:13446) [Homo sapiens]*
	14602531	*AAH09776.1*	*BC009776*	*92*	*AAH09776 Unknown (protein forMGC:13445) [Homo sapiens]*

Hs.143323
Gene: PLU Sequence count: 309

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	19923370	NP_006609.2	-	1681	putative DNA/chromatin bindingmotif [Homo sapiens]
	3970878	BAA34803.1	AB015348	431	HRIHFB2060 [Homo sapiens]
	4322488	AAD16061.1	AF087481	1580	retinoblastoma binding protein 2homolog 1 [Homo sapiens]
	4902724	CAB43532.1	AJ132440	1544	PLU-1 protein [Homo sapiens]

☐	6572291	CAB63108.1	AJ243706	1681	RB-binding protein [Homo sapiens]
☐	6453448	CAB61368.1	AL133040	1350	hypothetical protein [Homo sapiens]
☐	6453463	CAB61375.1	AL133048	1028	hypothetical protein [Homo sapiens]
☐	6453514	CAB61395.1	AL133072	916	hypothetical protein [Homo sapiens]
☐	6808379	CAB70847.1	AL137622	626	hypothetical protein [Homo sapiens]

Hs.144266
Gene: FLJ22612 Sequence count: 14

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	10439066	BAB15419.1	AK026265	516	unnamed protein product [Homosapiens]
☐	13376134	NP_079054.1	NM_024778	516	hypothetical protein FLJ22612[Homo sapiens]

Hs.144658
Gene: - Sequence count: 0

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	4	protlog4.0	-	729	hPOSH2 based on gi 18676780 with a changeof A->G [Homo sapiens]

Hs.146037
Gene: RNF32 Sequence count: 43

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	12276178	AAG50281.1	-	362	AF325690_1 FKSG33 [Homo sapiens]
☐	20278963	AAM18664.1	-	362	AF441222_1 ring finger protein RNF32[Homo sapiens]
☐	12053253	CAB66808.1	AL136874	362	hypothetical protein [Homo sapiens]
☐	13569903	NP_112198.1	NM_030936	362	ring finger protein 32 [Homosapiens]

Hs.149918
Gene: GASC1 Sequence count: 330

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	18573213	XP_034624.4	-	1056	gene amplified in squamous cellcarcinoma 1 [Homo sapiens]
☐	3882281	BAA34500.1	AB018323	1100	KIAA0780 protein [Homo sapiens]
☐	10567164	BAB16102.1	AB037901	1056	gene amplified in squamous cellcarcinoma-1 [Homo sapiens]

Hs.151237
Gene: FLJ12526 Sequence count: 18

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	13644171	XP_018257.1	-	155	hypothetical protein FLJ12526[Homo sapiens]
☐	10434064	BAB14115.1	AK022588	155	unnamed protein product [Homosapiens]
☐	13376152	NP_079063.1	NM_024787	155	hypothetical protein FLJ12526[Homo sapiens]

Hs.151411
Gene: KIAA0916 Sequence count: 229

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	4240321	BAA74939.1	AB020723	1210	KIAA0916 protein [Homo sapiens]
☐	3319326	AAC39928.1	AF075587	4641	protein associated with Myc [Homosapiens]
☐	7662380	NP_055872.1	NM_015057	4641	KIAA0916 protein [Homo sapiens]

Hs.151428
Gene: RFP2 Sequence count: 133

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	13124899	AAK13059.1	-	407	CAR [Homo sapiens]
	14009479	AAK51624.1	-	407	AAK51624 putative tumor suppressorRFP2 [Homo sapiens]

☐					
☐	14594775	CAC43391.1	-	407	bA34F20.1 (ret finger protein 2)[Homo sapiens]
☐	12407423	AAG53500.1	AF220127	407	AF220127_1 tripartite motif proteinTRIM13 alpha [Homo sapiens]
☐	12407425	AAG53501.1	AF220128	175	AF220128_1 tripartite motif proteinTRIM13 beta [Homo sapiens]
☐	9651927	AAF91315.1	AF241850	407	AF241850_1 ret finger protein 2 [Homosapiens]
☐	3133092	CAA12136.1	AJ224819	407	tumor suppressor [Homo sapiens]
☐	13097765	AAH03579.1	BC003579	407	AAH03579 ret finger protein 2 [Homosapiens]
☐	5031861	NP_005789.1	NM_005798	407	ret finger protein 2 candidatetumor suppressor involved in B-CLL tripartite motif protein 13CLL-associated RING finger [Homo sapiens]
☐	16445412	NP_434698.1	NM_052811	407	ret finger protein 2 candidatetumor suppressor involved in B-CLL tripartite motif protein 13CLL-associated RING finger [Homo sapiens]

Hs.153638
Gene: MLL2 Sequence count: 171

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	2358285	AAC51734.1	AF010403	5262	ALR [Homo sapiens]
☐	2358287	AAC51735.1	AF010404	4957	ALR [Homo sapiens]
☐	4505197	NP_003473.1	NM_003482	5262	myeloid/lymphoid or mixed-lineageleukemia 2 ALL1-related gene [Homo sapiens]

Hs.153639
Gene: SBB103 Sequence count: 230

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	3342562	AAC27647.1	AF077599	317	hypothetical SBBI03 protein [Homosapiens]
☐	5032071	NP_005776.1	NM_005785	317	hypothetical SBBI03 protein [Homosapiens]
☐	*9956003*	*AAG01988.1*	*AY007109*	*141*	*similar to Homo sapiens hypotheticalSBBI03 protein mRNA with GenBank Accession Number AF077599*

Hs.153685
Gene: KIAA0322 Sequence count: 18

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	2224585	BAA20780.1	AB002320	1562	KIAA0322 [Homo sapiens]
☐	10039443	BAB13352.1	AB048365	1585	NEDD4-like ubiquitin ligase 1 [Homosapiens]

Hs.15423
Gene: HDCMC04P Sequence count: 157

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	4153862	AAD04721.1	-	592	determined by GENSCAN prediction andspliced EST match to EST R84329 (NID:942735) [Homo sapiens]
☐	7021918	BAA91435.1	-	594	unnamed protein product [Homosapiens]
☐	8489023	AAF75564.1	AF067804	453	AF067804_5 HDCMC04P [Homo sapiens]
☐	8923726	NP_061152.1	NM_018682	453	hypothetical protein HDCMC04P [Homosapiens]

Hs.15467
Gene: FLJ20725 Sequence count: 105

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	11434324	XP_007335.1	-	305	hypothetical protein FLJ20725[Homo sapiens]
	7021002	BAA91346.1	AK000732	305	unnamed protein product

					[Homosapiens]
	8923651	NP_060413.1	NM_017943	305	hypothetical protein FLJ20725 [Homosapiens]

Hs.154680
Gene: DKFZP434M154 Sequence count: 48

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	14761055	XP_051330.1	-	427	DKFZP434M154 protein [Homosapiens]
	5262621	CAB45750.1	AL080159	361	hypothetical protein [Homo sapiens]
	13543342	AAH05834.1	BC005834	515	AAH05834 Unknown (protein forIMAGE:2821841) [Homo sapiens]

Hs.15470
Gene: LOC51132 Sequence count: 66

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	10944884	CAC14228.1	-	624	RING zinc finger LIM domain bindingprotein [Homo sapiens]
	5360113	AAD42875.1	AF155109	483	AF155109_1 putative ring zinc fingerprotein NY-REN-43 antigen [Homo sapiens]
	7022528	BAA91632.1	AK001334	624	unnamed protein product [Homosapiens]
	15426504	AAH13357.1	BC013357	624	AAH13357 Unknown (protein forMGC:15161) [Homo sapiens]
	7705835	NP_057204.1	NM_016120	483	putative ring zinc finger proteinNY-REN-43 antigen putative ring zinc finger protein NY-REN-43antigenRING zinc finger LIM domain binding protein [Homo sapiens]

Hs.155287
Gene: KIAA0010 Sequence count: 243

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	11422249	XP_004990.1	-	1083	ubiquitin-protein isopeptideligase (E3) [Homo sapiens]
☐	285983	BAA02799.1	D13635	1083	KIAA0010 [Homo sapiens]
☐	7661856	NP_055486.1	NM_014671	1083	ubiquitin-protein isopeptide ligase(E3) [Homo sapiens]
☐	*15559332*	*AAH14029.1*	*BC014029*	*649*	*AAH14029 Unknown (protein forMGC:19944) [Homo sapiens]*

Hs.155313
Gene: DATF1 Sequence count: 252

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	12733867	CAC28883.1	-	379	dJ885L7.9.3 (Death associatedtranscription factor 1 (contains KIAA0333), isoform 3) [Homo sapiens]
☐	15680267	AAH14489.1	-	562	AAH14489 death associatedtranscription factor 1 [Homo sapiens]
☐	18375617	NP_071388.2	-	562	death associated transcriptionfactor 1, isoform a death inducer-obliterator 1 [Homo sapiens]
☐	18375619	NP_542986.1	-	562	death associated transcriptionfactor 1, isoform a death inducer-obliterator 1 [Homo sapiens]
☐	18375621	NP_542987.1	-	544	death associated transcriptionfactor 1, isoform b death inducer-obliterator 1 [Homo sapiens]
☐	2224607	BAA20791.1	AB002331	991	KIAA0333 [Homo sapiens]
☐	7023815	BAA92094.1	AK002127	562	unnamed protein product [Homosapiens]
☐	12653953	AAH00770.1	BC000770	544	AAH00770 hypothetical proteinFLJ11265 similar to death inducer-obliterator-1 [Homo sapiens]
☐	13278981	AAH04237.1	BC004237	562	AAH04237 hypothetical proteinFLJ11265 similar to death

					inducer-obliterator-1 [Homo sapiens]

Hs.155968
Gene: ZFP103 Sequence count: 167

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	12728697	XP_002551.2	-	685	zinc finger protein 103 homolog(mouse) [Homo sapiens]
	1945615	BAA19739.1	D76444	685	hkf-1 [Homo sapiens]
	5031825	NP_005658.1	NM_005667	685	zinc finger protein 103 homolog(mouse) zinc finger protein homologous to Zfp103 in mouse Zincfinger protein expressed in cerebellum [Homo sapiens]

Hs.155983
Gene: KIAA0677 Sequence count: 163

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	3327168	BAA31652.1	AB014577	1064	KIAA0677 protein [Homo sapiens]
	12803467	AAH02558.1	BC002558	1064	AAH02558 KIAA0677 gene product [Homosapiens]
	7662246	NP_055478.1	NM_014663	1064	KIAA0677 gene product [Homosapiens]

Hs.156276
Gene: KIAA0783 Sequence count: 218

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	3882287	BAA34503.1	AB018326	888	KIAA0783 protein [Homo sapiens]
	7662304	NP_055475.1	NM_014660	888	KIAA0783 gene product [Homosapiens]

Hs.1565
Gene: NEDD4 Sequence count: 104

Select	GI	Protein Acc.	DNA Acc.	Length	Description

☐	1171682	P46934	-	927	NED4_HUMAN NEDD-4 protein
☐	577313	BAA07655.1	D42055	927	KIAA0093 gene product is related toNEDD-4 protein. [Homo sapiens]

Hs.156637
Gene: CBLC Sequence count: 46

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	20149596	NP_036248.2	-	474	Cas-Br-M (murine) ectropicretroviral transforming sequence c CBL-3 [Homo sapiens]
☐	6291532	BAA86298.1	AB028645	474	Cbl-c [Homo sapiens]
☐	4959421	AAD34341.1	AF117646	474	AF117646_1 long CBL-3 protein [Homosapiens]
☐	4959423	AAD34342.1	AF117647	428	AF117647_1 short CBL-3 protein [Homosapiens]

Hs.157427
Gene: RFPL2 Sequence count: 7

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	18593967	XP_009938.3	-	378	ret finger protein-like 2 [Homosapiens]
☐	3417317	CAA09045.1	AJ010231	288	RET finger protein-like 2 [Homosapiens]
☐	5730011	NP_006596.1	NM_006605	288	ret finger protein-like 2 [Homosapiens]

☐

Hs.15772
Gene: ZNF147 Sequence count: 41

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	16877339	AAH16924.1	-	630	AAH16924 zinc finger protein 147(estrogen-responsive finger protein) [Homo sapiens]
	458726	BAA04747.1	D21205	630	estrogen responsive finger

					protein(efp) [Homo sapiens]
	4827065	NP_005073.1	NM_005082	630	zinc finger protein 147 Zincfinger protein-147 estrogen-responsive finger protein tripartitemotif protein 25 [Homo sapiens]

Hs.158761
Gene: LOC93349 Sequence count: 37

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	14724167	XP_050693.1	-	245	similar to unnamed protein product[Homo sapiens]
	20149711	NP_612411.2	-	245	hypothetical protein BC004921[Homo sapiens]
	10434890	BAB14413.1	AK023116	245	unnamed protein product [Homosapiens]
	13436236	*AAH04921.1*	*BC004921*	*129*	*AAH04921 Unknown (protein forMGC:4821) [Homo sapiens]*

Hs.15921
Gene: FLJ10759 Sequence count: 80

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	7022987	BAA91792.1	AK001621	475	unnamed protein product [Homosapiens]
	12654759	AAH01222.1	BC001222	475	AAH01222 hypothetical proteinFLJ10759 [Homo sapiens]
	14124950	AAH07999.1	BC007999	475	AAH07999 hypothetical proteinFLJ10759 [Homo sapiens]
	15079758	AAH11689.1	BC011689	475	AAH11689 Unknown (protein forMGC:19672) [Homo sapiens]
	15082476	AAH12152.1	BC012152	475	AAH12152 Unknown (protein forMGC:20370) [Homo sapiens]
	8922648	NP_060677.1	NM_018207	475	hypothetical protein FLJ10759 [Homosapiens]

Hs.159589
Gene: NEUD4 Sequence count: 48

Select	GI	Protein Acc.	DNA Acc.	Length	Description

☐	4758798	NP_004638.1	NM_004647	353	Neuro-d4 (rat) homolog [Homosapiens]
☐	1532121	AAC50685.1	U43843	353	h-neuro-d4 protein [Homo sapiens]

Hs.16036
Gene: FLJ12565 Sequence count: 112

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	10434127	BAB14139.1	AK022627	622	unnamed protein product [Homosapiens]
☐	10439957	BAB15607.1	AK026968	772	unnamed protein product [Homosapiens]
☐	12052977	CAB66663.1	AL136729	442	hypothetical protein [Homo sapiens]
☐	11545773	NP_071347.1	NM_022064	772	hypothetical protein FLJ12565[Homo sapiens]

Hs.16537
Gene: ZNF364 Sequence count: 112

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	17488930	XP_039714.2	-	304	hypothetical protein, similar to(U06944) PRAJA1 [Homo sapiens]
☐	5102894	CAB45280.1	AL079314	232	hypothetical protein, similar to(U06944) PRAJA1 [Mus musculus] [Homo sapiens]

Hs.165662
Gene: KIAA0675 Sequence count: 131

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	3327164	BAA31650.1	AB014575	1208	KIAA0675 protein [Homo sapiens]
☐	7662244	NP_055463.1	NM_014648	1208	KIAA0675 gene product [Homosapiens]
☐	*14582392*	*AAK69484.1*	*AF279370*	*508*	*AF279370_1 DZIP3 [Homo sapiens]*

Hs.16577
Gene: FBXO3 Sequence count: 170

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	12052776	CAB66560.1	-	471	hypothetical protein [Homo sapiens]
☐	6164733	AAF04516.1	AF174595	173	AF174595_1 F-box protein Fbx3 [Homosapiens]
☐	6103643	AAF03702.1	AF176702	410	F-box protein FBX3 [Homo sapiens]
☐	7023521	BAA91991.1	AK001943	471	unnamed protein product [Homosapiens]
☐	15812186	NP_036307.2	NM_012175	471	F-box only protein 3, isoform 1F-box protein FBX3 [Homo sapiens]
☐	15812188	NP_208385.1	NM_033406	415	F-box only protein 3, isoform 2F-box protein FBX3 [Homo sapiens]

Hs.166204
Gene: PHF1 Sequence count: 195

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	3169118	CAA16158.1	-	457	cICK0721Q.4.1 (PHD finger protein 1)(isoform 1) [Homo sapiens]
☐	3169119	CAA16159.1	-	567	cICK0721Q.4.1 (PHD finger protein 2)(isoform 2) [Homo sapiens]
☐	2660720	AAC52062.1	AF029678	457	PHF1 [Homo sapiens]
☐	3044064	AAC13273.1	AF052205	567	PHD finger protein 2 [Homo sapiens]
☐	14250730	AAH08834.1	BC008834	567	AAH08834 PHD finger protein 1 [Homosapiens]
☐	4505777	NP_002627.1	NM_002636	457	PHD finger protein 1, isoform a[Homo sapiens]
☐	13435397	NP_077084.1	NM_024165	567	PHD finger protein 1, isoform b[Homo sapiens]

Hs.167750
Gene: RFPL1 Sequence count: 4

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	3417312	CAA09043.1	AJ010228	288	RFPL1L [Homo sapiens]
☐	3417314	CAA09044.1	AJ010229	287	RFPL1S [Homo sapiens]
☐	10440558	NP_066306.1	NM_021026	288	ret finger protein-like 1 [Homosapiens]

Hs.167751
Gene: RFPL3 Sequence count: 6

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	4468862	CAB38256.1	-	288	dJ149A16.2 (Ret finger protein-like3) [Homo sapiens]
☐	3417319	CAA09046.1	AJ010232	288	RET finger protein-like 3 [Homosapiens]
☐	5730013	NP_006595.1	NM_006604	288	ret finger protein-like 3 [Homosapiens]

Hs.168095
Gene: RNF20 Sequence count: 101

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	18572254	XP_084272.1	-	975	ring finger protein 20 [Homosapiens]
☐	14279233	AAK58539.1	AF265230	975	AF265230_1 RING finger protein 20[Homo sapiens]
☐	7023699	BAA92057.1	AK002051	333	unnamed protein product [Homosapiens]
☐	10433666	BAB14005.1	AK022300	746	unnamed protein product [Homosapiens]
☐	10433974	BAB14081.1	AK022532	975	unnamed protein product [Homosapiens]
☐	16554453	NP_062538.4	NM_019592	975	ring finger protein 20 [Homosapiens]

Hs.168159
Gene: LOC51283 Sequence count: 202

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	18605049	XP_027311.3	-	450	apoptosis regulator [Homo sapiens]
☐	7329979	AAF59975.1	AF173003	450	AF173003_1 apoptosis regulator [Homosapiens]
☐	12804383	AAH03054.1	BC003054	450	AAH03054 apoptosis regulator [Homosapiens]
☐	7706091	NP_057645.1	NM_016561	450	apoptosis regulator [Homo sapiens]

Hs.170610
Gene: MAP3K1 Sequence count: 86

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	2815888	AAC97073.1	AF042838	1495	MEK kinase 1 [Homo sapiens]

Hs.170822
Gene: DKFZP564A022 Sequence count: 32

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	14042657	BAB55340.1	AK027748	258	unnamed protein product [Homosapiens]
☐	12052766	CAB66555.1	AL136620	167	hypothetical protein [Homo sapiens]
☐	13569926	NP_112216.1	NM_030954	167	hypothetical protein DKFZp564A022[Homo sapiens]

Hs.172084
Gene: PYGO2 Sequence count: 124

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	16160297	XP_034083.2	-	406	similar to Unknown (protein forIMAGE:3627860) [Homo sapiens]
☐	19550451	AAL91371.1	-	406	AF457208_1 pygopus 2 [Homo sapiens]
	13543991	AAH06132.1	BC006132	463	AAH06132 Unknown (protein

					forIMAGE:3627860) [Homo sapiens]
	15489242	AAH13725.1	BC013725	233	AAH13725 Unknown (protein forIMAGE:3859726) [Homo sapiens]

Hs.172700
Gene: NEURL Sequence count: 99

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	20070955	AAH26336.1	-	574	neuralized-like (Drosophila) [Homosapiens]
	4103928	AAD01887.1	AF029729	574	neuralized [Homo sapiens]
	4758800	NP_004201.1	NM_004210	574	neuralized-like (Drosophila)neuralized (Drosophila)-like [Homo sapiens]
	3157991	AAC17474.1	U87864	574	neuralized homolog [Homo sapiens]

Hs.172777
Gene: BIRC4 Sequence count: 17

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	13649024	XP_013050.3	-	497	similar to baculoviral IAPrepeat-containing 4 (H. sapiens) [Homo sapiens]
	4502143	NP_001158.1	NM_001167	497	baculoviral IAP repeat-containingprotein 4 apoptosis inhibitor 3 X-linked inhibitor of apoptosis[Homo sapiens]
	1016688	AAC50518.1	U32974	497	IAP-like protein ILP
	1184320	AAC50373.1	U45880	497	X-linked inhibitor of apotosisprotein

Hs.173980
Gene: NMP200 Sequence count: 217

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	17391461	AAH18665.1	-	504	AAH18665 nuclear matrix proteinNMP200 related to splicing factor PRP19 [Homo sapiens]

	17391520	AAH18698.1	-	504	AAH18698 nuclear matrix proteinNMP200 related to splicing factor PRP19 [Homo sapiens]
	5689738	CAB51857.1	AJ131186	504	nuclear matrix protein NMP200 [Homosapiens]
	14250536	AAH08719.1	BC008719	504	AAH08719 nuclear matrix proteinNMP200 related to splicing factor PRP19 [Homo sapiens]
	7657381	NP_055317.1	NM_014502	504	nuclear matrix protein NMP200related to splicing factor PRP19 [Homo sapiens]

Hs.17639
Gene: UBE3B Sequence count: 318

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	13507059	AAK28419.1	AF251046	185	AF251046_1 ubiquitin protein ligase[Homo sapiens]

Hs.177635
Gene: KIAA1095 Sequence count: 117

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	5689527	BAA83047.1	AB029018	1098	KIAA1095 protein [Homo sapiens]
	7018547	*CAB75679.1*	*AL157498*	*480*	*hypothetical protein [Homo sapiens]*

Hs.17767
Gene: KIAA1554 Sequence count: 696

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	10047173	BAB13380.1	AB046774	1320	KIAA1554 protein [Homo sapiens]
	10438750	*BAB15330.1*	*AK026038*	*216*	*unnamed protein product [Homosapiens]*
	10438576	*BAB15280.1*	*AK025914*	*919*	*unnamed protein product [Homosapiens]*
	10438270	*BAB15212.1*	*AK025676*	*1036*	*unnamed protein product [Homosapiens]*
	10435940	*BAB14708.1*	*AK023871*	*509*	*unnamed protein product*

☐					*[Homosapiens]*

Hs.179260
Gene: C14orf4 Sequence count: 72

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	10636484	CAC10539.1	-	796	polyglutamine-containing protein[Homo sapiens]
☐	14784721	XP_041104.1	-	423	chromosome 14 open reading frame 4[Homo sapiens]
☐	14017947	BAB47494.1	AB058768	723	KIAA1865 protein [Homo sapiens]
☐	*12002026*	*AAG43156.1*	*AF063597*	*103*	*AF063597_1 brain my039 protein [Homosapiens]*

Hs.179669
Gene: FLJ20637 Sequence count: 50

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	7020871	BAA91303.1	AK000644	379	unnamed protein product [Homosapiens]
☐	8923590	NP_060382.1	NM_017912	379	hypothetical protein FLJ20637 [Homosapiens]

Hs.179946
Gene: KIAA1100 Sequence count: 174

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	5689537	BAA83052.1	AB029023	432	KIAA1100 protein [Homo sapiens]
☐	7662486	NP_055716.1	NM_014901	432	KIAA1100 protein [Homo sapiens]

Hs.179982
Gene: TP53BPL Sequence count: 134

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	9664146	BAB03714.1	AB045732	1045	RING-finger protein [Homo sapiens]
☐	9664148	BAB03715.1	AB045733	980	RING-finger protein [Homo sapiens]

	4566495	AAD23379.1	AF098300	1045	AF098300_1 topoisomerase I-binding RSprotein [Homo sapiens]
	15489083	*AAH13655.1*	*BC013655*	*30*	*AAH13655 Unknown (protein forIMAGE:4152599) [Homo sapiens]*
	5032191	*NP_005793.1*	*NM_005802*	*815*	*tumor protein p53-binding proteintopoisomerase I binding protein [Homo sapiens]*
	2656123	*AAC98530.1*	*U82939*	*815*	*p53 binding protein [Homo sapiens]*

Hs.180403
Gene: STRIN Sequence count: 143

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	6468773	AAD46623.2	AF162680	245	AF162680_1 HSD-4 protein [Homosapiens]
	7706723	NP_057355.1	NM_016271	245	STRIN protein [Homo sapiens]
	10435554	*BAB14614.1*	*AK023579*	*151*	*unnamed protein product [Homosapiens]*
	6599126	*CAB63712.1*	*AL133557*	*183*	*hypothetical protein [Homo sapiens]*

Hs.180612
Gene: PXMP3 Sequence count: 198

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	9719228	AAF97687.1	-	305	AF133826_1 35 kDa peroxisomal membraneprotein [Homo sapiens]
	12653751	AAH00661.1	BC000661	305	AAH00661 peroxisomal membrane protein3 (35kD, Zellweger syndrome) [Homo sapiens]
	13529227	AAH05375.1	BC005375	305	AAH05375 peroxisomal membrane protein3 (35kD, Zellweger syndrome) [Homo sapiens]
	190190	AAA60141.1	M85038	305	peroxisomal membrane protein
	189849	AAC12785.1	M86852	305	peroxisome assembly factor-1

☐					[Homosapiens]
☐	4506343	NP_000309.1	NM_000318	305	peroxisomal membrane protein 3Peroxisomal membrane protein-3 (35kD) [Homo sapiens]

Hs.180686
Gene: UBE3A Sequence count: 522

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	1495436	CAA66653.1	-	852	E6-AP [Homo sapiens]
☐	2361031	AAB69154.1	-	852	E6-AP ubiquitin-protein ligase [Homosapiens]
☐	2853320	AAC39580.1	-	39	E6-AP ubiquitin-protein ligase [Homosapiens]
☐	3421128	CAA04536.1	-	48	E6-AP ubiquitin-protein ligase [Homosapiens]
☐	3421130	CAA04537.1	-	68	E6-AP ubiquitin-protein ligase [Homosapiens]
☐	3421136	CAA04538.1	-	55	E6-AP ubiquitin-protein ligase [Homosapiens]
☐	3421142	CAA04539.1	-	76	E6-AP ubiquitin-protein ligase [Homosapiens]
☐	3421159	CAA04540.1	-	39	E6-AP ubiquitin-protein ligase [Homosapiens]
☐	19718762	NP_570853.1	-	852	ubiquitin protein ligase E3A,isoform 1 human papilloma virus E6-associated protein oncogenicprotein-associated protein E6-AP CTCL tumor antigen se37-2 [Homosapiens]
☐	19718764	NP_570854.1	-	872	ubiquitin protein ligase E3A,isoform 3 human papilloma virus E6-associated protein oncogenicprotein-associated protein E6-AP CTCL tumor antigen se37-2 [Homosapiens]
☐	19718766	NP_000453.2	-	875	ubiquitin protein ligase E3A,isoform 2 human papilloma virus E6-associated protein

					oncogenicprotein-associated protein E6-AP CTCL tumor antigen se37-2 [Homosapiens]
☐	11385658	AAG34910.1	AF273050	852	AF273050_1 CTCL tumor antigen se37-2[Homo sapiens]
☐	12803511	AAH02582.1	BC002582	852	AAH02582 ubiquitin protein ligase E3A(human papilloma virus E6-associated protein, Angelman syndrome) [Homosapiens]
☐	14424503	AAH09271.1	BC009271	585	AAH09271 Unknown (protein forMGC:15720) [Homo sapiens]
☐	178745	AAA35542.1	L07557	874	oncogenic protein-associated protein
☐	1872514	AAB49301.1	U84404	852	E6-associated proteinE6-AP/ubiquitin-protein ligase [Homo sapiens]
☐	1495432	CAA66654.1	X98031	852	isoform II [Homo sapiens]
☐	1495430	CAA66655.1	X98032	852	isoform I [Homo sapiens]
☐	1495434	CAA66656.1	X98033	852	isoform III [Homo sapiens]

Hs.180933
Gene: CGBP Sequence count: 226

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	8100075	BAA96307.1	AB031069	656	protein containing CXXC domain 1[Homo sapiens]
☐	7188556	AAF37799.1	AF149758	656	AF149758_1 CpG binding protein [Homosapiens]
☐	12053229	CAB66796.1	AL136862	656	hypothetical protein [Homo sapiens]
☐	7656975	NP_055408.1	NM_014593	656	CpG binding protein DNA-bindingprotein with PHD finger and CXXC domain [Homo sapiens]

Hs.180941
Gene: VPS41 Sequence count: 159

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	7657677	NP_055211.1	NM_014396	854	vacuolar protein sorting 41 (yeasthomolog), isoform 1 vacuolar assembly protein 41 [Homo sapiens]
☐	1842093	AAB47563.1	U87309	854	hVps41p [Homo sapiens]
☐	*12002286*	*AAG43279.1*	*AF135593*	*779*	*AF135593_1 hVps41p [Homo sapiens]*
☐	*887370*	*AAC42004.1*	*L40398*	*130*	*ORF putative*
☐	*1843570*	*AAB47758.1*	*U87281*	*149*	*hVps41p [Homo sapiens]*

Hs.181077
Gene: DKFZp586I021 Sequence count: 253

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	18999397	AAH24267.1	-	594	hypothetical protein DKFZp586I021 [Homo sapiens]
☐	12053337	CAB66855.1	AL136921	594	hypothetical protein [Homo sapiens]
☐	14150011	NP_115647.1	NM_032271	594	hypothetical protein DKFZp586I021 [Homo sapiens]

Hs.181161
Gene: KIAA1972 Sequence count: 114

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	18916845	BAB85558.1	-	576	KIAA1972 protein [Homo sapiens]
☐	15341960	AAH13173.1	BC013173	576	AAH13173 Unknown (protein forMGC:17340) [Homo sapiens]

Hs.183180
Gene: ANAPC11 Sequence count: 282

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	7106818	AAF36134.1	-	132	AF151048_1 HSPC214 [Homo sapiens]

Hs.348263
Gene: - Sequence count: 0

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	15042064	AAK81892.1	-	236	AF164682_1 IAP-like protein 2 [Homosapiens]
☐	16902898	AAL30369.1	-	236	AF420440_1 testis-specific inhibitorof apoptosis [Homo sapiens]
☐	16974128	NP_203127.2	-	236	baculoviral IAP repeat-containing8 IAP-like protein 2 [Homo sapiens]
☐	18590254	XP_084020.1	-	236	baculoviral IAP repeat-containing8 [Homo sapiens]

Hs.348716
Gene: - Sequence count: 0

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	6164616	AAF04467.1	-	434	AF129533_1 F-box protein Fbl3b [Homosapiens]

