

MAMMALIAN GENES INVOLVED IN INFECTION

This application claims priority to U.S. provisional application Serial No. 60/622,486, filed October 27, 2004, which is herein incorporated by this reference in its entirety.

ACKNOWLEDGEMENTS

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FIELD OF THE INVENTION

The present invention relates to nucleic acid sequences and cellular proteins encoded by these sequences that are involved in infection or are otherwise associated with the life cycle of one or more pathogens, such as a virus, a bacteria, a fungus or a parasite. The invention also relates to modulators of nucleic acid sequences and cellular proteins encoded by these sequences that are involved in infection or are otherwise associated with the life cycle of a pathogen.

BACKGROUND

Traditional treatments for viral infection include pharmaceuticals aimed at specific virus derived proteins, such as HIV protease or reverse transcriptase, or recombinant (cloned) immune modulators (host derived), such as the interferons. However, the current methods have several limitations and drawbacks which include high rates of viral mutations which render anti-viral pharmaceuticals ineffective. For immune modulators, limited effectiveness, limiting side effects, a lack of specificity all limit the general applicability of these agents. Also the rate of success with current antivirals and immune-modulators has been disappointing.

The current invention focuses on genes that are not essential for cellular survival when disrupted in one or both alleles, but which are required for virus replication. This may occur with a dose effect, in which one allele knock-out may confer the phenotype of virus resistance for the cell. As targets for therapeutic intervention, inhibition of these cellular gene products, including: proteins, parts of proteins (modification enzymes that include, but are not restricted to glycosylation, lipid modifiers [myristylation, etc.]), lipids, transcription

elements and RNA regulatory molecules, may be less likely to have profound toxic side effects and virus mutation is less likely to overcome the 'block' to replicate successfully.

The present invention provides a significant improvement over previous methods of attempted therapeutic intervention against viral infection by addressing the cellular genes required by the virus for growth. Therefore, the present invention also provides an innovative therapeutic approach to intervention in viral infection by providing methods to treat viruses by inhibiting the cellular genes necessary for viral infection. Inhibition of these cellular genes can also be useful in treating infection by other pathogens such as bacteria, fungi and parasites. Because these genes are nonessential to the cell's survival, these treatment methods can be used in a subject without serious detrimental effects to the subject, as has been found with previous methods.

SUMMARY OF THE INVENTION

The present invention provides nucleic acid sequences and cellular proteins encoded by these sequences that are involved in infection or are otherwise associated with the life cycle of one or more pathogens, such as a virus, a bacteria, a fungus or a parasite. The invention also provides methods of identifying modulators of nucleic acid sequences and cellular proteins encoded by these sequences that are involved in infection or are otherwise associated with the life cycle of a pathogen. Also provided are modulators of nucleic acid sequences and cellular proteins encoded by these sequences that are involved in infection or are otherwise associated with the life cycle of a pathogen.

BRIEF DESCRIPTION OF THE FIGURES

Figure 1 shows the characterization of phenotypic properties of cloned RIE-1 cells resistant to reovirus type 1 infection. (A) Cells were stained for reovirus antigen as previously described [3]. Only the PI cells contain reovirus antigen as detected by immunohistochemistry (dark wells). Upper wells are cloned mutant RIE-1 cells from two sets of RIE-1 mutant cell lines selected for reovirus resistance. Lower wells, PI RIE-1 (left), and uninfected wild type RIE-1 (right). (B) Reovirus susceptible L-cell monolayers, maintained in 1 ml of completed medium, were used to detect the presence of virus in a 100 µl lysate obtained of mutant cells (upper two wells), PI RIE-1 cells (lower left) or uninfected parental RIE-1 cells (lower right). Note, that only L- cell monolayers exposed to a lysate from PI RIE-1 cells lysed within one week of exposure (gentian violet stain).

Figure 2 shows RIE-1 mutant cells resist lytic infection by reovirus. The columns contain an unselected RIE-1 cell library, RIE-1 40°C, and representative reovirus resistant mutant cell clones. Serial two-fold dilutions of reovirus were made with the highest titer in the upper row, MOI= 1×10^4 . Resistance to reovirus type 1 infection was observed in the mutant cells 3 to 7 days post-infection. The bottom row of cells, denoted "C", were not infected to serve as controls for cell viability and proliferation. Cells were stained with gentian violet four days post-infection. A clear well indicates cell death following virus infection.

Figure 3 shows a model of the life cycle of reovirus and proposed checkpoints based on function of the cellular genes identified by insertional mutagenesis in the present application. The virus life cycle begins (top, clockwise) with virus binding to cell surface receptor and being endocytosed into early endosomes. These endosomes then associate with annexin-II (*Anax2*) [85] and fuse with annexin-II-associated vesicles containing newly synthesized lysosomal enzymes migrating from the Golgi [86], which further fuse with the lysosome. The vacuolar H^+ -ATPase acidifies the lysosome, allowing acid-dependent proteases to digest the outer coat from the virus particles and activate them [87]. These activated particles then pass through the lysosomal membrane and begin transcription of mRNA. The Golgi protein gm 130 (*Golga2*) is believed to mediate the docking of vesicles as they carry their newly synthesized cargo through the Golgi stack [88, 89]. *N*-acetylglucosaminyl transferase I (*Mgat1*) initiates the glycosylation of cell surface proteins (for example, receptors) and may play a major role, through kinship recognition, in helping maintain the correct assortment of lysosomal enzymes [90-94]. The *Igf2r* shuttles enzymes bound for the lysosome from the Golgi [95] and transfer *cathepsins* to the lysosome. *Igf2* over expression may alter the delivery of *igf2r* bound cargo to the lysosome (Sheng J, Organ EL, Hao C, Wells, KS, Ruley HE, Rubin DH. 2004. Mutations in the IGF-II pathway that confer resistance to lytic reovirus infection. BMC Cell Biology, 5:32 (27 August 2004). Calcyclin and the α -tropomyosins specifically bind each other, and calcyclin is known to bind *Anxa2* [16, 20]. Thus, they could be involved in endosome fusion. *Eif3s10* specifically binds the virus message to begin its preferential translation. The *DnaJal1* protein could facilitate the proper folding of virus proteins with its chaperone function [96]. However, *DnaJal1* protein and *Eif3* could play additional roles in virus trafficking or apoptosis, respectively. Eventually, morphogenesis is complete when crystalline-like arrays of new virions form, cell lysis occurs, and virus is released. Many of the cellular proteins encoded by mutated genes

have direct or indirect roles in trafficking of endosomes or lysosomal fusion and thus could play roles in the early disassembly or delivery of transcriptionally active virions to the appropriate cell location.

DETAILED DESCRIPTION OF THE INVENTION

5 The present invention may be understood more readily by reference to the following detailed description of preferred embodiments of the invention and the Examples included therein.

Before the present compounds, compositions, articles, devices, and/or methods are disclosed and described, it is to be understood that this invention is not limited to specific
10 nucleic acids, specific polypeptides, or to particular methods, as such may, of course, vary. It is also to be understood that the terminology used herein is for the purpose of describing particular embodiments only and is not intended to be limiting.

As used in the specification and the appended claims, the singular forms “a,” “an” and “the” include plural referents unless the context clearly dictates otherwise. The term “or”
15 refers to a single element of stated alternative elements or a combination of two or more elements, unless the context clearly indicates otherwise. As used herein, “comprises” means “includes.” Thus, “comprising A or B,” means “including A, B, or A and B,” without excluding additional elements.

Ranges may be expressed herein as from “about” one particular value, and/or to
20 “about” another particular value. When such a range is expressed, another embodiment includes from the one particular value and/or to the other particular value. Similarly, when values are expressed as approximations, by use of the antecedent “about,” it will be understood that the particular value forms another embodiment. It will be further understood that the endpoints of each of the ranges are significant both in relation to the other endpoint,
25 and independently of the other endpoint.

“Optional” or “optionally” means that the subsequently described event or circumstance may or may not occur, and that the description includes instances where said event or circumstance occurs and instances where it does not. For example, the phrase
30 “optionally obtained prior to treatment” means obtained before treatment, after treatment, or not at all.

As used throughout, by “subject” is meant an individual. Preferably, the subject is a mammal such as a primate, and, more preferably, a human. The term “subject” includes domesticated animals, such as cats, dogs, etc., livestock (for example, cattle, horses, pigs,

sheep, goats, etc.), laboratory animals (for example, mouse, rabbit, rat, gerbil, guinea pig, etc.) and avian species (for example, chickens, turkeys, ducks, pheasants, pigeons, doves, parrots, cockatoos, geese, etc.). The subjects of the present invention can also include, but are not limited to fish, amphibians and reptiles.

5 The present method provides several cellular genes that are necessary for viral growth in the cell but are not essential for the cell to survive. As used herein, a cellular gene "nonessential for cellular survival" means a gene for which disruption of one or both alleles results in a cell viable for at least a period of time which allows viral replication to be decreased or inhibited in a cell. Such a decrease can be utilized for preventative or
10 therapeutic uses or used in research. A gene "necessary for viral growth" means the gene product of this gene, either protein or RNA, secreted or not, is necessary, either directly or indirectly in some way for the virus to grow, and therefore, in the absence of that gene product (*i.e.*, a functionally available gene product), at least some of the cells containing the virus die. As utilized throughout, "gene product" is the RNA or protein resulting from the
15 expression of a gene.

 These cellular genes or host nucleic acid sequences involved in viral infection were identified using gene trap methods. These gene trap methods are set forth in the Examples as well as in U.S. Patent No. 6,448,000 and 6,777,177. U.S. Patent Nos. 6,448,000 and 6,777,177 are both incorporated herein in their entireties by this reference. For example, the
20 host nucleic acid sequences set forth herein can be identified by a method of identifying a cellular gene necessary for viral growth in a cell and nonessential for cellular survival, comprising: (a) transferring into a cell culture a vector encoding a selective marker gene lacking a functional promoter, (b) selecting cells expressing the marker gene, (c) infecting the cell culture with the virus, and (d) isolating from the surviving cells a cellular gene
25 within which the marker gene is inserted, thereby identifying a gene necessary for viral growth in a cell and nonessential for cellular survival. The host nucleic acid sequences can also be identified by a method of identifying a cellular gene necessary for viral growth in a cell and nonessential for cellular survival, comprising (a) transferring into a cell culture growing in serum-containing medium a vector encoding a selective marker gene lacking a
30 functional promoter, (b) selecting cells expressing the marker gene, (c) removing serum from the culture medium, (d) infecting the cell culture with the virus, and (e) isolating from the surviving cells a cellular gene within which the marker gene is inserted, thereby identifying a gene necessary for viral growth in a cell and nonessential for cellular survival.

 The identification of these host sequences and their encoded proteins permits the
35 identification of sequences that can be targeted for modulation (for example, decreasing gene

expression and/or activity of the gene product or increasing gene expression and/or activity of the gene product) and/or therapeutic intervention.

Table 1 sets forth host nucleic acid sequences that are involved in viral infection or otherwise associated with the life cycle of a virus. For example, these nucleic acids and their encoded proteins can be involved in all phases of viral life cycles including, but not limited to, viral attachment to cellular receptors, viral infection, viral entry, internalization, disassembly of the virus, viral replication, genomic integration of viral sequences, translation of mRNA, assembly of viral particles, cell lysis and egress of virus from the cells.

As used herein, a gene is a nucleic acid sequence that encodes a polypeptide under the control of a regulatory sequence, such as a promoter or operator. The coding sequence of the gene is the portion transcribed and translated into a polypeptide (*in vivo*, *in vitro* or *in situ*) when placed under the control of an appropriate regulatory sequence. The boundaries of the coding sequence can be determined by a start codon at the 5' (amino) terminus and a stop codon at the 3' (carboxyl) terminus. If the coding sequence is intended to be expressed in a eukaryotic cell, a polyadenylation signal and transcription termination sequence can be included 3' to the coding sequence.

Transcriptional and translational control sequences include, but are not limited to, DNA regulatory sequences such as promoters, enhancers, and terminators that provide for the expression of the coding sequence, such as expression in a host cell. A polyadenylation signal is an exemplary eukaryotic control sequence. A promoter is a regulatory region capable of binding RNA polymerase and initiating transcription of a downstream (3' direction) coding sequence. Additionally, a gene can include a signal sequence at the beginning of the coding sequence of a protein to be secreted or expressed on the surface of a cell. This sequence can encode a signal peptide, N-terminal to the mature polypeptide, which directs the host cell to translocate the polypeptide.

Table 1 (column 2) also provides the protein encoded by the genes listed in Table 1. In several instances, the gene trap vector utilized to trap the genes disrupted two genes, one of which is due to location of the vector as it resides in a gene transcribed off the negative strand. An example of such an occurrence is the disruption of the gene encoding aprataxin and the gene encoding DnaJ (Hsp40) homolog, subfamily A, member 1 by the same vector.

Table 1 also provides the chromosomal location of the gene in the rat and human genome (columns 3 and column 4, respectively). Thus, the present invention identifies the genomic loci of genes associated with viral infection. By identifying the gene and its location

in the genome, the invention provides both the gene and its product(s) as targets for therapies such as antiviral, antibacterial, antifungal and antiparasitic therapies, to name a few.

Also provided in Table 1 are the GenBank Accession Nos. for the rat mRNA sequences (column 5), the GenBank Accession Nos. for the human mRNA sequences (column 6) and the GenBank Accession Nos. for the human protein sequences (column 7). The nucleic acid sequences and protein sequences provided under the GenBank Accession Nos. mentioned herein are hereby incorporated in their entireties by this reference. One of skill in the art would know that the nucleotide sequences provided under the GenBank Accession Nos. set forth herein can be readily obtained from the National Center for Biotechnology Information at the National Library of Medicine (<http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=nucleotide>). Similarly, the protein sequences set forth herein can be readily obtained from the National Center for Biotechnology Information at the National Library of Medicine (<http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=protein>). The nucleic acid sequences and protein sequences provided under the GenBank Accession Nos. mentioned herein are hereby incorporated in their entireties by this reference.

Table 1 also provides the GenBank Accession Nos. for the partial sequences of the rat genes obtained upon the insertion of the gene trap vector (column 9). Briefly, these genes were isolated by generating gene trap libraries by infecting cells with a retrovirus gene trap vector and selecting for cells in which a gene trap event occurred (*i.e.*, in which the vector had inserted such that the promoterless marker gene was inserted such that a cellular promoter promotes transcription of the marker gene, *i.e.*, inserted into a functioning gene). Genes into which the retrovirus gene trap vector inserted were then isolated from the colonies using probes specific for the retrovirus gene trap vector. Thus nucleic acids isolated by this method are isolated portions of genes. These portions were then utilized to identify the complete sequences of each gene via sequence comparisons and other bioinformatics methods.

Further provided are the Entrez Gene numbers for the rat gene and human gene (columns 10 and 11, respectively). The information provided under the Entrez Gene numbers listed in Table 1 is also hereby incorporated entirely by this reference. One of skill in the art can readily obtain this information from the National Center for Biotechnology Information at the National Library of Medicine (<http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=gene>). By accessing Entrez Gene, one of skill in the art can readily obtain additional information about every gene listed in Table 1,

such as the genomic location of the gene, a summary of the properties of the protein encoded by the gene, information on homologs of the gene as well as numerous reference sequences, such as the genomic, mRNA and protein sequences for each gene. Thus, in addition to the sequences set forth under the GenBank Accession Nos. in Table 1, one of skill in the art can readily obtain additional sequences, such as genomic, mRNA and protein sequences by accessing additional information available under the Entrez Gene number provided for each gene. Thus, all of the information readily obtained from the Entrez Gene Nos. set forth herein is also hereby incorporated by reference in its entirety.

Table 2 provides classification of numerous genes set forth in Table 1 according to their cellular roles. Several examples of regulatory sequences (e.g., transcription factors) are provided in Table 2 (for example, Brd2, Brd3, Ctf, E2f2, Gtf2e1, Hnrpl, Hoxc13, Hp1-bp74, Id3, Znf207 and Zfp7). Therefore, these transcription factors control multi-gene pathways. In some cases, disruption of the transcription factor has a direct impact on viral growth. In other cases disruption of the transcription factor affects viral growth by affecting transcription or translation of the gene or genes that are under its control. Therefore, the genes that are under the control of the transcription factors set forth in Table 1 and Table 2 are also provided by the present invention as targets for therapy, such as antiviral, antibacterial, antiparasitic and antifungal therapy. Table 2 also provides examples of genes involved in other pathways such as vesicular trafficking, ubiquitination, apoptosis, metabolism etc. Thus, other genes in these pathways, either upstream or downstream of the genes set forth for these pathways in Table 2 are also provided herein as targets for therapeutic intervention (therapy). For example, a gene that produces a gene product that interacts with Ube1c either upstream or downstream in the ubiquitination pathway is considered a target for therapy against intracellular pathogens. For example, this can be a transcription factor that regulates expression of Ube1c or another protein that binds to Ube1c. These examples are merely exemplary as this applies to all of the genes set forth herein and the cellular pathways that they are involved in.

When referring to a gene(s) in Table 1, this includes any gene, nucleic acid, cDNA or RNA from any organism that can function as the gene or nucleic acid listed in Table 1.

When referring to a protein(s) listed in Table 1 this includes any protein or fragment thereof from any organism that can function as the protein listed in Table 1. For example, the term ANXA1 (annexin 1) includes any ANXA1 gene, nucleic acid, cDNA or RNA, from any organism that can function as an ANXA1 gene or ANXA1 nucleic acid. The term ANXA1 also includes any protein from any organism that can function as an ANXA1 protein.

As used herein, the term "nucleic acid" refers to single or multiple stranded molecules which may be DNA or RNA, or any combination thereof, including modifications to those nucleic acids. The nucleic acid may represent a coding strand or its complement, or any combination thereof. Nucleic acids may be identical in sequence to the sequences which are naturally occurring for any of the moieties discussed herein or may include alternative codons which encode the same amino acid as that which is found in the naturally occurring sequence. These nucleic acids can also be modified from their typical structure. Such modifications include, but are not limited to, methylated nucleic acids, the substitution of a non-bridging oxygen on the phosphate residue with either a sulfur (yielding phosphorothioate deoxynucleotides), selenium (yielding phosphorselenoate deoxynucleotides), or methyl groups (yielding methylphosphonate deoxynucleotides), a reduction in the AT content of AT rich regions, or replacement of non-preferred codon usage of the expression system to preferred codon usage of the expression system. The nucleic acid can be directly cloned into an appropriate vector, or if desired, can be modified to facilitate the subsequent cloning steps. Such modification steps are routine, an example of which is the addition of oligonucleotide linkers which contain restriction sites to the termini of the nucleic acid. General methods are set forth in in Sambrook *et al.* (2001) *Molecular Cloning - A Laboratory Manual* (3rd ed.) Vol. 1-3, Cold Spring Harbor Laboratory, Cold Spring Harbor Press, NY, (Sambrook).

Once the nucleic acid sequence is obtained, the sequence encoding the specific amino acids can be modified or changed at any particular amino acid position by techniques well known in the art. For example, PCR primers can be designed which span the amino acid position or positions and which can substitute any amino acid for another amino acid. Alternatively, one skilled in the art can introduce specific mutations at any point in a particular nucleic acid sequence through techniques for point mutagenesis. General methods are set forth in Smith, M. "In vitro mutagenesis" *Ann. Rev. Gen.*, 19:423-462 (1985) and Zoller, M.J. "New molecular biology methods for protein engineering" *Curr. Opin. Struct. Biol.*, 1:605-610 (1991), which are incorporated herein in their entirety for the methods. These techniques can be used to alter the coding sequence without altering the amino acid sequence that is encoded.

The sequences contemplated herein include full-length wild-type (or native) sequences, as well as allelic variants, variants, fragments, homologs or fusion sequences that retain the ability to function as the cellular nucleic acid or protein involved in viral infection. In certain examples, a protein or nucleic acid sequence has at least 70% sequence identity, for

example at least 75%, 80%, 85%, 90%, 95%, or 98% sequence identity to a native sequence set forth in Table 1. In other examples, a nucleic acid sequence involved in viral infection has a sequence that hybridizes to a sequence set forth in Table 1 and retains the activity of the sequence set forth in Table 1. For example, a nucleic acid that hybridizes to an ANXA1
 5 nucleic acid sequence set forth in Table 1 (for example the nucleic acid sequence set forth under GenBank Accession No. NM_000700) and encodes a protein that retains ANXA1 activity is contemplated by the present invention. Such sequences include the genomic sequence for the genes set forth in Table 1. The examples set forth above for ANXA1 are merely illustrative and should not be limited to ANXA1 as these examples would apply to
 10 every nucleic acid and protein listed in Table 1.