Hs.350321
Gene: RET Sequence count: 68

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	340026	AAA36786.1	M16029	805	tyrosine kinase
☐	*13279041*	*AAH04257.1*	*BC004257*	*1072*	*AAH04257 ret proto-oncogene (multipleendocrine neoplasia MEN2A, MEN2B and medullary thyroid carcinoma 1,Hirschsprung disease) [Homo sapiens]*
☐	*13111770*	*AAH03072.1*	*BC003072*	*458*	*AAH03072 Similar to retproto-oncogene (multiple endocrine neoplasia MEN2A, MEN2B andmedullary thyroid carcinoma 1, Hirschsprung disease) [Homo sapiens]*
☐	*10862705*	*NP_000314.1*	*NM_000323*	*1114*	*ret proto-oncogene, isoform aprecursor, hydroxyaryl-protein kinase RET51 oncogene RET RETtransforming sequence*

					cadherin family member 12 [Homo sapiens]
☐	*10862703*	*NP_066124.1*	*NM_020975*	*1114*	*ret proto-oncogene, isoform aprecursor hydroxyaryl-protein kinase RET51 oncogene RET RETtransforming sequence cadherin family member 12 [Homo sapiens]*
☐	*10862701*	*NP_065681.1*	*NM_020630*	*1072*	*ret proto-oncogene, isoform cprecursor hydroxyaryl-protein kinase RET51 oncogene RET RETtransforming sequence cadherin family member 12 [Homo sapiens]*
☐	*10862699*	*NP_065680.1*	*NM_020629*	*1106*	*ret proto-oncogene, isoform bprecursor hydroxyaryl-protein kinase RET51 oncogene RET RETtransforming sequence cadherin family member 12 [Homo sapiens]*
☐	*38275*	*CAA31408.1*	*X12949*	*860*	*ret tyrosine kinase (AA 1 - 860) [Homosapiens]*
☐	*190700*	*AAA36524.1*	*M31213*	*503*	*papillary thyroid carcinoma-encodedprotein*

Hs.350518
Gene: TRIM6 Sequence count: 60

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	18079262	NP_477514.1	-	488	tripartite motif protein 6 [Homosapiens]
☐	12407391	AAG53484.1	AF220030	488	AF220030_1 tripartite motif proteinTRIM6 [Homo sapiens]
☐	14042509	BAB55276.1	AK027664	488	unnamed protein product [Homosapiens]

Hs.35384
Gene: RING1 Sequence count: 119

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	3820982	CAA20235.1	-	377	dJ1033B10.8.1 (Ring finger protein 1(RNF1), isoform 1)

					[Homo sapiens]
☐	12804137	AAH02922.1	BC002922	377	AAH02922 ring finger protein 1 [Homosapiens]
☐	4506535	NP_002922.1	NM_002931	377	ring finger protein 1 [Homosapiens]
☐	296064	CAA78389.1	Z14000	377	RING1 [Homo sapiens]

Hs.355726
Gene: HT011 Sequence count: 13

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	13650239	XP_017935.1	-	357	uncharacterized hypothalamusprotein HT011 [Homo sapiens]
☐	7689021	AAF67650.1	AF220185	360	AF220185_1 uncharacterizedhypothalamus protein HT011 [Homo sapiens]
☐	8923810	NP_060942.1	NM_018472	360	uncharacterized hypothalamusprotein HT011 [Homo sapiens]
☐	*9437341*	*AAF87315.1*	*AF168713*	*222*	*AF168713_1 x 004 protein [Homosapiens]*

Hs.355977
Gene: - Sequence count: 0

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	2072501	AAC51324.1	-	684	WWP1 [Homo sapiens]
☐	15929915	AAH15380.1	-	304	AAH15380 Similar to WWdomain-containing protein 1 [Homo sapiens]
☐	18554931	XP_087357.1	-	922	WW domain-containing protein 1[Homo sapiens]

Hs.356868
Gene: - Sequence count: 0

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	20067026	AAM09503.1	-	229	AF489517_1 RNF35 [Homo

☐					sapiens]
☐	20162564	NP_619645.1	-	229	ring finger RNF35 [Homo sapiens]

Hs.35804
Gene: HERC3 Sequence count: 105

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	11436418	XP_003490.1	-	1050	hect domain and RLD 3 [Homosapiens]
☐	517115	BAA04945.1	D25215	1050	KIAA0032 [Homo sapiens]
☐	7657152	NP_055421.1	NM_014606	1050	hect domain and RLD 3 [Homosapiens]

Hs.38125
Gene: SP110 Sequence count: 155

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	1362890	B49515	-	371	B49515 phosphoprotein 75 - human
☐	17986254	NP_536349.1	-	713	SP110 nuclear body protein,isoform c interferon-induced protein 75, 52kD interferon-inducedprotein 41, 30kD transcriptional coactivator Sp110 phosphoprotein41 phosphoprotein 75 [Homo sapiens]
☐	17986256	NP_004500.2	-	689	SP110 nuclear body protein,isoform a interferon-induced protein 75, 52kD interferon-inducedprotein 41, 30kD transcriptional coactivator Sp110 phosphoprotein41 phosphoprotein 75 [Homo sapiens]
☐	9964115	AAG09826.1	AF280095	689	AF280095_1 transcriptional coactivatorSp110 [Homo sapiens]
☐	4239654	AAD13402.1	L22343	408	nuclear phosphoprotein [Homo sapiens]
☐	*9800494*	*AAF99318.1*	*AF280094*	*539*	*AF280094_1 transcriptional coactivatorSp110b [Homo sapiens]*
	402205	*AAA18806.1*	*L22342*	*248*	*phosphoprotein*

☐					

Hs.431
Gene: BMI1 Sequence count: 193

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	15341688	AAH11652.1	BC011652	326	AAH11652 Unknown (protein forMGC:12685) [Homo sapiens]
☐	291873	AAA19873.1	L13689	326	putative
☐	4885095	NP_005171.1	NM_005180	326	murine leukemia viral (bmi-1)oncogene homolog Oncogene BMI-1 [Homo sapiens]

Hs.43149
Gene: KIAA1214 Sequence count: 40

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	6330555	BAA86528.1	AB033040	462	KIAA1214 protein [Homo sapiens]

Hs.44685
Gene: ZFP26 Sequence count: 195

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	6856967	AAF30180.1	AF214680	230	C3HC4-like zinc finger protein [Homosapiens]
☐	7706777	NP_057506.1	NM_016422	230	C3HC4-like zinc finger protein[Homo sapiens]

Hs.46700
Gene: ING1 Sequence count: 112

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	16188451	XP_057109.1	-	422	inhibitor of growth family, member1 [Homo sapiens]
☐	19923771	NP_005528.2	-	422	inhibitor of growth family, member1 inhibitor of growth 1 inhibitor of growth 1 family, member 1 [Homosapiens]
☐	5689257	BAA82886.1	AB024401	279	p33 [Homo sapiens]

☐	5689259	BAA82887.1	AB024402	422	p47 [Homo sapiens]
☐	5771440	BAA83496.1	AB031269	210	p24 [Homo sapiens]
☐	2183221	AAB60879.1	AF001954	294	p33ING1 [Homo sapiens]
☐	2829208	AAC00501.1	AF044076	279	candidate tumor suppressor p33ING1[Homo sapiens]
☐	10039545	AAG12174.1	AF078835	279	AF078835_1 p33ING1 [Homo sapiens]
☐	7158365	AAF37421.1	AF149721	279	AF149721_1 ING1 tumor suppressor,variant A [Homo sapiens]
☐	7158367	AAF37422.1	AF149722	210	AF149722_1 ING1 tumor suppressor,variant B [Homo sapiens]
☐	7158369	AAF37423.1	AF149723	235	AF149723_1 ING1 tumor suppressor,variant C [Homo sapiens]
☐	6409278	AAF07920.1	AF181849	422	AF181849_1 p47ING1a [Homo sapiens]
☐	6409280	AAF07921.1	AF181850	279	AF181850_1 p33ING1b [Homo sapiens]
☐	13992539	CAC38067.1	AJ310392	279	p33ING1b [Homo sapiens]

Hs.4745
Gene: PSMC1 Sequence count: 530

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	15530249	AAH13908.1	BC013908	387	AAH13908 Unknown (protein forMGC:16498) [Homo sapiens]
☐	*12653481*	*AAH00512.1*	*BC000512*	*440*	*AAH00512 Similar to protease(prosome, macropain) 26S subunit, ATPase 1 [Homo sapiens]*
☐	*4506207*	*NP_002793.1*	*NM_002802*	*440*	*proteasome (prosome, macropain) 26Ssubunit, ATPase, 1 Proteasome 26S subunit, ATPase, 1 [Homo sapiens]*

☐	*403456*	*AAA35484.1*	*L02426*	*440*	*26S protease (S4) regulatory subunit*

Hs.48320
Gene: DORFIN Sequence count: 253

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	19923422	NP_056250.2	-	838	dorfin [Homo sapiens]
☐	13366024	BAB39353.1	AB029316	838	ring-IBR-ring domain containingprotein Dorfin [Homo sapiens]
☐	*10440099*	*BAB15647.1*	*AK027070*	*397*	*unnamed protein product [Homosapiens]*
☐	*10435397*	*BAB14581.1*	*AK023455*	*155*	*unnamed protein product [Homosapiens]*
☐	*7023254*	*BAA91900.1*	*AK001774*	*457*	*unnamed protein product [Homosapiens]*
☐	*6102910*	*CAB59264.1*	*AL122096*	*315*	*hypothetical protein [Homo sapiens]*
☐	*5817213*	*CAB53700.1*	*AL110253*	*101*	*hypothetical protein [Homo sapiens]*

Hs.49210
Gene: FBXO4 Sequence count: 65

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	6164618	AAF04468.1	AF129534	387	AF129534_1 F-box protein Fbx4 [Homosapiens]
☐	6103645	AAF03703.1	AF176703	305	F-box protein FBX4 [Homo sapiens]
☐	15834619	NP_036308.1	NM_012176	387	F-box only protein 4 F-boxprotein Fbx4 [Homo sapiens]
☐	15834621	NP_277019.1	NM_033484	307	F-box only protein 4, isoform 2F-box protein Fbx4 hypothetical protein FLJ10141 [Homo sapiens]
☐	*8655639*	*CAB94872.1*	*AL359579*	*244*	*hypothetical protein [Homo sapiens]*
	7022012	*BAA91463.1*	*AK001003*	*161*	*unnamed protein product*

☐					*[Homosapiens]*

☐

Hs.49526
Gene: FBXL4 Sequence count: 66

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	4468288	CAB37981.1	-	621	dJ273N12.1 (PUTATIVE protein basedon EST matches) [Homo sapiens]
☐	6164723	AAF04511.1	AF174590	621	AF174590_1 F-box protein Fbl4 [Homosapiens]
☐	6103637	AAF03699.1	AF176699	621	F-box protein FBL4 [Homo sapiens]
☐	6456735	AAF09247.1	AF199355	621	AF199355_1 F-box protein FBL5 [Homosapiens]
☐	16306588	NP_036292.2	NM_012160	621	F-box and leucine-rich repeatprotein 4 F-box protein FBL4 [Homo sapiens]

Hs.5094
Gene: RNF10 Sequence count: 616

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	5931614	BAA84708.1	AB027196	811	RIE2 sid2705 [Homo sapiens]
☐	9367867	CAB97533.1	AL389976	729	RNF10, ring finger 10 KIAA0262RIE2 alternatively spliced product [Homo sapiens]
☐	1665791	BAA13392.1	D87451	761	Contains C3HC4 type zinc fingersignature [Homo sapiens]
☐	7662653	NP_055683.1	NM_014868	761	ring finger protein 10 KIAA0262gene product [Homo sapiens]

Hs.53940
Gene: - Sequence count: 0

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	15982946	AAL11501.1	-	485	AF360739_1 SSA protein SS-56

☐					[Homosapiens]
☐	16923932	AAL31641.1	-	485	AF439153_1 Ro/SSA1 related proteinFLJ10369 [Homo sapiens]
☐	17511218	NP_060543.4	-	485	Ro/SSA1 related protein FLJ10369[Homo sapiens]
☐	18603787	XP_006063.4	-	485	Ro/SSA1 related protein FLJ10369[Homo sapiens]

Hs.54089
Gene: BARD1 Sequence count: 79

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	2828068	AAB99978.1	-	777	BRCA1-associated RING domain protein[Homo sapiens]
☐	4557349	NP_000456.1	NM_000465	777	BRCA1 associated RING domain 1BRCA1-associated RING domain gene 1 BRCA1-associated RING domain 1[Homo sapiens]
☐	1710175	AAB38316.1	U76638	777	BRCA1-associated RING domain protein[Homo sapiens]

Hs.54580
Gene: RNF27 Sequence count: 248

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	18314488	AAH21925.1	-	551	AAH21925 ring finger protein 27 [Homosapiens]
☐	12407399	AAG53488.1	AF220034	551	AF220034_1 tripartite motif proteinTRIM8 [Homo sapiens]
☐	12382258	AAG53087.1	AF281046	551	AF281046_1 glioblastoma-expressedRING finger protein GERP [Homo sapiens]
☐	13569866	NP_112174.1	NM_030912	551	ring finger protein 27 tripartitemotif protein TRIM8 glioblastoma expressed ring finger protein [Homosapiens]

Hs.5548
Gene: FBXL5 Sequence count: 280

Select	GI	Protein Acc.	DNA Acc.	Length	Description

☐	7672734	AAF66616.1	AF142481	691	AF142481_1 F-box protein FLR1 [Homosapiens]
☐	7688697	AAF67489.1	AF157323	674	AF157323_1 p45SKP2-like protein [Homosapiens]
☐	6164725	AAF04512.1	AF174591	535	AF174591_1 F-box protein Fbl5 [Homosapiens]
☐	6103639	AAF03700.1	AF176700	694	F-box protein FBL5 [Homo sapiens]
☐	6456739	AAF09249.1	AF199420	690	AF199420_1 F-box protein FBL4 [Homosapiens]
☐	7020055	BAA90978.1	AK000153	636	unnamed protein product [Homosapiens]
☐	16306572	NP_036293.1	NM_012161	691	F-box and leucine-rich repeatprotein 5, isoform 1 F-box protein FBL5 [Homo sapiens]
☐	16306574	NP_277077.1	NM_033535	565	F-box and leucine-rich repeatprotein 5, isoform 2 F-box protein FBL5 [Homo sapiens]

Hs.5912
Gene: FBXO7 Sequence count: 491

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	6164624	AAF04471.1	AF129537	482	AF129537_1 F-box protein Fbx7 [Homosapiens]
☐	7677409	AAF67155.1	AF233225	522	AF233225_1 F-box protein FBX [Homosapiens]
☐	4886423	CAB43356.1	AL050254	522	hypothetical protein [Homo sapiens]
☐	14249955	AAH08361.1	BC008361	522	AAH08361 F-box only protein 7 [Homosapiens]
☐	15812193	NP_036311.2	NM_012179	522	F-box only protein 7 F-boxprotein 7 F-box protein FBX F-box protein Fbx7 dJ149A16.8 [Homosapiens]

Hs.59545
Gene: RNF15 Sequence count: 142

Select	GI	Protein Acc.	DNA Acc.	Length	Description

☐	2088552	AAB82084.1	-	465	unknown [Homo sapiens]
☐	20070649	AAH26930.1	-	465	ring finger protein 15 [Homosapiens]
☐	5454014	NP_006346.1	NM_006355	465	ring finger protein 15 Ro/SSAribonucleoprotein homolog [Homo sapiens]
☐	2062696	AAB53425.1	U90547	465	Ro/SSA ribonucleoprotein homolog[Homo sapiens]

Hs.6092
Gene: FBXL2 Sequence count: 83

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	6164721	AAF04510.1	AF174589	423	AF174589_1 F-box protein Fbl2 [Homosapiens]
☐	6063090	AAF03128.1	AF176518	425	AF176518_1 F-box protein FBL2 [Homosapiens]
☐	5919219	AAD56248.1	AF186273	423	AF186273_1 leucine-rich repeatscontaining F-box protein FBL3 [Homo sapiens]
☐	7022695	BAA91691.1	AK001438	423	unnamed protein product [Homosapiens]
☐	16306582	NP_036289.2	NM_012157	423	F-box and leucine-rich repeatprotein 2 F-box protein containing leucine-rich repeats [Homosapiens]
☐	*4884202*	*CAB43222.1*	*AL049953*	*250*	*hypothetical protein [Homo sapiens]*

Hs.61515
Gene: RNF15 Sequence count: 65

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	14043332	AAH07661.1	BC007661	488	AAH07661 Similar to ring fingerprotein 23 [Homo sapiens]

Hs.62264
Gene: KIAA0937 Sequence count: 142

Select	GI	Protein Acc.	DNA Acc.	Length	Description

	4589518	BAA76781.1	AB023154	653	KIAA0937 protein [Homo sapiens]

Hs.62767
Gene: - Sequence count: 0

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	17450863	XP_048774.2	-	717	KIAA1332 protein [Homo sapiens]

Hs.64691
Gene: KIAA0483 Sequence count: 195

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	7022998	BAA91795.1	AK001628	368	unnamed protein product [Homosapiens]
	7662158	NP_055991.1	NM_015176	368	KIAA0483 protein [Homo sapiens]
	3413926	*BAA32327.1*	*AB007952*	*299*	*KIAA0483 protein [Homo sapiens]*

Hs.64794
Gene: ZNF183 Sequence count: 100

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	2341022	AAB67605.1	-	343	zinc-finger protein [Homo sapiens]
	11422613	XP_010437.1	-	343	zinc finger protein 183 (RINGfinger, C3HC4 type) [Homo sapiens]
	18089018	AAH20556.1	-	343	AAH20556 zinc finger protein 183(RING finger, C3HC4 type) [Homo sapiens]
	12654053	AAH00832.1	BC000832	343	AAH00832 zinc finger protein 183(RING finger, C3HC4 type) [Homo sapiens]
	5902158	NP_008909.1	NM_006978	343	zinc finger protein 183 (RINGfinger, C3HC4 type) [Homo sapiens]
	2274982	CAA66907.1	X98253	343	ZNF183 [Homo sapiens]

Hs.65238
Gene: RNF40 Sequence count: 320

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	14779695	XP_034375.1	-	1001	95 kDa retinoblastoma proteinbinding protein [Homo sapiens]
	17391423	AAH18647.1	-	1001	AAH18647 95 kDa retinoblastomaprotein binding protein [Homo sapiens]
	3327136	BAA31636.1	AB014561	1001	KIAA0661 protein [Homo sapiens]
	14042062	BAB55092.1	AK027406	901	unnamed protein product [Homosapiens]
	13325463	AAH04527.1	BC004527	271	AAH04527 Similar to 95 kDaretinoblastoma protein binding protein KIAA0661 gene product [Homosapiens]
	13543994	AAH06133.1	BC006133	1001	AAH06133 95 kDa retinoblastomaprotein binding protein KIAA0661 gene product [Homo sapiens]
	15079968	AAH11769.1	BC011769	1001	AAH11769 Similar to 95 kDaretinoblastoma protein binding protein [Homo sapiens]
	7662230	NP_055586.1	NM_014771	1001	95 kDa retinoblastoma proteinbinding protein [Homo sapiens]
	10179425	*AAG13723.1*	*AF122819*	*838*	*AF122819_1 Rb-associated protein[Homo sapiens]*

Hs.65736
Gene: TRIM4 Sequence count: 98

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	12407377	AAG53477.1	AF220023	500	AF220023_1 tripartite motif proteinTRIM4 isoform alpha [Homo sapiens]
	12407379	AAG53478.1	AF220024	474	AF220024_1 tripartite motif proteinTRIM4 isoform beta

					[Homo sapiens]
☐	14670266	NP_148977.1	NM_033017	500	tripartite motif protein TRIM4isoform alpha tripartite motif protein TRIM4 tripartite motifprotein 4 [Homo sapiens]
☐	15011941	NP_149082.1	NM_033091	474	tripartite motif protein TRIM4isoform beta tripartite motif protein TRIM4 tripartite motif protein4 [Homo sapiens]

Hs.66295
Gene: - Sequence count: 0

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	18557099	XP_030360.2	-	728	multi-PDZ-domain-containingprotein [Homo sapiens]

Hs.66394
Gene: RNF4 Sequence count: 327

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	1843401	BAA19122.1	AB000468	190	zinc finger protein [Homo sapiens]
☐	4506561	NP_002929.1	NM_002938	190	ring finger protein 4 [Homosapiens]
☐	2565164	AAC52022.1	U95140	190	RNF4 [Homo sapiens]

Hs.6900
Gene: RNF13 Sequence count: 312

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	2746333	AAC03769.1	AF037204	381	RING zinc finger protein [Homosapiens]
☐	3387925	AAC28641.1	AF070558	381	RING zinc finger protein RZF [Homosapiens]
☐	14602541	AAH09781.1	BC009781	381	AAH09781 ring finger protein 13 [Homosapiens]
☐	14602579	AAH09803.1	BC009803	381	AAH09803 ring finger protein 13 [Homosapiens]

☐	6005864	NP_009213.1	NM_007282	381	ring finger protein 13 RING zincfinger protein [Homo sapiens]

Hs.69554
Gene: FLJ20552 Sequence count: 232

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	2979531	AAC06149.1	-	103	R33683_3 [Homo sapiens]
☐	19263501	AAH25374.1	-	311	hypothetical protein FLJ20552 [Homosapiens]
☐	7020737	BAA91254.1	AK000559	311	unnamed protein product [Homosapiens]
☐	12655173	AAH01442.1	BC001442	326	AAH01442 hypothetical proteinFLJ20552 [Homo sapiens]
☐	15559245	AAH13977.1	BC013977	311	AAH13977 Similar to hypotheticalprotein FLJ20552 [Homo sapiens]
☐	8923522	NP_060346.1	NM_017876	311	hypothetical protein FLJ20552 [Homosapiens]

Hs.7158
Gene: DKFZP566H073 Sequence count: 485

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	10437824	BAB15113.1	AK025329	350	unnamed protein product [Homosapiens]
☐	4884104	CAB43253.1	AL050060	324	hypothetical protein [Homo sapiens]
☐	14603365	AAH10139.1	BC010139	350	AAH10139 DKFZP566H073 protein [Homosapiens]
☐	14149702	NP_056343.1	NM_015528	350	DKFZP566H073 protein [Homosapiens]
☐	*5102896*	*CAB45281.1*	*AL079315*	*158*	*hypothetical protein, similar to(AF037205) RING zinc finger protein [Mus musculus] [Homo sapiens]*

Hs.7236
Gene: NOSIP Sequence count: 263

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	4680689	AAD27734.1	AF132959	301	AF132959_1 CGI-25 protein [Homosapiens]
☐	14424550	AAH09299.1	BC009299	301	AAH09299 eNOS interacting protein[Homo sapiens]
☐	14603229	AAH10077.1	BC010077	301	AAH10077 eNOS interacting protein[Homo sapiens]
☐	15030017	AAH11249.1	BC011249	301	AAH11249 Similar to eNOS interactingprotein [Homo sapiens]
☐	7705716	NP_057037.1	NM_015953	301	eNOS interacting protein CGI-25protein [Homo sapiens]

Hs.7252
Gene: RAI17 Sequence count: 279

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	6330624	BAA86538.1	AB033050	635	KIAA1224 protein [Homo sapiens]

Hs.72964
Gene: MKRN3 Sequence count: 12

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	1001959	AAC13989.1	-	507	ZNF127 [Homo sapiens]
☐	5032243	NP_005655.1	NM_005664	507	makorin, ring finger protein, 3zinc finger protein 127 [Homo sapiens]

Hs.7299
Gene: RAI17 Sequence count: 185

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	6012973	CAB57324.1	AL121733	253	hypothetical protein [Homo sapiens]

Hs.7314
Gene: KIAA0614 Sequence count: 312

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	3327042	BAA31589.1	AB014514	1630	KIAA0614 protein [Homo sapiens]

☐	7108919	AAF36539.1	AF174498	1381	GR AF-1 specific protein phosphatase[Homo sapiens]
☐	5911937	CAB55944.1	AL117469	116	hypothetical protein [Homo sapiens]
☐	13623332	AAH06270.1	BC006270	116	AAH06270 Unknown (protein forMGC:11291) [Homo sapiens]

Hs.7316
Gene: KIAA0804 Sequence count: 125

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	3882329	BAA34524.1	AB018347	1211	KIAA0804 protein [Homo sapiens]
☐	10434628	BAB14322.1	AK022945	793	unnamed protein product [Homosapiens]
☐	*12654357*	*AAH01001.1*	*BC001001*	*92*	*AAH01001 Similar to hBKLF for basickruppel like factor [Homo sapiens]*

Hs.73958
Gene: RAG1 Sequence count: 13

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	14763521	XP_030299.1	-	1043	recombination activating gene 1[Homo sapiens]
☐	190843	AAA60248.1	M29474	1043	recombination activating protein
☐	4557841	NP_000439.1	NM_000448	1043	recombination activating gene 1[Homo sapiens]

☐

Hs.74441
Gene: CHD4 Sequence count: 644

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	4557453	NP_001264.1	NM_001273	1912	chromodomain helicase DNA bindingprotein 4 Mi-2b [Homo sapiens]
	1107696	CAA60384.1	X86691	1912	Mi-2 protein [Homo sapiens]

☐					

Hs.75090
Gene: TRIM9 Sequence count: 121

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	12407403	AAG53490.1	AF220036	664	AF220036_1 tripartite motif proteinTRIM9 isoform alpha [Homo sapiens]
☐	12407405	AAG53491.1	AF220037	710	AF220037_1 tripartite motif proteinTRIM9 isoform beta [Homo sapiens]
☐	12407407	AAG53492.1	AF220038	664	AF220038_1 tripartite motif proteinTRIM9 isoform gamma [Homo sapiens]
☐	15426583	AAH13414.1	BC013414	550	AAH13414 Unknown (protein forMGC:4626) [Homo sapiens]
☐	16519557	NP_055978.2	NM_015163	710	tripartite motif protein 9,isoform 1 homolog of rat RING finger Spring [Homo sapiens]
☐	16519559	NP_443210.1	NM_052978	550	tripartite motif protein 9,isoform 2 homolog of rat RING finger Spring [Homo sapiens]
☐	*1665803*	*BAA13398.1*	*D87458*	*550*	*Similar to Human estrogen-responsivefinger protein, efp (A49656) [Homo sapiens]*

Hs.75275
Gene: UBE4A Sequence count: 257

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	1469175	BAA09475.1	D50916	1073	The KIAA0126 gene is partiallyrelated to a yeast gene. [Homo sapiens]
☐	4759288	NP_004779.1	NM_004788	1073	ubiquitination factor E4A (UFD2homolog, yeast) homolog of yeast (S. cerevisiae) ufd2 ubiquitinationfactor E4A (homologous to yeast UFD2) [Homo sapiens]

Hs.7540
Gene: FBXL3A Sequence count: 165

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	6164614	AAF04466.1	-	428	AF129532_1 F-box protein Fbl3a [Homosapiens]
☐	17475754	XP_041209.2	-	428	F-box and leucine-rich repeatprotein 3A [Homo sapiens]
☐	7158286	AAF37383.1	AF126028	419	AF126028_1 unknown [Homo sapiens]
☐	16306584	NP_036290.1	NM_012158	428	F-box and leucine-rich repeatprotein 3A F-box protein Fbl3a [Homo sapiens]

Hs.75450
Gene: DSIPI Sequence count: 545

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	11527559	BAB18680.1	AB025432	134	GILZ [Homo sapiens]
☐	5231131	AAD41085.1	AF153603	134	AF153603_1 TSC-22 related protein[Homo sapiens]
☐	5919161	AAD56234.1	AF183393	134	AF183393_1 TSC-22-like Protein [Homosapiens]
☐	10086253	AAG12456.1	AF228339	134	glucocorticoid-induced GILZ [Homosapiens]
☐	5817106	CAB53669.1	AL110191	130	hypothetical protein [Homo sapiens]
☐	*4758198*	*NP_004080.1*	*NM_004089*	*77*	*delta sleep inducing peptide,immunoreactor [Homo sapiens]*
☐	*1834507*	*CAA90644.1*	*Z50781*	*77*	*leucine zipper protein [Homosapiens]*

Hs.75871
Gene: PRKCBP1 Sequence count: 337

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	*6329749*	BAA86439.1	AB032951	1205	KIAA1125 protein [Homo sapiens]
☐	*11037059*	*NP_036540.1*	*NM_012408*	*614*	*protein kinase C binding protein 1[Homo sapiens]*

	12654363	*AAH01004.1*	*BC001004*	*133*	*AAH01004 Unknown (protein forMGC:5439) [Homo sapiens]*
	11385648	*AAG34905.1*	*AF273045*	*764*	*AF273045_1 CTCL tumor antigen se14-3[Homo sapiens]*
	7960216	*AAF71262.1*	*AF233453*	*614*	*RACK-like protein PRKCBP1 [Homosapiens]*
	3142288	*AAC72244.1*	*U48251*	*553*	*protein kinase C-binding proteinRACK7 [Homo sapiens]*

Hs.76127
Gene: HERC1 Sequence count: 133

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	4557026	NP_003913.1	NM_003922	4861	guanine nucleotide exchange factorp532 [Homo sapiens]
	1477565	AAD12586.1	U50078	4861	p532 [Homo sapiens]

Hs.76272
Gene: RBBP2 Sequence count: 207

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	4826968	NP_005047.1	NM_005056	1722	retinoblastoma-binding protein 2[Homo sapiens]
	435778	AAB28544.1	S66431	1722	retinoblastoma binding protein 2 RBP2[Homo sapiens]

Hs.76798
Gene: FBXL7 Sequence count: 87

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	4240169	BAA74863.1	AB020647	483	KIAA0840 protein [Homo sapiens]
	6164729	AAF04514.1	AF174593	483	AF174593_1 F-box protein Fbl7 [Homosapiens]
	6456737	AAF09248.1	AF199356	491	AF199356_1 F-box protein FBL6 [Homosapiens]
	6912466	NP_036436.1	NM_012304	491	F-box and leucine-rich repeatprotein 7 F-box protein Fbl7 KIAA0840 protein [Homo sapiens]

Hs.76917
Gene: FBXO8 Sequence count: 170

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	6164735	AAF04517.1	AF174596	341	AF174596_1 F-box protein Fbx8 [Homosapiens]
☐	9295168	AAF86868.1	AF201932	319	AF201932_1 DC10 [Homo sapiens]
☐	7677406	AAF67154.1	AF233224	319	AF233224_1 F-box protein FBS [Homosapiens]
☐	15812208	NP_036312.1	NM_012180	319	F-box only protein 8 F-boxprotein Fbx8 [Homo sapiens]

Hs.7759
Gene: XAP135 Sequence count: 387

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	13487236	AAK27451.1	-	410	AF338735_1 hypothetical PHD zincfinger protein XAP135 [Homo sapiens]
☐	18088065	AAH20954.1	-	408	AAH20954 hypothetical proteinFLJ10975 [Homo sapiens]
☐	19747276	NP_579866.1	-	408	PHD zinc finger protein XAP135,isoform b [Homo sapiens]
☐	7023354	BAA91934.1	AK001837	410	unnamed protein product [Homosapiens]
☐	8922800	NP_060758.1	NM_018288	410	PHD zinc finger protein XAP135,isoform a [Homo sapiens]

Hs.77617
Gene: SP100 Sequence count: 232

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	13991103	AAK51202.1	AF255565	885	AF255565_1 nuclear body proteinSP100C [Homo sapiens]
☐	*15079448*	*AAH11562.1*	*BC011562*	*480*	*AAH11562 Similar to nuclear antigenSp100 [Homo sapiens]*
	1173656	*AAC50743.1*	*U36501*	*688*	*SP100-B*

	3252911	*AAC39790.1*	*AF056322*	*879*	*SP100-HMG nuclear autoantigen [Homosapiens]*
	178689	*AAA35537.1*	*M60618*	*480*	*nuclear autoantigen*

Hs.77823
Gene: FLJ21343 Sequence count: 211

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	14740318	XP_045035.1	-	332	hypothetical protein FLJ21343[Homo sapiens]
	10437428	BAB15050.1	AK024996	332	unnamed protein product [Homosapiens]
	12232471	NP_073618.1	NM_022781	332	hypothetical protein FLJ21343[Homo sapiens]
	12053145	*CAB66751.1*	*AL136817*	*394*	*hypothetical protein [Homo sapiens]*

Hs.7838
Gene: MKRN1 Sequence count: 473

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	6601434	AAF18979.1	-	482	makorin 1 [Homo sapiens]
	14739983	XP_035119.1	-	482	makorin, ring finger protein, 1[Homo sapiens]
	19684160	AAH25955.1	-	482	makorin, ring finger protein, 1[Homo sapiens]
	6563240	AAF17214.1	AF117233	328	AF117233_1 znf-xp protein [Homosapiens]
	6572964	AAF17487.1	AF192784	482	AF192784_1 makorin 1 [Homo sapiens]
	12053135	CAB66746.1	AL136812	482	hypothetical protein [Homo sapiens]
	7305273	NP_038474.1	NM_013446	482	makorin, ring finger protein, 1[Homo sapiens]

Hs.7885
Gene: PICALM Sequence count: 370

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	3139011	AAC16702.1	AF060930	104	type IV AF10/CALM fusion protein[Homo sapiens]
	3139013	AAC16703.1	AF060931	84	type V AF10/CALM fusion protein [Homosapiens]
	3139031	*AAC16712.1*	*AF060940*	*58*	*type II CALM protein [Homo sapiens]*
	3139029	*AAC16711.1*	*AF060939*	*78*	*type I CALM protein [Homo sapiens]*
	3139025	*AAC16709.1*	*AF060937*	*51*	*type IV AF10 protein [Homo sapiens]*
	3139009	*AAC16701.1*	*AF060929*	*51*	*type III AF10/CALM fusion protein[Homo sapiens]*
	6005733	*NP_009097.1*	*NM_007166*	*652*	*Clathrin assembly lymphoid-myeloidleukemia gene [Homo sapiens]*
	1373146	*AAB07762.1*	*U45976*	*652*	*CALM*

Hs.78893
Gene: PHF3 Sequence count: 221

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	6648928	AAF21292.1	AF091622	2039	AF091622_1 PHD finger protein 3 [Homosapiens]
	1663706	BAA13438.1	D87685	1723	similar to human transcriptionfactor TFIIS (S34159). [Homo sapiens]
	7662018	NP_055968.1	NM_015153	2039	PHD finger protein 3 [Homo sapiens]

Hs.792
Gene: ARFD1 Sequence count: 90

Select	GI	Protein Acc.	DNA Acc.	Length	Description

☐	18490296	AAH22510.1	-	574	ADP-ribosylation factor domainprotein 1, 64kD [Homo sapiens]
☐	12275883	AAG50176.1	AF230397	574	AF230397_1 tripartite motif proteinTRIM23 alpha [Homo sapiens]
☐	12275885	AAG50177.1	AF230398	569	AF230398_1 tripartite motif proteinTRIM23 beta [Homo sapiens]
☐	12275887	AAG50178.1	AF230399	546	AF230399_1 tripartite motif proteinTRIM23 gamma [Homo sapiens]
☐	292070	AAA35940.1	L04510	574	nucleotide binding protein
☐	4502197	NP_001647.1	NM_001656	574	ADP-ribosylation factor domainprotein 1 isoform alpha ARF domain protein 1 GTP-binding proteinARD-1 tripartite motif protein TRIM23 [Homo sapiens]
☐	15208641	NP_150230.1	NM_033227	569	ADP-ribosylation factor domainprotein 1 isoform beta ARF domain protein 1 GTP-binding proteinARD-1 tripartite motif protein TRIM23 [Homo sapiens]
☐	15208643	NP_150231.1	NM_033228	546	ADP-ribosylation factor domainprotein 1 isoform gamma ARF domain protein 1 GTP-binding proteinARD-1 tripartite motif protein TRIM23 [Homo sapiens]

Hs.79828
Gene: FLJ20333 Sequence count: 162

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	7243047	BAA92571.1	AB037754	741	KIAA1333 protein [Homo sapiens]
☐	7020359	BAA91095.1	AK000340	706	unnamed protein product [Homosapiens]
	10434508	BAB14280.1	AK022867	290	unnamed protein product

☐					[Homosapiens]
☐	13111835	AAH00973.2	BC000973	706	AAH00973 hypothetical proteinFLJ20333 [Homo sapiens]
☐	8923309	NP_060239.1	NM_017769	706	hypothetical protein FLJ20333 [Homosapiens]

Hs.80358
Gene: SMCY Sequence count: 64

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	11418363	XP_010478.1	-	1539	Smcy homolog, Y chromosome (mouse)[Homo sapiens]
☐	1510145	BAA13241.1	D87072	1482	similar to Human XE169protein(P41229) [Homo sapiens]
☐	4759150	NP_004644.1	NM_004653	1539	Smcy homolog, Y chromosome (mouse)histocompatibility Y antigen SMC (mouse) homolog, Y chromosomeSelected mouse cDNA on Y, human homolog of [Homo sapiens]
☐	1661016	AAC50806.1	U52191	1539	SMCY

Hs.80731
Gene: AMFR Sequence count: 298

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	19923132	NP_001135.2	-	643	autocrine motility factor receptor[Homo sapiens]
☐	5931955	AAD56722.1	AF124145	643	AF124145_1 autocrine motility factorreceptor [Homo sapiens]
☐	*521221*	*AAA79362.1*	*L35233*	*323*	*autocrine motility factor receptor*
☐	*338731*	*AAA36671.1*	*M63175*	*323*	*autocrine motility factor receptor*

Hs.81001
Gene: - Sequence count: 0

Select	GI	Protein Acc.	DNA	Length	Description

			Acc.		
☐	18700319	BAB85128.1	-	358	F-box domain Fbx25-containingprotein [Homo sapiens]

Hs.8164
Gene: TRIM37 Sequence count: 115

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	4240285	BAA74921.1	AB020705	979	KIAA0898 protein [Homo sapiens]
☐	15147333	NP_056109.1	NM_015294	964	tripartite motif-containing 37RING-B-box-coiled-coil protein MUL protein Mulibrey nanism [Homosapiens]

Hs.82023
Gene: DKFZP434B205 Sequence count: 375

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	10438817	BAB15354.1	AK026081	566	unnamed protein product [Homosapiens]
☐	15559537	AAH14130.1	BC014130	566	AAH14130 Unknown (protein forMGC:20962) [Homo sapiens]
☐	*14495644*	*AAH09429.1*	*BC009429*	*345*	*AAH09429 Unknown (protein forIMAGE:2988331) [Homo sapiens]*
☐	*13528687*	*AAH04541.1*	*BC004541*	*433*	*AAH04541 Unknown (protein forIMAGE:3951723) [Homo sapiens]*
☐	*12654081*	*AAH00850.1*	*BC000850*	*159*	*AAH00850 Similar to f-box and WD-40domain protein 5 [Homo sapiens]*
☐	*10441926*	*AAG17240.1*	*AF217998*	*159*	*AF217998_1 unknown [Homo sapiens]*
☐	*6808431*	*CAB70851.1*	*AL137631*	*192*	*hypothetical protein [Homo sapiens]*

Hs.82210
Gene: ZNF220 Sequence count: 167

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	5803098	NP_006757.1	NM_006766	2004	zinc finger protein 220

☐					Monocyticleukemia zinc finger protein [Homo sapiens]
☐	1517914	AAC50662.1	U47742	2004	monocytic leukaemia zinc fingerprotein
☐	*14041987*	*BAB55062.1*	*AK027361*	*205*	*unnamed protein product [Homosapiens]*

Hs.82292
Gene: KIAA0215 Sequence count: 73

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	14758564	XP_010180.4	-	823	KIAA0215 gene product [Homosapiens]
☐	5805248	AAD51905.1	AF127774	823	unknown [Homo sapiens]
☐	1504012	BAA13205.1	D86969	823	similar to Human zinc-fingerprotein, BR140(P1:JC2069) [Homo sapiens]
☐	7662006	NP_055550.1	NM_014735	823	KIAA0215 gene product [Homosapiens]

Hs.82380
Gene: MNAT1 Sequence count: 175

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	12654033	AAH00820.1	BC000820	309	AAH00820 menage a trois 1 (CAKassembly factor) [Homo sapiens]
☐	4505225	NP_002422.1	NM_002431	309	menage a trois 1 (CAK assemblyfactor) cyclin G1 interacting protein cyclin H assembly factor [Homosapiens]
☐	1470082	AAB05248.1	U61835	267	1500GX1 gene product
☐	1089848	CAA61112.1	X87843	309	cdk7/cyclin H assembly factor [Homosapiens]
☐	1109757	CAA63356.1	X92669	309	p35 [Homo sapiens]

Hs.82568
Gene: - Sequence count: 0

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	88399	A40044	-	560	A40044 PML-1 protein - human

Hs.83293
Gene: DKFZP434A0225 Sequence count: 287

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	7243153	BAA92624.1	AB037807	1214	KIAA1386 protein [Homo sapiens]
☐	*7022270*	*BAA91537.1*	*AK001179*	*509*	*unnamed protein product [Homosapiens]*
☐	*6807862*	*CAB70704.1*	*AL137349*	*541*	*hypothetical protein [Homo sapiens]*

Hs.8375
Gene: TRAF4 Sequence count: 220

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	3435256	AAC32376.1	AF082185	198	tumor necrosis factorreceptor-associated factor 4A [Homo sapiens]
☐	12804687	AAH01769.1	BC001769	470	AAH01769 TNF receptor-associatedfactor 4 [Homo sapiens]
☐	4759252	NP_004286.1	NM_004295	470	TNF receptor-associated factor 4[Homo sapiens]
☐	951277	CAA56491.1	X80200	470	cystein rich domain associated toRING and TRAF protein [Homo sapiens]

Hs.8383
Gene: BAZ2B Sequence count: 189

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	6683500	BAA89212.1	AB032255	1972	bromodomain adjacent to zinc fingerdomain 2B [Homo sapiens]
☐	7959213	BAA96000.1	AB040909	1220	KIAA1476 protein [Homo sapiens]
☐	5262644	CAB45759.1	AL080173	449	hypothetical protein [Homo sapiens]
	7304923	NP_038478.1	NM_013450	1972	bromodomain adjacent to zinc

					fingerdomain, 2B [Homo sapiens]
	15214874	*AAH12576.1*	*BC012576*	*643*	*AAH12576 Unknown (protein forMGC:13472) [Homo sapiens]*

Hs.85273
Gene: RBBP6 Sequence count: 118

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	18585666	XP_056260.3	-	1560	retinoblastoma-binding protein 6[Homo sapiens]
	5902044	NP_008841.1	NM_006910	948	retinoblastoma-binding protein 6[Homo sapiens]
	755748	CAA59445.1	X85133	948	RB protein binding protein [Homosapiens]
	10439936	*BAB15600.1*	*AK026954*	*628*	*unnamed protein product [Homosapiens]*

Hs.85524
Gene: RNF29 Sequence count: 51

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	13160385	CAC32839.1	-	436	ring finger protein 29 [Homosapiens]
	14588846	CAC43019.1	AJ243488	452	titin zinc-finger anchoring protein[Homo sapiens]
	14588848	CAC43020.1	AJ243489	548	titin zinc-finger anchoring protein[Homo sapiens]
	13160386	CAC32840.1	AJ291712	532	ring finger protein 29 [Homosapiens]
	14043532	AAH07750.1	BC007750	436	AAH07750 Unknown (protein forMGC:12836) [Homo sapiens]
	14916469	NP_149047.1	NM_033058	532	for muscle specific ring finger 2[Homo sapiens]

Hs.85844
Gene: NTRK1 Sequence count: 1572

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	339918	AAA36770.1	M23102	790	trk tyrosine-specific protein kinase

	14250052	*AAH08425.1*	*BC008425*	*285*	*AAH08425 Unknown (protein forMGC:14582) [Homo sapiens]*
	14250022	*AAH08407.1*	*BC008407*	*285*	*AAH08407 Unknown (protein forMGC:14532) [Homo sapiens]*
	12653955	*AAH00771.1*	*BC000771*	*248*	*AAH00771 Similar to tropomyosin 4[Homo sapiens]*
	4585712	*NP_002520.2*	*NM_002529*	*796*	*neurotrophic tyrosine kinase,receptor, type 1 Oncogene TRK [Homo sapiens]*
	9508585	*AAF87083.1*	*AY004867*	*247*	*tropomyosin isoform [Homo sapiens]*
	37430	*CAA27798.1*	*X04201*	*285*	*skeletal muscle tropomyosin (AA 1-285)[Homo sapiens]*
	37405	*CAA44719.1*	*X62947*	*503*	*55 kd protein [Homo sapiens]*
	37403	*CAA27243.1*	*X03541*	*641*	*trk gene product (aa 1-641) [Homosapiens]*
	37400	*CAA29888.1*	*X06704*	*439*	*trk-2h polypeptide [Homo sapiens]*
	553799	*AAA36775.1*	*M12128*	*96*	*cytoskeletal tropomyosin isoform*

Hs.8707
Gene: KIAA1301 Sequence count: 21

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	14730213	XP_038999.1	-	1572	KIAA1301 protein [Homo sapiens]
	7242957	BAA92539.1	AB037722	1581	KIAA1301 protein [Homo sapiens]
	9368900	CAB99103.1	AL390186	221	hypothetical protein [Homo sapiens]

Hs.8834
Gene: RNF3 Sequence count: 339

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	2440074	CAA04477.1	AJ001019	247	ring finger protein [Homo sapiens]

☐	5454012	NP_006306.1	NM_006315	247	ring finger protein 3 [Homosapiens]

Hs.8858
Gene: BAZ1A Sequence count: 229

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	17454515	XP_007240.2	-	1556	bromodomain adjacent to zincfinger domain, 1A [Homo sapiens]
☐	6683494	BAA89209.1	AB032252	1674	bromodomain adjacent to zinc fingerdomain 1A [Homo sapiens]
☐	7920301	AAF70601.1	AF213467	1556	AF213467_1 ATP-dependent chromatinremodelling protein [Homo sapiens]
☐	6942227	AAF32366.1	AF221130	1556	AF221130_1 chromatin remodeling factorWCRF180 [Homo sapiens]
☐	4884108	CAB43261.1	AL050089	811	hypothetical protein [Homo sapiens]
☐	7304919	NP_038476.1	NM_013448	1674	bromodomain adjacent to zinc fingerdomain, 1A [Homo sapiens]

Hs.89135
Gene: DTX2 Sequence count: 170

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	19913508	AAH26059.1	-	622	deltex homolog 2 (Drosophila) [Homosapiens]
☐	7959323	BAA96052.1	AB040961	740	KIAA1528 protein [Homo sapiens]
☐	10436012	BAB14727.1	AK023924	622	unnamed protein product [Homosapiens]
☐	14250774	AAH08856.1	BC008856	622	AAH08856 Unknown (protein forMGC:14983) [Homo sapiens]

Hs.89633
Gene: PML Sequence count: 286

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	18088052	AAH20994.1	-	781	AAH20994 promyelocytic

					leukemia [Homosapiens]
	12275891	AAG50180.1	AF230401	882	AF230401_1 tripartite motif proteinTRIM19 alpha [Homo sapiens]
	12275893	AAG50181.1	AF230402	611	AF230402_1 tripartite motif proteinTRIM19 beta [Homo sapiens]
	12275895	AAG50182.1	AF230403	824	AF230403_1 tripartite motif proteinTRIM19 gamma [Homo sapiens]
	12275897	AAG50183.1	AF230404	854	AF230404_1 tripartite motif proteinTRIM19 delta [Homo sapiens]
	12275899	AAG50184.1	AF230405	560	AF230405_1 tripartite motif proteinTRIM19 epsilon [Homo sapiens]
	12275901	AAG50185.1	AF230406	633	AF230406_1 tripartite motif proteinTRIM19 zeta [Homo sapiens]
	12275903	AAG50186.1	AF230407	423	AF230407_1 tripartite motif proteinTRIM19 eta [Homo sapiens]
	12275905	AAG50187.1	AF230408	435	AF230408_1 tripartite motif proteinTRIM19 theta [Homo sapiens]
	12275907	AAG50188.1	AF230409	423	AF230409_1 tripartite motif proteinTRIM19 iota [Homo sapiens]
	12275909	AAG50189.1	AF230410	829	AF230410_1 tripartite motif proteinTRIM19 kappa [Homo sapiens]
	12275912	AAG50190.1	AF230411	585	AF230411_1 tripartite motif proteinTRIM19 lambda [Homo sapiens]
	12652663	AAH00080.1	BC000080	759	AAH00080 Similar to promyelocyticleukemia [Homo sapiens]
	190115	AAA60125.1	M73778	560	PML-1 protein
	190117	AAA60388.1	M79462	860	putative

☐	190119	AAA60351.1	M79463	589	putative
☐	190121	AAA60390.1	M79464	802	putative
☐	190123	AAA60352.1	M80185	538	putative
☐	4505903	NP_002666.1	NM_002675	633	promyelocytic leukemia protein,isoform 6 promyelocytic leukemia, inducer of tripartite motifprotein TRIM19 [Homo sapiens]
☐	15451763	NP_150241.1	NM_033238	882	promyelocytic leukemia protein,isoform 1 promyelocytic leukemia, inducer of tripartite motifprotein TRIM19 [Homo sapiens]
☐	15451765	NP_150242.1	NM_033239	829	promyelocytic leukemia protein,isoform 9 promyelocytic leukemia, inducer of tripartite motifprotein TRIM19 [Homo sapiens]
☐	15451767	NP_150243.1	NM_033240	611	promyelocytic leukemia protein,isoform 2 promyelocytic leukemia, inducer of tripartite motifprotein TRIM19 [Homo sapiens]
☐	15451769	NP_150245.1	NM_033242	824	promyelocytic leukemia protein,isoform 3 promyelocytic leukemia, inducer of tripartite motifprotein TRIM19 [Homo sapiens]
☐	15451771	NP_150247.1	NM_033244	560	promyelocytic leukemia protein,isoform 5 promyelocytic leukemia, inducer of tripartite motifprotein TRIM19 [Homo sapiens]
☐	15451773	NP_150248.1	NM_033245	611	promyelocytic leukemia protein,isoform 2 promyelocytic leukemia, inducer of tripartite motifprotein TRIM19 [Homo sapiens]
	15451775	NP_150249.1	NM_033246	423	promyelocytic leukemia

☐					protein,isoform 7 promyelocytic leukemia, inducer of tripartite motifprotein TRIM19 [Homo sapiens]
☐	15451777	NP_150250.1	NM_033247	435	promyelocytic leukemia protein,isoform 8 promyelocytic leukemia, inducer of tripartite motifprotein TRIM19 [Homo sapiens]
☐	15451779	NP_150252.1	NM_033249	585	promyelocytic leukemia protein,isoform 10 promyelocytic leukemia, inducer of tripartite motifprotein TRIM19 [Homo sapiens]
☐	15451781	NP_150253.1	NM_033250	781	promyelocytic leukemia protein,isoform 11 promyelocytic leukemia, inducer of tripartite motifprotein TRIM19 [Homo sapiens]
☐	8815562	AAB19601.2	S50913	641	PML [Homo sapiens]
☐	34814	CAA44841.1	X63131	633	My1 (PML) [Homo sapiens]

Hs.90375
Gene: FLJ10597 Sequence count: 350

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	7022730	BAA91704.1	AK001459	245	unnamed protein product [Homosapiens]
☐	8922542	NP_060620.1	NM_018150	245	hypothetical protein FLJ10597 [Homosapiens]
☐	*7706051*	*NP_057585.1*	*NM_016501*	*112*	*hypothetical protein FLJ10597 [Homosapiens]*
☐	*12653031*	*AAH00279.1*	*BC000279*	*112*	*AAH00279 hypothetical proteinFLJ10597 [Homo sapiens]*

Hs.90957
Gene: TRAF6 Sequence count: 44

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	4759254	NP_004611.1	NM_004620	522	TNF receptor-associated factor

☐					6[Homo sapiens]
☐	1732426	AAB38751.1	U78798	522	putative interleukin 1 signaltransducer [Homo sapiens]

Hs.91096
Gene: TRIM31 Sequence count: 52

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	12275860	AAG50165.1	AF230386	425	AF230386_1 tripartite motif proteinTRIM31 alpha [Homo sapiens]
☐	12275862	AAG50166.1	AF230387	267	AF230387_1 tripartite motif proteinTRIM31 beta [Homo sapiens]
☐	16445352	NP_008959.2	NM_007028	425	tripartite motif protein 31,isoform alpha ring finger protein HCGI protein tripartitemotif-containing 31 [Homo sapiens]
☐	16445354	NP_438111.1	NM_052816	267	tripartite motif protein 31,isoform beta ring finger protein HCGI protein tripartitemotif-containing 31 [Homo sapiens]
☐	1770499	CAA69165.1	Y07828	236	put. ring protein [Homo sapiens]

Hs.92236
Gene: MLL4 Sequence count: 145

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	4336749	AAD17932.1	-	1010	myeloid/lymphoid leukemia 2 [Homosapiens]
☐	6634011	BAA20763.2	AB002302	1900	KIAA0304 protein [Homo sapiens]
☐	5923931	AAD56420.1	AF186605	2605	AF186605_1 MLL2 protein [Homo sapiens]
☐	5123787	CAB45385.1	AJ007041	2715	trithorax homologue 2 [Homo sapiens]
☐	7662046	NP_055542.1	NM_014727	2715	KIAA0304 gene product [Homosapiens]
	14424624	*AAH09337.1*	*BC009337*	*798*	*AAH09337 Similar to KIAA0304 geneproduct [Homo sapiens]*

	13938427	*AAH07353.1*	*BC007353*	*175*	*AAH07353 Similar to KIAA0304 geneproduct [Homo sapiens]*
	4588365	*AAD26113.1*	*AF105279*	*64*	*AF105279_1 myeloid/lymphoid leukemia 2[Homo sapiens]*

Hs.9238
Gene: FLJ23516 Sequence count: 118

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	17485597	XP_016673.2	-	428	hypothetical protein FLJ23516[Homo sapiens]
	15011452	AAK77554.1	AF394689	428	AF394689_1 GRAIL [Homo sapiens]
	10440233	BAB15682.1	AK027169	156	unnamed protein product [Homosapiens]
	13375697	NP_078815.1	NM_024539	156	hypothetical protein FLJ23516[Homo sapiens]

Hs.93523
Gene: PPIL2 Sequence count: 309

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	13366579	AAH00022.1	BC000022	527	AAH00022 Similar to peptidylprolylisomerase (cyclophilin)-like 2 [Homo sapiens]
	7657473	NP_055152.1	NM_014337	520	peptidylprolyl isomerase(cyclophilin)-like 2 cyclophilin-like protein CyP-60 [Homo sapiens]
	1199598	AAC50376.1	U37219	520	cyclophilin-like protein CyP-60
	1199602	*AAC50378.1*	*U37221*	*311*	*cyclophilin-like protein*
	1199600	*AAC50377.1*	*U37220*	*282*	*cyclophilin-like protein*

Hs.94392
Gene: - Sequence count: 0

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	68992	TVHURF	-	513	TVHURF ret finger protein - human

Hs.95667
Gene: FBXO30 Sequence count: 90

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	13561413	AAK30299.1	AF248640	390	F-BOX domain protein [Homo sapiens]
☐	15812184	NP_115521.2	NM_032145	390	F-box only protein 30 [Homosapiens]

Hs.96264
Gene: ATRX Sequence count: 311

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	1778351	AAB40698.1	-	2375	putative DNA dependent ATPase andhelicase [Homo sapiens]
☐	1778352	AAB40699.1	-	2337	putative DNA dependent ATPase andhelicase [Homo sapiens]
☐	1778353	AAB40700.1	-	2288	putative DNA dependent ATPase andhelicase [Homo sapiens]
☐	2306766	AAC51655.1	-	2492	zinc finger helicase [Homo sapiens]
☐	2306809	AAC51657.1	-	2375	X-linked nuclear protein [Homosapiens]
☐	6274548	NP_000480.1	NM_000489	2492	transcriptional regulator ATRXalpha thalassemia/mental retardation syndrome X-linked (RAD54 (S.cerevisiae) homolog) RAD54 (Saccharomyces cerevisiae), human homologof [Homo sapiens]
☐	1778307	AAB49969.1	U72936	2288	putative DNA dependent ATPase andhelicase [Homo sapiens]
	6960326	AAB49970.2	U72937	2492	putative DNA dependent ATPase andhelicase [Homo sapiens]

☐					
☐	6960328	AAB49971.2	U72938	2454	putative DNA dependent ATPase andhelicase [Homo sapiens]
☐	*12803397*	*AAH02521.1*	*BC002521*	*90*	*AAH02521 Similar to alphathalassemia/mental retardation syndrome X-linked (RAD54 (S.cerevisiae) homolog) [Homo sapiens]*
☐	*606833*	*AAC50069.1*	*U09820*	*1641*	*helicase II*

Hs.96334
Gene: RNF11 Sequence count: 300

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	18089242	AAH20964.1	-	154	AAH20964 ring finger protein 11 [Homosapiens]
☐	5931545	BAA84683.1	AB024703	154	Sid1669p [Homo sapiens]
☐	4929715	AAD34118.1	AF151881	154	AF151881_1 CGI-123 protein [Homosapiens]
☐	7657520	NP_055187.1	NM_014372	154	ring finger protein 11 Sid1669protein [Homo sapiens]

Hs.97176
Gene: RNF25 Sequence count: 107

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	15990461	AAH15612.1	-	459	AAH15612 ring finger protein 25 [Homosapiens]
☐	10436180	BAB14743.1	AK023968	439	unnamed protein product [Homosapiens]
☐	11967989	NP_071898.1	NM_022453	439	ring finger protein 25 [Homosapiens]

Hs.9729
Gene: KIAA0239 Sequence count: 175

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	8670816	CAB94935.1	AJ251833	576	hypothetical protein [Homo sapiens]

	14424558	AAH09307.1	BC009307	577	AAH09307 KIAA0239 protein [Homosapiens]
	1510153	BAA13245.1	D87076	571	similar to human bromodomain proteinBR140(JC2069) [Homo sapiens]
	13375622	*NP_056103.1*	*NM_015288*	*246*	*KIAA0239 protein [Homo sapiens]*
	13279143	*AAH04292.1*	*BC004292*	*246*	*AAH04292 Unknown (protein forMGC:10883) [Homo sapiens]*

Hs.98074
Gene: ITCH Sequence count: 122

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	14285270	CAC09387.2	-	703	dJ468O1.1 (atrophin 1 interactingprotein 4 (AIP4)) [Homo sapiens]
	13366088	BAB39389.1	AB056663	862	ubiquitin protein ligase Itch [Homosapiens]
	2708329	AAC04845.1	AF038564	739	atrophin-1 interacting protein 4[Homo sapiens]
	13785518	AAK39399.1	AF095745	862	AF095745_1 ubiquitin protein ligaseITCH [Homo sapiens]
	13905122	AAH06848.1	BC006848	118	AAH06848 Similar to RIKEN cDNA1300010O06 gene [Homo sapiens]
	15079474	AAH11571.1	BC011571	903	AAH11571 Similar to itchy (mousehomolog) E3 ubiquitin protein ligase [Homo sapiens]
	14010859	NP_113671.1	NM_031483	862	itchy homolog E3 ubiquitin proteinligase (mouse) atrophin-1 interacting protein 4 itchy (mousehomolog) E3 ubiquitin protein ligase [Homo sapiens]

Hs.9877
Gene: NUP62 Sequence count: 398

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	7328113	CAB82399.1	AL162061	522	hypothetical protein [Homo

☐					sapiens]
☐	13177793	AAH03663.1	BC003663	522	AAH03663 hypothetical protein [Homosapiens]
☐	6912544	NP_036478.1	NM_012346	522	nucleoporin 62kD nucleoporin p62[Homo sapiens]
☐	7705355	NP_057637.1	NM_016553	522	nucleoporin 62kD nucleoporin p62[Homo sapiens]
☐	432654	CAA41411.1	X58521	522	nucleoporin p62 [Homo sapiens]

Hs.99010
Gene: NSD1 Sequence count: 111

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	16751269	AAL06645.1	-	2696	androgen receptor associatedcoregulator 267-b [Homo sapiens]
☐	16755530	AAL27991.1	-	2427	AF380302_1 androgenreceptor-associated coregulator 267-a [Homo sapiens]
☐	19923586	NP_071900.2	-	2696	hypothetical protein FLJ22263similar to nuclear receptor-bindin androgen receptor-associatedcoregulator 267 [Homo sapiens]
☐	15213542	AAK92049.1	AF322907	2596	AF322907_1 NSD1 [Homo sapiens]
☐	10438579	BAB15281.1	AK025916	699	unnamed protein product [Homosapiens]
☐	10438794	BAB15346.1	AK026066	1069	unnamed protein product [Homosapiens]

☐

Hs.99872
Gene: FALZ Sequence count: 286

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	6683492	BAA89208.1	AB032251	2781	bromodomain PHD finger transcriptionfactor [Homo

					sapiens]
☐	4758336	NP_004450.1	NM_004459	810	fetal Alzheimer antigen [Homosapiens]
☐	1276428	AAA97522.1	U05237	810	FAC1 gene product
☐	*10440252*	*BAB15686.1*	*AK027184*	*412*	*unnamed protein product [Homosapiens]*

Hs.99980
Gene: CBL Sequence count: 17

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	4885117	NP_005179.1	NM_005188	906	Cas-Br-M (murine) ecotropicretroviral transforming sequence Cas-Br-M ecotropic retroviraltransforming sequence (Oncogene CBL2) [Homo sapiens]
☐	29731	CAA40393.1	X57110	906	c-cbl protein [Homo sapiens]