Unless otherwise specified, any reference to a nucleic acid molecule includes the reverse complement of the nucleic acid. Except where single-strandedness is required by the text herein (for example, a ssRNA molecule), any nucleic acid written to depict only a single strand encompasses both strands of a corresponding double-stranded nucleic acid. For
 15 example, depiction of a plus-strand of a dsDNA also encompasses the complementary minus-strand of that dsDNA. Additionally, reference to the nucleic acid molecule that encodes a specific protein, or a fragment thereof, encompasses both the sense strand and its reverse complement. Fragments of the nucleic acids set forth in Table 1 and throughout the specification are also contemplated. These fragments can be utilized as primers and probes to
 20 amplify or detect any of the nucleic acids or genes set forth in Table 1.

Hybridization conditions resulting in particular degrees of stringency will vary depending upon the nature of the hybridization method and the composition and length of the hybridizing nucleic acid sequences. Generally, the temperature of hybridization and the ionic strength (such as the Na⁺ concentration) of the hybridization buffer will determine the
 25 stringency of hybridization. Calculations regarding hybridization conditions for attaining particular degrees of stringency are discussed in Sambrook *et al.*, (1989) Molecular Cloning, second edition, Cold Spring Harbor Laboratory, Plainview, NY (chapters 9 and 11). The following is an exemplary set of hybridization conditions and is not limiting:

30 Very High Stringency (detects sequences that share 90% identity)

Hybridization:	5x SSC at 65°C for 16 hours
Wash twice:	2x SSC at room temperature (RT) for 15 minutes each
Wash twice:	0.5x SSC at 65°C for 20 minutes each

High Stringency (detects sequences that share 80% identity or greater)

Hybridization: 5x-6x SSC at 65°C-70°C for 16-20 hours
 Wash twice: 2x SSC at RT for 5-20 minutes each
 5 Wash twice: 1x SSC at 55°C-70°C for 30 minutes each

Low Stringency (detects sequences that share greater than 50% identity)

Hybridization: 6x SSC at RT to 55°C for 16-20 hours
 Wash at least twice: 2x-3x SSC at RT to 55°C for 20-30 minutes each.

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Also provided is a vector, comprising a nucleic acid of the present invention. The vector can direct the *in vivo* or *in vitro* synthesis of any of the proteins or polypeptides described herein. The vector is contemplated to have the necessary functional elements that direct and regulate transcription of the inserted nucleic acid. These functional elements include, but are not limited to, a promoter, regions upstream or downstream of the promoter, such as enhancers that may regulate the transcriptional activity of the promoter, an origin of replication, appropriate restriction sites to facilitate cloning of inserts adjacent to the promoter, antibiotic resistance genes or other markers which can serve to select for cells containing the vector or the vector containing the insert, RNA splice junctions, a transcription termination region, or any other region which may serve to facilitate the expression of the inserted gene or hybrid gene. (See generally, *Sambrook et al.*). The vector, for example, can be a plasmid. The vectors can contain genes conferring hygromycin resistance, ampicillin resistance, gentamicin resistance, neomycin resistance or other genes or phenotypes suitable for use as selectable markers, or methotrexate resistance for gene amplification.

25 There are numerous other *E. coli* (*Escherichia coli*) expression vectors, known to one of ordinary skill in the art, which are useful for the expression of the nucleic acid insert. Other microbial hosts suitable for use include bacilli, such as *Bacillus subtilis*, and other enterobacteriaceae, such as *Salmonella*, *Serratia*, and various *Pseudomonas* species. In these prokaryotic hosts one can also make expression vectors, which will typically contain expression control sequences compatible with the host cell (e.g., an origin of replication). In addition, any number of a variety of well-known promoters will be present, such as the lactose promoter system, a tryptophan (Trp) promoter system, a beta-lactamase promoter system, or a promoter system from phage lambda. The promoters will typically control

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expression, optionally with an operator sequence, and have ribosome binding site sequences for example, for initiating and completing transcription and translation. If necessary, an amino terminal methionine can be provided by insertion of a Met codon 5' and in-frame with the downstream nucleic acid insert. Also, the carboxy-terminal extension of the nucleic acid insert can be removed using standard oligonucleotide mutagenesis procedures. Also, nucleic acid modifications can be made to promote amino terminal homogeneity.

Additionally, yeast expression can be used. The invention provides a nucleic acid encoding a polypeptide of the present invention, wherein the nucleic acid can be expressed by a yeast cell. More specifically, the nucleic acid can be expressed by *Pichia pastoris* or *S. cerevisiae*. There are several advantages to yeast expression systems, which include, for example, *Saccharomyces cerevisiae* and *Pichia pastoris*. First, evidence exists that proteins produced in a yeast secretion systems exhibit correct disulfide pairing. Second, efficient large scale production can be carried out using yeast expression systems. The *Saccharomyces cerevisiae* pre-pro-alpha mating factor leader region (encoded by the *MF α -1* gene) can be used to direct protein secretion from yeast (Brake, et al.). The leader region of pre-pro-alpha mating factor contains a signal peptide and a pro-segment which includes a recognition sequence for a yeast protease encoded by the *KEX2* gene: this enzyme cleaves the precursor protein on the carboxyl side of a Lys-Arg dipeptide cleavage signal sequence. The nucleic acid coding sequence can be fused in-frame to the pre-pro-alpha mating factor leader region. This construct can be put under the control of a strong transcription promoter, such as the alcohol dehydrogenase I promoter, alcohol oxidase I promoter, a glycolytic promoter, or a promoter for the galactose utilization pathway. The nucleic acid coding sequence is followed by a translation termination codon which is followed by transcription termination signals. Alternatively, the nucleic acid coding sequences can be fused to a second protein coding sequence, such as Sj26 or beta-galactosidase, used to facilitate purification of the fusion protein by affinity chromatography. The insertion of protease cleavage sites to separate the components of the fusion protein is applicable to constructs used for expression in yeast. Efficient post translational glycosylation and expression of recombinant proteins can also be achieved in Baculovirus systems.

Mammalian cells permit the expression of proteins in an environment that favors important post-translational modifications such as folding and cysteine pairing, addition of complex carbohydrate structures, and secretion of active protein. Vectors useful for the expression of active proteins in mammalian cells are characterized by insertion of the protein coding sequence between a strong viral promoter and a polyadenylation signal. The vectors

can contain genes conferring hygromycin resistance, gentamicin or G418 resistance, or other genes or phenotypes suitable for use as selectable markers, or methotrexate resistance for gene amplification. The chimeric protein coding sequence can be introduced into a Chinese hamster ovary (CHO) cell line using a methotrexate resistance-encoding vector, or other cell lines using suitable selection markers. Presence of the vector DNA in transformed cells can be confirmed by Southern blot analysis. Production of RNA corresponding to the insert coding sequence can be confirmed by Northern blot analysis. A number of other suitable host cell lines capable of secreting intact human proteins have been developed in the art, and include the CHO cell lines, HeLa cells, myeloma cell lines, Jurkat cells, etc. Expression vectors for these cells can include expression control sequences, such as an origin of replication, a promoter, an enhancer, and necessary information processing sites, such as ribosome binding sites, RNA splice sites, polyadenylation sites, and transcriptional terminator sequences. Preferred expression control sequences are promoters derived from immunoglobulin genes, SV40, Adenovirus, Bovine Papilloma Virus, etc.

The expression vectors described herein can also include nucleic acids of the present invention under the control of an inducible promoter such as the tetracycline inducible promoter or a glucocorticoid inducible promoter. The nucleic acids of the present invention can also be under the control of a tissue-specific promoter to promote expression of the nucleic acid in specific cells, tissues or organs. Any regulatable promoter, such as a metallothionein promoter, a heat-shock promoter, and other regulatable promoters, of which many examples are well known in the art are also contemplated. Furthermore, a Cre-loxP inducible system can also be used, as well as a FLP recombinase inducible promoter system, both of which are known in the art.

Alternative vectors for the expression of genes or nucleic acids in mammalian cells, those similar to those developed for the expression of human gamma-interferon, tissue plasminogen activator, clotting Factor VIII, hepatitis B virus surface antigen, protease Nexin1, and eosinophil major basic protein, can be employed. Further, the vector can include CMV promoter sequences and a polyadenylation signal available for expression of inserted nucleic acids in mammalian cells (such as COS-7).

Insect cells also permit the expression of mammalian proteins. Recombinant proteins produced in insect cells with baculovirus vectors undergo post-translational modifications similar to that of wild-type proteins. Briefly, baculovirus vectors useful for the expression of active proteins in insect cells are characterized by insertion of the protein coding sequence downstream of the *Autographica californica* nuclear polyhedrosis virus (AcNPV) promoter

for the gene encoding polyhedrin, the major occlusion protein. Cultured insect cells such as *Spodoptera frugiperda* cell lines are transfected with a mixture of viral and plasmid DNAs and the viral progeny are plated. Deletion or insertional inactivation of the polyhedrin gene results in the production of occlusion negative viruses which form plaques that are

5 distinctively different from those of wild-type occlusion positive viruses. These distinctive plaque morphologies allow visual screening for recombinant viruses in which the AcNPV gene has been replaced with a hybrid gene of choice.

The invention also provides for the vectors containing the contemplated nucleic acids in a host suitable for expressing the nucleic acids. The host cell can be a prokaryotic cell, including, for example, a bacterial cell. More particularly, the bacterial cell can be an *E. coli* cell. Alternatively, the cell can be a eukaryotic cell, including, for example, a Chinese hamster ovary (CHO) cell, a COS-7 cell, a HELA cell, an avian cell, a myeloma cell, a *Pichia* cell, or an insect cell. The coding sequence for any of the polypeptides described herein can be introduced into a Chinese hamster ovary (CHO) cell line, for example, using a

15 methotrexate resistance-encoding vector, or other cell lines using suitable selection markers. Presence of the vector DNA in transformed cells can be confirmed by Southern blot analysis. Production of RNA corresponding to the insert coding sequence can be confirmed by Northern blot analysis. A number of other suitable host cell lines have been developed and include myeloma cell lines, fibroblast cell lines, and a variety of tumor cell lines such as

20 melanoma cell lines. Expression vectors for these cells can include expression control sequences, such as an origin of replication, a promoter, an enhancer, and necessary information processing sites, such as ribosome binding sites, RNA splice sites, polyadenylation sites, and transcriptional terminator sequences. Preferred expression control sequences are promoters derived from immunoglobulin genes, SV40, Adenovirus, Bovine

25 Papilloma Virus, etc. The vectors containing the nucleic acid segments of interest can be transferred into the host cell by well-known methods, which vary depending on the type of cellular host. For example, calcium chloride transformation is commonly utilized for prokaryotic cells, whereas calcium phosphate, DEAE dextran, Lipofectamine, or lipofectin mediated transfection, electroporation or any method now known or identified in the future

30 can be used for other eukaryotic cellular hosts.

Polypeptides

The present invention provides isolated polypeptide comprising the polypeptide or protein sequences set forth under GenBank Accession Nos. in Table 1. The present invention

also provides fragments of these polypeptides, for example, fragments of an annexin A1 protein, fragments of an annexin A2 protein, fragments of an annexin A3 protein, etc. These fragments can be of sufficient length to serve as antigenic peptides for the generation of antibodies. The present invention also contemplates functional fragments of the proteins set forth in Table 1 that possess at least one activity of the protein, for example, necessary for viral infection, but not necessary for survival of the cell. It will be known to one of skill in the art that the polypeptides set forth in Table 1 possess other properties. For example, ABCA4 is a member of the superfamily of ATP-binding cassette transporters. Therefore one of skill in the art could assess a ABCA4 fragment for its ability to function as an ATP-binding cassette transporter. If there is ATP-binding cassette transporter activity, one of skill in the art would know that the ABCA4 is a functional fragment of ABCA4. Fragments and variants of the polypeptides listed in Table 1 can include one or more conservative amino acid residues as compared to the amino acid sequence listed under their respective GenBank Accession Nos.

By "isolated polypeptide" or "purified polypeptide" is meant a polypeptide that is substantially free from the materials with which the polypeptide is normally associated in nature or in culture. The polypeptides of the invention can be obtained, for example, by extraction from a natural source if available (for example, a mammalian cell), by expression of a recombinant nucleic acid encoding the polypeptide (for example, in a cell or in a cell-free translation system), or by chemically synthesizing the polypeptide. In addition, polypeptide may be obtained by cleaving full length polypeptides. When the polypeptide is a fragment of a larger naturally occurring polypeptide, the isolated polypeptide is shorter than and excludes the full-length, naturally-occurring polypeptide of which it is a fragment.

The polypeptides of the invention can be prepared using any of a number of chemical polypeptide synthesis techniques well known to those of ordinary skill in the art including solution methods and solid phase methods. One method of producing the polypeptides of the present invention is to link two or more peptides or polypeptides together by protein chemistry techniques. For example, peptides or polypeptides can be chemically synthesized using currently available laboratory equipment using either Fmoc (9-fluorenylmethyloxycarbonyl) or Boc (tert -butyloxycarbonyl) chemistry. (Applied Biosystems, Inc., Foster City, CA). One skilled in the art can readily appreciate that a peptide or polypeptide corresponding to the antibody of the present invention, for example, can be synthesized by standard chemical reactions. For example, a peptide or polypeptide can be synthesized and not cleaved from its synthesis resin, whereas the other fragment of an

antibody can be synthesized and subsequently cleaved from the resin, thereby exposing a terminal group which is functionally blocked on the other fragment. By peptide condensation reactions, these two fragments can be covalently joined via a peptide bond at their carboxyl and amino termini, respectively, to form an antibody, or fragment thereof. (Grant GA (1992) Synthetic Peptides: A User Guide. W.H. Freeman and Co., N.Y. (1992); Bodansky M and Trost B., Ed. (1993) Principles of Peptide Synthesis. Springer-Verlag Inc., NY. Alternatively, the peptide or polypeptide is independently synthesized in vivo as described above. Once isolated, these independent peptides or polypeptides may be linked to form an antibody or fragment thereof via similar peptide condensation reactions.

For example, enzymatic ligation of cloned or synthetic peptide segments allow relatively short peptide fragments to be joined to produce larger peptide fragments, polypeptides or whole protein domains (Abrahmsen L et al., *Biochemistry*, 30:4151 (1991)). Alternatively, native chemical ligation of synthetic peptides can be utilized to synthetically construct large peptides or polypeptides from shorter peptide fragments. This method consists of a two-step chemical reaction (Dawson et al. *Synthesis of Proteins by Native Chemical Ligation*. *Science*, 266:776-779 (1994)). The first step is the chemoselective reaction of an unprotected synthetic peptide-alpha-thioester with another unprotected peptide segment containing an amino-terminal Cys residue to give a thioester-linked intermediate as the initial covalent product. Without a change in the reaction conditions, this intermediate undergoes spontaneous, rapid intramolecular reaction to form a native peptide bond at the ligation site. Application of this native chemical ligation method to the total synthesis of a protein molecule is illustrated by the preparation of human interleukin 8 (IL-8) (Baggiolini M et al. (1992) *FEBS Lett.* 307:97-101; Clark-Lewis I et al., *J.Biol.Chem.*, 269:16075 (1994); Clark-Lewis I et al., *Biochemistry*, 30:3128 (1991); Rajarathnam K et al., *Biochemistry* 33:6623-30 (1994)).

Alternatively, unprotected peptide segments are chemically linked where the bond formed between the peptide segments as a result of the chemical ligation is an unnatural (non-peptide) bond (Schnolzer, M et al. *Science*, 256:221 (1992)). This technique has been used to synthesize analogs of protein domains as well as large amounts of relatively pure proteins with full biological activity (deLisle Milton RC et al., *Techniques in Protein Chemistry IV*. Academic Press, New York, pp. 257-267 (1992)).

The polypeptides of the invention can also be prepared by other means including, for example, recombinant techniques. Examples of appropriate cloning and sequencing techniques, and instructions sufficient to direct persons of skill through many cloning

exercises are found in Sambrook *et al.* (2001) *Molecular Cloning - A Laboratory Manual* (3rd ed.) Vol. 1-3, Cold Spring Harbor Laboratory, Cold Spring Harbor Press, NY, (Sambrook).

Also provided by the present invention is a polypeptide comprising an amino acid sequence at least about 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98% or 99% identical to the polypeptide sequences set forth under GenBank Accession Nos. in Table 1 or fragments of these polypeptide sequences.

It is understood that as discussed herein the use of the terms "homology" and "identity" mean the same thing as similarity. Thus, for example, if the use of the word homology is used to refer to two non-natural sequences, it is understood that this is not necessarily indicating an evolutionary relationship between these two sequences, but rather is looking at the similarity or relatedness between their nucleic acid sequences. Many of the methods for determining homology between two evolutionarily related molecules are routinely applied to any two or more nucleic acids or proteins for the purpose of measuring sequence similarity regardless of whether they are evolutionarily related.

In general, it is understood that one way to define any known variants and derivatives or those that might arise, of the disclosed nucleic acids and polypeptides herein, is through defining the variants and derivatives in terms of homology to specific known sequences. In general, variants of nucleic acids and polypeptides herein disclosed typically have at least, about 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99 percent homology to the stated sequence or the native sequence. Those of skill in the art readily understand how to determine the homology of two polypeptides or nucleic acids. For example, the homology can be calculated after aligning the two sequences so that the homology is at its highest level.

Another way of calculating homology can be performed by published algorithms. Optimal alignment of sequences for comparison may be conducted by the local homology algorithm of Smith and Waterman *Adv. Appl. Math.* 2: 482 (1981), by the homology alignment algorithm of Needleman and Wunsch, *J. Mol. Biol.* 48: 443 (1970), by the search for similarity method of Pearson and Lipman, *Proc. Natl. Acad. Sci. U.S.A.* 85: 2444 (1988), by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Dr., Madison, WI; the BLAST algorithm of Tatusova and Madden *FEMS Microbiol. Lett.* 174: 247-250 (1999) available from the National Center for Biotechnology Information (<http://www.ncbi.nlm.nih.gov/blast/bl2seq/bl2.html>)), or by inspection.

The same types of homology can be obtained for nucleic acids by for example the algorithms disclosed in Zuker, M. *Science* 244:48-52, 1989, Jaeger et al. *Proc. Natl. Acad. Sci. USA* 86:7706-7710, 1989, Jaeger et al. *Methods Enzymol.* 183:281-306, 1989 which are herein incorporated by reference for at least material related to nucleic acid alignment. It is understood that any of the methods typically can be used and that in certain instances the results of these various methods may differ, but the skilled artisan understands if identity is found with at least one of these methods, the sequences would be said to have the stated identity.

For example, as used herein, a sequence recited as having a particular percent homology to another sequence refers to sequences that have the recited homology as calculated by any one or more of the calculation methods described above. For example, a first sequence has 80 percent homology, as defined herein, to a second sequence if the first sequence is calculated to have 80 percent homology to the second sequence using the Zuker calculation method even if the first sequence does not have 80 percent homology to the second sequence as calculated by any of the other calculation methods. As another example, a first sequence has 80 percent homology, as defined herein, to a second sequence if the first sequence is calculated to have 80 percent homology to the second sequence using both the Zuker calculation method and the Pearson and Lipman calculation method even if the first sequence does not have 80 percent homology to the second sequence as calculated by the Smith and Waterman calculation method, the Needleman and Wunsch calculation method, the Jaeger calculation methods, or any of the other calculation methods. As yet another example, a first sequence has 80 percent homology, as defined herein, to a second sequence if the first sequence is calculated to have 80 percent homology to the second sequence using each of calculation methods (although, in practice, the different calculation methods will often result in different calculated homology percentages).