Proteins not included in UniGene:

GI	Accession	Length	Description
1	protlog1.0	888	predicted Full Human POSH [Homo sapiens]
66829	TVHUTT	790	TVHUTT nerve growth factor receptorprecursor, high affinity - human
88547	A33754	1043	A33754 recombination-activating protein 1 -human
105146	A37241	475	A37241 52K autoantigen Ro/SS-A - human
106090	S19244	633	S19244 gene My1 protein - human
107399	A40045	641	A40045 probable transcription factor PML L- human
107473	S16954	464	S16954 retinoblastoma-binding protein 2 -human (fragment)
115855	P22681	906	CBL_HUMAN Signal transduction protein CBL(Proto-oncogene c-CBL)
129554	P28328	305	PEX2_HUMAN Peroxisome assembly factor-1(PAF-1) (Peroxin-2) (Peroxisomal membrane protein 3) (35 kDaperoxisomal membrane protein)
131827	P15918	1043	RAG1_HUMAN V(D)J recombination activatingprotein 1 (RAG-1)
132517	P14373	513	RFP_HUMAN Zinc-finger protein RFP (Retfinger protein) (Tripartite motif protein 27)
133250	P19474	475	RO52_HUMAN 52 kDa Ro protein (Sjogrensyndrome type A antigen (SS-A)) (Ro(SS-A)) (52 kDa ribonucleoproteinautoantigen Ro/SS-A)
190125	AAA60126.1	797	PML-RAR protein
227915	1713406B	464	1713406B retinoblastoma-binding protein2 [Homo sapiens]
239750	AAB20463.1	860	PML-1=putative zinc finger protein[human, Peptide, 860 aa]
239751	AAB20464.1	589	PML-2=putative zinc finger protein[human, Peptide, 589 aa]
239752	AAB20465.1	802	PML-3=putative zinc finger protein[human, Peptide, 802 aa]
280833	A60198	589	A60198 Myl protein - human
280867	A43817	906	A43817 transforming protein (cbl) - human
284349	A41812	305	A41812 peroxisome assembly factor-1, PAF-1- human
345731	A44264	3910	A44264 trithorax homolog HTX, version 1 -human (fragment)
345890	A44265	3968	A44265 trithorax homolog HTX, version 2 -human
388374	AAB27059.1	289	flvi-2/bmi-1 [Homo sapiens]
422756	A46054	574	A46054 GTP-binding protein ARD 1 - human
451555	AAA18644.1	288	BCR11q23
461632	P35226	326	BMI1_HUMAN Polycomb complex protein BMI-1
462585	P35227	344	ME18_HUMAN DNA-binding protein Mel-18 (Zincfinger protein 144)

476952	A47380	377	A47380 RING finger-containing DNA bindingprotein RING1 - human
542805	JN0717	344	JN0717 DNA-binding Mel-18 protein - human
542812	A49656	630	A49656 estrogen-responsive finger protein,efp (RING finger, coiled-coil domains) - human
542955	S41819	522	S41819 nucleoporin p62 - human
543063	JC2069	1214	JC2069 zinc-finger protein, BR140 - human
543839	P36406	574	ARD1_HUMAN GTP-binding protein ARD-1
548733	Q06587	377	RNG1_HUMAN Polycomb complex protein RING1(RNF1)
553800	AAA92511.1	1012	trithorax
575251	CAA86571.1	1009	helicase-like transcription factor[Homo sapiens]
585593	P37198	522	NU62_HUMAN Nuclear pore glycoprotein p62(62 kDa nucleoporin)
627392	A54652	1863	A54652 breast/ovarian cancersusceptibility protein BRCA1 - human
627427	A38920	874	A38920 E6-associated protein - human(fragment)
627468	A38919	1083	A38919 hypothetical protein 1 - human
627469	B38919	1054	B38919 hypothetical protein 2 - human(fragment)
631330	S42516	860	S42516 PML protein, splice form 1 - human
631331	S44380	860	S44380 PML protein, splice form 1 - human
631332	S42517	589	S42517 PML protein, splice form 2 - human
631333	S44381	589	S44381 PML protein, splice form 2 - human
631334	S42518	802	S42518 PML protein, splice form 3 - human
631335	S44382	802	S44382 PML protein, splice form 3 - human
728984	P38398	1863	BRC1_HUMAN Breast cancer type 1susceptibility protein
731161	P41229	1560	SMCX_HUMAN SmcX protein (Xe169 protein)
899268	CAA58584.1	395	ALL-1 protein [Homo sapiens]
1042097	AAB34770.1	366	trx Zinc-finger region homolog [Homosapiens]
1082312	A55501	786	A55501 cyclin F - human
1082438	S49618	1009	S49618 helicase-like transcription factor- human
1082441	A56095	1009	A56095 HIP116 protein - human
1082838	A55649	568	A55649 TNFR-associated protein LAP1 -human
1170364	Q03164	3969	HRX_HUMAN Zinc finger protein HRX (ALL-1)(Trithorax-like protein)
1362759	S56145	562	S56145 BS69 protein - human
1490271	CAA93625.1	4005	ALL-1 protein [Homo sapiens]
1585696	2201456A	529	2201456A Mi-2 autoantigen [Homosapiens]
1586946	2205253A	618	2205253A c-IAP1 protein [Homo sapiens]

1586947	2205253B	604	2205253B c-IAP2 protein [Homo sapiens]
1587642	2207180A	520	2207180A cyclophilin:ISOTYPE=CyP-60[Homo sapiens]
1658307	CAA86572.1	887	helicase-like transcription factor[Homo sapiens]

1658307	CAA86572.1	887	helicase-like transcription factor[Homo sapiens]
1703190	P55197	1027	AF10_HUMAN AF-10 protein
1703191	P55198	1093	AF17_HUMAN AF-17 protein
1705500	P55201	1214	BRF1_HUMAN Peregrin (Bromodomain and PHDfinger-containing protein 1) (BR140 protein)
1708932	P51948	309	MAT1_HUMAN CDK-activating kinase assemblyfactor MAT1 (RING finger protein MAT1) (Menage a trois) (CDK7/cyclin Hassembly factor) (p36) (p35) (Cyclin G1 interacting protein)
1710032	P29375	1722	RBB2_HUMAN Retinoblastoma-binding protein2 (RBBP-2)
1730008	P53804	2025	TTC3_HUMAN Tetratricopeptide repeatprotein 3 (TPR repeat protein D)
1871160	AAC51135.1	457	SMCY
2134713	I38533	1093	I38533 AF17 protein - human
2134780	S69544	497	S69544 apoptosis inhibitor IAP homolog -human
2134811	I38485	288	I38485 BCR11q23 - human (fragment)
2134879	A55960	568	A55960 CD40 receptor-associated factor 1- human
2134880	I53498	543	I53498 CD40-associated protein - human
2134952	I39171	435	I39171 cyclin A/CDK2-associated p45 -human
2134962	S64705	520	S64705 cyclophilin-like protein CyP-60 -human
2135088	I54361	1560	I54361 SMCX protein - human
2135185	I58373	289	I58373 gene flvi-2/bmi-1 protein - human(fragment)
2135739	I38558	530	I38558 Mi-2 autoantigen 240 kDa protein -human (fragment)
2135748	I38026	470	I38026 MLN 62 protein - human
2135749	S60681	470	S60681 MLN 62 protein - human
2135999	I54339	326	I54339 proto-oncogene bmi-1 - human
2136106	I78879	1722	I78879 retinoblastoma binding protein 2 -human
2136108	A57640	948	A57640 retinoblastoma binding proteinRBQ-1 - human
2136123	S60157	309	S60157 RING finger protein MAT1 - human
2136262	JC5020	2025	JC5020 tetratricopeptide repeat protein -human
2136310	A57041	442	A57041 transcription regulator Staf-50 -human

2136323	I53035	366	I53035 trithorax homolog HTX - human(fragment)
2160396	BAA03407.1	1909	MLL [Homo sapiens]
2477513	AAB81198.1	903	F25965_3 [Homo sapiens]
2495699	Q15034	1050	Y032_HUMAN Hypothetical protein KIAA0032
2495703	Q14139	1073	Y126_HUMAN HYPOTHETICAL PROTEIN KIAA0126
2497236	Q13489	604	BIR2_HUMAN Baculoviral IAPrepeat-containing protein 1 (Inhibitor of apoptosis protein 1) (HIAP1)(HIAP-1) (C-IAP2) (TNFR2-TRAF signaling complex protein 1) (IAPhomolog C)
2497238	Q13490	618	BIR3_HUMAN Baculoviral IAPrepeat-containing protein 3 (Inhibitor of apoptosis protein 2) (HIAP2)(HIAP-2) (C-IAP1) (TNFR2-TRAF signaling complex protein 2) (IAPhomolog B)
2499839	Q14669	1992	TRIB_HUMAN Thyroid receptor interactingprotein 12 (TRIP12)
2500145	Q92782	353	REQN_HUMAN Zinc-finger protein neuro-d4
2506924	P49754	854	VP41_HUMAN Vacuolar assembly protein VPS41homolog (S53)
2842711	Q92785	391	REQU_HUMAN Zinc-finger protein ubi-d4(Requiem) (Apoptosis response zinc finger protein)
3024371	O00623	359	PEXC_HUMAN Peroxisome assembly protein 12(Peroxin-12) (Peroxisome assembly factor-3) (PAF-3)
3123165	O15541	343	Z183_HUMAN Zinc finger protein 183
3183179	Q13263	835	TF1B_HUMAN Transcription intermediaryfactor 1-beta (TIF1-beta) (Nuclear corepressor KAP-1) (KRAB-associatedprotein 1)
3334119	O43918	545	AIRE_HUMAN Autoimmune regulator (APECEDprotein)
3647182	CAA20122.1	327	dJ341E18.2.1 (novel PUTATIVE protein(isoform 1)) [Homo sapiens]

3694627	AAC62428.1	420	R31343_1 [Homo sapiens]
3914299	O60683	326	PEXA_HUMAN Peroxisome assembly protein 10(Peroxin-10)
4107440	CAB06488.1	805	dJ524E15.1 (PEREGRIN (BR140PROTEIN)) [Homo sapiens]
5420465	BAA82324.1	345	SC1-1 [Homo sapiens]
5420467	BAA82325.1	345	SCI(TCF19)-4 [Homo sapiens]
5420469	BAA82326.1	345	SC1(TCF19)-6 [Homo sapiens]
5420471	BAA82327.1	345	SC1(TCF19)-7 [Homo sapiens]

5679463	CAB51756.1	288	dJ90G24.1 (RET finger protein-like2) [Homo sapiens]
5689263	BAA82889.1	233	p33 [Homo sapiens]
5739033	BAA83462.1	210	p24 is an alternatively splicedtranscript of p33/ING1. [Homo sapiens]
5788103	AAD51450.1	146	AC006978_1 supported by human androdent ESTs match to AA454028 (NID:g2167697), similar to AA9255224(NID:g4236415) and AA023712 (NID:g1487627) [Homo sapiens]
5788106	AAD51453.1	415	AC004975_1 hypothetical protein 1[Homo sapiens]
5921743	Q12873	1944	CHD3_HUMAN Chromodomainhelicase-DNA-binding protein 3 (CHD-3) (Mi-2 autoantigen 240 kDaprotein) (Mi2-alpha)
5921744	Q14839	1912	CHD4_HUMAN Chromodomainhelicase-DNA-binding protein 4 (CHD-4) (Mi-2 autoantigen 218 kDaprotein) (Mi2-beta)
6015129	Q12830	810	FALZ_HUMAN Fetal alzheimer antigen (FetalAlz-50-reactive clone 1)
6103649	AAF03705.1	551	F-box protein FBX10 [Homo sapiens]
6164739	AAF04519.1	178	AF174598_1 F-box protein Fbx10 [Homosapiens]
6166538	Q13342	882	LY10_HUMAN LYSP100 protein(Lymphoid-restricted homolog of Sp100) (Nuclear autoantigen Sp-140)(Speckled 140 kDa) (Nuclear body protein Sp140)
6226673	P29590	882	PML_HUMAN Probable transcription factorPML (Tripartite motif protein 19)
6573516	1C4Z	358	A Chain A, Structure Of E6ap: Insights IntoUbiquitination Pathway
6573517	1C4Z	358	B Chain B, Structure Of E6ap: Insights IntoUbiquitination Pathway
6573518	1C4Z	358	C Chain C, Structure Of E6ap: Insights IntoUbiquitination Pathway
6573528	1D5F	358	A Chain A, Structure Of An E6ap-Ubch7Complex: Insights Into The Ubiquitination Pathway
6573529	1D5F	358	B Chain B, Structure Of An E6ap-Ubch7Complex: Insights Into The Ubiquitination Pathway
6573530	1D5F	358	C Chain C, Structure Of An E6ap-Ubch7Complex: Insights Into The Ubiquitination Pathway
6580492	CAB63143.1	231	cN28H9.1 (novel protein) [Homosapiens]
6648106	Q05086	875	UE3A_HUMAN Ubiquitin-protein ligase E3A(Oncogenic protein-associated protein E6-AP) (Human papillomavirusE6-associated protein)

6683809	AAF23370.1	1365	MMSET type II [Homo sapiens]
6686035	Q13114	568	TRA3_HUMAN TNF receptor associated factor3 (CD40 receptor associated factor 1) (CRAF1) (CD40 binding protein)(CD40BP) (LMP1 associated protein) (LAP1) (CAP-1)
6706657	CAB65993.1	421	dJ101K10.3 (novel protein) [Homosapiens]
7018402	CAB75689.1	485	dJ744I24.1 (KIAA0646 (new zincfinger protein)) [Homo sapiens]
7022417	BAA91591.1	572	unnamed protein product [Homosapiens]
7280338	AAF44794.1	457	U82671_7 LIM domain ZNF185 peptide[Homo sapiens]
7428553	A58881	1863	A58881 breast/ovarian cancersusceptibility protein BRCA1 - human
7443545	T12495	449	T12495 hypothetical proteinDKFZp434H071.1 - human (fragment)
7444286	G02764	267	G02764 cyclin G1 interacting protein -human
7447800	S68451	497	S68451 apoptosis inhibitor xiap, X-linked- human
7459637	T14749	130	T14749 hypothetical proteinDKFZp566A093.1 - human
7460240	T03454	5262	T03454 ALR protein - human
7460242	S71752	4861	S71752 giant protein p619 - human
7512280	T03455	4957	T03455 ALR protein - human
7512287	S68449	604	S68449 apoptosis inhibitor hiap-1 - human
7512288	S68450	618	S68450 apoptosis inhibitor hiap-2 - human
7512333	S68467	543	S68467 CD40 receptor-associated proteinCAP-1 - human
7512499	G01950	350	G01950 hypothetical protein - human(fragment)
7512637	T14761	959	T14761 hypothetical proteinDKFZp434K233.1 - human (fragment)
7512658	T12543	361	T12543 hypothetical proteinDKFZp434M154.1 - human (fragment)
7512740	T12461	110	T12461 hypothetical proteinDKFZp564G092.1 - human
7512872	T08738	811	T08738 hypothetical proteinDKFZp586E0518.1 - human (fragment)
7512938	T17254	116	T17254 hypothetical proteinDKFZp586O1022.1 - human (fragment)
7512951	T17260	473	T17260 hypothetical proteinDKFZp727G051.1 - human (fragment)
7512983	T00064	708	T00064 hypothetical protein KIAA0438 -human
7513001	T00082	792	T00082 hypothetical protein KIAA0517 -human

			(fragment)
7513062	T00362	1208	T00362 hypothetical protein KIAA0675 -human
7513101	T00390	1630	T00390 KIAA0614 protein - human(fragment)
7513172	T00705	903	T00705 N-chimerin homolog F25965_3 -human
7513262	S71821	522	S71821 probable interleukin 1signal-transducing protein TRAF6 - human
7513317	T09482	667	T09482 ring finger protein FXY - human
7513318	T08729	324	T08729 RING zinc finger protein homologDKFZp566H073.1 - human (fragment)
7513336	G01252	810	G01252 small GTP binding protein SEC4homolog - human
7513405	JC6539	557	JC6539 tumor necrosis factorreceptor-associated factor 5 homolog - human
7513436	G01614	507	G01614 zinc finger protein 127 - human
7513438	JC5392	685	JC5392 zinc finger protein KF-1 precursor- human
7513439	I38759	1027	I38759 zinc finger/leucine zipper protein- human
7768776	BAA95560.1	545	autoimmune regulator (APECEDprotein) [Homo sapiens]
7981255	CAB92088.1	731	dJ1174N9.1 (novel protein with IBRdomain) [Homo sapiens]
8488988	Q13233	1495	M3K1_HUMAN Mitogen-activated proteinkinase kinase kinase 1 (MAPK/ERK kinase kinase 1) (MEK kinase 1) (MEKK1)
8744934	CAB95312.1	497	dJ315G1.2 (apoptosis inhibitor 3(XIAP, HILP)) [Homo sapiens]
8920240	CAB96178.1	163	AK000559 hypothetical protein,similar to (U06944) PRAJA1 [Mus musculus] [Homo sapiens]
8928017	Q13191	982	CBLB_HUMAN Signal transduction proteinCBL-B (SH3-binding protein CBL-B)
8928035	Q9ULV8	474	CBLC_HUMAN Signal transduction proteinCBL-C (SH3-binding protein CBL-C) (CBL-3)
8928179	O60858	407	RPF2_HUMAN Ret finger protein 2 (Leukemiaassociated protein 5) (B-cell chronic lymphocytic leukemia tumorsuppressor Leu5) (Putative tumor suppressor RFP2) (Tripartite motifprotein 13)
9588429	CAC00611.1	336	bG120K12.2 (ring finger protein DINGor BAP-1) [Homo sapiens]
9712188	BAB08101.1	279	p33ING1b [Homo sapiens]
9712189	BAB08102.1	422	p47ING1a [Homo sapiens]
9712190	BAB08103.1	210	p24ING1c [Homo sapiens]

9857987	AAG00951.1	1539	AF273841_1 SMCY [Homo sapiens]
9944280	AAG02578.1	279	growth inhibitory protein ING1 [Homosapiens]
9944281	AAG02579.1	283	growth inhibitory protein ING1 [Homosapiens]

9992842	AAG11396.1	280	p33 [Homo sapiens]
10039549	AAG12175.1	279	p33ING1 [Homo sapiens]
10120668	1FBV	388	A Chain A, Structure Of A Cbl-Ubch7Complex: Ring Domain Function In Ubiquitin-Protein Ligases
10279683	CAC09909.1	541	dJ1187M17.1.1 (KIAA0860 (isoform1))[Homo sapiens]
10334637	CAC10183.1	545	bA416N2.1 (neuralized(Drosophila)-like) [Homo sapiens]
10432612	BAB13822.1	712	unnamed protein product [Homosapiens]
10432934	BAB13877.1	790	unnamed protein product [Homosapiens]
10719919	Q15326	562	BS69_HUMAN Adenovirus 5 E1A-bindingprotein (BS69 protein)
10720409	O94822	1818	Z294_HUMAN Zinc finger protein 294
10834662	AAG23761.1	484	AF258558_1 PP3476 [Homo sapiens]
11037476	AAG27595.1	416	Makorin RING zinc-finger protein 2 [Homo sapiens]
11072099	AAG26335.2	380	MLL protein [Homo sapiens]
11125661	CAB90429.3	1574	containing human KIAA0714 protein[Homo sapiens]
11141531	AAG31985.1	204	MLL protein [Homo sapiens]
11272422	T46412	820	T46412 ubiquitin--protein ligase (EC6.3.2.19) NEDD4 - human (fragment)
11277002	T42697	1350	T42697 hypothetical proteinDKFZp434N0335.1 - human (fragment)
11282675	JC7155	632	JC7155 brain finger protein BFP/ZNF179 -human
11359888	T43490	392	T43490 hypothetical proteinDKFZp434A139.1 - human (fragments)
11359923	T46366	547	T46366 hypothetical proteinDKFZp434C0118.1 - human (fragment)
11359940	T43444	381	T43444 hypothetical proteinDKFZp434C1715.1 - human (fragment)
11359975	T43451	180	T43451 hypothetical proteinDKFZp434E1818.1 - human (fragment)
11359988	T43459	366	T43459 hypothetical proteinDKFZp434F0721.1 - human (fragment)
11360167	T43460	630	T43460 hypothetical proteinDKFZp434P1721.1 - human (fragment)

11360225	T46904	137	T46904 hypothetical proteinDKFZp761D081.1 - human
11360292	T47165	55	T47165 hypothetical proteinDKFZp762M1215.1 - human (fragment)
11434957	XP_007430.1	823	KIAA0317 gene product [Homosapiens]
11437205	XP_003605.1	462	hypothetical nuclear factor SBBI22[Homo sapiens]
11513315	1FQV	336	A Chain A, Insights Into Scf UbiquitinLigases From The Structure Of The Skp1-Skp2 Complex
11513317	1FQV	336	C Chain C, Insights Into Scf UbiquitinLigases From The Structure Of The Skp1-Skp2 Complex
11513319	1FQV	336	E Chain E, Insights Into Scf UbiquitinLigases From The Structure Of The Skp1-Skp2 Complex
11513321	1FQV	336	G Chain G, Insights Into Scf UbiquitinLigases From The Structure Of The Skp1-Skp2 Complex
11513323	1FQV	336	I Chain I, Insights Into Scf UbiquitinLigases From The Structure Of The Skp1-Skp2 Complex
11513325	1FQV	336	K Chain K, Insights Into Scf UbiquitinLigases From The Structure Of The Skp1-Skp2 Complex
11513327	1FQV	336	M Chain M, Insights Into Scf UbiquitinLigases From The Structure Of The Skp1-Skp2 Complex
11513329	1FQV	336	O Chain O, Insights Into Scf UbiquitinLigases From The Structure Of The Skp1-Skp2 Complex
11513332	1FS1	53	A Chain A, Insights Into Scf UbiquitinLigases From The Structure Of The Skp1-Skp2 Complex
11513334	1FS1	53	C Chain C, Insights Into Scf UbiquitinLigases From The Structure Of The Skp1-Skp2 Complex
11513337	1FS2	272	A Chain A, Insights Into Scf UbiquitinLigases From The Structure Of The Skp1-Skp2 Complex
11513339	1FS2	272	C Chain C, Insights Into Scf UbiquitinLigases From The Structure Of The Skp1-Skp2 Complex
11596070	CAC18513.1	491	dJ976O13.2.1 (M96 protein isoform1) [Homo sapiens]
11596071	CAC18514.1	593	dJ976O13.2.3 (M96 protein isoform3) [Homo sapiens]
12082389	BAB20900.1	685	KF-1 protein [Homo sapiens]

12084193	1F62	51	A Chain A, Wstf-Phd
12229697	O95696	1058	BRD1_HUMAN Bromodomain-containing protein1 (BR140-like protein)
12229723	Q9ULD4	1214	BRF3_HUMAN Bromodomain and PHDfinger-containing protein 3
12310669	CAC22477.1	443	unnamed protein product [Homosapiens]

12310671	CAC22478.1	522	unnamed protein product [Homosapiens]
12310673	CAC22479.1	327	unnamed protein product [Homosapiens]
12310675	CAC22480.1	447	unnamed protein product [Homosapiens]
12314005	CAC12756.1	1042	dJ885L7.9.1 (Death associatedtranscription factor 1 (contains KIAA0333), isoform 1) [Homo sapiens]
12314016	CAB99358.1	1957	dJ22I17.1 (KIAA0244) [Homo sapiens]
12406760	CAC25010.1	352	unnamed protein product [Homosapiens]
12406778	CAC25019.1	305	unnamed protein product [Homosapiens]
12541205	CAC25087.1	793	unnamed protein product [Homosapiens]
12541211	CAC25090.1	174	unnamed protein product [Homosapiens]
12585547	Q14258	630	Z147_HUMAN Zinc finger protein 147(Estrogen responsive finger protein) (Efp)
12643365	Q9UPN9	1127	TF1G_HUMAN Transcription intermediaryfactor 1-gamma (TIF1-gamma) (RET-fused gene 7 protein) (Rfg7 protein)(Tripartite motif protein 33)
12643387	P98170	497	BIR4_HUMAN Baculoviral IAPrepeat-containing protein 4 (Inhibitor of apoptosis protein 3)(X-linked inhibitor of apoptosis protein) (X-linked IAP) (IAP-likeprotein) (HILP)
12643555	O43189	567	PHF1_HUMAN PHD finger protein 1 (PHF1protein)
12643893	Q9UKT8	422	FBW2_HUMAN F-box/WD-repeat protein 2
12643900	Q9UMN6	2715	TRX2_HUMAN Trithorax homolog 2 (Mixedlineage leukemia gene homolog 2 protein)
12643952	Q9Y483	593	MTF2_HUMAN Metal-response element-bindingtranscription factor 2 (Metal-response element DNA-binding proteinM96)
12746552	O15164	1050	TF1A_HUMAN Transcription intermediaryfactor 1-alpha (TIF1-alpha)
13096372	1FP0	88	A Chain A, Solution Structure Of The PhdDomain From The Kap-1 Corepressor
13123980	Q99728	777	BAR1_HUMAN BRCA1-associated RING domainprotein 1 (BARD-1)
13124142	Q9NRD0	319	FBX8_HUMAN F-box only protein 8(F-box/SEC7 protein FBS) (DC10)
13124191	P57775	412	FBW4_HUMAN F-box/WD-repeat protein 4(Dactylin)
13124236	Q9UK22	295	FBX2_HUMAN F-box only protein 2
13124237	Q9UK96	551	FX10_HUMAN F-box only protein 10
13124238	Q9UK97	447	FBX9_HUMAN F-box only protein 9

13124239	Q9UK99	471	FBX3_HUMAN F-box only protein 3
13124249	Q9Y3I1	522	FBX7_HUMAN F-box only protein 7
13124258	O75426	318	FX24_HUMAN F-box only protein 24
13124267	Q9UKB1	542	FW1B_HUMAN F-box/WD-repeat protein 1B(F-box and WD-repeats protein beta-TrCP2)
13124522	Q9NVW2	624	RN12_HUMAN RING finger protein 12 (LIMdomain interacting RING finger protein) (RING finger LIMdomain-binding protein) (R-LIM) (NY-REN-43 antigen)
13124536	Q9Y252	685	RNF6_HUMAN RING finger protein 6
13171051	CAC33173.1	340	ring finger protein 28 [Homosapiens]
13185169	CAC33273.1	419	unnamed protein product [Homosapiens]
13185271	CAC33309.1	400	unnamed protein product [Homosapiens]
13509324	CAC35389.1	1214	KIAA0298 protein [Homo sapiens]
13560104	CAC36111.1	298	bA261N11.1.2 (baculoviral IAPrepeat-containing protein 7 (livin), isoform 2) [Homo sapiens]
13560106	CAC36113.1	210	bA261N11.1.3 (baculoviral IAPrepeat-containing protein 7 (livin), isoform 3) [Homo sapiens]
13626320	XP_002013.2	438	putative DNA binding protein [Homosapiens]
13637361	XP_018178.1	459	ring finger protein 25 [Homosapiens]

13637478	XP_016444.1	452	similar to ring finger protein 18(H. sapiens) [Homo sapiens]
13641902	XP_012034.2	452	similar to ring finger protein 18(H. sapiens) [Homo sapiens]
13645747	XP_011709.2	159	similar to ring finger protein 5(H. sapiens) [Homo sapiens]
13648156	XP_016607.1	1214	bromodomain-containing protein[Homo sapiens]
13652653	XP_006998.2	1418	retinoblastoma-binding protein 2[Homo sapiens]
13677198	CAC19780.1	524	dJ569M23.1.3 (protein kinase Cbinding protein 1, isoform 3 (DKFZp564P1772)) [Homo sapiens]
13677199	CAC19781.1	521	dJ569M23.1.1 (protein kinase Cbinding protein 1, isoform 1 (KIAA1125)) [Homo sapiens]
13677201	CAC19782.1	516	dJ569M23.1.2 (protein kinase Cbinding protein 1, isoform 2) [Homo sapiens]
13785205	CAC37338.1	298	inhibitor of apoptosis [Homosapiens]
13872241	CAC37490.1	673	bA400I20.1 (ligand of numb-proteinX) [Homo sapiens]
13921166	CAC37714.1	236	unnamed protein product [Homosapiens]

14035802	CAC38497.1	216	unnamed protein product [Homosapiens]
14035848	CAC38520.1	336	unnamed protein product [Homosapiens]
14036080	CAC38636.1	247	unnamed protein product [Homosapiens]
14041698	CAC38442.1	281	dJ1033B10.8.2 (Ring finger protein1 (RNF1), isoform 2) [Homo sapiens]
14041701	CAC38366.1	567	dJ570F3.3.2 (PHD finger protein 1,isoform b) [Homo sapiens]
14041702	CAC38367.1	457	dJ570F3.3.1 (PHD finger protein 1,isoform a) [Homo sapiens]
14195584	Q99576	134	GILZ_HUMAN Glucocorticoid-induced leucinezipper protein (Delta sleep-inducing peptide immunoreactor)(DSIP-immunoreactive peptide) (DIP protein) (hDIP) (TSC-22-likeprotein) (TSC-22R)
14270990	CAC39514.1	979	unnamed protein product [Homosapiens]
14272796	CAC39836.1	433	unnamed protein product [Homosapiens]
14286186	O15231	457	Z185_HUMAN Zinc finger protein 185(LIM-domain protein ZNF185) (P1-A)
14336710	AAK61242.1	303	AE006464_10 carboxy terminus ofHSP70-interacting protein [Homo sapiens]
14336713	AAK61245.1	581	AE006464_13 possible G-proteinreceptor [Homo sapiens]
14530760	CAC42394.1	1061	dJ575L21.1 (KIAA0684 protein) [Homosapiens]
14532913	CAC42525.1	337	bA10G5.1 (similar to ZNF183: zincfinger protein 183 (RING finger, C3HC4 type)) [Homo sapiens]
14571621	CAC42798.1	225	unnamed protein product [Homosapiens]
14571623	CAC42796.1	294	Partial sequence of vectorpMT2SM-AAP-2-II [Homo sapiens]
14721080	XP_031695.1	444	F-box and leucine-rich repeatprotein 7 [Homo sapiens]
14721529	XP_033946.1	509	hypothetical protein FLJ22479[Homo sapiens]
14727790	XP_017311.2	386	ring finger protein 13 [Homosapiens]
14730826	XP_003492.4	687	cyclin-E-binding protein 1-[Homosapiens]
14740775	XP_035773.1	854	vacuolar protein sorting 41 (yeasthomolog), isoform 1 [Homo sapiens]
14740919	XP_033465.1	723	similar to Unknown (protein forMGC:2867) [Homo sapiens]
14743603	XP_042050.1	838	dorfin [Homo sapiens]
14743703	XP_039070.1	618	KIAA1224 protein [Homo sapiens]
14747007	XP_031361.1	326	murine leukemia viral (bmi-1)oncogene homolog [Homo

			sapiens]
14748240	XP_052223.1	947	DKFZP564G092 protein [Homosapiens]
14748841	XP_052430.1	582	E3 ubiquitin ligase SMURF1 [Homosapiens]
14749959	XP_035829.1	167	hypothetical protein DKFZp564A022[Homo sapiens]
14750538	XP_045232.1	1585	KIAA0322 protein [Homo sapiens]
14752844	XP_050821.1	309	menage a trois 1 (CAK assemblyfactor) [Homo sapiens]
14753738	XP_030186.1	706	hypothetical protein FLJ20333[Homo sapiens]
14754867	XP_041207.1	4640	KIAA0916 protein [Homo sapiens]

14757226	XP_029280.1	235	similar to p33ING1b [Homo sapiens]
14757738	XP_041186.1	1488	transcriptional regulator ATRX[Homo sapiens]
14759105	XP_028909.1	359	hypothetical protein DKFZp434O1427[Homo sapiens]
14759543	XP_048948.1	926	bromodomain adjacent to zincfinger domain, 2A [Homo sapiens]
14761170	XP_027578.1	131	hypothetical protein [Homosapiens]
14761230	XP_004547.3	425	HCGI protein [Homo sapiens]
14761234	XP_041688.1	481	similar to ring finger protein 9,isoform 1 hematopoietic RING finger 1 tripartite motif protein 10[Homo sapiens]
14764024	XP_035627.1	793	ubiquitin-like, containing PHD andRING finger domains, 1 [Homo sapiens]
14765961	XP_032867.1	1772	similar to tetratricopeptiderepeat domain 3 (H. sapiens) [Homo sapiens]
14767212	XP_049185.1	838	hypothetical protein DKFZp434A1010[Homo sapiens]
14767420	XP_048020.1	1591	KIAA0614 protein [Homo sapiens]
14767571	XP_017350.2	208	similar to hypothetical proteinMGC4827 (H. sapiens) [Homo sapiens]
14768903	XP_047568.1	276	similar to MBLR protein (H.sapiens) [Homo sapiens]
14769553	XP_029000.1	813	myeloid/lymphoid or mixed-lineageleukemia (trithorax homolog, Drosophila) translocated to, 6 [Homosapiens]
14773919	XP_006078.4	380	Cas-Br-M (murine) ecotropicretroviral transforming sequence [Homo sapiens]
14778293	XP_028151.1	488	Nedd-4-like ubiquitin-proteinligase [Homo sapiens]
14778307	XP_018516.2	192	similar to Unknown (protein forMGC:19394) [Homo sapiens]
14778831	XP_027758.1	576	similar to hypothetical protein[Homo sapiens]
14782132	XP_004567.3	345	transcription factor 19 (SC1)[Homo sapiens]
14783019	XP_043363.1	1205	bromodomain and PHD fingercontaining, 3 [Homo

			sapiens]
14784892	XP_044060.1	619	KIAA0937 protein [Homo sapiens]
14785499	XP_046129.1	733	neural precursor cell expressed,developmentally down-regulated 4 [Homo sapiens]
14916696	Q9NV58	838	RN19_HUMAN RING finger protein 19(Dorfin) (Double ring-finger protein) (p38 protein)
15143895	CAC50806.1	205	unnamed protein product [Homosapiens]
15209774	CAC51176.1	352	unnamed protein product [Homosapiens]
15277219	BAB63312.1	345	DNA binding protein required forlate cell cycle progression [Homo sapiens]
15277240	BAB63333.1	420	Testis expressed gene [Homosapiens]
15295936	XP_053122.1	162	erythroblast macrophage attacher[Homo sapiens]
15319118	XP_053428.1	531	similar to dJ127B20.3 (novel PHDfinger protein) [Homo sapiens]
15524186	CAC69320.1	663	unnamed protein product [Homosapiens]
15667627	BAB68317.1	802	Np95-like ring finger protein [Homosapiens]
15679978	AAH14297.1	566	AAH14297 Unknown (protein forMGC:14899) [Homo sapiens]
15680142	AAH14414.1	374	AAH14414 Unknown (protein forMGC:19959) [Homo sapiens]
15680171	AAH14432.1	360	AAH14432 Similar to semaF cytoplasmicdomain associated protein 3 [Homo sapiens]
15680187	AAH14442.1	462	AAH14442 Unknown (protein forMGC:22964) [Homo sapiens]
15680241	AAH14475.1	298	AAH14475 Similar to baculoviral IAPrepeat-containing 7 (livin) [Homo sapiens]
15705403	AAL05625.1	1616	AF352051_1 proliferationpotential-related protein [Homo sapiens]
15778899	AAH14527.1	283	AAH14527 Similar to f-box onlyprotein 17 [Homo sapiens]
15809702	AAL07271.1	707	F-box protein CDC4 [Homo sapiens]
15822537	AAG16640.1	589	F-box protein SEL10 [Homo sapiens]

15824269	BAB69424.1	955	NEDD4-like ubiquitin ligase 3 [Homosapiens]
15862396	CAC88597.1	305	unnamed protein product [Homosapiens]
15928394	AAH14679.1	319	AAH14679 Unknown (protein forMGC:9368) [Homo sapiens]
15928767	AAH14842.1	522	AAH14842 Unknown (protein forMGC:21169) [Homo

			sapiens]
15928941	AAH14940.1	656	AAH14940 Unknown (protein forMGC:18007) [Homo sapiens]
15929975	AAH15416.1	235	AAH15416 Similar to hypotheticalprotein DKFZp434C135 [Homo sapiens]
15988069	1JM7	112	A Chain A, Solution Structure Of TheBrca1BARD1 RING-Domain Heterodimer
15991882	AAH13036.1	192	AAH13036 Unknown (protein forMGC:4734) [Homo sapiens]
16041694	AAH15715.1	416	AAH15715 Unknown (protein forMGC:16931) [Homo sapiens]
16041715	AAH15733.1	660	AAH15733 Unknown (protein forMGC:22977) [Homo sapiens]
16158210	XP_055989.1	137	similar to CHIMP [Homo sapiens]
16160621	XP_057408.1	1258	thyroid hormone receptorinteractor 12 [Homo sapiens]
16161752	XP_055929.1	802	similar to ubiquitin-like,containing PHD and RING finger domains, 1 transcription factor ICBP90[Homo sapiens]
16179285	XP_057150.1	237	similar to RIKEN cDNA 1700045I19gene [Homo sapiens]
16182204	XP_055873.1	410	similar to KIAA1542 protein (H.sapiens) [Homo sapiens]
16188503	XP_057122.1	221	similar to tripartitemotif-containing 7 (H. sapiens) [Homo sapiens]
16194541	XP_057462.1	228	zinc finger protein 313 [Homosapiens]
16303800	AAL16809.1	180	AF416715_1 unknown [Homo sapiens]
16306918	AAH09527.1	288	AAH09527 Similar to E3 ubiquitinligase SMURF2 [Homo sapiens]
16307167	AAH09672.1	304	AAH09672 Unknown (protein forMGC:8795) [Homo sapiens]
16511339	CAD10225.1	416	unnamed protein product [Homosapiens]
16549336	BAB70801.1	405	unnamed protein product [Homosapiens]
16549414	BAB70809.1	297	unnamed protein product [Homosapiens]
16549858	BAB70868.1	1059	unnamed protein product [Homosapiens]
16550104	BAB70913.1	802	unnamed protein product [Homosapiens]
16551542	BAB71119.1	696	unnamed protein product [Homosapiens]
16551669	BAB71144.1	303	unnamed protein product [Homosapiens]
16551933	BAB71200.1	691	unnamed protein product [Homosapiens]
16552334	BAB71291.1	728	unnamed protein product [Homosapiens]
16552560	BAB71338.1	247	unnamed protein product [Homosapiens]

16552616	BAB71354.1	668	unnamed protein product [Homosapiens]
16741642	AAH16622.1	811	AAH16622 Unknown (protein forMGC:17738) [Homo sapiens]
16877522	AAH17017.1	425	AAH17017 Similar to tripartitemotif-containing 31 [Homo sapiens]
16877903	AAH17178.1	303	AAH17178 Unknown (protein forMGC:1397) [Homo sapiens]
16878026	AAH17226.1	237	AAH17226 Unknown (protein forMGC:14381) [Homo sapiens]
17068413	AAH17585.1	322	AAH17585 Unknown (protein forMGC:26599) [Homo sapiens]
17068424	AAH17592.1	420	AAH17592 Unknown (protein forMGC:27006) [Homo sapiens]
17221827	AAL36460.1	964	AF213365_1 POB1 [Homo sapiens]
17223689	AAK77940.1	255	F-box protein FBG3 [Homo sapiens]
17368438	Q13064	507	MKR3_HUMAN Makorin 3 (Zinc-finger protein127)
17368441	Q13434	485	MKR4_HUMAN Makorin 4 (Zinc-finger protein127-Xp) (ZNF127-Xp)
17368706	Q9BY66	1539	SMCY_HUMAN SmcY protein(Histocompatibility Y antigen) (H-Y)
17368929	Q9H000	416	MKR2_HUMAN Makorin 2 (HSPC070)
17369682	Q9UHC7	482	MKR1_HUMAN Makorin 1
17380344	Q12899	539	Z173_HUMAN Zinc finger protein 173 (Acidfinger protein) (AFP)
17380348	Q9ULX5	632	Z179_HUMAN Zinc finger protein 179 (Brainfinger protein)
17380440	P46100	2492	ATRX_HUMAN Transcriptional regulator ATRX(X-linked helicase II) (X-linked nuclear protein) (XNP) (Znf-HX)
17389319	AAH17707.1	685	AAH17707 Unknown (protein forMGC:21197) [Homo sapiens]
17390228	AAH18104.1	230	AAH18104 Unknown (protein forMGC:8715) [Homo sapiens]
17390234	AAH18107.1	245	AAH18107 Unknown (protein forMGC:8758) [Homo sapiens]
17390786	AAH18337.1	206	AAH18337 Unknown (protein forMGC:17233) [Homo sapiens]
17433305	O75678	288	RFL2_HUMAN Ret finger protein-like 2
17435836	XP_065369.1	107	similar to Plenty of SH3s [Homosapiens]

17438178	XP_042066.3	1350	mitogen-activated protein kinasekinase kinase 1 [Homo sapiens]
17439802	XP_060236.1	131	similar to hypothetical proteinMGC4827 [Homo sapiens]
17442514	XP_059381.1	446	similar to ring finger protein 18testis-specific RING Finger protein [Homo sapiens]
17442529	XP_059379.1	446	similar to ring finger protein 18testis-specific RING Finger protein [Homo sapiens]
17446393	XP_060755.1	812	similar to dopamine receptor D5dopamine receptor D1B D1beta dopamine receptor [Homo sapiens]
17448282	XP_059966.1	117	similar to unnamed protein product[Homo sapiens]
17449055	XP_068823.1	252	similar to unnamed protein product[Homo sapiens]
17452617	XP_055933.2	623	deltex (Drosophila) homolog 2[Homo sapiens]
17454894	XP_047569.2	350	MBLR protein [Homo sapiens]
17456692	XP_059045.1	283	similar to unnamed protein product[Homo sapiens]
17457501	XP_036076.2	638	gene overexpressed in astrocytoma[Homo sapiens]
17460052	XP_059304.1	103	similar to ubiquitin proteinligase E3A (human papilloma virus E6-associated protein, Angelmansyndrome) [Homo sapiens]
17461546	XP_060022.1	671	synaptotagmin-like 4(granuphilin-a) [Homo sapiens]
17461624	XP_044477.3	538	similar to tripartitemotif-containing 34 (H. sapiens) [Homo sapiens]
17461639	XP_066248.1	400	similar to KIAA1629 protein [Homosapiens]
17462125	XP_059478.1	188	similar to RIKEN cDNA 1110020F21[Homo sapiens]
17463484	XP_052206.2	1532	rab3 interacting protein [Homosapiens]
17463526	XP_069211.1	395	similar to TAT-interactiveprotein, 72-KD tripartite motif protein TRIM32 zinc-finger proteinHT2A [Homo sapiens]
17463570	XP_069216.1	263	similar to ret finger protein-like1 [Homo sapiens]
17464383	XP_069474.1	229	similar to tripartite motifprotein TRIM4 isoform beta tripartite motif protein TRIM4 tripartitemotif protein 4 [Homo sapiens]
17464385	XP_069475.1	145	similar to putative acid fingerprotein [Homo sapiens]
17464511	XP_069496.1	272	similar to dJ109F14.3 (PUTATIVEZNF127 LIKE protein) [Homo sapiens]
17464695	XP_029192.2	1089	hypothetical protein [Homosapiens]
17467810	XP_059940.1	192	similar to Unknown (protein forMGC:4734) [Homo sapiens]

17468320	XP_070821.1	131	similar to hypothetical proteinMGC4827 [Homo sapiens]
17468328	XP_070822.1	131	similar to hypothetical proteinMGC4827 [Homo sapiens]
17472115	XP_061504.1	225	similar to TNF receptor-associatedfactor 6 [Homo sapiens]
17472509	XP_058425.1	391	requiem [Homo sapiens]
17472898	XP_040025.2	507	F-box and leucine-rich repeatprotein 11 [Homo sapiens]
17472959	XP_051010.2	681	KIAA1696 protein [Homo sapiens]
17473078	XP_061877.1	450	similar to ring finger protein 18testis-specific RING Finger protein [Homo sapiens]
17473137	XP_015378.3	285	similar to hypothetical proteinMGC4827 (H. sapiens) [Homo sapiens]
17474005	XP_038352.2	946	protein containing CXXC domain 2[Homo sapiens]
17474904	XP_058558.1	205	similar to Unknown (protein forIMAGE:3158218) [Homo sapiens]
17475027	XP_027038.3	454	BRCA1 associated protein [Homosapiens]
17475442	XP_058598.1	322	similar to bA10G5.1 (similar toZNF183: zinc finger protein 183 (RING finger, C3HC4 type)) [Homosapiens]
17478549	XP_064292.1	302	similar to ankyrin-repeatcontaining protein [Homo sapiens]
17482849	XP_053720.2	301	eNOS interacting protein [Homosapiens]
17483005	XP_064983.1	217	similar to ret finger protein-like1 [Homo sapiens]
17483067	XP_009172.5	397	Neuro-d4 (rat) homolog [Homosapiens]
17484837	XP_066217.1	311	similar to ring finger protein(C3H2C3 type) 6 [Homo sapiens]
17485136	XP_066294.1	272	similar to data source:SPTR,source key:Q9Y6U7, evidence:ISS~homolog to WUGSC:H_DJ130H16.6 PROTEIN(FRAGMENT)~putative [Homo sapiens]
17486200	XP_066792.1	378	similar to seven in absentiahomolog 1 (Drosophila) seven in absentia (Drosophila) homolog 1 [Homosapiens]
17489149	XP_044166.2	343	similar to PEM-3 [Homo sapiens]
17490177	XP_062300.1	656	similar to ring finger protein 18testis-specific RING Finger protein [Homo sapiens]
17511774	AAH18738.1	454	AAH18738 Unknown (protein forMGC:31869) [Homo sapiens]
17511961	AAH18938.1	256	AAH18938 Similar to RIKEN cDNA2510027N19 gene [Homo sapiens]
17530097	AAL40694.1	2696	AF395588_1 putative nuclear proteinNSD1 [Homo sapiens]

17644498	CAD19005.1	485	unnamed protein product [Homosapiens]
17736769	CAD19102.1	252	dJ820B18.2 (midline 1 (Opitz/BBBsyndrome)) [Homo sapiens]
17865624	Q9HAU4	748	SUF2_HUMAN Smad ubiquitination regulatoryfactor 2 (Ubiquitin--protein ligase SMURF2) (Smad-specific E3ubiquitin ligase 2) (hSMURF2)
17865625	Q9HCE7	757	SUF1_HUMAN Smad ubiquitination regulatoryfactor 1 (Ubiquitin--protein ligase SMURF1) (Smad-specific E3ubiquitin ligase 1) (hSMURF1)
17865680	Q9BYM8	500	U7I3_HUMAN Ubiquitin conjugating enzyme 7interacting protein 3 (Hepatitis B virus X-associated protein 4) (HBVassociated factor 4)
17939575	AAH19355.1	426	AAH19355 Unknown (protein forIMAGE:3956746) [Homo sapiens]
17939587	AAH19345.1	855	AAH19345 Unknown (protein forIMAGE:3604024) [Homo sapiens]
18070851	CAD20146.1	620	bA146B14.1 (KIAA0780) [Homosapiens]
18088108	AAH20984.1	441	AAH20984 Similar to arkadia [Homosapiens]
18088178	AAH20516.1	226	AAH20516 Unknown (protein forIMAGE:3882977) [Homo sapiens]
18088942	AAH21144.1	740	AAH21144 Unknown (protein forIMAGE:4873344) [Homo sapiens]
18202144	O75677	288	RFL1_HUMAN RET finger protein-like 1
18202145	O75679	288	RFL3_HUMAN RET finger protein-like 3

18202358	P78317	190	RNF4_HUMAN RING finger protein 4
18202744	Q9BZR9	551	RN27_HUMAN RING finger protein 27(Glioblastoma-expressed ring finger protein) (Tripartitemotif-containing protein 8)
18202944	Q9H4M3	224	FX30_HUMAN F-box protein FBX30
18202956	Q9HCM9	518	RN23_HUMAN RING finger protein 23(Testis-abundant finger protein)
18203498	Q9UDY6	482	RNF9_HUMAN RING finger protein 9(B30-RING finger protein) (Tripartite motif protein 10)
18203505	Q9UKT5	387	FBX4_HUMAN F-box only protein 4
18204309	AAH21570.1	653	AAH21570 Unknown (protein forIMAGE:4125718) [Homo sapiens]
18314446	AAH22038.1	376	AAH22038 Unknown (protein forMGC:27072) [Homo sapiens]

18490863	AAH22374.1	207	Similar to RIKEN cDNA 3321402G02gene [Homo sapiens]
18544646	XP_092184.1	363	hypothetical protein XP_092184[Homo sapiens]
18544707	XP_093996.1	471	hypothetical protein XP_093996[Homo sapiens]
18544711	XP_093998.1	468	hypothetical protein XP_093998[Homo sapiens]
18545056	XP_087521.1	186	hypothetical protein XP_087521[Homo sapiens]
18545452	XP_060178.2	1007	similar to putative [Homo sapiens]
18545719	XP_086204.1	300	similar to hypothetical protein[Homo sapiens]
18547314	XP_049820.2	346	peroxisome biogenesis factor 10[Homo sapiens]
18548542	XP_086461.1	224	F-box protein FBX30 [Homo sapiens]
18549241	XP_086542.1	210	hypothetical protein FLJ21156[Homo sapiens]
18550559	XP_092267.1	358	similar to keratin 8 [Homosapiens]
18551312	XP_092388.1	93	similar to serologically definedcolon cancer antigen 7 heat shock protein A binding protein 2(c-terminal) carboxy terminus of Hsp70p-interacting protein [Homosapiens]
18553366	XP_087231.1	476	similar to putative [Homo sapiens]
18553368	XP_043487.3	1972	bromodomain adjacent to zincfinger domain, 2B [Homo sapiens]
18553585	XP_087258.1	213	similar to Deltex3 [Homo sapiens]
18553893	XP_093381.1	676	hypothetical protein XP_093381[Homo sapiens]
18554646	XP_045469.2	868	Cas-Br-M (murine) ectropicretroviral transforming sequence b [Homo sapiens]
18555440	XP_093641.1	403	hypothetical protein XP_093641[Homo sapiens]
18557077	XP_093886.1	171	hypothetical protein XP_093886[Homo sapiens]
18557347	XP_093925.1	179	hypothetical protein XP_093925[Homo sapiens]
18559891	XP_094260.1	557	hypothetical protein XP_094260[Homo sapiens]
18562080	XP_087784.1	643	hypothetical protein XP_087784[Homo sapiens]
18562682	XP_087829.1	247	hypothetical protein XP_087829[Homo sapiens]
18563557	XP_084193.1	481	similar to tripartitemotif-containing 10 (H. sapiens) [Homo sapiens]
18564803	XP_087967.1	420	similar to HZFw1 protein (H.sapiens) [Homo sapiens]
18565756	XP_070560.2	144	similar to ring finger protein 11Sid1669 protein [Homo sapiens]
18565766	XP_042712.2	111	similar to myeloid/lymphoid ormixed-lineage leukemia3 ALR-like protein [Homo sapiens]
18566382	XP_095096.1	376	hypothetical protein XP_095096[Homo sapiens]

18568011	XP_059810.2	487	hypothetical protein XP_059810[Homo sapiens]
18568744	XP_004843.4	609	hypothetical protein FLJ10078[Homo sapiens]
18569417	XP_095426.1	341	hypothetical protein XP_095426[Homo sapiens]
18570268	XP_088333.1	328	hypothetical protein XP_088333[Homo sapiens]
18571802	XP_095735.1	131	hypothetical protein XP_095735[Homo sapiens]
18572388	XP_044856.4	1019	membrane-associated nucleic acidbinding protein [Homo sapiens]
18572885	XP_088531.1	192	hypothetical protein XP_088531[Homo sapiens]
18572887	XP_088529.1	192	hypothetical protein XP_088529[Homo sapiens]
18574236	XP_089479.1	228	hypothetical protein XP_089479[Homo sapiens]
18574971	XP_043168.3	969	hypothetical protein FLJ14590[Homo sapiens]
18576356	XP_084478.1	175	hypothetical protein MGC16202[Homo sapiens]
18576763	XP_084498.1	142	similar to murine leukemia viral(bmi-1) oncogene homolog Oncogene BMI-1 [Homo sapiens]
18577278	XP_006007.2	285	similar to HYPOTHETICAL 47.6 KDPROTEIN C16C10.5 IN CHROMOSOME III [Homo sapiens]
18577962	XP_061892.2	246	similar to hypothetical proteinMGC4827 [Homo sapiens]
18577964	XP_061893.2	624	similar to ring finger protein 18testis-specific RING Finger protein [Homo sapiens]
18578040	XP_089985.1	373	hypothetical protein XP_089985[Homo sapiens]
18578651	XP_083862.1	230	C3HC4-like zinc finger protein[Homo sapiens]
18578825	XP_062308.2	340	similar to ring finger protein 18testis-specific RING Finger protein [Homo sapiens]
18578829	XP_062304.2	427	similar to ring finger protein 18testis-specific RING Finger protein [Homo sapiens]
18578831	XP_090209.1	283	similar to ring finger protein 18testis-specific RING Finger protein [Homo sapiens]
18579150	XP_090259.1	740	hypothetical protein XP_090259[Homo sapiens]
18579285	XP_090288.1	510	hypothetical protein XP_090288[Homo sapiens]
18579431	XP_071738.2	278	similar to Deltex3 [Homo sapiens]
18580894	XP_084940.1	401	similar to Unknown (protein forIMAGE:3601186) [Homo sapiens]
18580925	XP_084941.1	495	similar to KIAA0010 gene product(H. sapiens) [Homo sapiens]
18581254	XP_084968.1	137	similar to ring finger protein(C3H2C3 type) 6 (H. sapiens) [Homo sapiens]
18581301	XP_090532.1	1243	hypothetical protein XP_090532[Homo sapiens]

18582645	XP_085034.1	407	similar to ret finger protein 2(H. sapiens) [Homo sapiens]
18583889	XP_090929.1	562	ring finger protein 36 [Homosapiens]
18584250	XP_090986.1	469	hypothetical protein XP_090986[Homo sapiens]
18585873	XP_048233.2	380	autocrine motility factor receptor[Homo sapiens]
18586221	XP_091412.1	154	hypothetical protein XP_091412[Homo sapiens]
18586239	XP_091413.1	173	hypothetical protein XP_091413[Homo sapiens]
18586453	XP_083950.1	227	hypothetical protein DKFZp434E229[Homo sapiens]
18587767	XP_091619.1	168	hypothetical protein XP_091619[Homo sapiens]
18588283	XP_091687.1	210	hypothetical protein XP_091687[Homo sapiens]
18588670	XP_091751.1	260	hypothetical protein XP_091751[Homo sapiens]
18588683	XP_085770.1	612	ubiquitin-protein ligaseNEDD4-like [Homo sapiens]
18589463	XP_091850.1	493	hypothetical protein XP_091850[Homo sapiens]
18590847	XP_086031.1	420	similar to R31343_1 [Homo sapiens]
18591483	XP_086109.1	326	hypothetical protein FLJ20552[Homo sapiens]
18591892	XP_086643.1	949	similar to protein kinase Cbinding protein 1 (H. sapiens) [Homo sapiens]
18593513	XP_044052.2	271	similar to myeloid/lymphoid ormixed-lineage leukemia3 ALR-like protein [Homo sapiens]
18594684	XP_092977.1	566	hypothetical protein XP_092977[Homo sapiens]
18595004	XP_093022.1	95	hypothetical protein XP_093022[Homo sapiens]
18595894	XP_088687.1	160	similar to praja 1 (H. sapiens)[Homo sapiens]
18595981	XP_084295.1	624	putative ring zinc finger proteinNY-REN-43 antigen [Homo sapiens]
18595990	XP_088700.1	1995	similar to tetratricopeptiderepeat domain 3 (H. sapiens) [Homo sapiens]
18596115	XP_093154.1	713	hypothetical protein XP_093154[Homo sapiens]
18600308	XP_001764.5	238	similar to hypothetical proteinFLJ10759 (H. sapiens) [Homo sapiens]
18600766	XP_004762.10	208	similar to myeloid/lymphoid ormixed-lineage leukemia3 (H. sapiens) [Homo sapiens]
18600886	XP_058284.2	616	similar to myeloid/lymphoid ormixed-lineage leukemia3 ALR-like protein [Homo sapiens]
18600912	XP_089300.1	1131	similar to myeloid/lymphoid ormixed-lineage leukemia3 (H. sapiens) [Homo sapiens]
18601599	XP_084023.1	522	similar to nucleoporin 62kD (H.sapiens) [Homo sapiens]
18601907	XP_028760.2	3492	myeloid/lymphoid or mixed-lineageleukemia 2 [Homo

			sapiens]
18603462	XP_008699.6	656	CpG binding protein [Homo sapiens]
18603766	XP_084540.1	108	similar to 52kD Ro/SSAautoantigen Sjogren syndrome antigen A1 Sicca syndrome antigen Atripartite motif protein TRIM21 [Homo sapiens]
18604709	XP_051402.5	941	vacuolar protein sorting 11 (yeasthomolog) [Homo sapiens]
18604912	XP_046292.3	713	similar to hypothetical proteinMGC10977 (H. sapiens) [Homo sapiens]
18605230	XP_090177.1	975	similar to nuclear matrix proteinNMP200 related to splicing factor PRP19 (H. sapiens) [Homo sapiens]
18605350	XP_044513.3	489	tripartite motif-containing 3,isoform alpha [Homo sapiens]
18605520	AAH22788.1	303	Unknown (protein for MGC:15443)[Homo sapiens]
18605735	AAH22983.1	728	Similar tomulti-PDZ-domain-containing protein [Homo sapiens]
18676408	BAB84856.1	1438	FLJ00039 protein [Homo sapiens]
18676594	BAB84949.1	639	FLJ00195 protein [Homo sapiens]
18676644	BAB84974.1	298	FLJ00221 protein [Homo sapiens]
18676781	BAB85025.1	457	unnamed protein product [Homosapiens]
18676819	BAB85033.1	428	unnamed protein product [Homosapiens]
18676903	BAB85052.1	291	unnamed protein product [Homosapiens]
18677022	BAB85078.1	240	unnamed protein product [Homosapiens]
18694703	CAD23756.1	690	unnamed protein product [Homosapiens]
18999367	AAH24256.1	365	Unknown (protein for MGC:13101)[Homo sapiens]
19168942	CAD26707.1	464	unnamed protein product [Homosapiens]
19169911	CAD26769.1	1191	Native DNA and protein sequence[Homo sapiens]
19169913	CAD26770.1	1191	DNA with C to G substitutionchanging second codon to alanine [Homo sapiens]
19263982	AAH25388.1	322	similar to bA10G5.1 (similar toZNF183: zinc finger protein 183 (RING finger, C3HC4 type)) [Homosapiens]
19263985	AAH25394.1	291	Similar to RIKEN cDNA 1300017E09gene [Homo sapiens]
19344028	AAH25712.1	266	Similar to odd-skipped related 1(Drosophila) [Homo sapiens]
19353084	AAH24326.1	745	Similar to RIKEN cDNA 1700026A16gene [Homo sapiens]
19421766	AAL86610.1	447	early mitotic inhibitor [Homosapiens]

19548926	AAL90859.1	740	AF484416_1 rhysin 2 [Homo sapiens]
19584372	CAD28480.1	238	hypothetical protein [Homo sapiens]
19584408	CAD28495.1	1213	hypothetical protein [Homo sapiens]
19718810	AAH06426.2	365	Unknown (protein for MGC:12908)[Homo sapiens]
19773960	AAL98962.1	1954	AF425231_1 chromodomain helicase DNAbinding protein 5 [Homo sapiens]
19851936	AAL99927.1	303	AF432221_1 CLL-associated antigenKW-8 [Homo sapiens]
19909898	BAB87121.1	1028	RIM short form [Homo sapiens]
19909962	BAB87200.1	424	SKP2-like protein type alpha [Homosapiens]
19909964	BAB87201.1	410	SKP2-like protein type beta [Homosapiens]
19909966	BAB87202.1	442	SKP2-like protein type gamma [Homosapiens]
19909970	BAB87242.1	1470	RIM long form [Homo sapiens]
19923717	NP_612144.1	740	rhysin 2 [Homo sapiens]
20137621	O95071	2799	EDD_HUMAN Ubiquitin--protein ligase EDD(Hyperplastic discs protein homolog) (hHYD) (Progestin inducedprotein)
20138037	Q9P0U4	656	CGBP_HUMAN CpG binding protein (Proteincontaining PHD finger and CXXC domain 1)
20139692	Q9BY78	433	RN26_HUMAN RING finger protein 26
20139803	Q9NS80	452	RN18_HUMAN RING finger protein 18(Testis-specific ring-finger protein)
20139860	Q9Y225	148	RN24_HUMAN RING finger protein 24
20141070	Q9Y508	228	Z313_HUMAN Zinc finger protein 313
20162318	AAM14566.1	145	MLL/AF4 fusion protein [Homosapiens]
20178283	P41002	786	CG2F_HUMAN G2/mitotic-specific cyclin F
20178303	Q13049	653	HT2A_HUMAN Zinc-finger protein HT2A (72kDa Tat-interacting protein) (Tripartite motif-containing protein 32)
20306314	AAH28397.1	503	similar to ubiquitin-like,containing PHD and RING finger domains, 1 transcription factor ICBP90[Homo sapiens]
20306373	AAH28385.1	520	peptidylprolyl isomerase(cyclophilin)-like 2 [Homo sapiens]