Also provided by the present invention are polypeptides set forth under GenBank Accession Nos. in Table 1, with one or more conservative amino acid substitutions. These conservative substitutions are such that a naturally occurring amino acid is replaced by one having similar properties. Such conservative substitutions do not alter the function of the polypeptide. For example, conservative substitutions can be made according to the following table:

TABLE 1: Amino Acid Substitutions

Original Residue	Exemplary Substitutions
Arg	Lys
Asn	Gln
Asp	Glu
Cys	Ser
Gln	Asn
Glu	Asp
Gly	Pro
His	Gln
Ile	leu; val
Leu	ile; val
Lys	arg; gln
Met	leu; ile
Phe	met; leu; tyr
Ser	Thr
Thr	Ser
Trp	Tyr
Tyr	trp; phe
Val	ile; leu

Thus, it is understood that, where desired, modifications and changes may be made in the nucleic acid encoding the polypeptides of this invention and/or amino acid sequence of the polypeptides of the present invention and still obtain a polypeptide having like or otherwise desirable characteristics. Such changes may occur in natural isolates or may be

synthetically introduced using site-specific mutagenesis, the procedures for which, such as mis-match polymerase chain reaction (PCR), are well known in the art. For example, certain amino acids may be substituted for other amino acids in a polypeptide without appreciable loss of functional activity. It is thus contemplated that various changes may be made in the amino acid sequence of the polypeptides of the present invention (or underlying nucleic acid sequence) without appreciable loss of biological utility or activity and possibly with an increase in such utility or activity. Thus, it is clear that naturally occurring variations in the polypeptide sequences set forth herein as well as genetically engineered variations in the polypeptide sequences set forth herein are contemplated by the present invention. By providing the genomic location of genes that are involved in viral infection, the present invention has also provided the genomic location of any variant sequences of these genes. Thus, based on the information provided herein, it would be routine for one of skill in the art to identify and sequence the genomic region identified by applicants and identify variant sequences of the genes set forth herein. It would also be routine for one of skill in the art to utilize comparison tools and bioinformatics techniques to identify sequences from other species that are homologs of the genes set forth herein and are also necessary for infection, but not necessary for survival of the cell.

Antibodies

The present invention also provides antibodies that specifically bind to the gene products, polypeptides, proteins and fragments thereof set forth in Table 1. The antibody of the present invention can be a polyclonal antibody or a monoclonal antibody. The antibody of the invention selectively binds a polypeptide. By "selectively binds" or "specifically binds" is meant an antibody binding reaction which is determinative of the presence of the antigen (in the present case, a polypeptide set forth in Table 1 or antigenic fragment thereof among a heterogeneous population of proteins and other biologics). Thus, under designated immunoassay conditions, the specified antibodies bind preferentially to a particular peptide and do not bind in a significant amount to other proteins in the sample. Preferably, selective binding includes binding at about or above 1.5 times assay background and the absence of significant binding is less than 1.5 times assay background.

This invention also contemplates antibodies that compete for binding to natural interactors or ligands to the proteins set forth in Table 1. In other words, the present invention provides antibodies that disrupt interactions between the proteins set forth in Table 1 and their binding partners. For example, an antibody of the present invention can compete

with a protein for a binding site (e.g. a receptor) on a cell or the antibody can compete with a protein for binding to another protein or biological molecule, such as a nucleic acid that is under the transcriptional control of a transcription factor set forth in Table 1. The antibody optionally can have either an antagonistic or agonistic function as compared to the antigen.

5 Preferably, the antibody binds a polypeptide *ex vivo* or *in vivo*. Optionally, the antibody of the invention is labeled with a detectable moiety. For example, the detectable moiety can be selected from the group consisting of a fluorescent moiety, an enzyme-linked moiety, a biotin moiety and a radiolabeled moiety. The antibody can be used in techniques or procedures such as diagnostics, screening, or imaging. Anti-idiotypic antibodies and affinity
10 matured antibodies are also considered to be part of the invention.

As used herein, the term "antibody or fragments thereof" encompasses chimeric antibodies and hybrid antibodies, with dual or multiple antigen or epitope specificities, and fragments, such as F(ab')₂, Fab', Fab and the like, including hybrid fragments. Thus, fragments of the antibodies that retain the ability to bind their specific antigens are provided.
15 Such antibodies and fragments can be made by techniques known in the art and can be screened for specificity and activity according to the methods set forth in the Examples and in general methods for producing antibodies and screening antibodies for specificity and activity (See Harlow and Lane. Antibodies, A Laboratory Manual. Cold Spring Harbor Publications, New York, (1988)).

20 Also included within the meaning of "antibody or fragments thereof" are conjugates of antibody fragments and antigen binding proteins (single chain antibodies) as described, for example, in U.S. Pat. No. 4,704,692, the contents of which are hereby incorporated by reference.

Optionally, the antibodies are generated in other species and "humanized" for
25 administration in humans. In one embodiment of the invention, the "humanized" antibody is a human version of the antibody produced by a germ line mutant animal. Humanized forms of non-human (e.g., murine) antibodies are chimeric immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')₂, or other antigen-binding subsequences of antibodies) which contain minimal sequence derived from non-human
30 immunoglobulin. Humanized antibodies include human immunoglobulins (recipient antibody) in which residues from a CDR of the recipient are replaced by residues from a CDR of a non-human species (donor antibody) such as mouse, rat or rabbit having the desired specificity, affinity and capacity. In one embodiment, the present invention provides a humanized version of an antibody, comprising at least one, two, three, four, or up to all CDRs

of a monoclonal antibody that specifically binds to a protein set forth in Table 1. In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies may also comprise residues that are found neither in the recipient antibody nor in the imported CDR or framework sequences.

5 In general, the humanized antibody will comprise substantially all of or at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the FR regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc),
10 typically that of a human immunoglobulin (Jones et al., Nature, 321:522-525 (1986); Riechmann et al., Nature, 332:323-327 (1988); and Presta, Curr. Op. Struct. Biol., 2:593-596 (1992)).

Methods for humanizing non-human antibodies are well known in the art. Generally, a humanized antibody has one or more amino acid residues introduced into it from a source
15 that is non-human. These non-human amino acid residues are often referred to as "import" residues, which are typically taken from an "import" variable domain. Humanization can be essentially performed following the method of Winter and co-workers (Jones et al., Nature, 321:522-525 (1986); Riechmann et al., Nature, 332:323-327 (1988); Verhoeyen et al., Science, 239:1534-1536 (1988)), by substituting rodent CDRs or CDR sequences for the
20 corresponding sequences of a human antibody. Accordingly, such "humanized" antibodies are chimeric antibodies (U.S. Pat. No. 4,816,567), wherein substantially less than an intact human variable domain has been substituted by the corresponding sequence from a non-human species. In practice, humanized antibodies are typically human antibodies in which some CDR residues and possibly some FR residues are substituted by residues from
25 analogous sites in rodent antibodies.

Identification of Agents

A method of identifying an antiviral agent comprising a) administering the agent to a cell containing a cellular gene listed in Table 1, b) detecting the level and/or activity of the gene product produced by the cellular gene, a decrease or elimination of the gene product and/or gene product activity indicating a compound with antiviral activity.

The present invention also provides a method of identifying an antiviral agent comprising: a) administering the agent to a cell containing a cellular gene listed in Table 1, b) contacting the cell with a virus; c) detecting the level of viral infection; and d) associating the level of viral infection with the level of expression of the gene from Table 1 or the activity of the protein encoded by the gene from Table 1, a decrease or elimination of viral infection associated with a decrease or elimination of gene expression and/or activity indicating that the agent is an antiviral agent. For example, the agent can interfere with gene expression and/or the activity of the protein or polypeptide product of the gene. In the methods of the present invention, the test compounds or antiviral agents of the invention can be delivered before or after contacting a cell with a virus or simultaneously with the virus.

The methods described above can be utilized to identify any agent with an activity that decreases infection, prevents infection or promotes cell survival after infection with a pathogen(s). Therefore, in the methods of the present invention, the step of contacting the cell with the virus can be replaced with contacting the cell with any infectious pathogen. Infection includes the introduction of an infectious agent, such as a non-recombinant virus, recombinant virus, plasmid, bacteria, prion, eukaryotic microbe, or other agent capable of infecting a host, such as a cell in cell culture or a cell of a subject. Such infection can be *in vitro*, *ex vivo* or *in vivo*.

The test compounds used in the methods described herein can be, but are not limited to, chemicals, small molecules, drugs, proteins, cDNAs, antibodies, morpholinos, triple helix molecule, siRNAs, shRNAs, antisense RNAs, ribozymes or any other compound now known or identified in the future that interferes with the expression and/or function of the cellular genes described herein. The test compounds can also modulate the activity of the gene products of the cellular genes set forth herein.

Short interfering RNAs (siRNAs) are double-stranded RNAs that can induce sequence-specific post-transcriptional gene silencing, thereby decreasing or even inhibiting gene expression. In some examples, siRNA molecules are about 19-23 nucleotides in length, such as at least 21 nucleotides, for example at least 23 nucleotides. In one example, siRNA

triggers the specific degradation of homologous RNA molecules, such as mRNAs, within the region of sequence identity between both the siRNA and the target RNA. For example, WO 02/44321 discloses siRNAs capable of sequence-specific degradation of target mRNAs when base-paired with 3' overhanging ends. The direction of dsRNA processing determines whether a sense or an antisense target RNA can be cleaved by the produced siRNA endonuclease complex. Thus, siRNAs can be used to modulate transcription, for example, by silencing genes, such as one or more genes set forth in Table 1. The effects of siRNAs have been demonstrated in cells from a variety of organisms, including *Drosophila*, *C. elegans*, insects, frogs, plants, fungi, mice and humans (for example, WO 02/44321; Gitlin *et al.*, *Nature* 418:430-4, 2002; Caplen *et al.*, *Proc. Natl. Acad. Sci.* 98:9742-9747, 2001; and Elbashir *et al.*, *Nature* 411:494-8, 2001).

In certain examples, siRNAs are directed against certain target genes, to confirm results of the gene-trap method used against the same nucleic acid sequence. Utilizing sequence analysis tools, one of skill in the art can design siRNAs to specifically target any gene set forth in Table 1 for decreased gene expression. siRNAs that inhibit or silence gene expression of any gene set forth in Table 1 can be obtained from Ambion Inc. 2130 Woodward Austin, TX 78744-1832

USA. The siRNAs synthesized by Ambion Inc. can be readily obtained by providing the GenBank Accession No. for a coding sequence or the Entrez Gene number for a gene, both of which are provided for rat and human coding sequences in Table 1.

Also provided herein are examples of sequences that can be utilized to decrease gene expression of the genes listed in Table 1. Specifically, Table 3 provides sense RNA sequences and antisense RNA sequences for the genes listed in Table 1. Therefore, any of the sense or antisense sequences set forth in Table 3 can be used alone or in combination with other sequences to inhibit gene expression. These sequences can comprise a 3' TT overhang and/or additional sequences that allow efficient cloning and expression of the siRNA sequences. These sequences were obtained by analyzing the open reading frames of the genes listed in Table 3. Therefore, Table 3 provides the name of each gene analyzed, the GenBank Accession No. for the mRNA of the gene, the length of the mRNA, the ORF region of the mRNA and the Locus number for each gene. The Locus number for each gene is equivalent to the Entrez Gene number listed in Table 1. Table 3 also provides the start site of the sequence in the open reading frame of the gene that is targeted by the sense RNA sequence and/or the antisense RNA sequence set forth in Table 3. The start site for the target

sequence is indicated in the Name column and in the Start column. The Name column also provides a GenBank Accession No. identifier for each target sequence. Thus, it would be clear that a row in Table 3 that had the Name NM_000350_siRNA_458 indicates that the sense and antisense sequences correspond to GenBank Accession No. NM_000350 and the start site for the target sequence is 458. For example, a target sequence for the ABCA4 gene starts at position 458. Therefore, a sequence comprising SEQ ID NO: 1 and/or a sequence comprising SEQ ID NO: 2 are two sequences that can be utilized to target ABCA4 and decrease ABCA4 gene expression. Similarly, a sequence comprising SEQ ID NO: 3 and/or a sequence comprising SEQ ID NO: 4 can be utilized to target ABCA4 expression. These examples are not meant to be limiting and pertain to every sense and antisense RNA sequence set forth in Table 3. Sequences comprising the sense and antisense RNA sequences set forth herein can be utilized to inhibit gene expression in any cell (eukaryotic or prokaryotic), animal or any other organism. These sequences can be cloned into vectors and utilized *in vitro*, *ex vivo* or *in vivo* to decrease gene expression.

shRNA (short hairpin RNA) is a DNA molecule that can be cloned into expression vectors to express siRNA (19-21nt RNA duplex) for RNAi interference studies. shRNA has the following structural features: a short nucleotide sequence ranging from about 19-29 nucleotides derived from the target gene, followed by a short spacer of about 4-15 nucleotides (*i.e.* loop) and about a 19-29 nucleotide sequence that is the reverse complement of the initial target sequence. For example, the sense siRNA sequence for any of the genes set forth in Table 3 can be utilized to design an shRNA. As an example, a sense RNA sequence for C10orf3 (SEQ ID NO: 292) was utilized to design an shRNA with an exemplary linker sequence (CGAA). As shown below, the sense sequence is linked via the linker (CGAA) to the antisense sequence to form the top strand. The top strand and the bottom strand are annealed to make a double stranded oligonucleotide that can be cloned into an appropriate vector for expression. The double stranded oligonucleotide can have nucleotide overhangs as depicted below to facilitate cloning. These sequences can be cloned into vectors and utilized *in vitro*, *ex vivo* or *in vivo* to decrease gene expression.

Top Strand	5'-CACCG*CCAGAAGTACCAAAGATTTTCGAAAAATCTTTGGTACTTCTGG-3' (SEQ ID NO: 837)
Bottom Strand	5'-AAAACCAGAAGTACCAAAGATTTTCGAAATCTTTGGTACTTCTGGC*-3' (SEQ ID NO: 838)
ds Oligo for c10orf3 shRNA	5'-CACCGCCAGAAGTACCAAAGATTTTCGAAAAATCTTTGGTACTTCTGG-3' (SEQ ID NO: 839)
	3'-CGGTCTTCATGGTTTCTAAAGCTTTTGTAAACCATGAAGACCAAAA-5' (SEQ ID NO: 840)

Therefore, any sense sequence set forth in Table 3 can be linked to its corresponding antisense sequence with a linker to make a top strand for an shRNA. The bottom strand is the reverse complement of the top strand. The “U”s in the sequence set forth in Table 3 are replaced with “T”s to make DNA strands. The top strand and the bottom strand are then annealed to form the double stranded shRNA. As mentioned above, the top and bottom strand can have overhangs or additional sequence to facilitate cloning into an expression vector.

Ribozymes are enzymatic RNA molecules capable of catalyzing the specific cleavage of RNA. The mechanism of ribozyme action involves sequence specific hybridization of the ribozyme molecule to complementary target RNA, followed by an endonucleolytic cleavage. Methods of using ribozymes to decrease or inhibit RNA expression are known in the art (for example see Kashani-Sabet, *J. Invest. Dermatol. Symp. Proc.*, 7:76-78, 2002).

Generally, the term “antisense” refers to a nucleic acid molecule capable of hybridizing to a portion of an RNA sequence (such as mRNA) by virtue of some sequence complementarity. The antisense nucleic acids disclosed herein can be oligonucleotides that are double-stranded or single-stranded, RNA or DNA or a modification or derivative thereof, which can be directly administered to a cell (for example by administering the antisense molecule to the subject), or which can be produced intracellularly by transcription of exogenous, introduced sequences (for example by administering to the subject a vector that includes the antisense molecule under control of a promoter).

Antisense nucleic acids are polynucleotides, for example nucleic acid molecules that are at least 6 nucleotides in length, at least 10 nucleotides, at least 15 nucleotides, at least 20 nucleotides, at least 100 nucleotides, at least 200 nucleotides, such as 6 to 100 nucleotides. However, antisense molecules can be much longer. In particular examples, the nucleotide is modified at one or more base moiety, sugar moiety, or phosphate backbone (or combinations thereof), and can include other appending groups such as peptides, or agents facilitating transport across the cell membrane (Letsinger *et al.*, *Proc. Natl. Acad. Sci. USA* 1989,

86:6553-6; Lemaitre *et al.*, *Proc. Natl. Acad. Sci. USA* 1987, 84:648-52; WO 88/09810) or blood-brain barrier (WO 89/10134), hybridization triggered cleavage agents (Krol *et al.*, *BioTechniques* 1988, 6:958-76) or intercalating agents (Zon, *Pharm. Res.* 5:539-49, 1988).

Examples of modified base moieties include, but are not limited to: 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, acetylcytosine, 5-(carboxyhydroxymethyl) 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, methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarbonylmethyluracil, 5-methoxyuracil, 2-methylthio-N⁶-isopentenyladenine, uracil-5-oxyacetic acid, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-S-oxyacetic acid, 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, and 2,6-diaminopurine.

Examples of modified sugar moieties include, but are not limited to: arabinose, 2-fluoroarabinose, xylose, and hexose, or a modified component of the phosphate backbone, such as phosphorothioate, a phosphorodithioate, a phosphoramidothioate, a phosphoramidate, a phosphordiamidate, a methylphosphonate, an alkyl phosphotriester, or a formacetal or analog thereof.

In a particular example, an antisense molecule is an α -anomeric oligonucleotide. An α -anomeric oligonucleotide forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual β -units, the strands run parallel to each other (Gautier *et al.*, *Nucl. Acids Res.* 15:6625-41, 1987). The oligonucleotide can be conjugated to another molecule, such as a peptide, hybridization triggered cross-linking agent, transport agent, or hybridization-triggered cleavage agent. Oligonucleotides can include a targeting moiety that enhances uptake of the molecule by host cells. The targeting moiety can be a specific binding molecule, such as an antibody or fragment thereof that recognizes a molecule present on the surface of the host cell.

In a specific example, antisense molecules that recognize a nucleic acid set forth herein, include a catalytic RNA or a ribozyme (for example see WO 90/11364; WO 95/06764; and Sarver *et al.*, *Science* 247:1222-5, 1990). Conjugates of antisense with a metal complex, such as terpyridylCu (II), capable of mediating mRNA hydrolysis, are described in

Bashkin *et al.* (*Appl. Biochem Biotechnol.* 54:43-56, 1995). In one example, the antisense nucleotide is a 2'-O-methylribonucleotide (Inoue *et al.*, *Nucl. Acids Res.* 15:6131-48, 1987), or a chimeric RNA-DNA analogue (Inoue *et al.*, *FEBS Lett.* 215:327-30, 1987).

The antiviral agents identified utilizing these methods can be used to inhibit viral infection in cells either *in vitro*, *ex vivo* or *in vivo*.

In the methods of the present invention any cell that can be infected with a virus or other pathogen, such as bacteria, parasite or fungi can be utilized. The cell can be prokaryotic or eukaryotic, such as a cell from an insect, fish, crustacean, mammal, bird, reptile, yeast or a bacterium, such as *E. coli*. The cell can be part of an organism, or part of a cell culture, such as a culture of mammalian cells or a bacterial culture.

The viruses of the present invention include all RNA viruses (including negative stranded RNA viruses, positive stranded RNA viruses, double stranded RNA viruses and retroviruses) and DNA viruses. Examples of viruses include, but are not limited to, HIV (including HIV-1 and HIV-2), parvovirus, papillomaviruses, measles, filovirus (for example, Marburg), SARS (severe acute respiratory syndrome) virus, hantaviruses, influenza viruses (*e.g.*, influenza A, B and C viruses), hepatitis viruses A to G, caliciviruses, astroviruses, rotaviruses, coronaviruses, (for example, human respiratory coronavirus), picornaviruses, (for example, human rhinovirus and enterovirus), Ebola virus, human herpesvirus (such as, HSV-1-9, including zoster, Epstein-Barr, and human cytomegalovirus), foot and mouth disease virus, human adenovirus, adeno-associated virus, smallpox virus (variola), cowpox, monkey pox, vaccinia, polio, viral meningitis and hantaviruses.