Hs.20815
Gene: MAEA Sequence count: 389

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	3789917	AAC67543.1	AF084928	395	erythroblast macrophage protein EMP[Homo sapiens]
	7022137	BAA91499.1	AK001088	396	unnamed protein product [Homosapiens]
	10433948	BAB14072.1	AK022515	328	unnamed protein product [Homosapiens]
	10434060	BAB14113.1	AK022586	355	unnamed protein product [Homosapiens]
	12654765	AAH01225.1	BC001225	385	AAH01225 Similar to erythroblastmacrophage protein [Homo sapiens]
	13623685	AAH06470.1	BC006470	385	AAH06470 Similar to macrophageerythroblast attacher [Homo sapiens]
	5031685	NP_005873.1	NM_005882	395	erythroblast macrophage attachererythroblast macrophage protein [Homo sapiens]

Hs.21036
Gene: DKFZp434A1010 Sequence count: 35

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	15559435	AAH14084.1	BC014084	298	AAH14084 Unknown (protein forIMAGE:4300179) [Homo sapiens]
	6808293	*CAB70821.1*	*AL137579*	*862*	*hypothetical protein [Homo sapiens]*

Hs.210850
Gene: KIAA1131 Sequence count: 291

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	15300020	XP_030175.2	-	1592	KIAA1131 protein [Homo sapiens]
	6329819	BAA86445.1	AB032957	1620	KIAA1131 protein [Homo sapiens]

	5817157	CAB53681.1	AL110222	959	hypothetical protein [Homo sapiens]
	13623275	AAH06237.1	BC006237	81	AAH06237 Similar to CG5604 geneproduct [Homo sapiens]
	15079684	AAH11658.1	BC011658	523	AAH11658 Unknown (protein forIMAGE:4122368) [Homo sapiens]

Hs.21122
Gene: PJA1 Sequence count: 115

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	10433181	BAB13928.1	AK021892	361	unnamed protein product [Homosapiens]
	11641293	NP_071763.1	NM_022368	361	hypothetical protein FLJ11830similar to Praja1 [Homo sapiens]

Hs.21229
Gene: FBXW1B Sequence count: 166

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	20070728	AAH26213.1	-	529	F-box and WD-40 domain protein 1B [Homo sapiens]
	3327206	BAA31671.1	AB014596	550	KIAA0696 protein [Homo sapiens]
	7209809	BAA92329.1	AB033279	508	F-box and WD-repeats proteinbeta-TRCP2 isoform A [Homo sapiens]
	7209811	BAA92330.1	AB033280	529	F-box and WD-repeats proteinbeta-TRCP2 isoform B [Homo sapiens]
	7209813	BAA92331.1	AB033281	542	F-box and WD-repeats proteinbeta-TRCP2 isoform C [Homo sapiens]
	6164757	AAF04528.1	AF176022	542	AF176022_1 F-box protein Fbw1b [Homosapiens]
	16306494	NP_036432.1	NM_012300	542	F-box and WD-40 domain protein 1B,isoform C F-box protein Fbw1b beta-transducin repeat-containingprotein 2 [Homo sapiens]

☐	16306496	NP_387448.1	NM_033644	529	F-box and WD-40 domain protein 1B,isoform B F-box protein Fbw1b beta-transducin repeat-containingprotein 2 [Homo sapiens]
☐	16306498	NP_387449.1	NM_033645	508	F-box and WD-40 domain protein 1B,isoform A F-box protein Fbw1b beta-transducin repeat-containingprotein 2 [Homo sapiens]

Hs.21254
Gene: TRIP Sequence count: 57

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	17939477	AAH19283.1	-	469	AAH19283 TRAF interacting protein[Homo sapiens]
☐	12653089	AAH00310.1	BC000310	469	AAH00310 TRAF interacting protein[Homo sapiens]
☐	5032195	NP_005870.1	NM_005879	469	TRAF interacting protein [Homosapiens]
☐	2039304	AAB52993.1	U77845	469	hTRIP [Homo sapiens]

Hs.21320
Gene: RAD18 Sequence count: 84

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	8980617	BAA99284.1	AB035274	495	postreplication repair proteinhRAD18p [Homo sapiens]
☐	8895212	AAF80856.1	AF169796	484	AF169796_1 zinc finger DNA bindingprotein [Homo sapiens]
☐	10434828	BAB14392.1	AK023075	495	unnamed protein product [Homosapiens]
☐	11079224	AAF86618.1	AY004333	495	RAD18 [Homo sapiens]
☐	12654913	AAH01302.1	BC001302	495	AAH01302 postreplication repairprotein hRAD18p [Homo sapiens]
☐	14550405	NP_064550.2	NM_020165	495	postreplication repair proteinhRAD18p RAD18, S.

					cerevisiae, homolog [Homo sapiens]

Hs.216354
Gene: RNF5 Sequence count: 234

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	1841551	AAB47492.1	-	180	AAB47492 G16 [Homo sapiens]
	13366064	BAB39359.1	AB056869	180	HsRma1 [Homo sapiens]
	13278762	AAH04155.1	BC004155	180	AAH04155 ring finger protein 5 [Homosapiens]
	5902054	NP_008844.1	NM_006913	180	ring finger protein 5 [Homosapiens]

Hs.219614
Gene: FBXL11 Sequence count: 319

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	4589652	BAA76848.1	AB023221	496	KIAA1004 protein [Homo sapiens]
	5917730	AAD56012.1	AF179221	474	AF179221_1 F-box protein Lilina [Homosapiens]
	10440530	BAB15795.1	AK024505	757	FLJ00115 protein [Homo sapiens]
	16306580	NP_036440.1	NM_012308	1162	F-box and leucine-rich repeatprotein 11 F-box protein FBL11 [Homo sapiens]
	12654723	*AAH01203.1*	*BC001203*	*191*	*AAH01203 Similar to f-box andleucine-rich repeat protein 11 [Homo sapiens]*

Hs.22193
Gene: FBXL9 Sequence count: 24

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	6103641	AAF03701.1	AF176701	313	F-box protein FBL9 [Homo sapiens]
	16306591	*NP_036295.1*	*NM_012163*	*223*	*F-box and leucine-rich repeatprotein 9 F-box protein*

					FBL9 [Homo sapiens]

Hs.225984
Gene: - Sequence count: 0

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	19550449	AAL91370.1	-	419	AF457207_1 pygopus 1 [Homo sapiens]

Hs.226019
Gene: FBXL11 Sequence count: 1

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	5578773	CAB51286.1	AJ243936	180	protein G16 [Homo sapiens]

Hs.228059
Gene: TRIM28 Sequence count: 1144

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	13436401	AAH04978.1	BC004978	835	AAH04978 KRAB-associated protein 1[Homo sapiens]
	13938486	AAH07390.1	BC007390	373	AAH07390 Similar to KRAB-associatedprotein 1 [Homo sapiens]
	5032179	NP_005753.1	NM_005762	835	tripartite motif-containing 28protein KRAB-associated protein 1 transcriptional intermediaryfactor 1-beta nuclear corepressor KAP-1 [Homo sapiens]
	951332	AAA74954.1	U31657	350	unknown
	1699027	AAB37341.1	U78773	835	nuclear corepressor KAP-1 [Homosapiens]
	1930059	AAB51517.1	U95040	835	hKAP1/TIF1B [Homo sapiens]
	1524109	CAA66150.1	X97548	835	TIF1beta zinc finger protein [Homosapiens]

Hs.23158
Gene: - Sequence count: 0

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	18916721	BAB85526.1	-	821	KIAA1940 protein [Homo sapiens]

Hs.232026
Gene: - Sequence count: 0

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	15929862	AAH15353.1	-	446	AAH15353 Unknown (protein forMGC:21446) [Homo sapiens]
	20270353	NP_620155.1	-	446	hypothetical protein BC015353[Homo sapiens]

Hs.23348
Gene: SKP2 Sequence count: 112

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	12655171	AAH01441.1	BC001441	410	AAH01441 Similar to S-phasekinase-associated protein 2 (p45) [Homo sapiens]
	13938579	AAH07441.1	BC007441	410	AAH07441 Unknown (protein forMGC:4483) [Homo sapiens]
	16306595	NP_005974.2	NM_005983	424	S-phase kinase-associated protein2, isoform 1 cyclin A/CDK2-associated p45 F-box protein Skp2 [Homosapiens]
	14249170	NP_116026.1	NM_032637	410	S-phase kinase-associated protein2, isoform 2 cyclin A/CDK2-associated p45 F-box protein Skp2 [Homosapiens]
	995826	AAC50242.1	U33761	435	cyclin A/CDK2-associated p45

Hs.234282
Gene: VPS11 Sequence count: 200

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	17978477	NP_068375.3	-	941	vacuolar protein sorting 11 (yeasthomolog) vacuolar protein

					sorting protein 11 [Homo sapiens]
	11138093	BAA95163.2	AB027508	941	hVPS11 [Homo sapiens]
	11345380	AAG34677.1	AF308800	941	AF308800_1 vacuolar protein sortingprotein 11 [Homo sapiens]
	10438714	BAB15320.1	AK026012	331	unnamed protein product [Homosapiens]
	15082293	AAH12051.1	BC012051	331	AAH12051 Similar to vacuolar proteinsorting 11 (yeast homolog) [Homo sapiens]

Hs.236218
Gene: TRIM32 Sequence count: 104

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	8217434	CAB92723.1	-	653	bA67K19.2 (zinc-finger protein HT2A(72 kD TAT-interacting protein)) [Homo sapiens]
	11427566	XP_005335.1	-	653	TAT-interactive protein, 72-KD[Homo sapiens]
	13111963	AAH03154.1	BC003154	653	AAH03154 TAT-INTERACTIVE PROTEIN,72-KD [Homo sapiens]
	6912426	NP_036342.1	NM_012210	653	TAT-interactive protein, 72-KDtripartite motif protein TRIM32 zinc-finger protein HT2A [Homosapiens]
	758423	AAA86474.1	U18543	653	zinc-finger protein

Hs.23794
Gene: CHFR Sequence count: 140

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	18579557	XP_053913.2	-	664	checkpoint with forkhead and ringfinger domains [Homo sapiens]
	9651170	AAF91084.1	AF170724	664	AF170724_1 cell cycle checkpointprotein CHFR [Homo sapiens]
	7023051	BAA91817.1	AK001658	623	unnamed protein product [Homosapiens]

☐	14042553	BAB55297.1	AK027687	652	unnamed protein product [Homosapiens]
☐	15082330	AAH12072.1	BC012072	652	AAH12072 Unknown (protein forMGC:19963) [Homo sapiens]
☐	8922675	NP_060693.1	NM_018223	623	checkpoint with forkhead and ringfinger domains [Homo sapiens]
☐	*6808266*	*CAB70812.1*	*AL137561*	*306*	*hypothetical protein [Homo sapiens]*

Hs.238246
Gene: FLJ22479 Sequence count: 165

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	19923609	NP_079176.2	-	509	hypothetical protein FLJ22479[Homo sapiens]
☐	14017831	BAB47436.1	AB058710	702	KIAA1807 protein [Homo sapiens]
☐	14042423	BAB55239.1	AK027620	509	unnamed protein product [Homosapiens]
☐	*10438885*	*BAB15371.1*	*AK026132*	*289*	*unnamed protein product [Homosapiens]*

☐

Hs.24307
Gene: SHFM3 Sequence count: 220

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	10764488	AAG22739.1	AF281859	412	dactylin [Homo sapiens]
☐	11545739	NP_071322.1	NM_022039	412	split hand/foot malformation(ectrodactyly) type 3 [Homo sapiens]
☐	*13938471*	*AAH07380.1*	*BC007380*	*292*	*AAH07380 Similar to dactylaplasia[Homo sapiens]*

Hs.24439
Gene: RNF8 Sequence count: 248

Select	GI	Protein Acc.	DNA Acc.	Length	Description

☐	3721580	BAA33557.1	-	485	new zinc finger protein [Homosapiens]
☐	3327106	BAA31621.1	AB014546	485	KIAA0646 protein [Homo sapiens]
☐	13960155	AAH07517.1	BC007517	485	AAH07517 ring finger protein (C3HC4type) 8 [Homo sapiens]
☐	4504867	NP_003949.1	NM_003958	485	ring finger protein (C3HC4 type) 8C3HC4-type zinc finger protein zinc finger protein [Homo sapiens]

Hs.24594
Gene: UBE4B Sequence count: 334

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	17434568	XP_018317.4	-	1302	ubiquitination factor E4B (UFD2homolog, yeast) [Homo sapiens]
☐	6635133	BAA31659.2	AB014584	1072	KIAA0684 protein [Homo sapiens]
☐	13516467	BAB40446.1	AB028839	1173	homzygously deleted inneuroblastoma-1/UFD2 [Homo sapiens]
☐	4104976	AAD02233.1	AF043117	1302	ubiquitin-fusion degradation protein2 [Homo sapiens]
☐	3860024	AAC72962.1	AF091093	186	unknown [Homo sapiens]
☐	14582754	AAK69622.1	AF331520	1173	AF331520_1 ubiquitin-fusiondegradation protein 2 [Homo sapiens]
☐	5174483	NP_006039.1	NM_006048	1302	ubiquitination factor E4B (UFD2homolog, yeast) clone 686 protein ubiquitination factor E4B(homologous to yeast UFD2) [Homo sapiens]

Hs.246795
Gene: BRPF3 Sequence count: 140

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	6331389	BAA86600.1	AB033112	1214	KIAA1286 protein [Homo sapiens]

	7021034	*BAA91359.1*	*AK000751*	*168*	*unnamed protein product [Homosapiens]*

Hs.247220
Gene: PEX10 Sequence count: 254

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	17390443	AAH18198.1	-	326	AAH18198 peroxisome biogenesis factor10 [Homo sapiens]
	6518431	BAA87895.1	AB013818	326	peroxisome biogenesis factor(peroxin) 10 [Homo sapiens]
	3170653	AAC18133.1	AF060502	326	peroxisome assembly protein PEX10[Homo sapiens]
	12653541	AAH00543.1	BC000543	346	AAH00543 Similar to peroxisomebiogenesis factor 10 [Homo sapiens]
	4505715	NP_002608.1	NM_002617	326	peroxisome biogenesis factor 10[Homo sapiens]

Hs.247280
Gene: C20orf18 Sequence count: 324

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	12697476	CAC28312.1	-	500	dJ852M4.1.2 (HBV associated factor(isoform 2)) [Homo sapiens]
	15929590	AAH15219.1	-	510	AAH15219 HBV associated factor [Homosapiens]
	14043036	NP_112506.1	NM_031229	500	chromosome 20 open reading frame18, isoform 2 HBV associated factor [Homo sapiens]
	14043034	*NP_112505.1*	*NM_031228*	*262*	*chromosome 20 open reading frame18, isoform 3 HBV associated factor [Homo sapiens]*
	14043032	*NP_112504.1*	*NM_031227*	*230*	*chromosome 20 open reading frame18, isoform 4 HBV associated factor [Homo sapiens]*
	5454168	*NP_006453.1*	*NM_006462*	*468*	*chromosome 20 open reading frame18, isoform 1 HBV associated factor [Homo sapiens]*

	13784935	*AAH00983.3*	*BC000983*	*230*	*AAH00983 Similar to HBV associatedfactor [Homo sapiens]*
	4097712	*AAD00162.1*	*U67322*	*468*	*HBV associated factor*

Hs.247525
Gene: - Sequence count: 0

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	15928896	AAH14913.1	-	671	AAH14913 Similar tosynaptotagmin-like 4 [Homo sapiens]
	18152767	NP_542775.1	-	671	synaptotagmin-like 4(granuphilin-a) [Homo sapiens]

Hs.249184
Gene: TCF19 Sequence count: 110

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	12803349	AAH02493.1	BC002493	345	AAH02493 Similar to transcriptionfactor 19 (SC1) [Homo sapiens]
	6005892	*NP_009040.1*	*NM_007109*	*359*	*transcription factor 19 (SC1)transcription factor like # [Homo sapiens]*
	8714511	*AAB19475.2*	*S53374*	*358*	*putative trans-acting factor involvedin cell cycle control [Homo sapiens]*

Hs.249194
Gene: MLLT6 Sequence count: 169

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	5174577	NP_005928.1	NM_005937	1093	myeloid/lymphoid or mixed-lineageleukemia (trithorax homolog, Drosophila) translocated to, 6Myeloid/lymphoid or mixed-lineage leukemia, translocated to, 6myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila)homolog) translocated to, 6 [Homo sapiens]
	532762	AAA21145.1	U07932	1093	AF-17

	14043818	*AAH07859.1*	*BC007859*	*218*	*AAH07859 Unknown (protein forMGC:14385) [Homo sapiens]*
	13938230	*AAH07237.1*	*BC007237*	*462*	*AAH07237 Unknown (protein forMGC:15433) [Homo sapiens]*
	10440185	*BAB15670.1*	*AK027133*	*462*	*unnamed protein product [Homosapiens]*
	6599251	*CAB63772.1*	*AL133659*	*424*	*hypothetical protein [Homo sapiens]*

Hs.249727
Gene: FBG4 Sequence count: 57

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	16553918	BAB71616.1	-	287	unnamed protein product [Homosapiens]
	17226121	AAL37625.1	-	278	AF386743_1 F-box protein [Homosapiens]
	18643385	NP_079183.4	-	278	F-box protein FBG4 f-box onlyprotein 17 hypothetical protein FLJ11798 [Homo sapiens]
	15214527	AAH12385.1	BC012385	278	AAH12385 Similar to f-box onlyprotein 17 [Homo sapiens]
	10433138	*BAB13917.1*	*AK021860*	*251*	*unnamed protein product [Homosapiens]*

Hs.25197
Gene: STUB1 Sequence count: 559

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	18585371	XP_083939.1	-	303	serologically defined colon cancerantigen 7 [Homo sapiens]
	3170178	AAC18038.1	AF039689	303	antigen NY-CO-7 [Homo sapiens]
	4928064	AAD33400.1	AF129085	303	AF129085_1 carboxy terminus ofHsp70-interacting protein [Homo sapiens]
	10441867	AAG17211.1	AF217968	231	AF217968_1 unknown [Homo sapiens]

☐	14043119	AAH07545.1	BC007545	303	AAH07545 Unknown (protein forMGC:15444) [Homo sapiens]
☐	5031963	NP_005852.1	NM_005861	303	serologically defined colon cancerantigen 7 heat shock protein A binding protein 2 (c-terminal)carboxy terminus of Hsp70p-interacting protein [Homo sapiens]

Hs.25601
Gene: CHD3 Sequence count: 345

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	761718	AAC50228.1	-	530	Mi-2 autoantigen 240 kDa protein
☐	2645433	AAB87383.1	AF006515	1944	CHD3 [Homo sapiens]
☐	4557451	NP_001263.1	NM_001272	1944	chromodomain helicase DNA bindingprotein 3 Mi-2a zinc-finger helicase (Snf2-like) [Homo sapiens]
☐	3298562	AAC39923.1	U91543	2000	zinc-finger helicase [Homo sapiens]

Hs.256126
Gene: BIRC7 Sequence count: 31

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	11545503	AAG37878.1	AF301009	298	AF301009_1 inhibitor of apoptosisprotein KIAP [Homo sapiens]
☐	*11245453*	*AAG33622.1*	*AF311388*	*280*	*AF311388_1 livininhibitor-of-apotosis [Homo sapiens]*
☐	*11545910*	*NP_071444.1*	*NM_022161*	*280*	*livin inhibitor-of-apotosis [Homosapiens]*

Hs.25913
Gene: PEX12 Sequence count: 58

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	1938369	AAC68813.1	-	359	peroxin 12 [Homo sapiens]

☐	3308973	BAA31559.1	AB004546	359	peroxisome assembly factor-3 (PAF-3)[Homo sapiens]
☐	4505721	NP_000277.1	NM_000286	359	peroxisomal biogenesis factor 12peroxisome biogenesis factor 12 [Homo sapiens]
☐	1938367	AAC68812.1	U91521	359	peroxin 12 [Homo sapiens]

Hs.26009
Gene: UBCE7IP5 Sequence count: 89

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	4240209	BAA74883.1	AB020667	541	KIAA0860 protein [Homo sapiens]
☐	12653487	AAH00515.1	BC000515	541	AAH00515 KIAA0860 protein [Homosapiens]
☐	7662344	NP_055763.1	NM_014948	541	likely ortholog of mouse ubiquitinconjugating enzyme 7 interacting protein 5 KIAA0860 protein [Homosapiens]

Hs.26058
Gene: FLJ21156 Sequence count: 177

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	17512254	AAH19105.1	-	210	AAH19105 hypothetical proteinFLJ21156 [Homo sapiens]
☐	10437206	BAB15015.1	AK024809	210	unnamed protein product [Homosapiens]
☐	13375805	NP_078878.1	NM_024602	210	hypothetical protein FLJ21156[Homo sapiens]

Hs.26323
Gene: LOC57117 Sequence count: 133

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	9802046	AAF99604.1	AF242524	444	AF242524_1 hypothetical nuclear factorSBBI22 [Homo sapiens]
☐	9966873	NP_065128.1	NM_020395	444	hypothetical nuclear factor SBBI22[Homo sapiens]

Hs.26412
Gene: RNF26 Sequence count: 189

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	14774000	XP_051435.1	-	433	ring finger protein 26 [Homosapiens]
	13591593	BAB40955.1	AB055622	433	RING finger protein with leucinezipper RNF26 [Homo sapiens]
	14043099	AAH07534.1	BC007534	433	AAH07534 reserved [Homo sapiens]
	14042925	NP_114404.1	NM_032015	433	ring finger protein 26 [Homosapiens]

Hs.26663
Gene: LOC51191 Sequence count: 34

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	6630609	BAA88519.1	AB027289	1024	cyclin-E binding protein 1 [Homosapiens]
	7705931	NP_057407.1	NM_016323	1024	cyclin-E binding protein 1 [Homosapiens]

Hs.266933
Gene: HERC2 Sequence count: 185

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	4079809	AAD08657.1	AF071172	4834	HERC2 [Homo sapiens]
	4758520	NP_004658.1	NM_004667	4834	hect domain and RLD 2 [Homosapiens

Hs.267120
Gene: DKFZP434O1427 Sequence count: 150

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	7159799	CAB76254.1	-	359	dJ351K20.1.1 (novel C3HC4 type Zincfinger (RING finger) protein (isoform 1)) [Homo sapiens]

☐	7159800	CAB76255.1	-	358	dJ351K20.1.2 (novel C3HC4 type Zincfinger (RING finger) protein (isoform 2)) [Homo sapiens]
☐	18378125	CAC85986.1	-	358	dactylidin [Homo sapiens]
☐	14042108	BAB55108.1	AK027436	358	unnamed protein product [Homosapiens]
☐	14042318	BAB55196.1	AK027558	359	unnamed protein product [Homosapiens]
☐	14042704	BAB55359.1	AK027776	358	unnamed protein product [Homosapiens]
☐	12053167	CAB66763.1	AL136829	358	hypothetical protein [Homo sapiens]
☐	14198342	AAH08235.1	BC008235	358	AAH08235 hypothetical proteinDKFZp434O1427 [Homo sapiens]
☐	13624337	NP_112225.1	NM_030963	359	hypothetical protein DKFZp434O1427[Homo sapiens]

Hs.270549
Gene: HZFW1 Sequence count: 31

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	11875405	AAG40628.1	AF238315	420	AF238315_1 HZFw1 protein [Homosapiens]
☐	11875407	AAG40629.1	AF238316	354	AF238316_1 HZFw2 protein [Homosapiens]
☐	11875409	AAG40630.1	AF238317	256	AF238317_1 HZFw3 protein [Homosapiens]
☐	13376844	NP_079512.1	NM_025236	420	HZFw1 protein [Homo sapiens]

Hs.272027
Gene: FBXO5 Sequence count: 96

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	17511911	AAH18905.1	-	447	AAH18905 F-box only protein 5 [Homosapiens]
	6164620	AAF04469.1	AF129535	447	AF129535_1 F-box protein Fbx5

☐					[Homosapiens]
☐	6912366	NP_036309.1	NM_012177	447	F-box only protein 5 F-box proteinFbx5 homolog of xenopus EMI1 [Homo sapiens]

Hs.272314
Gene: DKFZP434C1715 Sequence count: 8

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	6599210	CAB63737.1	AL133602	381	hypothetical protein [Homo sapiens]

Hs.272564
Gene: LOC51725 Sequence count: 11

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	14727195	XP_045910.1	-	709	muscle disease-related protein[Homo sapiens]
☐	6330372	BAA86509.1	AB033021	717	KIAA1195 protein [Homo sapiens]
☐	6561831	AAF17085.1	AF204674	709	AF204674_1 muscle disease-relatedprotein [Homo sapiens]
☐	7706493	NP_057382.1	NM_016298	709	muscle disease-related protein[Homo sapiens]

Hs.272800
Gene: FLJ20456 Sequence count: 18

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	18588857	XP_008732.4	-	232	hypothetical protein FLJ20456[Homo sapiens]
☐	7020569	BAA91182.1	AK000463	232	unnamed protein product [Homosapiens]
☐	15080562	AAH12021.1	BC012021	232	AAH12021 Unknown (protein forMGC:21737) [Homo sapiens]
☐	8923429	NP_060301.1	NM_017831	232	hypothetical protein FLJ20456 [Homosapiens]

Hs.273385
Gene: - Sequence count: 0

Select	GI	Protein	DNA	Length	Description

		Acc.	Acc.		
	3024154	Q92794	-	2004	MOZ_HUMAN Monocytic leukemia zinc fingerprotein (Zinc finger protein 220)

Hs.274295
Gene: TRIM10 Sequence count: 40

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	5708210	CAB52384.1	-	481	RING finger protein [Homo sapiens]
	15277239	BAB63332.1	-	481	Zn-finger, interacts withchromatin-binding polycomb proteins [Homo sapiens]
	12407413	AAG53495.1	AF220122	482	AF220122_1 tripartite motif proteinTRIM10 alpha [Homo sapiens]
	12407415	AAG53496.1	AF220123	396	AF220123_1 tripartite motif proteinTRIM10 beta [Homo sapiens]
	5803147	NP_006769.1	NM_006778	481	ring finger protein 9, isoform 1hematopoietic RING finger 1 tripartite motif protein 10 [Homosapiens]
	16519561	NP_439893.1	NM_052828	395	ring finger protein 9, isoform 2hematopoietic RING finger 1 tripartite motif protein 10 [Homosapiens]

Hs.27590
Gene: MORF Sequence count: 196

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	18032212	AAL56647.1	-	2072	AF217500_1 histone acetyltransferaseMOZ2 [Homo sapiens]
	2224707	BAA20837.1	AB002381	1520	KIAA0383 [Homo sapiens]
	6002686	AAF00095.1	AF113514	1781	histone acetyltransferase MORF [Homosapiens]
	6002694	AAF00099.1	AF119230	1890	AF119230_1 histone acetyltransferaseMORF alpha [Homo sapiens]

☐	6002696	AAF00100.1	AF119231	2073	AF119231_1 histone acetyltransferaseMORF beta [Homo sapiens]
☐	6912512	NP_036462.1	NM_012330	2073	histone acetyltransferase [Homosapiens]
☐	*12718197*	*CAC28864.1*	*AJ299262*	*94*	*CBP/MORF protein [Homo sapiens]*

Hs.27695
Gene: MID1 Sequence count: 148

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	3462503	AAC32998.1	-	484	midline 1 cerebellar isoform 1 [Homosapiens]
☐	3462505	AAC32999.1	-	228	midline 1 cerebellar isoform 2 [Homosapiens]
☐	2827994	AAB99951.1	AF035360	667	ring finger protein [Homo sapiens]
☐	3462507	AAC33000.1	AF041208	667	midline 1 fetal kidney isoform 1[Homo sapiens]
☐	3462509	AAC33001.1	AF041209	667	midline 1 fetal kidney isoform 2[Homo sapiens]
☐	12275914	AAG50191.1	AF230976	667	AF230976_1 tripartite motif proteinTRIM18 alpha MID1 alpha [Homo sapiens]
☐	12275916	AAG50192.1	AF230977	552	AF230977_1 tripartite motif proteinTRIM18 beta MID1 beta [Homo sapiens]
☐	11228709	AAG33130.1	AF269101	667	AF269101_1 midline 1 [Homo sapiens]
☐	4557753	NP_000372.1	NM_000381	667	midline 1, isoform alphamidline-1 zinc finger X and Y putative transcription factor XPRFtripartite motif protein TRIM18 midline 1 ring finger gene midinfinger on X and Y, mouse, homolog of [Homo sapiens]
☐	15451852	NP_150632.1	NM_033290	667	midline 1, isoform alphamidline-1 zinc finger X and Y putative transcription factor XPRFtripartite

					motif protein TRIM18 midline 1 ring finger gene midinfinger on X and Y, mouse, homolog of [Homo sapiens]
	15451854	NP_150633.1	NM_033291	552	midline 1, isoform betamidline-1 zinc finger X and Y putative transcription factor XPRFtripartite motif protein TRIM18 midline 1 ring finger gene midinfinger on X and Y, mouse, homolog of [Homo sapiens]
	2612793	CAA74018.1	Y13667	667	putative transcription factor XPRF[Homo sapiens]
	3462511	*AAC33002.1*	*AF041210*	*630*	*midline 1 fetal kidney isoform 3[Homo sapiens]*

Hs.27721
Gene: WHSC1L1 Sequence count: 405

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	12642817	AAK00355.1	AF332469	1437	putative protein WHSC1L11 [Homosapiens]
	12697312	CAC28350.1	AJ295990	1437	putative chromatin modulator [Homosapiens]
	12697314	CAC28351.1	AJ295991	1388	Putative Chromatin modulator [Homosapiens]
	13699811	NP_075447.1	NM_023034	1437	WHSC1L1 protein isoform longWolf-Hirschhorn syndrome candidate 1-like 1 protein [Homo sapiens]
	12642815	*AAK00354.1*	*AF332468*	*645*	*putative protein WHSC1L1s [Homosapiens]*
	15082307	*AAH12059.1*	*BC012059*	*645*	*AAH12059 Wolf-Hirschhorn syndromecandidate 1-like 1 [Homo sapiens]*
	12697316	*CAC28352.1*	*AJ295992*	*645*	*putative chromatin modulator [Homosapiens]*
	13699813	*NP_060248.2*	*NM_017778*	*645*	*WHSC1L1 protein isoform shortWolf-Hirschhorn syndrome candidate 1-like 1 protein [Homo sapiens]*

	6912588	*NP_036359.1*	*NM_012227*	*403*	*Pseudoautosomal GTP-bindingprotein-like protein [Homo sapiens]*
	12005823	*AAG44637.1*	*AF255649*	*561*	*AF255649_1 DC28 [Homo sapiens]*
	10434020	*BAB14099.1*	*AK022560*	*645*	*unnamed protein product [Homosapiens]*
	7020394	*BAA91110.1*	*AK000360*	*161*	*unnamed protein product [Homosapiens]*
	6562623	*CAA74749.2*	*Y14391*	*403*	*GTP-binding protein [Homo sapiens]*