For animals, viruses include, but are not limited to, the animal counterpart to any above listed human virus, avian influenza (for example, strains H5N1, H5N2, H7N1, H7N7 and H9N2), and animal retroviruses, such as simian immunodeficiency virus, avian immunodeficiency virus, pseudocowpox, bovine immunodeficiency virus, feline immunodeficiency virus, equine infectious anemia virus, caprine arthritis encephalitis virus and visna virus.

The methods of the present invention can also be used to assess bacterial infection and identify antibacterial agents. Specifically, the same methods are employed but instead of contacting a cell with a virus, the cell is contacted with a bacterium. Therefore, the present invention provides a method of identifying an antibacterial agent comprising a) administering the agent to a cell containing a cellular gene listed in Table 1, b) detecting the level and/or activity of the gene product produced by the cellular gene, a decrease or elimination of the gene product and/or gene product activity indicating a compound with antibacterial activity.

The present invention also provides a method of identifying an antibacterial agent comprising: a) administering the agent to a cell containing a cellular gene listed in Table 1, b) contacting the cell with a bacteria; c) detecting the level of bacterial infection; and d) associating the level of bacterial infection with the level of expression of the gene from Table 1 or the activity of the protein encoded by the gene from Table 1, a decrease or elimination of bacterial infection associated with a decrease or elimination of gene expression and/or activity indicating that the agent is an antibacterial agent.

Examples of bacteria include, but are not limited to, the following: *Listeria* (sp.), *Mycobacterium tuberculosis*, *Rickettsia* (all types), *Ehrlichia*, *Chlamydia*. Further examples of bacteria that can be targeted by the present methods include *M. tuberculosis*, *M. bovis*, *M. bovis* strain BCG, BCG substrains, *M. avium*, *M. intracellulare*, *M. africanum*, *M. kansasii*, *M. marinum*, *M. ulcerans*, *M. avium* subspecies *paratuberculosis*, *Nocardia asteroides*, other *Nocardia* species, *Legionella pneumophila*, other *Legionella* species, *Salmonella typhi*, other *Salmonella* species, *Shigella* species, *Yersinia pestis*, *Pasteurella haemolytica*, *Pasteurella multocida*, other *Pasteurella* species, *Actinobacillus pleuropneumoniae*, *Listeria monocytogenes*, *Listeria ivanovii*, *Brucella abortus*, other *Brucella* species, *Cowdria ruminantium*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Chlamydia psittaci*, *Coxiella burnetti*, other *Rickettsia* species, *Ehrlichia* species, *Staphylococcus aureus*, *Staphylococcus epidermidis*, *Streptococcus pyogenes*, *Streptococcus agalactiae*, *Bacillus anthracis*, *Escherichia coli*, *Vibrio cholerae*, *Campylobacter* species, *Neisseria meningitidis*, *Neisseria gonorrhea*, *Pseudomonas aeruginosa*, other *Pseudomonas* species, *Haemophilus influenzae*, *Haemophilus ducreyi*, other *Haemophilus* species, *Clostridium tetani*, other *Clostridium* species, *Yersinia enterocolitica*, and other *Yersinia* species.

Antibacterial agents found to be effective for one bacterium, can also be effective for other bacteria, particularly bacteria from the same family. Therefore, antibacterial agents identified for one bacteria can be tested utilizing the methods of the present invention for antibacterial activity against other bacteria.

The methods of the present invention can also be used to assess parasitic infection and identify antiparasitic agents. Specifically, the same methods are employed but instead of contacting a cell with a virus, the cell is contacted with a parasite. Therefore, the present invention provides a method of identifying an antiparasitic agent comprising a) administering the agent to a cell containing a cellular gene listed in Table 1, b) detecting the level and/or activity of the gene product produced by the cellular gene, a decrease or elimination of the gene product and/or gene product activity indicating a compound with antiparasitic activity.

The present invention also provides a method of identifying an antiparasitic agent comprising: a) administering the agent to a cell containing a cellular gene listed in Table 1, b) contacting the cell with a parasite; c) detecting the level of parasitic infection; and d) associating the level of parasitic infection with the level of expression of the gene from Table 1 or the activity of the protein encoded by the gene from Table 1, a decrease or elimination of parasitic infection associated with a decrease or elimination of gene expression and/or activity indicating that the agent is an antiparasitic agent.

Examples of parasites include, but are not limited to, the following: *Cryptosporidium*, *Plasmodium* (all species), American trypanosomes (*T. cruzi*). Furthermore, examples of protozoan and fungal species contemplated within the present methods include, but are not limited to, *Plasmodium falciparum*, other *Plasmodium* species, *Toxoplasma gondii*, *Pneumocystis carinii*, *Trypanosoma cruzi*, other trypanosomal species, *Leishmania donovani*, other *Leishmania* species, *Theileria annulata*, other *Theileria* species, *Eimeria tenella*, other *Eimeria* species, *Histoplasma capsulatum*, *Cryptococcus neoformans*, *Blastomyces dermatitidis*, *Coccidioides immitis*, *Paracoccidioides brasiliensis*, *Penicillium marneffei*, and *Candida* species.

Antiparasitic agents found to be effective for one parasite, can also be effective for other parasite, particularly parasites from the same family. Therefore, antiparasitic agents identified for one parasite can be tested utilizing the methods of the present invention for antiparasitic activity against other parasites.

In the methods described herein, once the cell containing a cellular gene listed in Table 1 has been contacted with an agent, the level of infection can be associated with the level of gene expression and/or activity, such that a decrease or elimination of infection associated with a decrease or elimination of gene expression and/or activity indicates that the agent is effective against the pathogen. These methods can be utilized to assess the effects of an agent on bacterial infection, antiviral infection, antifungal infection, antiparasitic infection, to name a few. For example, the level of viral infection can be measured in a cell after administration of siRNA that inhibits expression of a gene set forth in Table 1. If there is a decrease in viral infection, then the siRNA is an effective antiviral agent. The level of viral infection can be assessed by measuring an antigen or other product associated with a particular viral infection (for example, p24 for HIV infection). If there is a decrease in p24 levels after administration of an siRNA directed to a gene set forth in Table 1, the siRNA targeting that gene is an effective antiviral agent against HIV. The level of viral infection can

also be measured by real-time quantitative reverse transcription-polymerase chain reaction (RT-PCR) assay (See for example, Payungporn et al. "Single step multiplex real-time RT-PCR for H5N1 influenza A virus detection." *J Virol Methods*. Sep 22, 2005; Landolt et al. "Use of real-time reverse transcriptase polymerase chain reaction assay and cell culture methods for detection of swine influenza A viruses" *Am J Vet Res*. 2005 Jan;66(1):119-24)

Similarly, the level of viral infection can be measured in a cell, utilizing the methods set forth above and known in the art, after administration of a chemical, small molecule, drug, protein, cDNA, antibody, morpholino, antisense RNA, ribozyme or any other compound. If there is a decrease in viral infection, then the chemical, small molecule, drug, protein, cDNA, antibody, morpholino, antisense RNA, ribozyme or any other compound is an effective antiviral agent. Similar methods can be utilized to measure the levels of other types of infection such as bacterial infection, fungal infection and parasitic infection.

Antiviral agents found to be effective for one virus, can also be effective for other viruses, particularly viruses from the same family. However, it is also contemplated that an agent found to be effective against HIV can also be effective against influenza or avian flu or any other virus. Therefore, antiviral agents identified for one virus can be tested utilizing the methods of the present invention for antiviral activity against other viruses. The level of the gene product can be measured by any standard means, such as by detection with an antibody specific for the protein. The nucleic acids set forth herein and fragments thereof can be utilized as primers to amplify nucleic acid sequences, such as a gene transcript of one of the genes set forth in Table 1 by standard amplification techniques. For example, expression of a gene transcript can be quantified by RT-PCR using RNA isolated from cells. A variety of PCR techniques are familiar to those skilled in the art. For a review of PCR technology, see White (1997) and the publication entitled "PCR Methods and Applications" (1991, Cold Spring Harbor Laboratory Press), which is incorporated herein by reference in its entirety for amplification methods. In each of these PCR procedures, PCR primers on either side of the nucleic acid sequences to be amplified are added to a suitably prepared nucleic acid sample along with dNTPs and a thermostable polymerase such as Taq polymerase, Pfu polymerase, or Vent polymerase. The nucleic acid in the sample is denatured and the PCR primers are specifically hybridized to complementary nucleic acid sequences in the sample. The hybridized primers are extended. Thereafter, another cycle of denaturation, hybridization, and extension is initiated. The cycles are repeated multiple times to produce an amplified fragment containing the nucleic acid sequence between the primer sites. PCR has further been

described in several patents including U.S. Pat. Nos. 4,683,195, 4,683,202 and 4,965,188. Each of these publications is incorporated herein by reference in its entirety for PCR methods. One of skill in the art would know how to design and synthesize primers that amplify any of the nucleic acid sequences set forth in Table 1 or a fragment thereof.

5 A detectable label may be included in an amplification reaction. Suitable labels include fluorochromes, e.g. fluorescein isothiocyanate (FITC), rhodamine, Texas Red, phycoerythrin, allophycocyanin, 6-carboxyfluorescein (6-FAM), 2',7'-dimethoxy-4',5'-dichloro-6-carboxyfluorescein (JOE), 6-carboxy-X-rhodamine (ROX), 6-carboxy-2',4',7',4',7-hexachlorofluorescein (HEX), 5-carboxyfluorescein (5-FAM) or N,N,N',N'-tetramethyl-6-carboxyrhodamine (TAMRA), radioactive labels, e.g., ^{32}P , ^{35}S , ^3H ; etc. The label may be a
10 two stage system, where the amplified DNA is conjugated to biotin, haptens, etc. having a high affinity binding partner, e.g. avidin, specific antibodies, etc., where the binding partner is conjugated to a detectable label. The label may be conjugated to one or both of the primers. Alternatively, the pool of nucleotides used in the amplification is labeled, so as to incorporate
15 the label into the amplification product.

The sample nucleic acid, e.g. amplified fragment, can be analyzed by one of a number of methods known in the art. The nucleic acid can be sequenced by dideoxy or other methods. Hybridization with the sequence can also be used to determine its presence, by Southern blots, dot blots, etc.

20 The genes and nucleic acids of the invention can also be used in polynucleotide arrays. Polynucleotide arrays provide a high throughput technique that can assay a large number of polynucleotide sequences in a single sample. This technology can be used, for example, to identify samples with reduced expression of a nucleic acid set forth in Table 1 as compared to a control sample. This technology can also be utilized to determine the effects of
25 reduced expression of a nucleic acid set forth in Table 1. In this way, one of skill in the art can identify genes that are upregulated or downregulated upon reduction of expression of a nucleic acid set forth in Table 1. Similarly, one of skill in the art can identify genes that are upregulated or downregulated upon increased expression of a nucleic acid set forth in Table 1. In this way, other genes can be identified as targets for therapy, such as antiviral therapy,
30 antibacterial therapy, antiparasitic therapy or antifungal therapy.

To create arrays, single-stranded polynucleotide probes can be spotted onto a substrate in a two-dimensional matrix or array. Each single-stranded polynucleotide probe can comprise at least 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 25, or 30 or more

contiguous nucleotides selected from the nucleotide sequences set forth under GenBank Accession Nos. in Table 1.

The array can also be a microarray that includes probes to different polymorphic alleles of one or more genes set forth in Table 1. A polymorphism exists when two or more versions of a nucleic acid sequence exist within a population of subjects. For example, a polymorphic nucleic acid can be one where the most common allele has a frequency of 99% or less. Different alleles can be identified according to differences in nucleic acid sequences, and genetic variations occurring in more than 1% of a population (which is the commonly accepted frequency for defining polymorphism) are useful polymorphisms for certain applications.

The allelic frequency (the proportion of all allele nucleic acids within a population that are of a specified type) can be determined by directly counting or estimating the number and type of alleles within a population. Polymorphisms and methods of determining allelic frequencies are discussed in Hartl, D.L. and Clark, A.G., Principles of Population Genetics, Third Edition (Sinauer Associates, Inc., Sunderland Massachusetts, 1997), particularly in chapters 1 and 2.

These microarrays can be utilized to detect polymorphic alleles in samples from subjects. Such alleles may indicate that a subject is more susceptible to viral infection or less susceptible to viral infection. For example, since the present invention shows that a disruption in any of the genes set forth in Table 1 results in decreased viral infection, such microarrays can be utilized to detect polymorphic versions of the genes set forth in Table 1 that result in decreased gene expression and/or decreased activity of the gene product to identify subjects that are less susceptible to viral infection.

The substrate can be any substrate to which polynucleotide probes can be attached, including but not limited to glass, nitrocellulose, silicon, and nylon. Polynucleotide probes can be bound to the substrate by either covalent bonds or by non-specific interactions, such as hydrophobic interactions. Techniques for constructing arrays and methods of using these arrays are described in EP No. 0 799 897; PCT No. WO 97/29212; PCT No. WO 97/27317; EP No. 0 785 280; PCT No. WO 97/02357; U.S. Pat. Nos. 5,593,839; 5,578,832; EP No. 0 728 520; U.S. Pat. No. 5,599,695; EP No. 0 721 016; U.S. Pat. No. 5,556,752; PCT No. WO 95/22058; and U.S. Pat. No. 5,631,734. Commercially available polynucleotide arrays, such as Affymetrix GeneChip.TM., can also be used. Use of the GeneChip.TM. to detect gene expression is described, for example, in Lockhart et al., Nature Biotechnology 14:1675

(1996); Chee et al., Science 274:610 (1996); Hacia et al., Nature Genetics 14:441, 1996; and Kozal et al., Nature Medicine 2:753, 1996.

The level of gene product can be compared to the level of the gene product in a control cell not contacted with the compound. The level of gene product can be compared to the level of the gene product in the same cell prior to addition of the compound. Activity or function, can be measured by any standard means, such as by enzymatic assays that measure the conversion of a substrate to a product or binding assays that measure the binding of a protein to a nucleic acid, for example.

Moreover, the regulatory region of the gene can be functionally linked to a reporter gene and compounds can be screened for inhibition of the reporter gene. Such regulatory regions can be isolated from the genomic sequences and identified by any characteristics observed that are characteristic for regulatory regions of the species and by their relation to the start codon for the coding region of the gene. As used herein, a reporter gene encodes a reporter protein. A reporter protein is any protein that can be specifically detected when expressed. Reporter proteins are useful for detecting or quantitating expression from expression sequences. Many reporter proteins are known to one of skill in the art. These include, but are not limited to, β -galactosidase, luciferase, and alkaline phosphatase that produce specific detectable products. Fluorescent reporter proteins can also be used, such as green fluorescent protein (GFP), cyan fluorescent protein (CFP), red fluorescent protein (RFP) and yellow fluorescent protein (YFP).

Viral infection can also be measured via cell based assays. Briefly, cells (20,000 to 2,500,000) are infected with the desired pathogen, and the incubation continued for 3-7 days. The antiviral agent can be applied to the cells before, during, or after infection with the pathogen. The amount of virus and agent administered can be determined by skilled practitioners. In some examples, several different doses of the potential therapeutic agent can be administered, to identify optimal dose ranges. Following transfection, assays are conducted to determine the resistance of the cells to infection by various agents.

For example, if analyzing viral infection, the presence of a viral antigen can be determined by using antibody specific for the viral protein then detecting the antibody. In one example, the antibody that specifically binds to the viral protein is labeled, for example with a detectable marker such as a fluorophore. In another example, the antibody is detected by using a secondary antibody containing a label. The presence of bound antibody is then detected, for example using microscopy, flow cytometry and ELISA.

Alternatively, or in addition, the ability of the cells to survive viral infection is determined, for example, by performing a cell viability assay, such as trypan blue exclusion.

The amount of a protein listed in Table 1, in a cell, can be determined by methods standard in the art for quantitating proteins in a cell, such as Western blotting, ELISA, ELISPOT, immunoprecipitation, immunofluorescence (e.g., FACS), immunohistochemistry, immunocytochemistry, etc., as well as any other method now known or later developed for quantitating protein in or produced by a cell.

The amount of a nucleic acid listed in Table 1, in a cell, can be determined by methods standard in the art for quantitating nucleic acid in a cell, such as *in situ* hybridization, quantitative PCR, RT-PCR, Taqman assay, Northern blotting, ELISPOT, dot blotting, etc., as well as any other method now known or later developed for quantitating the amount of a nucleic acid in a cell.

The ability of an antiviral agent to prevent or decrease infection by a virus, such as HIV, Ebola, influenza A, SARS, smallpox, to name a few, can be assessed in animal models. Several animal models for viral infection are known in the art. For example, mouse HIV models are disclosed in Sutton *et al.* (*Res. Initiat Treat. Action*, 8:22-4, 2003) and Pincus *et al.* (*AIDS Res. Hum. Retroviruses* 19:901-8, 2003); guinea pig models for Ebola infection are disclosed in Parren *et al.* (*J. Virol.* 76:6408-12, 2002) and Xu *et al.* (*Nat. Med.* 4:37-42, 1998); and cynomolgus monkey (*Macaca fascicularis*) models for influenza infection are disclosed in Kuiken *et al.* (*Vet. Pathol.* 40:304-10, 2003). Such animal models can also be used to test agents for an ability to ameliorate symptoms associated with viral infection. In addition, such animal models can be used to determine the LD₅₀ and the ED₅₀ in animal subjects, and such data can be used to determine the *in vivo* efficacy of potential agents. Animal models can also be used to assess antibacterial, antifungal and antiparasitic agents.

Animals of any species, including, but not limited to, birds, mice, rats, rabbits, guinea pigs, pigs, micro-pigs, goats, and non-human primates, e.g., baboons, monkeys, and chimpanzees, can be used to generate an animal model of viral infection, bacterial infection, fungal infection or parasitic infection if needed.

For example, for a model of viral infection, the appropriate animal is inoculated with the desired virus, in the presence or absence of the antiviral agent. The amount of virus and agent administered can be determined by skilled practitioners. In some examples, several different doses of the potential therapeutic agent (for example, an antiviral agent) can be administered to different test subjects, to identify optimal dose ranges. The therapeutic agent can be administered before, during, or after infection with the virus. Subsequent to the

treatment, animals are observed for the development of the appropriate viral infection and symptoms associated therewith. A decrease in the development of the appropriate viral infection, or symptoms associated therewith, in the presence of the agent provides evidence that the agent is a therapeutic agent that can be used to decrease or even inhibit viral infection in a subject.

The present invention also provides a method of making compound that reduces infection, comprising: a) synthesizing a compound; b) administering the compound to a cell containing a cellular gene set forth in Table 1, c) contacting the cell with an infectious pathogen; c) detecting the level of infection; d) associating the level of infection with the level of expression of the gene from Table 1 or the activity of the protein encoded by the gene from Table 1, a decrease or elimination of infection associated with a decrease or elimination of gene expression and/or activity indicating that a compound that reduces infection was made.

Also provided is a method of making compound that reduces infection, comprising: a) administering the compound to a cell containing a cellular gene set forth in Table 1, b) contacting the cell with an infectious pathogen; c) detecting the level of infection; d) associating the level of infection with the level of expression of the gene from Table 1 or the activity of the protein encoded by the gene from Table 1, a decrease or elimination of infection associated with a decrease or elimination of gene expression and/or activity indicating that a compound is a compound that reduces infection; and e) placing the compound in a pharmaceutically acceptable carrier. The compounds that reduce infection can be antiviral, antibacterial, antifungal or antiparasitic compounds or any compound that reduces infection by an infectious agent..

Transgenic Cells and Non-Human Mammals

Transgenic animal models, including recombinant and knock-out animals, can be generated from the host nucleic acids described herein. Exemplary transgenic non-human mammals include, but are not limited to, mice, rabbits, rats, chickens, cows, and pigs. The present invention provides a transgenic non-human mammal that has a knock-out of one or more genes listed in Table 1 and has a decreased susceptibility to infection by pathogens, such as viruses, bacteria, fungi and parasites. Such knock-out animals are useful for reducing the transmission of viruses from animals to humans. In the transgenic animals of the present invention one or both alleles of one or more genes set forth in Table 1 can be knocked out.

By "decreased susceptibility" is meant that the animal is less susceptible to infection or experiences decreased infection by a pathogen as compared to an animal that does not have one or both alleles of a gene of Table 1 knocked out or functionally deleted. The animal does not have to be completely resistant to the pathogen. For example, the animal can be 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 100% or any percentage in between less susceptible to infection by a pathogen as compared to an animal that does not have a functional deletion of a gene set forth in Table 1. Furthermore, decreasing infection or decreasing susceptibility to infection includes decreasing entry, replication, pathogenesis, insertion, lysis, or other steps in the replication strategy of a virus or other pathogen into a cell or subject, or combinations thereof.

Therefore, the present invention provides a non-human transgenic mammal comprising a functional deletion of one or more genes listed in Table 1, wherein the mammal has decreased susceptibility to infection by a pathogen, such as a virus, a bacterium, a parasite or a fungus. A functional deletion is a mutation, partial or complete deletion, insertion, or other variation made to a gene sequence that inhibits production of the gene product or renders a gene product that is not completely functional or non-functional.

Expression of the sequence used to knock-out or functionally delete the desired gene can be regulated by an appropriate promoter sequence. For example, constitutive promoters can be used to ensure that the functionally deleted gene is not expressed by the animal. In contrast, an inducible promoter can be used to control when the transgenic animal does or does not express the gene of interest. Exemplary inducible promoters include tissue-specific promoters and promoters responsive or unresponsive to a particular stimulus (such as light, oxygen, chemical concentration, such as a tetracycline inducible promoter).

For example, a transgenic mouse or other transgenic animal including a disrupted gene listed in Table 1 can be examined during exposure to various pathogens. Comparison data can provide insight into the life cycles of pathogens. Moreover, knock-out animals (such as pigs) that are otherwise susceptible to an infection (for example influenza) can be made to resist infection, conferred by disruption of the gene. If disruption of the gene in the transgenic animal results in an increased resistance to infection, these transgenic animals can be bred to establish flocks or herds that are less susceptible to infection.

Transgenic animals, including methods of making and using transgenic animals, are described in various patents and publications, such as WO 01/43540; WO 02/19811; U.S. Pub. Nos: 2001-0044937 and 2002-0066117; and U.S. Pat. Nos: 5,859,308; 6,281,408; and 6,376,743; and the references cited therein.

The transgenic animals of this invention also include conditional gene knockdown animals produced, for example, by utilizing the SIRIUS-Cre system that combines siRNA for specific gene-knockdown, Cre-loxP for tissue-specific expression and tetracycline-on for inducible expression. These animals can be generated by mating two parental lines that contain a specific siRNA of interest gene and tissue-specific recombinase under tetracycline control. See Chang et al. "Using siRNA Technique to Generate Transgenic Animals with Spatiotemporal and Conditional Gene Knockdown." American Journal of Pathology 165: 1535-1541 (2004) which is hereby incorporated in its entirety by this reference regarding production of conditional gene knockdown animals.

The present invention also provides cells including an altered or disrupted gene listed in Table 1 that are resistant to infection by a pathogen. These cells can be *in vitro*, *ex vivo* or *in vivo* cells and can have one or both alleles altered. Such cells therefore include cells having decreased susceptibility to HIV infection, Ebola infection, avian flu, influenza A or any of the other pathogens described herein, including bacteria, parasites and fungi.

Screening for Resistance to Infection

Also provided herein are methods of screening host subjects for resistance to infection by characterizing a nucleotide sequence of a host nucleic acid or the amino acid sequence of a host polypeptide (such as those shown in Table 1). For example, a ANXA1 nucleic acid of a subject can be isolated, sequenced, and compared to the wildtype sequence for ANXA1. The greater the similarity between that subject's ANXA1 nucleic acid and the wildtype ANXA1 sequence, the more susceptible that person is to infection, while a decrease in similarity between that subject's ANXA1 nucleic acid and the wildtype ANXA1 sequence, the more resistant that subject may be to infection. Such screens can be performed for any host nucleic acid or the amino acid sequence of a host polypeptide set forth in Table 1, in any species.

Assessing the genetic characteristics of a population can provide information about the susceptibility or resistance of that population to viral infection. For example, polymorphic analysis of alleles in a particular human population, such as the population of a particular city or geographic area, can indicate how susceptible that population is to infection. A higher percentage of alleles substantially similar to wild-type sequences listed in Table 1 indicates that the population is more susceptible to infection, while a large number of polymorphic alleles that are substantially different than wild-type sequences listed in Table 1 indicates that a population is more resistant to infection. Such information can be used, for example, in making public health decisions about vaccinating susceptible populations.

The present invention also provides a method of screening a cell for a variant form of a gene listed in Table 1. A variant can be a gene with a functional deletion, mutation or alteration in the gene such that the amount or activity of the gene product is altered. These cells containing a variant form of a gene listed in Table 1 can be contacted with a pathogen to determine if cells comprising a naturally occurring variant of a gene listed in Table 1 differ in their resistance to infection. For example, cells from an animal, for example, a chicken, can be screened for a variant form of a gene listed in Table 1. If a naturally occurring variant is found and chickens possessing a variant form of the gene in their genome are less susceptible to infection, these chickens can be selectively bred to establish flocks that are resistant to infection. By utilizing these methods flocks of chickens that are resistant to avian flu can be established. Similarly, other animals can be screened for a variant form of a gene listed in Table 1. If a naturally occurring variant is found and animals possessing a variant form of the gene in their genome are less susceptible to infection, these animals can be selectively bred to establish populations that are resistant to infection. These animals include, but are not limited to, cats, dogs, livestock (for example, cattle, horses, pigs, sheep, goats, etc.), laboratory animals (for example, mouse, rabbit, rat, gerbil, guinea pig, etc.) and avian species (for example, flocks of chickens, geese, turkeys, ducks, pheasants, pigeons, doves etc.). Therefore, the present application provides populations of animals that comprise a naturally occurring variant of a gene listed in Table 1 that results in decreased susceptibility to viral infection, thus providing populations of animals that are less susceptible to viral infection. Similarly, if a naturally occurring variant is found and animals possessing a variant form of the gene in their genome are less susceptible to bacterial, parasitic or fungal infection, these animals can be selectively bred to establish populations that are resistant to bacterial, parasitic or fungal infection.

Methods of Inhibiting Infection

Also provided by the present invention is a method of inhibiting infection in a cell comprising inhibiting expression or activity of a gene or a gene product listed in Table 1. As discussed throughout, infection can be a viral infection, bacterial infection, fungal infection or a parasitic infection, to name a few. Inhibition can occur in a cell, *in vitro*, *ex vivo* or *in vivo*. Expression of one or more genes from Table 1 can be inhibited. Similarly, the activity of one or more gene products listed in Table 1 can be inhibited. Inhibition or a decrease in expression does not have to be complete as this can range from a slight decrease in expression to complete ablation of expression. For example, expression can be inhibited by

about 5%, 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95%, 99%, 100% or any percentage in between as compared to a control cell wherein the expression of a gene listed in Table 1 has not been inhibited. Similarly, inhibition or decrease in the activity of a gene product does not have to be complete as this can range from a slight decrease to complete ablation of the activity of the gene product. For example, the activity of a gene product can be inhibited by about 5%, 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95%, 99%, 100% or any percentage in between as compared to a control cell wherein activity of a gene product listed in Table 1 has not been inhibited.

Antisense oligonucleotides, RNAi molecules, ribozymes and siRNA molecules can be utilized to disrupt expression and/or decrease the activity of a gene product. Small molecules, drugs, antibodies, proteins and chemicals can also be utilized to inhibit expression and/or the activity of a gene product. Antisense oligonucleotides, RNAi molecules, ribozymes, siRNA, small molecules, chemicals, antibodies proteins, cDNAs, and any other compound now known or identified in the future to decrease expression of a gene and/or activity of a gene product set forth in Table 1 can be used alone or in combination with other therapeutic agents such as anti-viral compounds, antibacterial agents, antifungal agents, antiparasitic agents, anti-inflammatory agents, anti-cancer agents, etc.

Examples of antiviral compounds include, but are not limited to, amantadine, rimantadine, zanamavir and oseltamavir (Tamiflu) for the treatment of flu and its associated symptoms. Antiviral compounds useful in the treatment of HIV include Combivir® (lamivudine-zidovudine), Crixivan® (indinavir), Emtriva® (emtricitabine), Epivir® (lamivudine), Fortovase® (saquinavir-sg), Hivid® (zalcitabine), Invirase® (saquinavir-hg), Kaletra® (lopinavir-ritonavir), Lexiva™ (fosamprenavir), Norvir® (ritonavir), Retrovir® (zidovudine) Sustiva® (efavirenz), Videx EC® (didanosine), Videx® (didanosine), Viracept® (nelfinavir) Viamune® (nevirapine), Zerit® (stavudine), Ziagen® (abacavir), Fuzeon® (enfuvirtide) Rescriptor® (delavirdine), Reyataz® (atazanavir), Trizivir® (abacavir-lamivudine-zidovudine) Viread® (tenofovir disoproxil fumarate) and Agenerase® (amprenavir). Other antiviral compounds useful in the treatment of Ebola and other filoviruses include ribavirin and cyanovirin-N (CV-N). For the treatment of herpes virus, Zovirax® (acyclovir) is available. Antibacterial agents include, but are not limited to, antibiotics (for example, penicillin and ampicillin), sulfa Drugs and folic acid Analogs, Beta-Lactams, aminoglycosides, tetracyclines, macrolides, lincosamides, streptogramins, fluoroquinolones, rifampin, mupirocin, cycloserine, aminocyclitol and oxazolidinones.

Antifungal agents include, but are not limited to, amphotericin, nystatin, terbinafine, itraconazole, fluconazole, ketoconazole, griseofulvin.

Antiparasitic agents include, but are not limited to, anthelmintics, antinematodal Agents, antiplatyhelminthic agents, antiprotozoal agents, amebicides, antimalarials, antitrichomonal agents, aoccidiostats and trypanocidal agents.

The present invention provides a method of reducing or inhibiting infection in a subject comprising administering to the subject an amount of a composition that inhibits expression or activity of a gene or a gene product in Table 1. As discussed throughout, the infection can be from any pathogen, for example, a virus, a bacteria, a fungus or a parasite.

The reduction or inhibition of infection does not have to be complete as this can range from a slight reduction in infection to elimination of the infection. For example, in the methods described herein, there can be a reduction of infection of 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95%, 100% or any percentage in between. The reduction can result in amelioration of the symptoms associated with the infection to complete amelioration of the infection. However, complete amelioration of the infection is not necessary for a reduction or inhibition of infection in a subject to be effective in reducing the symptoms associated with the infection or effective in making the subject less susceptible to infection.

As utilized throughout, preventing infection refers to inhibiting the development of an infection. When referring to treatment, this refers to a method that ameliorates a sign or symptom of a disease or pathological condition related to a infection, such as inhibiting or decreasing viral infection and does not require a complete amelioration of symptoms or of the infection.

The present invention also provides a method of reducing or inhibiting infection in a subject comprising mutating *ex vivo* in a selected cell from the subject a gene listed in Table 1 to a mutated gene incapable of producing a functional gene product of the gene or to a mutated gene producing a reduced amount of a functional gene product of the gene and replacing the cell in the subject, thereby reducing infection of cells in the subject.

Any cell that can be infected with a virus or other pathogen, such as a bacterium, a fungus or a parasite is contemplated herein. A host cell can be prokaryotic or eukaryotic, such as a cell from an insect, crustacean, mammal, bird, reptile, yeast, or a bacterium such as *E. coli*. Exemplary host cells include, but are not limited to, mammalian B-lymphocyte cells, hematopoietic cells, embryonic stem cells, embryonic germ line cells, pluripotent stem cells and totipotent stem cells.

For example, a subject susceptible to or suffering from an infection can be treated with a therapeutically effective amount of an antisense oligonucleotide, a RNAi molecule, a ribozyme or a siRNA molecule (or combinations thereof). After the antisense oligonucleotide, an RNAi molecule, a ribozyme or a siRNA molecule has taken effect (a decreased level of viral infection is observed, or symptoms associated with viral infection decrease), for example after 24-48 hours, the subject can be monitored for symptoms associated with viral infection.

Similarly, other agents, such as an antibody, polypeptide, small molecule or other drug that interacts with a host protein from Table 1 can also be used to decrease or viral infection. This interaction can be direct, such as binding to the host protein or indirect, such as binding to or modulating a protein that interacts with a host protein from Table 1. After the antibody, polypeptide, small molecule or other drug has taken effect (a decreased level of infection is observed, or symptoms associated with infection decrease), for example after 24-48 hours, the subject can be monitored for symptoms associated with infection. Other agents such as peptides and organic or inorganic molecules can also be administered to a subject in a therapeutically effective amount.

The treatments disclosed herein can also be used prophylactically, for example, to inhibit or prevent infection, such as viral infection, bacterial infection, fungal infection or parasitic infection. Such administration is indicated where the treatment is shown to have utility for treatment or prevention of the disorder. The prophylactic use is indicated in conditions known or suspected of progressing to disorders associated with infection.

In certain instances, some genes when disrupted by the present method of retrovirus insertion, resulted in overexpression of the gene product, and this overexpression inhibited viral replication. For example, upon disrupting the genomic locus comprising the sequence of CTCF this resulted in an overexpression of IGF2 which led to decreased viral replication. Therefore, the present invention provides a method of decreasing or inhibiting viral replication by overexpressing genes that lead to decreased viral replication. The present invention also provides a method of increasing the expression of genes whose overexpression decreases viral replication by disrupting the a gene, or inhibiting the gene product of a gene that results in increased expression of the gene whose overexpression decreases viral replication. For example, one could inhibit CTCF in order to increase expression of IGF2. This would be similar for any gene found to increase the expression of another gene and results in decreased viral replication.

Once a gene is found that upon disruption results in overexpression of another gene, the gene that is overexpressed can be modulated directly, i.e., via the overexpressed gene, or indirectly, i.e., via the gene that was originally disrupted (or its gene product) or via another gene (or its gene product) associated with the overexpressed gene.

5 Therefore, the present invention provides a method of identifying an agent that increases the expression of a gene and/or the activity of a gene product comprising contacting a cell with the agent and measuring an increase in gene expression and/or activity of the gene product.

10 The present invention also provides a method of identifying an agent that decreases or inhibits infection via overexpression of a gene and/or an increase in the activity of a gene product comprising administering the agent to the cell, contacting the cell with a pathogen and associating an increase in gene expression and/or activity of the gene product with the level of infection such that an increase in gene expression and/or activity of the gene product accompanied by a decrease in infection indicates that the agent inhibits infection by the
15 pathogen via overexpression of the gene and/or an increase in the activity of the gene product.

For example, one of skill in the art can administer a compound that results in the overexpression of IGF2. This compound may interact with the IGF2 gene, IGF2 mRNA, the IGF2 protein or a fragment thereof. Information for the human IGF 2 gene and its related
20 sequences can be found under Entrez Gene number 3481. The compound could also interact with the CTCF gene, CTCF mRNA, the CTCF protein or a fragment thereof to increase IGF2 expression. The compound can also interact with other genes, mRNAs or proteins involved in the IGF2 pathway, resulting in increased IGF2 expression.

Therefore, if disruption of gene X results in overexpression of gene Y, the gene that is
25 overexpressed (Y) can be modulated directly, i.e. via the overexpressed gene (Y), or indirectly, i.e., via the gene that was originally disrupted (X) (or its gene product) or via another gene (or its gene product) associated with the overexpressed gene (Y). For example, one of skill in the art can administer a compound that results in the overexpression of Y. This compound may interact with the Y gene, Y mRNA or the Y protein. The compound could
30 also interact with the X gene, X mRNA or the X protein to increase Y expression. The compound can also interact with other genes, mRNAs or proteins involved in the gene Y pathway (i.e. a cellular pathway in which gene Y is involved), resulting in increased Y expression.

Pharmaceutical Compositions and Modes of Administration

Various delivery systems for administering the therapies disclosed herein are known, and include encapsulation in liposomes, microparticles, microcapsules, expression by
5 recombinant cells, receptor-mediated endocytosis (Wu and Wu, *J. Biol. Chem.* 1987, 262:4429-32), and construction of therapeutic nucleic acids as part of a retroviral or other vector. Methods of introduction include, but are not limited to, mucosal, topical, intradermal, intramuscular, intraperitoneal, vaginal, rectal, intravenous, subcutaneous, intranasal, and oral routes. The compounds can be administered by any convenient route, for example by
10 infusion or bolus injection, by absorption through epithelial or mucocutaneous linings (for example, oral mucosa, rectal, vaginal and intestinal mucosa, etc.) and can be administered together with other biologically active agents. Administration can be systemic or local. Pharmaceutical compositions can be delivered locally to the area in need of treatment, for example by topical application or local injection.

15 Pharmaceutical compositions are disclosed that include a therapeutically effective amount of a RNA, DNA, antisense molecule, ribozyme, siRNA, molecule, drug, protein, antibody or other therapeutic agent, alone or with a pharmaceutically acceptable carrier. Furthermore, the pharmaceutical compositions or methods of treatment can be administered in combination with (such as before, during, or following) other therapeutic treatments, such
20 as other antiviral agents, antibacterial agents, antifungal agents and antiparasitic agents.

Delivery systems

The pharmaceutically acceptable carriers useful herein are conventional. *Remington's Pharmaceutical Sciences*, by Martin, Mack Publishing Co., Easton, PA, 15th Edition (1975),
25 describes compositions and formulations suitable for pharmaceutical delivery of the therapeutic agents herein disclosed. In general, the nature of the carrier will depend on the mode of administration being employed. For instance, parenteral formulations usually include injectable fluids that include pharmaceutically and physiologically acceptable fluids such as water, physiological saline, balanced salt solutions, aqueous dextrose, sesame oil,
30 glycerol, ethanol, combinations thereof, or the like, as a vehicle. The carrier and composition can be sterile, and the formulation suits the mode of administration. In addition to biologically-neutral carriers, pharmaceutical compositions to be administered can contain minor amounts of non-toxic auxiliary substances, such as wetting or emulsifying agents,

preservatives, and pH buffering agents and the like, for example sodium acetate or sorbitan monolaurate.

The composition can be a liquid solution, suspension, emulsion, tablet, pill, capsule, sustained release formulation, or powder. For solid compositions (for example powder, pill, tablet, or capsule forms), conventional non-toxic solid carriers can include, for example, pharmaceutical grades of mannitol, lactose, starch, sodium saccharine, cellulose, magnesium carbonate, or magnesium stearate. The composition can be formulated as a suppository, with traditional binders and carriers such as triglycerides.

Embodiments of the disclosure including medicaments can be prepared with conventional pharmaceutically acceptable carriers, adjuvants and counterions as would be known to those of skill in the art.

The amount of therapeutic agent effective in decreasing or inhibiting infection can depend on the nature of the pathogen and its associated disorder or condition, and can be determined by standard clinical techniques. Therefore, these amounts will vary depending on the type of virus, bacteria, fungus, parasite or other pathogen. In addition, *in vitro* assays can be employed to identify optimal dosage ranges. The precise dose to be employed in the formulation will also depend on the route of administration, and the seriousness of the disease or disorder, and should be decided according to the judgment of the practitioner and each subject's circumstances. Effective doses can be extrapolated from dose-response curves derived from *in vitro* or animal model test systems.

The disclosure also provides a pharmaceutical pack or kit comprising one or more containers filled with one or more of the ingredients of the pharmaceutical compositions. Optionally associated with such container(s) can be a notice in the form prescribed by a governmental agency regulating the manufacture, use or sale of pharmaceuticals or biological products, which notice reflects approval by the agency of manufacture, use or sale for human administration. Instructions for use of the composition can also be included.

In an example in which a nucleic acid is employed to reduce infection, for example, a viral infection, such as an antisense or siRNA molecule, the nucleic acid can be delivered intracellularly (for example by expression from a nucleic acid vector or by receptor-mediated mechanisms), or by an appropriate nucleic acid expression vector which is administered so that it becomes intracellular, for example by use of a retroviral vector (see U.S. Patent No. 4,980,286), or by direct injection, or by use of microparticle bombardment (such as a gene gun; Biolistic, Dupont), or coating with lipids or cell-surface receptors or transfecting agents, or by administering it in linkage to a homeobox-like peptide which is known to enter the

nucleus (for example Joliot *et al.*, *Proc. Natl. Acad. Sci. USA* 1991, 88:1864-8). The present disclosure includes all forms of nucleic acid delivery, including synthetic oligos, naked DNA, plasmid and viral delivery, integrated into the genome or not.