Hs.277401
Gene: BAZ2A Sequence count: 499

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	2224569	BAA20773.1	AB002312	1240	KIAA0314 [Homo sapiens]
	6683498	BAA89211.1	AB032254	1878	bromodomain adjacent to zinc fingerdomain 2A [Homo sapiens]
	14286328	AAH08965.1	BC008965	840	AAH08965 Similar to bromodomainadjacent to zinc finger domain, 2A [Homo sapiens]
	7304921	NP_038477.1	NM_013449	1878	bromodomain adjacent to zinc fingerdomain, 2A TTF-I interacting peptide 5 [Homo sapiens]

Hs.278428
Gene: DD5 Sequence count: 328

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	4240281	BAA74919.1	AB020703	1230	KIAA0896 protein [Homo sapiens]
	15029597	AAD01259.2	AF006010	2799	progestin induced protein [Homosapiens]
	15147337	NP_056986.2	NM_015902	2799	progestin induced proteinubiquitin-protein ligase [Homo sapiens]
	9545980	AAF88143.1	U95000	2798	U95000_1 hyd protein [Homo

☐					sapiens]

Hs.279025
Gene: MKRN4 Sequence count: 1

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	1304599	AAA99070.1	-	485	ZNF127-Xp
☐	14767567	XP_035379.1	-	485	makorin, ring finger protein, 4[Homo sapiens]
☐	13540509	NP_110384.1	NM_030757	485	makorin, ring finger protein, 4zinc finger protein 127-like 1 [Homo sapiens]

Hs.279474
Gene: MKRN2 Sequence count: 229

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	8714513	AAF29042.2	-	416	AF161555_1 HSPC070 [Homo sapiens]
☐	14730765	XP_051580.1	-	416	makorin, ring finger protein, 2[Homo sapiens]
☐	11118885	AAG30426.1	AF302084	416	AF302084_1 MAKORIN2 [Homo sapiens]
☐	12804735	AAH01799.1	BC001799	373	AAH01799 Unknown (protein forIMAGE:3354600) [Homo sapiens]
☐	8850223	NP_054879.2	NM_014160	416	HSPC070 protein [Homo sapiens]

Hs.279535
Gene: AGTRL2 Sequence count: 237

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	14550508	AAH09504.1	BC009504	192	AAH09504 Similar to CG8974 geneproduct [Homo sapiens]
☐	*4885059*	*NP_005153.1*	*NM_005162*	*71*	*angiotensin receptor-like 2angiotensin II receptor-like [Homo sapiens]*

Hs.279709
Gene: RNF28 Sequence count: 25

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	16041697	AAH15717.1	-	346	AAH15717 Similar to ring fingerprotein 28 [Homo sapiens]
☐	16552480	BAB71318.1	-	353	unnamed protein product [Homosapiens]
☐	18073356	CAC81706.1	-	353	muscle specific RING finger 2(MURF2) [Homo sapiens]
☐	19924163	NP_115977.2	-	353	muscle specific ring fingerprotein 1 striated muscle RING zinc finger protein iris ring fingerprotein muscle specific ring finger protein 2 [Homo sapiens]
☐	13785924	AAK39519.1	AF353673	353	AF353673_1 iris ring finger protein[Homo sapiens]
☐	14028787	AAK52497.1	AF361946	288	AF361946_1 RING zinc finger proteinSMRZ [Homo sapiens]

Hs.279849
Gene: KIAA0438 Sequence count: 279

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	16157382	XP_003693.3	-	708	KIAA0438 gene product [Homosapiens]
☐	2662157	BAA23710.1	AB007898	708	KIAA0438 [Homo sapiens]
☐	7662124	NP_055634.1	NM_014819	708	KIAA0438 gene product [Homosapiens]

Hs.279919
Gene: RBX1 Sequence count: 219

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	4769004	AAD29715.1	-	108	AF140598_1 ring-box protein 1 [Homosapiens]
☐	4809216	AAD30146.1	-	108	AF142059_1 RING finger protein [Homosapiens]
☐	6572304	CAB62925.1	-	108	bA554C12.1 (RBX1 or ROC1 (ring-boxor ring finger protein 1)) [Homo sapiens]

	12655215	AAH01466.1	-	108	AAH01466 ring-box 1 [Homo sapiens]
	16924202	AAH17370.1	-	108	AAH17370 ring-box 1 [Homo sapiens]

Hs.28285
Gene: TRC8 Sequence count: 120

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	18204312	AAH21571.1	-	664	AAH21571 patched related proteintranslocated in renal cancer [Homo sapiens]
	3395787	AAC39930.1	AF064801	664	multiple membrane spanning receptorTRC8 [Homo sapiens]
	6005912	NP_009149.1	NM_007218	664	patched related proteintranslocated in renal cancer [Homo sapiens]

Hs.283103
Gene: RNF18 Sequence count: 3

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	15308359	XP_053475.1	-	452	ring finger protein 18 [Homosapiens]
	9650982	BAB03503.1	AB037682	452	testis-specific RING Finger protein[Homo sapiens]
	9966829	NP_065091.1	NM_020358	452	ring finger protein 18testis-specific RING Finger protein [Homo sapiens]

Hs.283429
Gene: SMCX Sequence count: 212

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	12743425	XP_013101.1	-	1560	Smcx homolog, X chromosome (mouse)[Homo sapiens]
	457137	AAA61302.1	L25270	1560	escapes X-chromosome inactivation
	11321605	NP_004178.1	NM_004187	1560	Smcx homolog, X chromosome(mouse) SMC (mouse) homolog, X chromosome XE169 gene (selected

					mousecDNA on X, human homolog of) [Homo sapiens]

Hs.283764
Gene: FBXO24 Sequence count: 18

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	3135317	AAC78801.1	-	318	ORF4 [Homo sapiens]
☐	6164751	AAF04525.1	AF174604	318	AF174604_1 F-box protein Fbx24 [Homosapiens]
☐	12053133	CAB66745.1	AL136811	580	hypothetical protein [Homo sapiens]
☐	11024696	NP_036304.1	NM_012172	318	F-box only protein 24 F-boxprotein Fbx24 [Homo sapiens]
☐	15812196	NP_277041.1	NM_033506	580	F-box only protein 24 F-boxprotein Fbx24 [Homo sapiens]

Hs.284204
Gene: FBXO29 Sequence count: 19

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	6063092	AAF03129.1	AF176707	551	AF176707_1 F-box protein FBX29 [Homosapiens]

Hs.284226
Gene: FBXO6 Sequence count: 34

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	18088629	AAH20880.1	-	293	AAH20880 F-box only protein 6 [Homosapiens]
☐	6164622	AAF04470.1	AF129536	338	AF129536_1 F-box protein Fbx6 [Homosapiens]
☐	7677403	AAF67153.1	AF233223	293	AF233223_1 F-box protein FBG2 [Homosapiens]
☐	8922188	NP_060908.1	NM_018438	293	F-box only protein 6 F-box proteinFbx6 F-box protein FBG2 [Homo sapiens]

Hs.284251
Gene: KIAA0544 Sequence count: 167

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	3043612	BAA25470.1	AB011116	583	KIAA0544 protein [Homo sapiens]

Hs.285641
Gene: KIAA1111 Sequence count: 146

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	5689559	BAA83063.1	AB029034	1084	KIAA1111 protein [Homo sapiens]
☐	*3860000*	*AAC72950.1*	*AF091081*	*303*	*unknown [Homo sapiens]*

Hs.287414
Gene: TRIM33 Sequence count: 249

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	5689563	BAA83065.1	AB029036	1131	KIAA1113 protein [Homo sapiens]
☐	4325109	AAD17259.1	AF119043	1120	transcriptional intermediary factor 1gamma TIF1gamma [Homo sapiens]
☐	12407441	AAG53509.1	AF220136	1127	AF220136_1 tripartite motif proteinTRIM33 alpha [Homo sapiens]
☐	12407443	AAG53510.1	AF220137	1110	AF220137_1 tripartite motif proteinTRIM33 beta [Homo sapiens]
☐	5834582	CAB55313.1	AJ132948	1052	rfg7 protein [Homo sapiens]
☐	10432686	BAB13834.1	AK021491	120	unnamed protein product [Homosapiens]
☐	14971413	NP_056990.2	NM_015906	1127	tripartite motif-containing 33protein transcriptional intermediary factor 1 gamma ret-fused gene 7[Homo sapiens]
☐	14971411	NP_148980.1	NM_033020	1110	tripartite motif-containing 33protein transcriptional

					intermediary factor 1 gamma ret-fused gene 7[Homo sapiens]

Hs.287735
Gene: FLJ23229 Sequence count: 5

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	10439844	BAB15580.1	AK026882	551	unnamed protein product [Homosapiens]
	13376593	NP_079334.1	NM_025058	551	hypothetical protein FLJ23229[Homo sapiens]

Hs.288217
Gene: MGC2941 Sequence count: 199

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	12803377	AAH02509.1	BC002509	403	AAH02509 Unknown (protein forMGC:2941) [Homo sapiens]
	14250395	AAH08630.1	BC008630	315	AAH08630 Similar to RIKEN cDNA2410141M05 gene [Homo sapiens]
	13236520	*NP_077273.1*	*NM_024297*	*265*	*hypothetical protein MGC2941 [Homosapiens]*
	10439417	*BAB15498.1*	*AK026537*	*265*	*unnamed protein product [Homosapiens]*

Hs.288773
Gene: ZNF294 Sequence count: 75

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	14780121	XP_047829.1	-	1071	zinc finger protein 294 [Homosapiens]
	3882149	BAA34434.1	AB018257	1112	KIAA0714 protein [Homo sapiens]

Hs.288971
Gene: MLL3 Sequence count: 317

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	5630077	AAD45822.1	-	1813	AC006017_2 similar to ALR similar toAAC51735 (PID:g2358287) [Homo sapiens]

☐	10568112	AAF74766.2	AF264750	4025	ALR-like protein [Homo sapiens]
☐	10434227	BAB14179.1	AK022687	452	unnamed protein product [Homosapiens]
☐	10864041	NP_067053.1	NM_021230	4025	myeloid/lymphoid or mixed-lineageleukemia 3 ALR-like protein [Homo sapiens]

Hs.289074
Gene: FBXO22 Sequence count: 145

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	6164747	AAF04523.1	-	81	AF174602_1 F-box protein Fbx22 [Homosapiens]
☐	10436317	BAB14798.1	AK024048	276	unnamed protein product [Homosapiens]
☐	13443000	NP_036302.1	NM_012170	276	F-box only protein 22hypothetical protein FLJ13986 F-box protein Fbx22 [Homo sapiens]

Hs.289107
Gene: BIRC2 Sequence count: 254

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	14770187	XP_040717.1	-	618	baculoviral IAP repeat-containingprotein 2 [Homo sapiens]
☐	16740585	AAH16174.1	-	618	AAH16174 baculoviral IAPrepeat-containing 2 [Homo sapiens]
☐	1160973	AAC41942.1	L49431	618	TNFR2-TRAF signalling complex protein
☐	4502141	NP_001157.1	NM_001166	618	baculoviral IAP repeat-containingprotein 2 cIAP1 hiap-2 apoptosis inhibitor 1 NFR2-TRAF signallingcomplex protein [Homo sapiens]
☐	1145293	AAC50508.1	U37547	618	MIHB
☐	1184318	AAC50372.1	U45879	618	inhibitor of apoptosis protein 2

Hs.292767
Gene: HAKAI Sequence count: 96

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	13644708	XP_018098.1	-	491	hypothetical protein FLJ23109[Homo sapiens]
	20072755	AAH27460.1	-	491	hypothetical protein FLJ23109 [Homosapiens]
	10439688	BAB15544.1	AK026762	491	unnamed protein product [Homosapiens]
	13376204	NP_079090.1	NM_024814	491	hypothetical protein FLJ23109likely ortholog of mouse E-cadherin binding protein E7 [Homo sapiens]

Hs.293660
Gene: - Sequence count: 0

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	15741221	AAK07687.1	-	638	gene overexpressed in astrocytoma[Homo sapiens]

Hs.294151
Gene: KIAA1917 Sequence count: 132

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	13278963	AAH04231.1	BC004231	268	AAH04231 Unknown (protein forIMAGE:3603836) [Homo sapiens]
	15620893	*BAB67810.1*	*AB067504*	*593*	*KIAA1917 protein [Homo sapiens]*

Hs.29736
Gene: TRAF5 Sequence count: 84

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	2982671	BAA25262.1	AB000509	557	TRAF5 [Homo sapiens]
	11321603	NP_004610.1	NM_004619	557	TNF receptor-associated factor 5[Homo sapiens]
	2138180	AAC51329.1	U69108	538	TNF receptor associated factor

					5[Homo sapiens]

Hs.297660
Gene: TRAF3 Sequence count: 110

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	14754079	XP_040913.1	-	568	TNF receptor-associated factor 3[Homo sapiens]
	695358	AAA68195.1	L38509	543	CD40-associated protein
	4507679	NP_003291.1	NM_003300	568	TNF receptor-associated factor 3[Homo sapiens]
	595911	AAA56753.1	U15637	567	CD40 binding protein [Homo sapiens]
	675460	AAA65732.1	U19260	568	LMP1 associated protein
	726088	AAC50112.1	U21092	568	CD40 receptor associated factor 1
	4761210	*AAD29276.1*	*AF110908*	*33*	*AF110908_1 TNF-receptor associatedfactor-3 [Homo sapiens]*

Hs.297681
Gene: - Sequence count: 0

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	107400	B40045	-	593	B40045 probable transcription factor PML S- human

Hs.29874
Gene: MGC13061 Sequence count: 65

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	13477235	AAH05084.1	BC005084	210	AAH05084 Similar to RIKEN cDNA0610037N03 gene [Homo sapiens]
	14150096	NP_115698.1	NM_032322	210	hypothetical protein MGC13061[Homo sapiens]

Hs.301011
Gene: KIAA0876 Sequence count: 237

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	6910563	AAF31271.1	-	819	AC022517_1 KIAA0876 protein [Homosapiens]
	14764011	XP_035625.1	-	1096	KIAA0876 protein [Homo sapiens]
	14133223	BAA74899.2	AB020683	1119	KIAA0876 protein [Homo sapiens]
	6599260	CAB63748.1	AL133622	630	hypothetical protein [Homo sapiens]

Hs.301055
Gene: C20orf104 Sequence count: 138

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	10241461	CAC09389.1	-	584	dJ1121G12.1.2 (A novel proteincontaining a putative PHD finger domain, isoform 2) [Homo sapiens]
	18034775	NP_057520.2	-	1012	transcription factor TZPhepatocellular carcinoma-associated antigen 58 C2H2 zinc fingerprotein glioma-expressed antigen 2 [Homo sapiens]
	13195151	AAK13046.1	AY027523	1012	transcription factor TZP [Homosapiens]
	13346457	*AAK19748.1*	*AF348207*	*639*	*AF348207_1 C2H2 zinc finger protein[Homo sapiens]*
	6970064	*AAF34184.1*	*AF220416*	*260*	*hepatocellular carcinoma-associatedantigen 58 HCA58 [Homo sapiens]*

Hs.301173
Gene: TRIM4 Sequence count: 13

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	19683990	AAH25949.1	-	294	tripartite motif-containing 4 [Homosapiens]

☐	15079952	AAH11763.1	BC011763	294	AAH11763 Similar to tripartite motifprotein 4 [Homo sapiens]

Hs.301209
Gene: MLLT10 Sequence count: 104

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	4757726	NP_004632.1	NM_004641	1027	myeloid/lymphoid or mixed-lineageleukemia (trithorax (Drosophil ALL1 fused gene from chromosome 10myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila)homolog) translocated to, 10 [Homo sapiens]
☐	538277	AAA79972.1	U13948	1027	zinc finger/leucine zipper protein
☐	*3139027*	*AAC16710.1*	*AF060938*	*58*	*type V AF10 protein [Homo sapiens]*
☐	*3139005*	*AAC16699.1*	*AF060927*	*49*	*type I AF10/CALM fusion protein [Homosapiens]*

Hs.301449
Gene: BS69 Sequence count: 233

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	14745546	XP_005891.3	-	562	adenovirus 5 E1A binding protein[Homo sapiens]
☐	5729746	NP_006615.1	NM_006624	562	adenovirus 5 E1A binding protein[Homo sapiens]
☐	899294	CAA60052.1	X86098	562	binds directly to adenovirus type 5E1A protein [Homo sapiens]

Hs.301526
Gene: FLJ13181 Sequence count: 21

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	13638242	XP_018333.1	-	580	hypothetical protein FLJ13181[Homo sapiens]
☐	10435088	BAB14484.1	AK023243	580	unnamed protein product [Homosapiens]
	13376780	NP_079464.1	NM_025188	580	hypothetical protein

☐					FLJ13181 [Homo sapiens]

Hs.30154
Gene: - Sequence count: 0

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	17478957	XP_027805.2	-	435	PTD016 protein [Homo sapiens]

Hs.302136
Gene: RIM Sequence count: 22

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	2224621	BAA20798.1	AB002338	1053	KIAA0340 [Homo sapiens]
☐	*10799020*	*AAG23167.1*	*AF263310*	*516*	*AF263310_1 rab3 interacting proteinvariant 6 [Homo sapiens]*
☐	*10799018*	*AAG23166.1*	*AF263309*	*567*	*AF263309_1 rab3 interacting proteinvariant 5 [Homo sapiens]*
☐	*10799016*	*AAG23165.1*	*AF263308*	*596*	*AF263308_1 rab3 interacting proteinvariant 4 [Homo sapiens]*
☐	*10799014*	*AAG23164.1*	*AF263307*	*700*	*AF263307_1 rab3 interacting proteinvariant 3 [Homo sapiens]*
☐	*10799012*	*AAG23163.1*	*AF263306*	*740*	*AF263306_1 rab3 interacting proteinvariant 2 [Homo sapiens]*
☐	*10799010*	*AAG23162.1*	*AF263305*	*766*	*AF263305_1 rab3 interacting proteinvariant 1 [Homo sapiens]*

Hs.30445
Gene: TRIM5 Sequence count: 88

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	18204217	AAH21258.1	-	347	AAH21258 tripartite motif-containing5 [Homo sapiens]
☐	12407381	AAG53479.1	AF220025	493	AF220025_1 tripartite motif proteinTRIM5 isoform alpha [Homo sapiens]
☐	12407383	AAG53480.1	AF220026	400	AF220026_1 tripartite motif proteinTRIM5 isoform beta [Homo sapiens]

	12407385	AAG53481.1	AF220027	347	AF220027_1 tripartite motif proteinTRIM5 isoform gamma [Homo sapiens]
	12407387	AAG53482.1	AF220028	326	AF220028_1 tripartite motif proteinTRIM5 isoform delta [Homo sapiens]
	12407389	AAG53483.1	AF220029	271	AF220029_1 tripartite motif proteinTRIM5 isoform epsilon [Homo sapiens]
	14042375	BAB55218.1	AK027593	493	unnamed protein product [Homosapiens]
	14719418	NP_149023.1	NM_033034	493	tripartite motif protein TRIM5;isoform alpha tripartite motif protein TRIM5 tripartite motifprotein 5 [Homo sapiens]
	15011944	NP_149083.1	NM_033092	347	tripartite motif protein TRIM5isoform gamma tripartite motif protein TRIM5 tripartite motifprotein 5 [Homo sapiens]
	15011946	NP_149084.1	NM_033093	326	tripartite motif protein TRIM5isoform delta tripartite motif protein TRIM5 tripartite motifprotein 5 [Homo sapiens]

Hs.30524
Gene: RNF24 Sequence count: 72

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	4883435	CAB43182.1	-	148	dJ681N20.1 (ring finger protein 24)[Homo sapiens]
	5102892	CAB45279.1	AL079313	104	hypothetical protein, similar to(M97204) goliath protein [Drosophila melanogaster] [Homo sapiens]
	5420200	CAB46627.1	AL096778	148	hypothetical protein [Homo sapiens]
	12802986	AAH00213.1	BC000213	148	AAH00213 ring finger protein 24 [Homosapiens]
	6857791	NP_009150.1	NM_007219	148	ring finger protein 24goliath-like protein (C3HC4 type) [Homo sapiens]

Hs.3068
Gene: SMARCA3 Sequence count: 212

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	16943790	CAD10805.1	-	1009	SWI/SNF related, matrix associated,actin dependent regulator of chromatin, subfamily a, member 3 [Homosapiens]
☐	531196	AAA67436.1	L34673	1009	ATPase
☐	4507071	NP_003062.1	NM_003071	1009	SWI/SNF related, matrix associated,actin dependent regulator of chromatin, subfamily a, member 3 SWI/SNFrelated, matrix associated, actin dependent regulator of SNF2(sucrose nonfermenting, yeast, homolog)-like 3 helicase-liketranscription factor [Homo sapiens]

Hs.30773
Gene: MBLR Sequence count: 65

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	16307386	AAH10235.1	-	352	AAH10235 MBLR protein [Homo sapiens]
☐	13537206	BAB40779.1	AB047006	352	Mel18 and Bmi1 like ring finger[Homo sapiens]
☐	14042885	BAB55431.1	AK027885	220	unnamed protein product [Homosapiens]
☐	14043225	AAH07602.1	BC007602	277	AAH07602 Unknown (protein forMGC:15678) [Homo sapiens]
☐	14149831	NP_115530.1	NM_032154	352	MBLR protein [Homo sapiens]

Hs.309943
Gene: SP140 Sequence count: 43

Select	GI	Protein Acc.	DNA Acc.	Length	Description
☐	14724149	XP_050691.1	-	867	SP140 nuclear body protein [Homosapiens]

	6005880	NP_009168.1	NM_007237	753	SP140 nuclear body protein nuclearbody protein Sp140 [Homo sapiens]
	1173654	AAB18617.1	U36500	882	LYSP100-B
	1669498	AAC50817.1	U63420	753	Sp140 protein [Homo sapiens]
	1173652	*AAB18616.1*	*U36499*	*412*	*LYSP100-A*

Hs.31016
Gene: M96 Sequence count: 198

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	3342452	AAC27618.1	AF072814	491	PHD finger DNA binding proteinisoform 1 [Homo sapiens]
	3402197	CAA08970.1	AJ010014	593	M96A protein [Homo sapiens]
	14603084	AAH10013.1	BC010013	536	AAH10013 Similar to putative DNAbinding protein [Homo sapiens]
	6678764	NP_031384.1	NM_007358	593	putative DNA binding protein [Homosapiens]
	3283994	*AAC27080.1*	*AF073293*	*262*	*M962 protein spliced isoform 2 [Homosapiens]*

Hs.3144
Gene: CBLB Sequence count: 94

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	4757920	NP_004342.1	NM_004351	770	Cas-Br-M (murine) ectropicretroviral transforming sequence b [Homo sapiens]
	862407	AAB09291.1	U26710	982	cbl-b
	862409	AAB09292.1	U26711	810	cbl-b truncated form 1
	862411	AAB09293.1	U26712	770	cbl-b truncated form 2

Hs.316750
Gene: MGC10882 Sequence count: 65

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	13436326	AAH04952.1	BC004952	247	AAH04952 Unknown (protein forMGC:10882) [Homo sapiens]
	14249240	NP_116062.1	NM_032673	247	hypothetical protein MGC10882[Homo sapiens]

Hs.318501
Gene: TRIM22 Sequence count: 130

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	13639761	XP_015243.1	-	442	tripartite motif-containing 22[Homo sapiens]
	5174699	NP_006065.1	NM_006074	442	tripartite motif-containing 22stimulated trans-acting factor (50 kDa) tripartite motif proteinTRIM22 [Homo sapiens]
	899300	CAA57684.1	X82200	442	gpStaf50 [Homo sapiens]

Hs.318584
Gene: KIAA1133 Sequence count: 70

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	13195721	BAB33319.1	AB051436	891	KIAA1133 protein [Homo sapiens]
	14328086	*AAH09252.1*	*BC009252*	*647*	*AAH09252 Unknown (protein forIMAGE:3028041) [Homo sapiens]*

Hs.31945
Gene: FBXW7 Sequence count: 115

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	15721927	AAL06290.1	-	707	AF411971_1 archipelago alpha form[Homo sapiens]
	15721929	AAL06291.1	-	627	AF411972_1 archipelago beta form[Homo sapiens]

	14326447	AAK60269.1	AF383178	561	AF383178_1 F-box protein FBX30 [Homosapiens]
	7023505	BAA91986.1	AK001933	553	unnamed protein product [Homosapiens]
	14280321	AAK57547.1	AY033553	627	F-box protein FBW7 [Homo sapiens]
	16117779	NP_060785.2	NM_018315	627	F-box protein FBW7, isoform 2hypothetical protein FLJ11071 F-box protein FBW7 F-box proteinSEL-10 homolog of C elegans sel-10 archipelago, Drosophila, homologof [Homo sapiens]
	16117781	NP_361014.1	NM_033632	707	F-box protein FBW7, isoform 1hypothetical protein FLJ11071 F-box protein FBW7 F-box proteinSEL-10 homolog of C elegans sel-10 archipelago, Drosophila, homologof [Homo sapiens]

Hs.320834
Gene: NIN283 Sequence count: 199

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	14583079	AAK69753.1	AF378524	227	AF378524_1 nin283 [Homo sapiens]
	12053303	CAB66837.1	AL136903	227	hypothetical protein [Homo sapiens]
	13938227	AAH07235.1	BC007235	227	AAH07235 Unknown (protein forMGC:15430) [Homo sapiens]
	14150005	NP_115644.1	NM_032268	227	hypothetical protein DKFZp434E229hypothetical protein FLJ14846 [Homo sapiens]
	14042664	*BAB55343.1*	*AK027752*	*155*	*unnamed protein product [Homosapiens]*

Hs.321576
Gene: TRIM3 Sequence count: 111

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	3273699	AAC24809.1	AF045239	744	brain expressed ring finger

					protein[Homo sapiens]
	12407371	AAG53474.1	AF220020	744	AF220020_1 tripartite motif proteinTRIM3 isoform alpha [Homo sapiens]
	12407373	AAG53475.1	AF220021	733	AF220021_1 tripartite motif proteinTRIM3 isoform beta [Homo sapiens]
	12407375	AAG53476.1	AF220022	665	AF220022_1 tripartite motif proteinTRIM3 isoform gamma [Homo sapiens]
	5453569	NP_006449.1	NM_006458	744	ring finger protein 22, isoformalpha brain expressed ring finger tripartite motif protein TRIM3[Homo sapiens]
	15451753	NP_150594.1	NM_033278	733	ring finger protein 22, isoformbeta brain expressed ring finger tripartite motif protein TRIM3[Homo sapiens]
	15451755	NP_150595.1	NM_033279	665	ring finger protein 22, isoformgamma brain expressed ring finger tripartite motif protein TRIM3[Homo sapiens]

Hs.321687
Gene: FBX30 Sequence count: 95

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	9988958	AAG09623.1	AY007380	224	F-box protein FBX30 [Homo sapiens]
	14043744	AAH07832.1	BC007832	224	AAH07832 Similar to F-box onlyprotein 6 [Homo sapiens]
	15055515	NP_149438.1	NM_033182	224	F-box protein FBX30 [Homo sapiens]

Hs.323813
Gene: LOC90678 Sequence count: 91

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	19923897	NP_612370.1	-	723	hypothetical protein BC009239[Homo sapiens]

	14328050	AAH09239.1	BC009239	723	AAH09239 Unknown (protein forMGC:2867) [Homo sapiens]

Hs.323835
Gene: PHF2 Sequence count: 8

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	4529843	AAD21791.1	AF043725	1099	PHD-finger protein [Homo sapiens]
	4885547	NP_005383.1	NM_005392	1099	PHD finger protein 2 [Homo sapiens]

Hs.324275
Gene: WWP1 Sequence count: 27

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	12052997	CAB66673.1	AL136739	922	hypothetical protein [Homo sapiens]
	15419011	AAK94668.1	AY043361	922	WW domain-containing protein 1 [Homosapiens]
	13654239	NP_008944.1	NM_007013	922	WW domain-containing protein 1suppressor of deltex related protein 1 Nedd-4-like ubiquitin-proteinligase atrophin-1 interacting protein 5 [Homo sapiens]

Hs.32597
Gene: RNF6 Sequence count: 140

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	4583652	CAB40413.1	AJ010346	685	RING-H2 [Homo sapiens]
	4583654	CAB40414.1	AJ010347	685	RING-H2 [Homo sapiens]
	6599239	CAB63747.1	AL133621	366	hypothetical protein [Homo sapiens]
	12331002	AAG49400.1	AY009109	685	ring-H2 protein [Homo sapiens]
	5174653	NP_005968.1	NM_005977	685	ring finger protein (C3H2C3 type) 6[Homo sapiens]

	12656363	*AAK00848.1*	*AF293342*	*142*	*AF293342_1 RNF6 protein [Homosapiens]*

Hs.330407
Gene: FLJ13962 Sequence count: 28

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	10436278	BAB14783.1	AK024024	350	unnamed protein product [Homosapiens]
	13376292	NP_079138.1	NM_024862	350	hypothetical protein FLJ13962[Homo sapiens]

Hs.331561
Gene: RNF30 Sequence count: 10

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	13160388	CAC32841.1	-	342	ring finger protein 30 [Homosapiens]
	13160389	CAC32842.1	AJ291714	384	ring finger protein 30 [Homosapiens]
	14211839	NP_115935.1	NM_032546	384	muscle-specific RING-fingerprotein 3 muscle-specific RING-finger protein homolog [Homo sapiens]

Hs.333382
Gene: WWP2 Sequence count: 123

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	15489060	AAH13645.1	BC013645	870	AAH13645 Nedd-4-likeubiquitin-protein ligase [Homo sapiens]
	5902156	NP_008945.1	NM_007014	870	Nedd-4-like ubiquitin-proteinligase WW domain-containing protein 2 [Homo sapiens]
	2072503	AAC51325.1	U96114	870	WWP2 [Homo sapiens]

Hs.334583
Gene: RNF23 Sequence count: 19

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	10716076	BAB16374.1	AB046381	518	testis-abundant finger

					protein[Homo sapiens]
	10864061	NP_067076.1	NM_021253	518	ring finger protein 23 [Homosapiens]