As mentioned above, vector delivery can be via a viral system, such as a retroviral vector system which can package a recombinant retroviral genome (see e.g., Pastan *et al.*, *Proc. Natl. Acad. Sci. U.S.A.* 85:4486, 1988; Miller *et al.*, *Mol. Cell. Biol.* 6:2895, 1986). The recombinant retrovirus can then be used to infect and thereby deliver to the infected cells a nucleic acid, for example an antisense molecule or siRNA. The exact method of introducing the altered nucleic acid into mammalian cells is, of course, not limited to the use of retroviral vectors. Other techniques are widely available for this procedure including the use of adenoviral vectors (Mitani *et al.*, *Hum. Gene Ther.* 5:941-948, 1994), adeno-associated viral (AAV) vectors (Goodman *et al.*, *Blood* 84:1492-1500, 1994), lentiviral vectors (Naidini *et al.*, *Science* 272:263-267, 1996), and pseudotyped retroviral vectors (Agrawal *et al.*, *Exper. Hematol.* 24:738-747, 1996). Other nonpathogenic vector systems such as the foamy virus vector can also be utilized (Park *et al.* "Inhibition of simian immunodeficiency virus by foamy virus vectors expressing siRNAs." *Virology*. 2005 Sep 20). It is also possible to deliver short hairpin RNAs (shRNAs) via vector delivery systems in order to inhibit gene expression (See Pichler *et al.* "In vivo RNA interference-mediated ablation of MDR1 P-glycoprotein." *Clin Cancer Res.* 2005 Jun 15;11(12):4487-94; Lee *et al.* "Specific inhibition of HIV-1 replication by short hairpin RNAs targeting human cyclin T1 without inducing apoptosis." *FEBS Lett.* 2005 Jun 6;579(14):3100-6.).

Physical transduction techniques can also be used, such as liposome delivery and receptor-mediated and other endocytosis mechanisms (see, for example, Schwartzenberger *et al.*, *Blood* 87:472-478, 1996) to name a few examples. This invention can be used in conjunction with any of these or other commonly used gene transfer methods.

Throughout this application, various publications are referenced. The disclosures of these publications in their entireties are hereby incorporated by reference into this application in order to more fully describe the state of the art to which this invention pertains.

It will be apparent to those skilled in the art that various modifications and variations can be made in the present invention without departing from the scope or spirit of the invention. Other embodiments of the invention will be apparent to those skilled in the art from consideration of the specification and practice of the invention disclosed herein. It is intended that the specification and examples be considered as exemplary only, with a true scope and spirit of the invention being indicated by the following claims.

EXAMPLES

Viruses are obligate intracellular parasites that rely upon the host cell for different steps in their life cycles. The characterization of cellular genes required for virus infection and/or cell killing will be essential for understanding viral life cycles, and can provide cellular targets for new antiviral therapies.

Candidate genes required for lytic reovirus infection were identified by tagged sequence mutagenesis, a process that permits rapid identification of genes disrupted by gene entrapment. One hundred fifty-one reovirus resistant clones were selected from cell libraries containing 2×10^5 independently disrupted genes, of which 111 contained mutations in previously characterized genes and functionally anonymous transcription units. Collectively, the genes associated with reovirus resistance differed from genes targeted by random gene entrapment in that known mutational hot spots were under represented, and a number of mutations appeared to cluster around specific cellular processes, including: IGF-II expression/signaling, vesicular transport/cytoskeletal trafficking and apoptosis.

Tagged sequence mutagenesis provides a rapid, genome-wide strategy to identify candidate cellular genes required for virus infection.

Cellular genes are likely to participate in all phases of viral life cycles including attachment to cellular receptors, internalization, disassembly, translation of mRNA, assembly and egress from the cells [1]. The susceptibility to virus infection varies greatly among different cell types, and virus-resistant cells frequently emerge post-infection [2-4]. This suggests that genetic determinants can influence host cell contributions to the virus life cycle. Despite examples of mammalian genes that influence virus infection, the identification of such genes has been hampered by the lack of practical methods for genetic analysis in cultured cells. In the present study, whether tagged sequence mutagenesis- a gene entrapment strategy widely used to mutate genes in mouse embryonic stem cells [5-10] could be used to identify candidate cellular genes required for lytic infection by reovirus, a small cytolytic RNA virus that replicates in the cytoplasm was tested. The mammalian reoviruses serve as useful models for virus-host cell interaction due to their capacity to replicate preferentially in proliferating and undifferentiated cells [3].

Gene traps are efficient mutagens as assessed by studies in mice of mutations induced originally in embryonic stem cells. In somatic cells, the approach assumes that loss-of-function mutations induced by gene entrapment may confer reovirus resistance as a result of

gene dosage effects (e.g. haploinsufficiency), pre-existing heterozygosity or loss of heterozygosity. Following infection with the U3NeoSV1 retrovirus gene trap shuttle vector, libraries of mutagenized rat intestinal epithelial (RIE)-1 cell clones were isolated in which each clone contained a single gene disrupted by provirus integration [6]. The entrapment libraries were infected with reovirus type 1, and virus-resistant clones were selected under conditions that also selected against the emergence of persistently infected cells (PI) that may express virus resistance in the absence of cellular mutations [4]. Genes disrupted in a total of 151 reovirus resistant cells were identified by sequencing regions of genomic DNA adjacent to the entrapment vector [6]; of these, 111 contained mutations in previously characterized genes and anonymous transcription units.

Reovirus-resistant clones were selected at higher frequencies from entrapment libraries than from non-mutagenized cells, suggesting that reovirus-resistant phenotypes were induced by gene trap mutagenesis. However in any genetic screen, clones with the selected phenotype may arise from spontaneous mutations, and consequently, additional experiments are required to demonstrate that individual genes disrupted by gene entrapment actually contribute to the reovirus-resistant phenotype. For example, a mutation in *Ctcf*, a transcriptional repressor of insulin growth factor II (IGF-II), was one of 4 mutations associated with reovirus resistance that affected IGF-II expression and/or signaling. Subsequent experiments demonstrated that enforced IGF-II expression is sufficient to confer high levels of reovirus resistance [4]. In short, genes collectively identified by tagged sequence mutagenesis in a panel of reovirus resistant clones provide candidates for mechanistic studies of cellular processes that participate in the virus lifecycle. Since the disrupted genes do not adversely affect cell survival, drugs that inhibit proteins encoded by the genes are not expected to be overtly toxic to cells. Hence, the candidate genes also include targets for novel anti-viral therapies.

RIE-1, L-Cells and Virus:

Reovirus type 1, strain Lang, was initially obtained from Bernard N. Fields. Virus was passaged in L-cells and a third passaged stock was purified over a CsCl gradient as previously described and was used for these experiments [59]. To develop PI cell lines, RIE-1 cells were infected with reovirus type 1, at a multiplicity of infection (MOI) of 5, and surviving cells were maintained in Dulbecco's modification of Eagle's minimum essential medium (DMEM) (Irvine Scientific, Santa Ana, CA, USA). The herpes simplex virus (HSV)-1 clone, HSV-1 KOSTk12, that expresses a reporter gene, lacZ, as an immediate-early

gene [46] was a generous gift of Patricia Spear, Northwestern University, USA. For RIE-1 and L-cells, medium was supplemented with 10% fetal bovine serum, 2 mM per ml, L-Glutamine 100 units per ml, Penicillin, and 100 μ g per ml Streptomycin (Irvine Scientific, Santa Ana, CA, USA) [complete medium]. In some experiments, serum was omitted from the medium. The continuance of cell monolayers following infection with reovirus or HSV-1 was determined by staining with gentian violet.

Tagged sequence mutagenesis and selection for reovirus resistance:

Following infection of RIE-1 cells with the U3neoSV1 vector, MOI of 0.1, mutagenized cells were selected for neomycin resistance in medium containing 1 mg/ml G418 sulfate (Clontech, Palo Alto, CA, USA) [6]. Twenty libraries of mutant RIE-1 cells, and one library of A549 human adenocarcinoma cells, each consisting of 10^4 gene entrapment events, were expanded until approximately 10^3 sibling cells represented each mutant clone. These cells were plated at a sub-confluent density and incubated in serum-free media for 3 days until they became quiescent, and infected with reovirus serotype 1, MOI of 35 plaque forming units (pfu) per cell. Eighteen hours following infection, the cells were detached with trypsin, and plated in DMEM medium containing 10% fetal bovine serum (FBS) (Hyclone Laboratories, Inc., Logan, Utah, USA). After 6 hrs, the medium was removed and cells were maintained in serum-free medium until only a few cells remained attached to the flask. On average, one to ten clones were recovered from a library consisting of 10^7 mutant cells, an enrichment for selected cells of six orders of magnitude. Cells that survived the selection were transferred to cell culture plates in media containing 10% FBS and cells were divided for extraction of DNA and cryopreservation.

Transcription and translation of HSV-1 immediate early gene reporter:

The transcription and translation of the HSV-1 immediate early gene reporter gene, *lacZ*, was determined by standard northern blot techniques and β -galactosidase assay, respectively.

Generation of libraries of mutagenized RIE-1 cells:

Libraries of mutagenized cells were infected with reovirus serotype-1, strain Lang, to select for clones resistant to lytic infection. Selection of virus-resistant clones was performed in serum-free medium to suppress the emergence of persistently infected (PI) cells [4]. This is important since PI cells, which arise by a process involving adaptive mutations in both the

virus and the cell genomes [60], provide a means whereby RIE-1 cells can acquire virus resistance in the absence of cellular mutations. Uninfected RIE-1 cells undergo growth arrest, whereas PI RIE-1 cells are killed in serum-free medium.

5 DNA sequence analysis:

Genomic DNA immediately adjoining the 5' end of the proviral insert in each of 130 cell lines was cloned by plasmid rescue [6]. Approximately 300 to 600 base pairs of this flanking DNA were sequenced and compared with the non-redundant (nr) and expressed sequence tag (dbEST) nucleic acid databases [61]. The probability of a match with orthologous sequences in the databases varies due to interspecies variation, the amount of exon in the flanking DNA (in cases where the flanking DNA matches cDNA sequences), alternative splicing and sequencing errors. Matches with sequences in the database were considered potentially significant if probability score was $<10^{-5}$ and the sequence was non-repetitive. In most cases, the matching gene was in the same transcriptional orientation as the provirus. Moreover, matches involving cDNA sequences were co-linear across exons present in the flanking genomic DNA and diverged at splice sites. As indicated, virtually all of the genes identified had matches to murine, rat, or human gene sequences with $p < 10^{-10}$.

Tagged sequence mutagenesis and selection of reovirus resistant clones

Twenty libraries of mutagenized RIE-1 cells, each representing approximately 10^4 independent gene trap events, were isolated following infection with the U3NeoSV1 gene trap retrovirus. U3NeoSV1 contains coding sequences for a neomycin resistance gene in the U3 region of the viral long terminal repeat (LTR). Selection for neomycin resistance generates clones with proviruses inserted within actively transcribed genes. Cells pooled from each entrapment library were separately infected with Type 1 reovirus at a multiplicity of infection of 35, and reovirus-resistant clones were selected in serum-free media to suppress the emergence of persistently infected (PI) cells (ref). A total of 151 reovirus-resistant clones were isolated--approximately 1 mutant per 10^3 gene trap clones or 1 mutant per 10^7 reovirus infected cells. For comparison, the frequency of recovering resistant clones from RIE-1 cells not mutagenized by gene entrapment was less than 10^{-8} . This suggests that reovirus-resistant phenotypes were induced by gene trap mutagenesis.

Reovirus-resistant cells selected in serum-free media did not express viral antigens (Figure 1) and did not produce infectious virus as assessed by plaque assay. Most clones were resistant to infection by high titer reovirus and were further analyzed (Figure 2). While

reovirus resistance did not initially result from the establishment of a persistent infection, many clones became persistently infected upon subsequent passages, presumably because mutant cells that display virus resistance are susceptible to the establishment of a PI state [2] from residual virus used in selection.

5

Identification of genes disrupted in reovirus-resistant clones

The U3NeoSV1 gene trap vector contains a plasmid origin of replication and ampicillin resistance gene; thus, regions of genomic DNA adjacent to the targeting vector were readily cloned by plasmid rescue and sequenced [6]. The flanking sequences were compared to the nucleic acid databases to identify candidate cellular genes that confer resistance to lytic infection by reovirus when altered by gene entrapment. Altogether, the 151 cloned flanking sequences matched 111 annotated gene and transcription units in the public DNA sequence databases [non-redundant (nr), high-throughput genomic sequences (htgs), and human, mouse, and rat genome sequences [6]. 40 flanking sequences were

uninformative because they matched repetitive elements or regions of genomic DNA not associated with any annotated transcription unit.

Table I lists genes disrupted in reovirus resistant clones for which some functional information is available. The Table also includes genes that encode proteins that are known to physically interact. Genes associated with particular metabolic or signaling pathways are shown in Table 2. These include gene products that could play potential roles in all aspects of virus replication: entry, disassembly, transcription, translation, and reassembly (Table 1, 2, Figure 3). Eleven genes encoding calcyclin, insulin growth factor binding protein 5 protease (prss11), type C-like lectin protein (*Clr*)-f and -C, *Dnaja1*-/Aprataxin+ (*Aprx*), GATA binding protein 4 (*Gata4*), Bcl2 like-1 (*Bcl2L1*); and chromosome 10 open reading frame 3 (*Chr10orf3*) and *myoferlin*, fer-1 like protein 3 (*Fer1l3*), S100a6 (encoding calcyclin), and two functionally anonymous cDNAs were independently mutated in separate cell libraries (Table 1). The proviruses in these independent of mutant clones were located within 7 to over 1500 nucleotides of each other.

Resistance to HSV-1

Experiments were conducted to determine if genes were resistant to HSV-1 infection. These experiments utilized HSV-1(KOS)tk12, an infectious virus that expresses a *lacZ* reporter as an immediate-early gene [46]. Four clones, with mutations in the *Eif3s10*, *Anxa1*, *Mgat1*, and *Igf2r* genes, were resistant to HSV-I infection and there was a diminished

capacity to express the immediate-early *lacZ* reporter gene. Clones with mutations in *Eif3s10*, *Mgat1*, and *Igf2r* also show decreases in transcription and translation of virus mRNA and cell death. Mutations in the *Igf2r* are known to affect HSV replication [15, 54, 58]; whereas, association of HSV replication with proteins encoded by the *Eif3s10*, *Anxa1*, and *Mgat1* are novel. These data show that some of the candidate genes discovered in clones surviving reovirus infection can affect common cellular processes that are used by other viruses.

TABLE I

GENE	Definition	Rat CHR	Human CHR	Rat Genbank Accession	Human Genbank Accession # for mRNA	Human GenBank Accession # for protein	Clone Designation	Genbank Accession # for Nucleic Acid Insert	Entrez Gene for Rat Gene	Entrez Gene for Human Gene
<i>Loc310836</i> (<i>Abca4</i>)	ATP-binding cassette, subfamily A (ABCA1), member 4	2q41	1p22.1-p21	XP_241525	NM_000350	NP_000341	6BE65_T7	AR228076 BD069426 SEQ ID NO: 69 from U.S. Patent No. 6,448,000;	310836	24
<i>Anxa1</i>	annexin A1	1q51	9q12-q21.2	U25159	NM_000700	NP_000691	6B37H_T7	AR228072 BD069422 sequence 65 from U.S. Patent No. 6,448,000	25380	301
<i>Anxa2</i>	annexin A2	8q24	15q21-q22	NM_019905	NM_001002857 NM_001002858 NM_004039	NP_001002857 NP_001002858 NP_004030	7A7_rE	AR228047 BD069397 sequence 40 from U.S. Patent No. 6,448,000;	56611	302

GENE	Definition	Rat CHR	Human CHR	Rat Genbank Accession	Human Genbank Accession # for mRNA	Human GenBank Accession # for protein	Clone Designation	Genbank Accession # for Nucleic Acid Insert	Entrez Gene for Rat Gene	Entrez Gene for Human Gene
								<u>BD078939</u> SEQ ID NO: 19 from U.S. Patent No. 6,777,177;		
<i>Anx3</i>	annexin A3	14p22	4q13-q22	NM_012823	NM_005139	NP_005130	70A-rE	<u>BD079025</u> SEQ ID NO: 105 from U.S. Patent No. 6,777,177	<u>25291</u>	<u>306</u>
<i>Aptx-1</i> <i>dnajl1</i> [Hsf2]	apataxin/DnaJ (Hsp40) homolog, subfamily A, member 1	5q22	9p13.3	NW_07454	NM_017692 NM_175069 NM_175071 NM_175072/ NM_001539	NP_060162 NP_778239 NP_778241 NP_778242/ NP_001530	12_3b#7-rE 12_3B#8-rE	<u>BD078944</u> SEQ ID NO: 24 U.S. Patent No. 6,777,177 <u>BD078943</u> SEQ ID NO: 23 from U.S. Patent No.	<u>25271</u> <u>65028</u>	<u>54840</u> <u>3301</u>
							9B27_2_rE			

GENE	Definition	Rat CHR	Human CHR	Rat Genbank Accession	Human Genbank Accession # for mRNA	Human GenBank Accession # for protein	Clone Designation	Genbank Accession # for Nucleic Acid Insert	Entrez Gene for Rat Gene	Entrez Gene for Human Gene
<i>Atp6v0c</i>	ATPase, H+ transporting, lysosomal 16kDa, V0 subunit c	10q12	16p13.3	NC_000016	NM_001694	NP_001685	6BE3_lac	6,777,177 BD078945 SEQ ID NO: 25 from U.S. Patent No. 6,777,177	170667	527
<i>Bcl2l1</i>	Bcl2-like1	3q41.2	20q11.21	NP_238186	NM_001191 NM_138578	NP_001182 NP_612815	L197B3E-rE L24 5-3-rE L24-4-4-rE	6,448,000 BD079008 SEQ ID NO: 88 from U.S. Patent No. 6,777,177 , BD079032 SEQ ID NO: 112, U.S. Patent	24888	598

GENE	Definition	Rat CHR	Human CHR	Rat Genbank Accession	Human Genbank Accession # for mRNA	Human GenBank Accession # for protein	Clone Designation	Genbank Accession # for Nucleic Acid Insert	Entrez Gene for Rat Gene	Entrez Gene for Human Gene
								No. 6,777,177		
<i>Brd2</i>	bromodomain- containing 2	20p12	6p21.3	XP_238186	NM_005104	NP_005095	36_5_2_6-rE	BD078987 SEQ ID NO: 67 from U.S. Patent No. 6,777,177	294276	6046
<i>Brd3/ Wdr5</i>	Bromodomain- containing 3/ WD repeat domain 5	3p12	9q34	XP_342398 XP_342397	NM_007371/ NM_017588 NM_052821	NP_031397/ NP_060058 NP_438172	1A_rE	AR228036, BD069386 SEQ ID NO: 29 from U.S. Patent No. 6,448,000	362093	8019/ 11091
<i>C9orf119+/ Golga2-</i>	gene of unknown function Golgi autoantigen, Golgin subfamily a, 2	3p11	9q34.13	NW_047652 NM_022596	XM_372143 BC029911 NM_004486	XP_372143 AAH29911 NP_004477	6_3_6_2E-rE	BD078967 SEQ ID NO: 47 from U.S. Patent No. 6,177,177	375757	375757 2801

GENE	Definition	Rat CHR	Human CHR	Rat Genbank Accession	Human Genbank Accession # for mRNA	Human GenBank Accession # for protein	Clone Designation	Genbank Accession # for Nucleic Acid Insert	Entrez Gene for Rat Gene	Entrez Gene for Human Gene
<i>C10orf3</i>	chromosome 10 open reading frame 3	1q54	10q23.33	XP_220034	NM_018131	NP_060601	14_24#6-rE L24 5-3-rE L192A3E-rE 6b52-rE	AR228054 BD069404 SEQ ID NO: 47 from U.S. Patent No. 6,448,000; BD078938 SEQ ID NO: 88 from U.S. Patent No. 6,777,177 BD078978 SEQ ID NO: 58 from U.S. Patent No. 6,777,177 AR228049 BD069399, SEQ ID NO: 42 from U.S.	55165	55165

GENE	Definition	Rat CHR	Human CHR	Rat Genbank Accession	Human Genbank Accession # for mRNA	Human GenBank Accession # for protein	Clone Designation	Genbank Accession # for Nucleic Acid Insert	Entrez Gene for Rat Gene	Entrez Gene for Human Gene
								Patent No. 6,448,000		
<i>Cald1</i>	caldesmon 1	4q22	7q33	NM_004342 NM_033138 NM_033139 NM_033140 NM_033157	NP_004333 NP_149129 NP_149130 NP_149131 NP_149347	191E2E-rE	BD078958 SEQ ID NO: 38 from U.S. Patent No. 6,777,177	25687	800	
<i>Calm2</i>	calmodulin 2 (phosphorylase kinase, delta)	6q11- q12	2p21	NM_001743	NP_001734	32-3-2#1E/-rE	BD078921 SEQ ID NO: 1 from U.S. Patent No. 6,777,177	50663	805	

GENE	Definition	Rat CHR	Human CHR	Rat Genbank Accession	Human Genbank Accession # for mRNA	Human GenBank Accession # for protein	Clone Designation	Genbank Accession # for Nucleic Acid Insert	Entrez Gene for Rat Gene	Entrez Gene for Human Gene
<i>Celsr2</i>	cadherin, EGF LAG seven-pass G-type receptor 2	4q11	1p21	NW_047687	NM_001408	NP_001399	12_4b_9-rE	AR228032, SEQ ID NO: 25 from U.S. Patent No. 6,448,000; AR228027 SEQ ID NO: 20 from U.S. Patent No. 6,448,000 BD069377; BD069382	83465	1952
<i>Ctr-f</i>	killer cell lectin- like receptor F1	4q12	N/A	XM_232399	N/A	N/A	36_7_1a-rE SCA9#14_rE	BD078982 SEQ ID NO: 62 from U.S. Patent No. 6,777,177 AR228038 SEQ ID NO: 31 from U.S.	312745	N/A

GENE	Definition	Rat CHR	Human CHR	Rat Genbank Accession	Human Genbank Accession # for mRNA	Human GenBank Accession # for protein	Clone Designation	Genbank Accession # for Nucleic Acid Insert	Entrez Gene for Rat Gene	Entrez Gene for Human Gene
<i>Copg2</i> / <i>Tsgal3</i>	coatamer protein complex, subunit gamma 2/ testis specific gene A13- variegated monoallelic expression 1	4q22	7q32	NW_047355/ XP_231582	NM_012133/ NM_052933	NP_036265 NP_443165	36_5_2-19b_lac 12cx#11-rE	Patent No. 6,448,000 AR228051, SEQ ID NO: 44 from U.S. Patent 6,448,000; BD078955 SEQ ID NO: 35 from U.S. Patent 6,777,177, BD078941, BD069401, BD078988 SEQ ID NO: 68 from U.S. Patent 6,777,177.	301742 312203	26958 114960

GENE	Definition	Rat CHR	Human CHR	Rat Genbank Accession	Human Genbank Accession # for mRNA	Human GenBank Accession # for protein	Clone Designation	Genbank Accession # for Nucleic Acid Insert	Entrez Gene for Rat Gene	Entrez Gene for Human Gene
<i>Csf2l</i>	cleavage stimulation factor, 3' pre-RNA, subunit 2, 64kDa	1q52	10q11	NW_047565	NM_015235	NP_056050	19_9BE_rE	BD078960 SEQ ID NO: 40 from U.S. Patent No. 6,777,177, BD078958 SEQ ID NO: 38 from U.S. Patent no. 6,777,177	309338	23283
<i>Csmd2</i>	CUB and sushi multiple domains 2	5q36	1p35.1-p34.3	XP_232753	NM_052896	NP_443128	L24_9_1-rE	BD079033 SEQ ID NO: 113 in U.S. Patent 6,777,177	313040	114784
<i>Ctcf</i>	CCCTC-binding factor (zinc finger protein)	19q12	16q21-q22.3	NP_114012	NM_006565	NP_006556	6BE72_rE	AR228009 BD069366 SEQ ID NO: 2 from U.S. Patent No. 6,448,000;;	83726	10664

GENE	Definition	Rat CHR	Human CHR	Rat Genbank Accession	Human Genbank Accession # for mRNA	Human GenBank Accession # for protein	Clone Designation	Genbank Accession # for Nucleic Acid Insert	Entrez Gene for Rat Gene	Entrez Gene for Human Gene
<i>Cutl1/ Mylc2pt⁺</i>	cut-like 1, CCAAT displacement protein (Drosophila) myosin light chain 2, precursor lymphocyte- specific	12q12	7q22.1	XP_341054 XP_344098	NM_001913 NM_181500 NM_181552/ NM_138403	NP_001904 NP_852477 NP_853530/ NP_612412	31_3_17_rE	BD079017 BD078994 SEQ ID NO: 74 from U.S. Patent No. 6,777,177	116639/ 363900	1523 93408
<i>Dlx2</i>	distal-less homeo box 2 similar to TES-1 homeobox	3q21	2q32	XP_230986	NM_004405	NP_004396	1.24_4_2BE_rE	BD079037 SEQ ID NO: 117 from U.S. Patent No. 6,777,177	296499	1746
<i>DnaJ1</i>	DnaJ (Hsp40) homolog, subfamily A, member 1	5q22	9p13-p12	NP_075223	NM_001539	NP_001530	10_46_4-Lac 12_3B#8-rE	BD078944 SEQ ID NO: 24 from U.S. Patent 6,777,177	65028	3301

GENE	Definition	Rat CHR	Human CHR	Rat Genbank Accession	Human Genbank Accession # for mRNA	Human GenBank Accession # for protein	Clone Designation	Genbank Accession # for Nucleic Acid Insert	Entrez Gene for Rat Gene	Entrez Gene for Human Gene
<i>Dre1</i> Also known as <i>KLHL24</i>	Dre1 protein	11q23	3q27.1	NM_181473	NM_017644	NP_060114	10_4b_4-rE	AR228014, SEQ ID NO: 7 from U.S. Patent No. 6,448,000; BD069364 BD078933 SEQ ID NO: 13 from U.S. Patent No. 6,777,177	303803	54800
<i>E2ig2</i>	Estrogen induced gene 2	1q32	11q13.3	NP_057649	NM_016565	NP_057649	L197B3E-rE for	BD078972 SEQ ID NO: 52 from U.S. Patent No. 6,777,177		51287
<i>Eij3s10</i>	Elongation initiation factor 3 subunit 10	1q55	10q26	NW_047570	NM_003750	NP_003741	12PSA#6_rE	AR228011 BD069361 SEQ ID NO: 4 from U.S. Patent	292148	8661

GENE	Definition	Rat CHR	Human CHR	Rat Genbank Accession	Human Genbank Accession # for mRNA	Human GenBank Accession # for protein	Clone Designation	Genbank Accession # for Nucleic Acid Insert	Entrez Gene for Rat Gene	Entrez Gene for Human Gene
<i>ErbB2ip</i>	ErbB2 interacting protein	2q12	5q13.1	XP_345149	NM_018695	NP_061165	SCA9#14_rE ScB2#19-rE	No. 6,448,000 <u>AR228015</u> <u>BD069365</u> SEQ ID NO: 8 from U.S. Patent No. 6,448,000		<u>55914</u>
<i>Fer1l3</i>	fer-1-like protein 3, myoferlin	1q53	10q24	NW_047565	NM_013451 NM_133337	NP_038479 NP_579899	14_24_#6-rE 6b52-re	<u>AR228049</u> , <u>BD069399</u> SEQ ID NO: 42 from U.S. Patent No. 6,448,000		<u>26509</u>
<i>Fkbp8</i>	FK506 binding protein 8, 38kDa	16p14	19p12	XP_214316	NM_012181	NP_036313	31_3_15#1_Lac 31_3_15#1_rE 31_3_6_2-rE.	<u>BD079018</u> <u>BD078996</u> SEQ ID NO: 76 from U.S. Patent No. 6,777,177;		<u>23770</u>

GENE	Definition	Rat CHR	Human CHR	Rat Genbank Accession	Human Genbank Accession # for mRNA	Human GenBank Accession # for protein	Clone Designation	Genbank Accession # for Nucleic Acid Insert	Entrez Gene for Rat Gene	Entrez Gene for Human Gene
								<u>BD079016</u> , <u>BD078993</u> SEQ ID NO: 96 from U.S. Patent No. 6,777,177		
<i>Fusip1</i>	FUS interacting protein (serine- arginine rich) 1	5q36	1p36.11	XP_342949	NM_006625 <u>NM_054016</u>	NP_006616 <u>NP_473357</u>	L28ap-rE	<u>BD079009</u> SEQ ID NO: 89 from U.S. Patent No. 6,777,177	<u>362630</u>	<u>10772</u>
<i>Gas5</i>	Growth arrest specific 5	13q21	1q23.3	U77829	<u>AK025846</u> <u>AL110141</u> <u>BC038733</u>	N/A	10_4A_8_rE	<u>AR228010</u> <u>BD069360</u> SEQ ID NO: 3 from 6,448,000	<u>81714</u>	<u>60674</u>
<i>Gata4</i>	GATA binding protein 4	15p12	8p23.1-p22	NW_047454	<u>NM_002052</u>	NP_002043	10_2A_3_12-rE 10_2A_3-rE	<u>AR228023</u> SEQ ID NO: 16 from U.S. Patent No.		<u>2626</u>

GENE	Definition	Rat CHR	Human CHR	Rat Genbank Accession	Human Genbank Accession # for mRNA	Human GenBank Accession # for protein	Clone Designation	Genbank Accession # for Nucleic Acid Insert	Entrez Gene for Rat Gene	Entrez Gene for Human Gene
								6,448,000 BD069373; AR228024 SEQ ID NO: 17 from U.S. Patent No. 6,448,000		
<i>Grb2</i>	Growth factor receptor bound protein 2	10q32.2	17q24-q25	NP_110473	NM_002086 NM_203506..	NP_002077 NP_987102.	36_5_2_19a	In process	81504	2885
<i>Gtf2e1/</i>	General transcription factor III ϵ , polypeptide 1, alpha 56kDa;	11q22	3q21-q24	XP_221426	NM_005513/	NP_005504/	L195B1E	BD078975 SEQ ID NO: 55 from U.S. Patent No. 6,777,177		2960
<i>Rabl3</i>	RAB, member of RAS oncogene family-like 3			XP_340993	NM_173825	NP_776186			360720	285282
<i>HML3</i>	histocompatibility (minor) 13, human gene from A549 cell library		20q11.21		NM_030789.	NP_110416	RA3_A-rE RA2#C_rE			81502

GENE	Definition	Rat CHR	Human CHR	Rat Genbank Accession	Human Genbank Accession # for mRNA	Human GenBank Accession # for protein	Clone Designation	Genbank Accession # for Nucleic Acid Insert	Entrez Gene for Rat Gene	Entrez Gene for Human Gene
<i>HNRPL</i>	heterogeneous nuclear ribonucleoprotein L- human gene from A549 cell library	1q21	19q13.2		NM_001533	NP_001524	RA2_A-rE			3191
<i>Hoxc13</i>	Homeo box C13	7q36	12q13.3	XP_345881	NM_017410	NP_059106	L191B2E#3+_rE	BD078923 SEQ ID NO: 3 from U.S. Patent No. 6,777,177	366995	3229
<i>Hpl-bp74</i>	heterochromatin protein 1, binding protein 74	5q36	1p36.13	NM_199108	NM_016287	NP_057371	10_3bE	AR228022 ;BD069372 SEQ ID NO: 15 from U.S. Patent No. 6,448,000	313647	50809
<i>Hspc135⁺</i> <i>Mox2r</i>	HSPC135 protein homologue/ Cd200 receptor 2	11q21	3q13.2	XP_340986 NP_076443	NM_014170/ NM_138806 NM_138939	NP_054889/ NP_620161 NP_620385	14D#8	AR228059 BD069409 SEQ ID NO: 52 from U.S.	360714/ 29083	131450

GENE	Definition	Rat CHR	Human CHR	Rat Genbank Accession	Human Genbank Accession # for mRNA	Human GenBank Accession # for protein	Clone Designation	Genbank Accession # for Nucleic Acid Insert	Entrez Gene for Rat Gene	Entrez Gene for Human Gene
					NM_138940 NM_170780	NP_620386 NP_740750		Patent No. 6,448,000;		
<i>Id3</i>	Inhibitor of DNA binding 3, dominant negative helix-loop-helix protein	5q36	1p36.13- p36.12	NP_037190	NM_002167	NP_002158	21_5_8E-rE 21_5_7E-rE 21_5_9E-rE	BD078974 SEQ ID NO: 54 from U.S. Patent No. 6,777,177 BD078924 SEQ ID NO: 4 from U.S. Patent No. 6,777,177, BD079042 SEQ ID NO: 122 from U.S. Patent No. 6,777,177	25585	3399
<i>Igf2r</i>	Insulin-like	1q11	6q26	NW_047553	NM_000876	NP_000867	L192B3E#13 rE	BD078980	25151	3482

GENE	Definition	Rat CHR	Human CHR	Rat Genbank Accession	Human Genbank Accession # for mRNA	Human GenBank Accession # for protein	Clone Designation	Genbank Accession # for Nucleic Acid Insert	Entrez Gene for Rat Gene	Entrez Gene for Human Gene
	growth factor 2 receptor (IGF2R)							SEQ ID NO: 60 from U.S. Patent No. 6,777,177		
<i>Jak1</i>	Tyrosine-protein kinase JAK1	5q33	1p32.3-p31.3	XP_342873	NM_002227	NP_002218	18A_8_4E-rE	BD078969 BD079044 SEQ ID NO: 49 U.S. Patent No. 6,777,177	362552	3716
<i>Kif13b</i>	guanylate kinase associated kinesin	15p12	8p12	XP_224288	NM_015254	NP_056069	194c4e-rE	BD078976 SEQ ID NO: 56 from U.S. Patent No. 6,777,177	305967	23303
<i>Klhl6</i>	kelch-like 6	11q23	3q27.3	NW_047358	NM_130446	NP_569713	10_3b_2_rE 10_4b_4-rE	AR228020 BD069370 SEQ ID NO: 13		89857

GENE	Definition	Rat CHR	Human CHR	Rat Genbank Accession	Human Genbank Accession # for mRNA	Human GenBank Accession # for protein	Clone Designation	Genbank Accession # for Nucleic Acid Insert	Entrez Gene for Rat Gene	Entrez Gene for Human Gene
Ki-67	proliferation related antigen	2q26	10q25	XP_227096	NM_002417	NP_002408	12_4b#11_rE	from U.S. Patent No. 6,448,000;; BD078933 SEQ ID NO: 13 from U.S. Patent No. 6,777,177; AR228014 SEQ ID NO: 7 from U.S. Patent No. 6,448,000 AR228033, , BD069383 SEQ ID NO: 26 from U.S. Patent No. 6,448,000	310382	4288

GENE	Definition	Rat CHR	Human CHR	Rat Genbank Accession	Human Genbank Accession # for mRNA	Human GenBank Accession # for protein	Clone Designation	Genbank Accession # for Nucleic Acid Insert	Entrez Gene for Rat Gene	Entrez Gene for Human Gene
<i>Lipc</i> / LOC363090 Human Genbank accession Nos. and Entrez Gene correspond to Lipc gene	lipase, member H glyceroldehyde-3- phosphate dehydrogenase (phosphorylating)	8q24	15q21-q23	NM_012597XP_343422	NM_000236/	NP_000227/	6BSA12_rE	AR228018, BD069368 SEQ ID NO: 11 from U.S. Patent No. 6,448,000,, AR228046 BD069396 SEQ ID NO: 39 from U.S. Patent No. 6,448,000;	24538/ 363090	3990
<i>Madh7</i>	MAD, mothers against decapentaplegic homolog 7 (Drosophila)	18q12.3	18q21.1	NW_047516	NM_005904	NP_005895	14A7re	BD078950 SEQ ID NO: 30 from U.S. Patent No. 6,777,177		4092

GENE	Definition	Rat CHR	Human CHR	Rat Genbank Accession	Human Genbank Accession # for mRNA	Human GenBank Accession # for protein	Clone Designation	Genbank Accession # for Nucleic Acid Insert	Entrez Gene for Rat Gene	Entrez Gene for Human Gene
<i>IKBζ</i> (MAIL)	Molecule possessing ankyrin repeats induced by lipopolysaccharide	11q12	3p12-q12	NW_047355	NM_031419 NM_001005474	NP_113607 NP_001005474	31_3_9_rE	BD079015 BD078992 SEQ ID NO: 95 from U.S. Patent No. 6,777,177,		64332
<i>Map3k7ip1</i>	Mitogen-activated protein kinase kinase kinase 7 interacting protein 1	7q34	22q13.1	NW_047780	NM_006116 NM_153497	NP_006107 NP_705717	34X24_126-rE	BD078985 SEQ ID NO: 65 from U.S. Patent No. 6,777,177		10454
<i>Mapt</i>	Microtubule- associated protein TAU	10q32.1	17q21.1	NM_017212	NM_005910 NM_016834 NM_016835 NM_016841	NP_005901 NP_058518 NP_058519 NP_058525	12_3B#7	AR228033, BD069383 SEQ ID NO: 26 from U.S. Patent No. 6,448,000;	360248	4137

GENE	Definition	Rat CHR	Human CHR	Rat Genbank Accession	Human Genbank Accession # for mRNA	Human GenBank Accession # for protein	Clone Designation	Genbank Accession # for Nucleic Acid Insert	Entrez Gene for Rat Gene	Entrez Gene for Human Gene
<i>Mgat1</i>	mannosyl (alpha-1,3-)-glycoprotein beta-1,2-N-acetylglucosaminyltransferase	10q21	5q35	NW_047334	NM_002406	NP_002397	14_7#2E_rE	AR228012, BD069362, SEQ ID NO: 5 from U.S. Patent No. 6,448,000; BD079013 SEQ ID NO: 93 from U.S. Patent No. 6,777,177 BD078952 SEQ ID NO: 32 from U.S. Patent No. 6,777,177,	81519	4245
<i>Mical2</i>	flavoprotein oxidoreductase	1q33	11p15.3	NP_872610	NM_014632	NP_055447	12C#A_rE	AR228031, BD069381 SEQ ID NO: 24	365352	9645

GENE	Definition	Rat CHR	Human CHR	Rat Genbank Accession	Human Genbank Accession # for mRNA	Human GenBank Accession # for protein	Clone Designation	Genbank Accession # for Nucleic Acid Insert	Entrez Gene for Rat Gene	Entrez Gene for Human Gene
<i>Ocil</i>	osteoclast inhibitory lectin C-type	4q32	12p13	XP_342770	NM_001004419 NM_001004420 NM_013269	NP_001004419 NP_001004420 NP_037401	14XD#12E-rE 191E9E-rE	from U.S. Patent No. 6,448,000; <u>BD078931</u> SEQ ID NO: 11 form U.S. Patent No. 6,777,177,	<u>113937</u>	<u>29121</u>

GENE	Definition	Rat CHR	Human CHR	Rat Genbank Accession	Human Genbank Accession # for mRNA	Human GenBank Accession # for protein	Clone Designation	Genbank Accession # for Nucleic Acid Insert	Entrez Gene for Rat Gene	Entrez Gene for Human Gene
								<u>BD078951</u> SEQ ID NO: 31 from U.S. Patent No. 6,777,177		
<i>OL16</i> [<i>Asam</i> in <i>humans</i>]	adipocyte specific protein 5 and splice variant ol- 16	8q22	11q24.1	NM_173154	NM_024769	NP_079045	X236E1_T7 X236E1_T3		<u>286939</u>	<u>79827</u>
<i>Numb</i>	putative inhibitor of Notch signaling	6q31	14q24.3	XP_234394	NM_003744	NP_003735	SCA7#5_rE	<u>AR228078</u> SEQ ID NO: 71 from U.S. Patent No. 6,448,000;	<u>29419</u>	<u>8650</u>
<i>Pde4b-1</i>	phosphodiesterase 4B, cAMP- specific (phosphodiesterase E4 dunce homolog, Drosophila)	5q32	1p31	NP_058727	NM_002600	NP_002591	34X25_23_Lac	<u>BD078990</u> SEQ ID NO: 70 from U.S. Patent No. 6,777,177	<u>24626</u>	<u>5142</u>