Hs.334624
Gene: BTRC Sequence count: 45

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	13124271	Q9Y297	-	605	FW1A_HUMAN F-box/WD-repeat protein 1B(F-box and WD-repeats protein beta-TrCP) (E3RSIkappaB)(pIkappaBalpha-E3 receptor subunit)
	4165136	AAD08702.1	AF101784	605	b-TRCP variant E3RS-IkappaB [Homosapiens]
	6164610	AAF04464.1	AF129530	569	AF129530_1 F-box protein Fbw1A [Homosapiens]
	4502477	NP_003930.1	NM_003939	569	beta-transducin repeat containingprotein, isoform 2 F-box and WD40 domain protein 1A homolog ofDrosophila Slimb protein F-box protein Fbw1A F-box/WD-repeat protein1B F-box and WD-repeats protein beta-TRCP E3RSIKAPPABpikappabalpha-E3 receptor subunit E3 receptor subunit for IKB [Homosapiens]
	16117783	NP_378663.1	NM_033637	605	beta-transducin repeat containingprotein, isoform 1 F-box and WD40 domain protein 1A homolog ofDrosophila Slimb protein F-box protein Fbw1A F-box/WD-repeat protein1B F-box and WD-repeats protein beta-TRCP E3RSIKAPPABpikappabalpha-E3 receptor subunit E3 receptor subunit for IKB [Homosapiens]
	2995194	CAA74572.1	Y14153	569	beta-transducin repeats containingprotein [Homo sapiens]

Hs.334638
Gene: MGC16175 Sequence count: 17

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	13938457	AAH07372.1	BC007372	297	AAH07372 Unknown (protein forMGC:16175) [Homo sapiens]
	14249412	NP_116154.1	NM_032765	297	hypothetical protein MGC16175[Homo sapiens]

Hs.334819
Gene: HRD1 Sequence count: 220

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	2	protlog2.0	-	617	Proteologics hHrd1 CDS, from Eran [Homosapiens]
	3	protlog3.0	-	559	Proteologics hHrd1-53-CDS (As in Plasmid 53excluding the suspected PCR mutation) [Homo sapiens]
	16588806	AAL26903.1	-	616	AF317634_1 HRD1 [Homo sapiens]
	17472528	XP_045498.2	-	616	HRD1 protein [Homo sapiens]
	14017837	BAB47439.1	AB058713	579	KIAA1810 protein [Homo sapiens]

Hs.337461
Gene: TRIM15 Sequence count: 30

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	15277238	BAB63331.1	-	465	Zn-finger [Homo sapiens]
	12407433	AAG53505.1	AF220132	465	AF220132_1 tripartite motif proteinTRIM15 alpha [Homo sapiens]
	15100170	NP_150232.1	NM_033229	465	tripartite motif protein 15,isoform alpha tripartite motif-containing 15 [Homo sapiens]
	4096654	AAD03787.1	U34249	465	zinc finger protein [Homo sapiens]
	16445350	*NP_434699.1*	*NM_052812*	*115*	*tripartite motif protein 15,isoform beta tripartite motif-containing 15*

					[Homo sapiens]
	12407435	*AAG53506.1*	*AF220133*	*115*	*AF220133_1 tripartite motif proteinTRIM15 beta [Homo sapiens]*

Hs.3383
Gene: UREB1 Sequence count: 649

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	2370079	CAB09785.1	-	336	DNA binding protein [Homo sapiens]
	6841194	AAF28950.1	-	2011	AF161390_1 HSPC272 [Homo sapiens]
	2224565	BAA20771.1	AB002310	1906	KIAA0312 [Homo sapiens]
	3694922	AAC62492.1	AF057569	308	upstream regulatory element bindingprotein 1 [Homo sapiens]
	7328096	CAB82393.1	AL162050	55	hypothetical protein [Homo sapiens]
	12803545	AAH02602.1	BC002602	308	AAH02602 upstream regulatory elementbinding protein 1 [Homo sapiens]
	13929476	NP_113584.1	NM_031407	308	upstream regulatory elementbinding protein 1 [Homo sapiens]

Hs.343661
Gene: TRIM7 Sequence count: 47

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	12407395	AAG53486.1	AF220032	221	AF220032_1 tripartite motif proteinTRIM7 [Homo sapiens]
	15150298	AAK85377.1	AF396651	511	AF396651_1 glycogenin-interactingprotein 1 [Homo sapiens]
	15079463	AAH11567.1	BC011567	221	AAH11567 Unknown (protein forMGC:20185) [Homo sapiens]
	16076875	NP_203128.1	NM_033342	221	tripartite motif protein TRIM7glycogenin-interacting protein 1 [Homo sapiens]

	15150306	*AAK85381.1*	*AF396655*	*329*	*AF396655_1 glycogenin-interactingprotein 3 [Homo sapiens]*
	15150304	*AAK85380.1*	*AF396654*	*303*	*AF396654_1 glycogenin-interactingprotein 2 [Homo sapiens]*
	15150302	*AAK85379.1*	*AF396653*	*303*	*AF396653_1 glycogenin-interactingprotein 2 [Homo sapiens]*
	15150300	*AAK85378.1*	*AF396652*	*303*	*AF396652_1 glycogenin-interactingprotein 2 [Homo sapiens]*

Hs.346945
Gene: MGC1127 Sequence count: 137

Select	GI	Protein Acc.	DNA Acc.	Length	Description
	13436338	AAH04956.1	BC004956	361	AAH04956 Unknown (protein forIMAGE:3625550) [Homo sapiens]
	14602509	*AAH09762.1*	*BC009762*	*210*	*AAH09762 Unknown (protein forMGC:1127) [Homo sapiens]*
	6808335	*CAB70832.1*	*AL137593*	*210*	*hypothetical protein [Homo sapiens]*

WE CLAIM:

1. A method of identifying a potential drug target, comprising:

providing a database comprising nucleic acid or protein sequences, wherein said sequences are annotated with potential disease-associations of said sequences;

providing an assay for measuring the disease characteristic of a disease potentially associated to any one of said sequences;

decreasing expression or activity of at least one of the nucleic acid or protein sequences provided in the database; and

determining whether the decreased expression or activity results in a change in said assay wherein a change in said assay is indicative that said nucleic acid or protein sequence is a potential drug target for the associated disease.

2. A method of identifying a potential drug target comprising:

providing a database comprising nucleic acid or protein sequences, wherein said sequences are annotated with potential disease-associations of said sequences;

providing an assay for measuring the disease characteristic of a disease potentially associated to any one of said sequences;

increasing expression or activity of at least one of the nucleic acid or protein sequences provided in the database; and

determining whether the increased expression or activity results in a change in said assay wherein a change in said assay is indicative that said nucleic acid or protein sequence is a potential drug target for the associated disease.

3. A method of identifying a potential drug target comprising:

providing a database comprising nucleic acid or protein sequences, wherein said sequences are annotated with potential disease-associations of said sequences;

determining differential expression or activity of said nucleic acid or protein sequences in a cell exhibiting a disease characteristic of a potential associated disease and a corresponding normal cell;

decreasing expression or activity of said nucleic acid or protein sequences; and

determining the effect of decreased expression or activity on said cell exhibiting disease characteristics of the associated disease, wherein a change in said disease characteristics is indicative that said nucleic acid or protein sequence is a potential drug target for said associated disease.

4. A method of identifying a potential drug target comprising:

providing a database comprising nucleic acid or protein sequences, wherein said sequences are annotated with potential disease-associations of said sequences;

determining differential expression of said nucleic acid or protein sequences in a cell exhibiting disease characteristics of a potential associated disease and a corresponding normal cell;

increasing expression or activity of said nucleic acid or protein sequence; and

determining the effect of increased expression or activity on said cell exhibiting disease characteristics of the associated disease, wherein a change in said disease characteristics is indicative that said nucleic acid or protein sequence is a potential drug target for said associated disease.

5. The method of any one of claims 1-4, further comprising creating the database.

6. The method of any one of claims 1-4, wherein said database optionally contains domain analysis.

7. The method of claim 5, wherein creating the database comprises:

receiving a first set of information corresponding to a protein or nucleic acid;

receiving a second set of information identifying a characteristic of said nucleic acid or protein; and

conducting a clustering analysis to determine how said protein or nucleic acid should be clustered based on the first and second sets of information.

8. The method of claim 7, wherein the first set of information comprises sequence information and/or structural information.

9. The method of claim 7, wherein the second set of information comprises domain information.

10. The method of claim 9, wherein the second set of information indicates the presence or absence of one or more domains selected from the group of: Hect, Ring, Ubox, Fbox and PHD.

11. The method of any one of claims 1-4, wherein the nucleic acid or protein sequence is a human E3 sequence.

12. The method of any one of claims 1-4, wherein the potential disease associations are selected from the group consisting of viral diseases, proliferative disorders, and ubiquitin- mediated disorders.

13. The method of any one of claims 1-2, wherein the assay determines a disease characteristic of an associated disease.

14. The method of claim 13, wherein said disease characteristic is assessed by determining whether said protein interacts with an interacting-protein, and wherein said interacting-protein undergoes abnormal degradation in the disease characteristic.

15. The method of claim 13, wherein said disease characteristic is assessed by determining the cellular localization of said protein.

16. The method of claim 13, wherein said disease characteristic is assessed by determining the biological activity of said protein.

17. The method of claim 13, wherein the protein is a E3 protein.

18. The method of claim 17, wherein said disease characteristic is assessed by determining a biological activity of said E3 protein.

19. The method of claim 18, wherein the biological activity is the ligase activity of said E3 protein.

20. The method of claim 18, wherein said disease characteristic is assessed by determining whether said E3 interacts with a substrate that is ubiquitinated in the disease characteristic.

21. The method of claim 12, wherein said associated disease is a retroviral infection.

22. The method of claim 21, wherein said retroviral infection is HIV infection.

23. The method of claim 21, wherein said assay comprises determining the release of virus like particles (VLP) from infected cells.

24. The method of claim 23, wherein decreasing expression or activity of an E3 protein results in a change in the release of said VLPs.

25. The method of claim 24, wherein said E3 protein contains a WW domain.

26. The method of claim 24, wherein said E3 protein contains a HECT domain.

27. The method of claim 24, wherein said E3 protein contains a SH3 domain.

28. The method of claim 24, wherein said E3 protein contains a RING domain.

29. The method of any one of claims 1 or 3, wherein expression of said nucleic acid sequence is decreased using RNAi.

30. The method of any one of claims 1 or 3, wherein expression of said nucleic acid sequence is decreased using an antisense oligonucleotide construct.

31. The method of any one of claims 1 or 3, wherein expression of said nucleic acid sequence is decreased using ribozyme.

32. The method of any one of claims 1 or 3, wherein expression of said nucleic acid sequence is decreased using a DNA enzyme.

33. The method of claim 4, wherein the protein is a E3 protein.

34. The method of claim 33, wherein decreased expression of said E3 is indicative of a disease characteristic.

35. The method of claim 34, wherein said E3 is a tumor suppressor and the disease characteristic is tumorigenesis.

36. The method of claim 35, wherein an increase in expression or activity of said E3 protein results in a gain of function phenotype.

37. The method of claims 36, wherein said E3 is a potential drug target.

38. The method of claim 37, wherein the substrate of said E3 is also a potential drug target.

39. The method of claim 5, wherein access to the database is provided to subscribers.

40. A method for determining whether a test sequence is a potential drug target, comprising:

providing a database comprising nucleic acid or protein sequences, wherein said sequences are annotated with potential disease-associations of said sequences;

comparing said test sequence to the sequences provided in said database and predicting potential disease associations;

validating the predicted disease association by decreasing the activity of said nucleic acid or protein sequences; and

updating the database to include the test sequence and associated annotations.

41. A method of identifying a therapeutic ribozyme for treating viral infections comprising:

(a) providing an E3 drug target for treating viral infections;

(b) administering a ribozyme to decrease expression of said E3 in an infected cell;

(c) determining the release of virus like particles from said infected cell; and

wherein a decrease in the release of virus like particles is indicative that said ribozyme is a therapeutic ribozyme for treating said viral infections.

42. A method of identifying a therapeutic ribozyme for treating cancer comprising:

(a) providing an E3 drug target for treating cancer;

(b) administering a ribozyme to decrease expression of said E3 in a tumor cell;

(c) determining the rate of proliferation of said tumor cell;

wherein a decrease in the rate of proliferation is indicative that said ribozyme is a therapeutic ribozyme for treating said proliferative diseases.

43. A method of identifying a therapeutic RNAi construct for treating viral infections comprising:

(a) providing an E3 drug target for treating viral infections;

(b) administering a RNAi construct to decrease expression of said E3 in an infected cell;

(c) determining the release of virus like particles from said infected cell; and

wherein a decrease in the release of virus like particles is indicative that said RNAi construct is a therapeutic RNAi construct for treating said viral infections.

42. A method of identifying a therapeutic RNAi construct for treating cancer comprising:

(a) providing an E3 drug target for treating cancer;

(b) administering a RNAi construct to decrease expression of said E3 in a tumor cell;

(c) determining the rate of proliferation of said tumor cell;

wherein a decrease in the rate of proliferation is indicative that said RNAi construct is a therapeutic ribozyme for treating said proliferative diseases.

43. A method of screening E3 proteins as potential drug targets, comprising:

selecting an E3 protein;

decreasing expression or activity of said E3 protein in an viral-infected cell;

determining the release of virus like particles upon decreasing the expression or activity of said E3;

wherein a decrease the release of the virus like particles is indicative that said E3 protein is a potential drug target.

44. A method of creating a database of E3 proteins or nucleic acids, comprising:

receiving a first set of information corresponding to a protein or nucleic acid;

receiving a second set of information identifying a characteristic of said nucleic acid or protein sequence; and

conducting a clustering analysis to determine how said protein or nucleic acid sequences should be clustered based on the first and second sets of information.

45. The method of claim 44, wherein the first set of information comprises sequence information and/or structural information.

46. The method of claim 44, wherein the second set of information comprises domain information.

47. The method of claim 44, wherein the second set of information indicates the presence or absence of one or more domains selected from the group of: Hect, Ring, Ubox,, Fbox and PHD.

48. The method of claim 47, wherein all protein and nucleic acid sequences comprising one or more domains selected from the group of: Hect, Ring, Ubox,, Fbox and PHD are included within said database.

49. The method of claim 48, wherein the protein and nucleic acid sequences are further clustered based on the presence or absence of said domains.

50. The method of claim 48, wherein the protein and nucleic acid sequences are further clustered based on certain disease associations.

51. The method of claim 48, wherein the protein and nucleic acid sequences are further clustered based on the presence or absence of interacting motifs.

52. The method of claim 48, wherein the protein and nucleic acid sequences are further clustered based on one or more of the following: homology modeling, secondary structure, threading, transmembrane helices, signal peptide domains, and protein localization signals.

53. The method of claim 48, wherein said E3 sequences are evaluated as potential drug targets.

54. The method of claim 48, wherein said E3 sequences are screened is biological assays for testing disease associations. .

55. A method of creating a database of proteins or nucleic acid sequences containing the RING domain, comprising:

receiving a first set of information corresponding to a protein or nucleic acid;

receiving a second set of information identifying a characteristic of said nucleic acid or protein sequence; and

conducting a clustering analysis to determine how said protein or nucleic acid sequences should be clustered based on the first and second sets of information.

56. The method of claim 55, wherein all protein and nucleic acid sequences comprising one or more Ring domains included within said database.

57. A method of screening an E3 protein as potential drug target, comprising:

selecting an E3 protein;

decreasing expression or activity of said E3 protein in a tumor cell;

determining the rate of proliferation of said tumor cell upon decreasing the expression or activity of said E3;

wherein a decrease in the rate of proliferation is indicative that said E3 protein is a potential drug target.

58. A method of screening an E3 protein as a potential drug targets, comprising:

selecting an E3 protein;

decreasing expression or activity of said E3 protein in a diseased cell;

determining the effect of decreasing the expression or activity of said E3 on a Ubiquitin-mediated disorder;

wherein a change is indicative that said E3 protein is a potential drug target.

59. The method of any one of claims 1 or 3, wherein expression or activity is decreased by using a dominant negative mutant.

60. The method of any one of claims 1 or 3, wherein expression or activity is decreased by using a small molecule.

61. A method of identifying a potential drug target for an associated disease comprising:

(a) conducting a structure-function analysis to determine domain information and/or structural information involved in disease associations;

(b) providing a database comprising nucleic acid or protein sequence;

(c) selecting sequences containing the domains and/or structural information relevant to disease associations;

(d) providing an assay for measuring the disease characteristic;

(e) decreasing the expression or activity of the nucleic acid or protein sequence selected in step (c); and

(f) determining whether the decreased expression or activity results in change in said assay;

wherein a change in the disease characteristic is indicative of a potential drug target.

62. A method of identifying a potential drug target for an associated disease comprising:

(a) conducting a structure-function analysis to determine domain information and/or structural information involved in disease associations;

(b) providing a database comprising nucleic acid or protein sequence;

(c) selecting sequences containing the domains and/or structural information relevant to disease associations;

(d) providing an assay for measuring the disease characteristic;

(e) increasing the expression or activity of the nucleic acid or protein sequence selected in step (c); and

(f) determining whether the increased expression or activity results in change in said assay;

wherein a change in the disease characteristic is indicative of a potential drug target.

63. The method of claim 61 or claim 62, wherein the protein and nucleic acid sequences are E3 sequences.

64. The method of claim 63, wherein the protein and nucleic acid sequences comprise one or more domains selected from the group of: Hect, Ring, Ubox,, Fbox and PHD.

65. The method of claim 64, wherein the disease associations are selected from the group consisting of viral diseases, proliferative disorders, and ubiquitin- mediated disorders.

66. The method of claim 65, wherein the assay determines a disease characteristic of an associated disease.

67. The method of claim 66, wherein said disease characteristic is assessed by determining whether said protein interacts with an interacting-protein, and wherein said interacting-protein undergoes abnormal degradation in the disease characteristic.

68. The method of claim 66, wherein said disease characteristic is assessed by determining the cellular localization of said protein.

69. The method of claim 66, wherein said disease characteristic is assessed by determining whether said E3 interacts with a substrate that is ubiquitinated in the disease characteristic.

70. The method of claim 61, wherein expression of said nucleic acid sequence is decreased using RNAi construct.

71. The method of claim 61, wherein expression of said nucleic acid sequence is decreased using an antisense oligonucleotide construct.

72. The method of claim 61, wherein expression of said nucleic acid sequence is decreased using ribozyme.

73. The method of claim 61, wherein expression of said nucleic acid sequence is decreased using a DNA enzyme.

74. The method of claim 61, wherein activity of said protein is decreased by using a dominant negative mutant.

75. The method of claim 61, wherein expression or activity is decreased by using a small molecule.

76. The method of any one of claims 5, 44, or 55, wherein said database comprises at least 20, 25, 50, 75, 100, 125, 150, 200, 250, or 300 sequences.

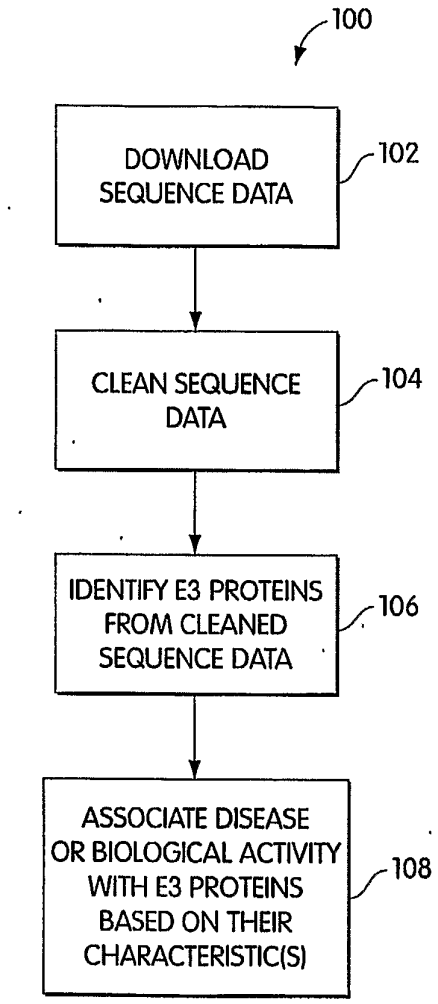

100
DOWNLOAD SEQUENCE DATA
102
CLEAN SEQUENCE DATA
104
IDENTIFY E3 PROTEINS FROM CLEANED SEQUENCE DATA
106
ASSOCIATE DISEASE OR BIOLOGICAL ACTIVITY WITH E3 PROTEINS BASED ON THEIR CHARACTERISTIC(S)
108

Fig. 1

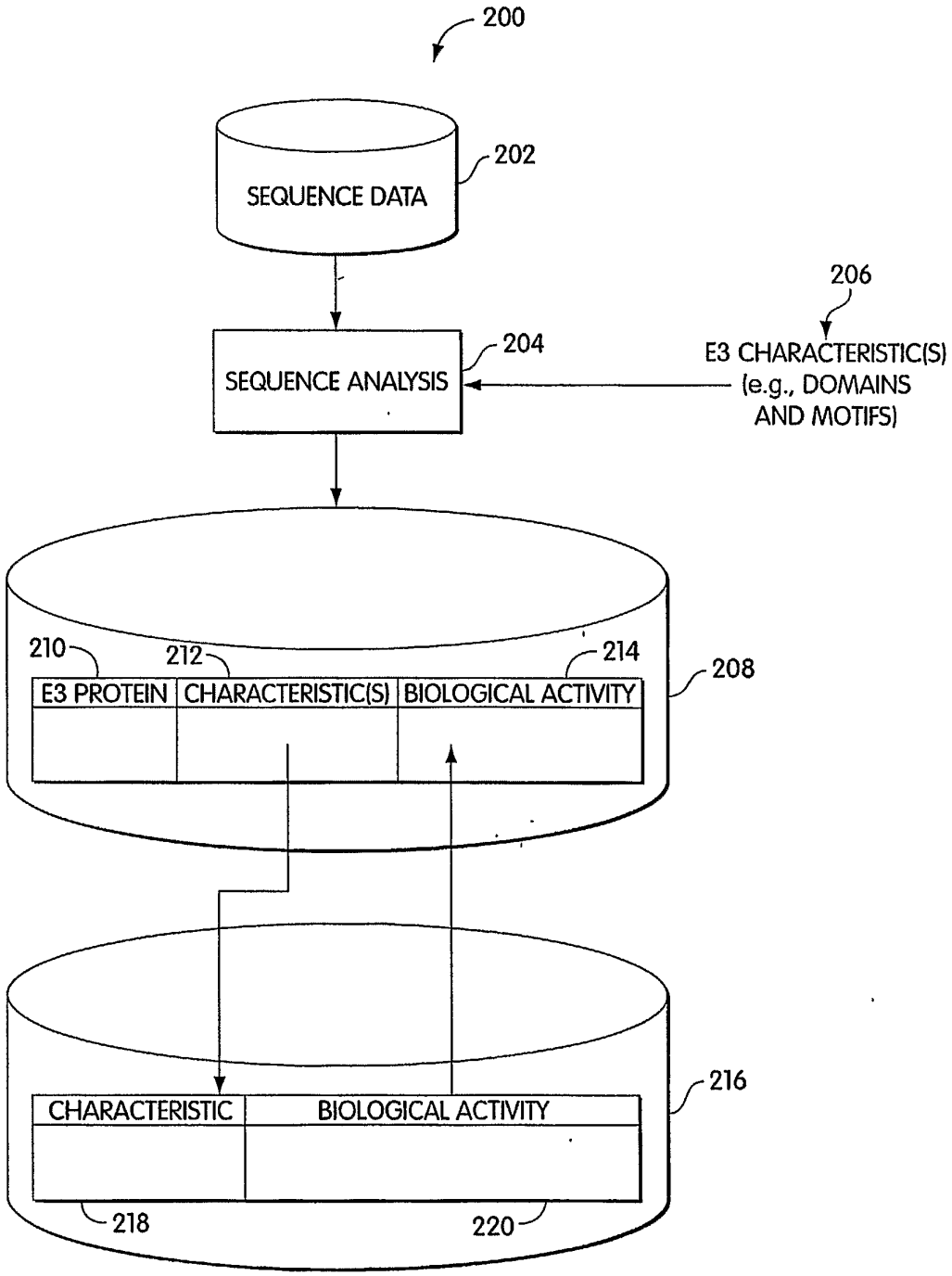

200
SEQUENCE DATA
202
206
E3 CHARACTERISTIC(S)
(e.g., DOMAINS
AND MOTIFS)
SEQUENCE ANALYSIS
204
210
212
214
E3 PROTEIN
CHARACTERISTIC(S)
BIOLOGICAL ACTIVITY
208
CHARACTERISTIC
BIOLOGICAL ACTIVITY
216
218
220

Fig. 2

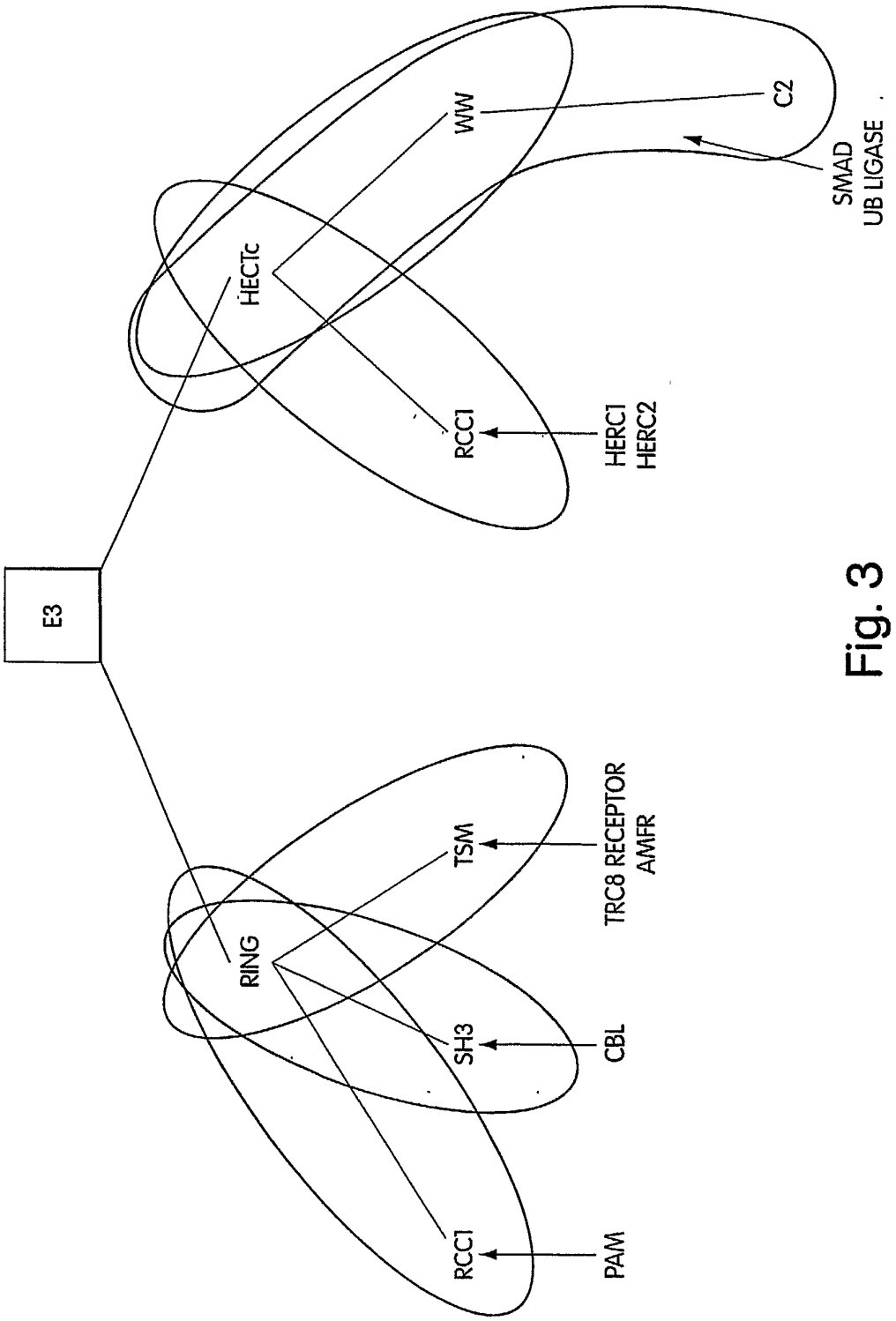

E3
HECTc
WW
C2
SMAD
UB LIGASE
RCC1
HERC1
HERC2
RING
TSM
TRC8 RECEPTOR
AMFR
SH3
CBL
RCC1
PAM

Fig. 3

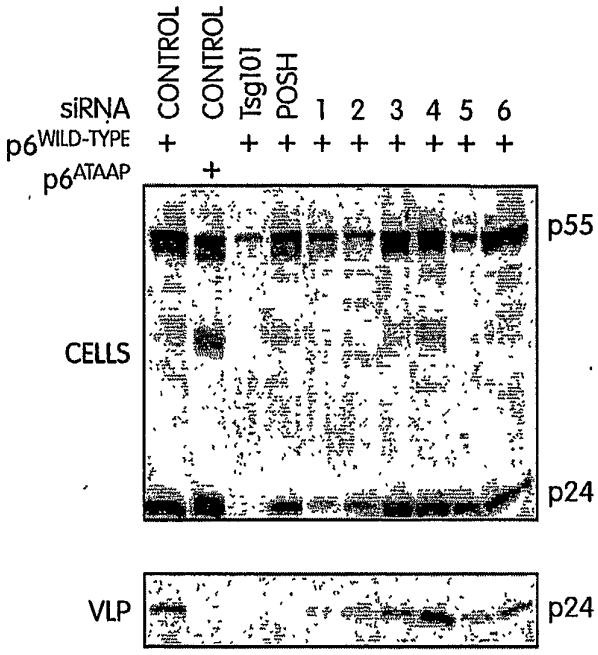

siRNA
CONTROL
CONTROL
Tsg101
POSH
1
2
3
4
5
6
p6WILD-TYPE
+
+
+
+
+
+
+
+
+
p6ATAAP
+
CELLS
p55
p24
VLP
p24

Fig. 4

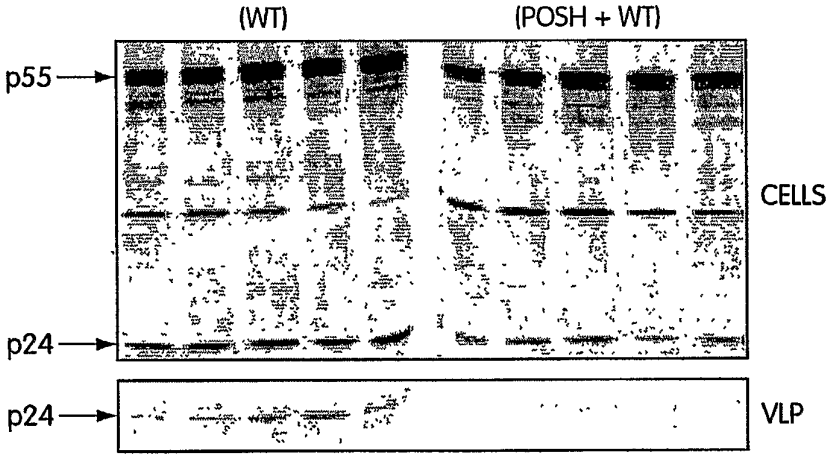


Fig. 5