GENE	Definition	Rat CHR	Human CHR	Rat Genbank Accession	Human Genbank Accession # for mRNA	Human GenBank Accession # for protein	Clone Designation	Genbank Accession # for Nucleic Acid Insert	Entrez Gene for Rat Gene	Entrez Gene for Human Gene
<i>Pgy1- (Abcb1)</i>	ATP-binding cassette, sub- family B (MDR/TAP), member 1	4q12	7q21.1	NM_012623	NM_000927	NP_000918	34X23_3-rE	BD078989 SEQ ID NO: 69 from U.S. Patent No. 6,777,177	24646	5243
<i>Prss11</i>	protease, serine, 11 (IGF binding)	1q37	10q26.3	NP_113909	NM_002775	NP_002766	12CXY#7_rE	BD069425 AR228075 SEQ ID NO: 68 from U.S. Patent No. 6,448,000	65164	5654
<i>Psa</i>	Aminopeptidase puromycin sensitive	10q31	17q21	NW-047338	NM_006310	NP_006301	8C5_6_rE	BD069403; AR228053 SEQ ID NO: 46 from U.S. Patent No. 6,448,000	50558	9520
<i>Psm7</i>	proteasome (prosome, macropain) subunit, alpha	3q43	20q13.33	XP_342599	NM_002792 NM_152255	NP_002783 NP_689468	12CX#11E_rE 35 5 1 4a-rE I	BD078983 SEQ ID NO: 62	29674	5688

GENE	Definition	Rat CHR	Human CHR	Rat Genbank Accession	Human Genbank Accession # for mRNA	Human GenBank Accession # for protein	Clone Designation	Genbank Accession # for Nucleic Acid Insert	Entrez Gene for Rat Gene	Entrez Gene for Human Gene
	type, 7							from U.S. Patent No. 6,777,177		
<i>Pts</i>	6-pyruvoyl- tetrahydropterin synthase	8q23	11q22.3- q23.3	NP_058916	NM_000317	NP_000308	19D5E_rE	BD078942 SEQ ID NO: 22 from U.S. Patent No. 6,777,177	29498	5805
<i>Rfp2</i>	ret finger protein 2 or Trim13	15p12	13q14	NM_005798	NM_005798 NM_052811 NM_213590	NP_005789 NP_434698 NP_998755	1A_A549_6_rE			10206
<i>Rps18</i>	S18 ribosomal protein, cytosolic, substrate for Ca2+/ calmodulin- activated protein kinase II	5q24	6p21.3	XP_232915	NM_022551	NP_072045	12_4b#11_rE 12_4b#7_rE	AR228028 BD069378 SEQ ID NO: 21 from U.S. Patent No. 6,448,000;	298014	6222

GENE	Definition	Rat CHR	Human CHR	Rat Genbank Accession	Human Genbank Accession # for mRNA	Human GenBank Accession # for protein	Clone Designation	Genbank Accession # for Nucleic Acid Insert	Entrez Gene for Rat Gene	Entrez Gene for Human Gene
<i>Rin2</i>	ras association (RalGDS/AF-6) domain containing protein JC265; RAB5 interacting protein 2	3q41	20p11	XP_230647	NM_018993	NP_061866	12_3B#10-rE	AR228026 BD069376 SEQ ID NO: 19 from 6,448,000	311494	54453
<i>Ror1</i>	Receptor tyrosine kinase-like orphan receptor 1	5q33	1p32-p31	XP_238402	NM_005012	NP_005003	12_6B#6_rE	AR228030, BD069380 SEQ ID NO: 23 from U.S. Patent No. 6,448,000	117094	4919
<i>Rraga</i>	Ras-related GTP binding A	5q32	9p21.3	NP_446425	NM_006570	NP_006561	L193A1E#A_rE	BD078977 SEQ ID NO: 57 from U.S. Patent No. 6,777,177	117044	10670
<i>Ryk</i>	Receptor-like tyrosine kinase	8q32	3q22	XP_343459	NM_002958	NP_002949	19-7ae_rE	BD078959 SEQ ID NO: 39 from U.S. Patent No.	140585	6259

GENE	Definition	Rat CHR	Human CHR	Rat Genbank Accession	Human Genbank Accession # for mRNA	Human Genbank Accession # for protein	Clone Designation	Genbank Accession # for Nucleic Acid Insert	Entrez Gene for Rat Gene	Entrez Gene for Human Gene
<i>S100a6</i>	S100 calcium binding protein A6 (calyculin)/	2q34	1q21	NP_445937	NM_014624/ NM_006271	NP_055439/ NP_006262	L25_10-Lac 18_3#3E-rE is SEQ ID NO: 6 and 3_2_4-rE is 61 and 110 from U.S. patent No. 6,777,177 SEQ ID NO: 111 is L25-10-rE SEQ ID NO: 114 is 17-L25-27#7- rE SEQ ID NO: 109 is 3_2_13-rE SEQ ID NO: 115 is L21C1E-rE	6,777,177	85247	6277
<i>S100a1</i>	S-100 protein, alpha chain			XP_215606				AR228013, SEQ ID NO: 6 from U.S. Patent No. 6,777,177 BD069363, BD079030 SEQ ID NO: from U.S. Patent Nos. 61 and 110 6,777,177 BD078981, BD079031 SEQ ID NO: 111 from U.S. Patent No. 6,777,177, BD079034	295214	6271

GENE	Definition	Rat CHR	Human CHR	Rat Genbank Accession	Human Genbank Accession # for mRNA	Human GenBank Accession # for protein	Clone Designation	Genbank Accession # for Nucleic Acid Insert	Entrez Gene for Rat Gene	Entrez Gene for Human Gene
<i>Scnh1</i>	sex comb on midleg homolog 1 (Drosophila)	5q36	1p34	XP_342901	NM_012236	NP_036368	38_17#2_rE	SEQ ID NO: 114 from U.S. Patent No. 6,777,177, BD079029 SEQ ID NO: 109 from U.S. Patent No. 6,777,177, BD079035 SEQ ID NO: 115 from U.S. Patent No. 6,777,177, In process		22955

GENE	Definition	Rat CHR	Human CHR	Rat Genbank Accession	Human Genbank Accession # for mRNA	Human GenBank Accession # for protein	Clone Designation	Genbank Accession # for Nucleic Acid Insert	Entrez Gene for Rat Gene	Entrez Gene for Human Gene
<i>Serp1</i>	Stress-associated endoplasmic reticulum protein 1	15q11	3q25.1	NM_030835	NM_014445	NP_055260	191E8E_rE	<u>BD078962</u> SEQ ID NO: 42 from U.S. Patent No. 6,777,177	<u>80881</u>	<u>27230</u>
<i>Srp19</i>	signal recognition particle 19kDa	18p12	5q21-q22	NW_047510	NM_003135	NP_003126	14C_2E_rE	<u>BD078963</u> SEQ ID NO: 43 from U.S. Patent No. 6,777,177,	<u>291685</u>	<u>6728</u>
<i>Stmn1</i>	Stathmin, microtubule- depolymerizing protein	8q31	1p36.1-p35	XP_343442	NM_005563 NM_203399 NM_203401	NP_005554 NP_981944 NP_981946	SCA6#1_rE	<u>AR228025</u> , <u>BD069375</u> SEQ ID NO: 18 from U.S. Patent No. 6,448,000;	<u>363108</u>	<u>3925</u>
<i>Tpm1</i>	tropomyosin 1 (alpha)	8q24	15q22.1	NW_047799	NM_000366	NP_000357	6BE60_rE	<u>BD078934</u> SEQ ID NO: 14	<u>24851</u>	<u>7168</u>

GENE	Definition	Rat CHR	Human CHR	Rat Genbank Accession	Human Genbank Accession # for mRNA	Human GenBank Accession # for protein	Clone Designation	Genbank Accession # for Nucleic Acid Insert	Entrez Gene for Rat Gene	Entrez Gene for Human Gene
<i>Trim52</i>	Tripartite motif- containing 52	15q22	5q35.3	XM_224468	NM_032765	NP_116154	L24_26_2A-rE L24_3_2B-rE L24_26_1-BL	from U.S. Patent No. 6,777,177 BD079011 SEQ ID NO: 91 from U.S. Patent No. 6,777,177; BD079005 SEQ ID NO: 85 from U.S. Patent No. 6,777,177; BD079002 SEQ ID NO: 82 from U.S. Patent No. 6,777,177	290458	84851

GENE	Definition	Rat CHR	Human CHR	Rat Genbank Accession	Human Genbank Accession # for mRNA	Human GenBank Accession # for protein	Clone Designation	Genbank Accession # for Nucleic Acid Insert	Entrez Gene for Rat Gene	Entrez Gene for Human Gene
<i>Tsec-2⁺</i> / <i>Mthfd1</i>	<i>tsec-2⁺</i> /C1- tetrahydrofolate synthase	6q24	14q24	NW_047761 NM_022508	NM_005956	NP_005947	36_5_2_196-rE 14D#18-rE	AR228055 BD069405 SEQ ID NO: 48 from U.S. Patent No. 6,448,000,	299152 64300	4522
<i>Ubelc</i>	ubiquitin- activating enzyme E1C	4q34	3p24.3-p13	NP_476553	NM_003968 NM_198195 NM_198197	NP_003959 NP_937838 NP_937840	12_3B#2_rE	AR228029 BD069379 SEQ ID NO: 22 from 6,448,000,	117553	9039
<i>Zfp207</i>	zinc finger protein 207	10q26	17q12	XP_221231	NM_003457	NP_003448	31_3_5-rE	BD078995 SEQ ID NO: 75 from U.S. Patent No. 6,777,177	303763	7756
<i>Znf7</i>	Zinc finger protein 7	7q34	8q24	XP_235457	NM_003416	NP_003407	1bw_lac		315101	7553

Table 2. Classification of trapped genes according to function.

Trapped genes are listed by the official HUGO Gene Nomenclature Committee names, when available. Functional placement of genes or their products are determined by literature assignments. Some genes perform more than one cellular role, and are classified arbitrarily and others have undefined roles.

Transcription	Cytoskeletal-Related	Membrane	Signaling	Vesicle/Trafficking	
<i>Brd2</i>	<i>Anx3</i>	<i>Abca4</i>	<i>E2ip2</i>	<i>Anxa1</i>	
<i>Brd3</i>	<i>Cald1</i>	<i>Csmd2</i>	<i>Fusip1</i>	<i>Anxa2</i>	
<i>Ctcf</i>	<i>Calm2</i>	<i>Celsr2</i>	<i>Fkbp8</i>	<i>Atp6v0c</i>	
<i>E2f2</i>	<i>Mapt</i>	<i>Erbp2ip</i>	<i>Gata4</i>	<i>Copg2</i>	
<i>Gtf2e1</i>	<i>Ppm1a</i>	<i>OL16</i>	<i>Grb2</i>	<i>Golga2</i>	
<i>Hnrpl</i>	<i>Rps18</i>	<i>Pgy1</i>	<i>Jak1</i>	<i>Hm13</i>	
<i>Hoxc13</i>	<i>Stmn1</i>	<i>Rab13</i>	<i>Madh7</i>	<i>Igf2r</i>	
<i>Hp1-bp74</i>	<i>Tpm1</i>	<i>Serp1</i>	<i>Map3k7ip1</i>	<i>Psa</i>	
<i>Id3</i>	<i>Kif13b</i>		<i>Pde4b</i>	<i>Rin2</i>	
<i>Znf207</i>			<i>Rraga</i>	<i>Rab13</i>	
<i>Zfp7</i>			<i>Ryk</i>	<i>S100a6</i>	
Translation	Apoptosis	Metabolism	Chaperonin		
			<i>Dnaja1</i>		
			Ubiquitination/Proteosome		
					<i>Ubelc</i>
					<i>Psma7</i>
Unassigned					
<i>Aptx</i>	<i>Hspc135</i>	<i>Ocil</i>	<i>Wdr5</i>		
<i>Clr-f</i>	<i>Klhl6</i>	<i>Ror1</i>			
<i>Dre1</i>	<i>Mox2r</i>	<i>Scmh1</i>			
<i>Dlx2</i>	<i>Numb</i>	<i>Trim52</i>			

Table 3

Gene Name:	ABCA4	GenBank Accession No:	NM_000350	GI:	4557875
Organism:	Homo sapiens	Length:	7318	ORF Region:	82-6903
Locus:	24	Blast database:	Human	ORF GC%	52.58
Definition:	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 4(ABCA4), mRNA.				
Name	Start	Sense RNA Sequence 5'-3'	Antisense RNA Sequence 5'-3'	Region	GC%
NM_000350_sirna_458	458	GGCAGAGCUCACACAUUU (SEQ ID NO: 1)	AAGAUGUGAGCUCUCUGUC (SEQ ID NO: 2)	ORF	47.36842105
NM_000350_sirna_869	869	GCCGUUCUCAAGGUAUCAA (SEQ ID NO: 3)	UUGAUACCUUGAGAACGGC (SEQ ID NO: 4)	ORF	47.36842105
NM_000350_sirna_880	880	GGUAUCAUCUGAGAUUU (SEQ ID NO: 5)	AAGAUCUCAGAUUGAUACC (SEQ ID NO: 6)	ORF	36.84210526
NM_000350_sirna_1734	1734	GGUAUCCUGACAUUU (SEQ ID NO: 7)	AUACAUUGCAGGGAUACC (SEQ ID NO: 8)	ORF	42.10526316
NM_000350_sirna_1864	1864	GCUGAUCCCGUGGAAGAUU (SEQ ID NO: 9)	AAUCUCCACGGGAUCAGC (SEQ ID NO: 10)	ORF	52.63157895
Gene Name:	ANXA1	GenBank Accession No:	NM_000700	GI:	4502100
Organism:	Homo sapiens	Length:	1399	ORF Region:	75-1115
Locus:	301	Blast database:	Human	ORF GC%	44.48
Definition:	Homo sapiens annexin A1 (ANXA1), mRNA.				
Name	Start	Sense RNA Sequence 5'-3'	Antisense RNA Sequence 5'-3'	Region	GC%
NM_000700_sirna_318	318	GCAGCAUAUCUCCAGGAAA (SEQ ID NO: 11)	UUUCCUGGAGAUUAGCUGC (SEQ ID NO: 12)	ORF	47.36842105
NM_000700_sirna_609	609	GCUUUGCCUUUCUCUUGCUA (SEQ ID NO: 13)	UAGCAAGAGAAAGCAAAGC (SEQ ID NO: 14)	ORF	42.10526316
NM_000700_sirna_775	775	GCAGAGUGUUUCAGAAUA (SEQ ID NO: 15)	UAUUUCUGAAACACUCUGC (SEQ ID NO: 16)	ORF	36.84210526
NM_000700_sirna_942	942	GGAAUCUGCAUAAGGCAU (SEQ ID NO: 17)	AUGCCUUAUGGGGAGUCC (SEQ ID NO: 18)	ORF	52.63157895
NM_000700_sirna_1058	1058	GGAUGAAACCAAGGAGAU (SEQ ID NO: 19)	AUCUCCUUUGGUUUCAUCC (SEQ ID NO: 20)	ORF	42.10526316

Gene Name:	ANXA2	GenBank Accession No.	NM_001002857	GI:	50845385
Organism:	Homo sapiens	Length:	1644	ORF Region:	137-1156
Locus:	302	Blast database:	Human	ORF GC%	48.14
Definition:	Homo sapiens annexin A2 (ANXA2), transcript variant 2, mRNA.				

Name	Start	Sense RNA Sequence 5'-3'	Antisense RNA Sequence 5'-3'	Region	GC%
NM_001002857_sirna_844	844	CCCUUUGACAUUGUGGAA (SEQ ID NO: 21)	UUCCAACAUUGUCAUAAAGG (SEQ ID NO: 22)	ORF	42.10526316
NM_001002857_sirna_845	845	CCUUAUGACAUUGUGGAAA (SEQ ID NO: 23)	UUUCCAAACAUUGUCAUAAAGG (SEQ ID NO: 24)	ORF	36.84210526
NM_001002857_sirna_1071	1071	GCAAGUCCUGUACUUAUUA (SEQ ID NO: 25)	UAAUAGUACAGGGACUUGC (SEQ ID NO: 26)	ORF	42.10526316

Gene Name:	ANXA2	GenBank Accession No.	NM_001002858	GI:	50845387
Organism:	Homo sapiens	Length:	1635	ORF Region:	74-1147
Locus:	302	Blast database:	Human	ORF GC%	48.89
Definition:	Homo sapiens annexin A2 (ANXA2), transcript variant 1, mRNA.				

Name	Start	Sense RNA Sequence 5'-3'	Antisense RNA Sequence 5'-3'	Region	GC%
NM_001002858_sirna_835	835	CCCUUUGACAUUGUGGAA (SEQ ID NO: 27)	UUCCAACAUUGUCAUAAAGG (SEQ ID NO: 28)	ORF	42.10526316
NM_001002858_sirna_836	836	CCUUAUGACAUUGUGGAAA (SEQ ID NO: 29)	UUUCCAAACAUUGUCAUAAAGG (SEQ ID NO: 30)	ORF	36.84210526
NM_001002858_sirna_1062	1062	GCAAGUCCUGUACUUAUUA (SEQ ID NO: 31)	UAAUAGUACAGGGACUUGC (SEQ ID NO: 32)	ORF	42.10526316

Gene Name:	ANXA2	GenBank Accession No.	NM_004039	GI:	50845389
Organism:	Homo sapiens	Length:	1563	ORF Region:	56-1075
Locus:	302	Blast database:	Human	ORF GC%	48.14
Definition:	Homo sapiens annexin A2 (ANXA2), transcript variant 3, mRNA.				

Name	Start	Sense RNA Sequence 5'-3'	Antisense RNA Sequence 5'-3'	Region	GC%
NM_004039_sirna_763	763	CCCUUUGACAUUGUGGAA (SEQ ID NO: 33)	UUCCAACAUUGUCAUAAAGG (SEQ ID NO: 34)	ORF	42.10526316
NM_004039_sirna_764	764	CCUUAUGACAUUGUGGAAA (SEQ ID NO: 35)	UUUCCAAACAUUGUCAUAAAGG (SEQ ID NO: 36)	ORF	36.84210526
NM_004039_sirna_990	990	GCAAGUCCUGUACUUAUUA (SEQ ID NO: 37)	UAAUAGUACAGGGACUUGC (SEQ ID NO: 38)	ORF	42.10526316

Gene Name:	ANXA3	GenBank Accession No.	NM_005139	GI:	4826642
Organism:	Homo sapiens	Length:	1339	ORF Region:	47-1018
Locus:	306	Blast database:	Human	ORF GC%	42.8
Definition:	Homo sapiens annexin A3 (ANXA3), mRNA.				
Name	Start	Sense RNA Sequence 5'-3'	Antisense RNA Sequence 5'-3'	Region	GC%
NM_005139_sRNA_317	317	CCAGCAGUCUUUGAUGCAA (SEQ ID NO: 39)	UUGCAUCAAAGACUGCUGG (SEQ ID NO: 40)	ORF	47.36842105
NM_005139_sRNA_332	332	GCAAAGCAGCUAAAGAAU (SEQ ID NO: 41)	AUUUCUUUAGCUGCUUUGC (SEQ ID NO: 42)	ORF	36.84210526
NM_005139_sRNA_405	405	GGACAAAGCAGGCAAUGAA (SEQ ID NO: 43)	UUCAUUUUGCCUGCUUGUCC (SEQ ID NO: 44)	ORF	47.36842105
NM_005139_sRNA_411	411	GCAGGCAAAGGGAUUAU (SEQ ID NO: 45)	AUAUCCUUAUUUUGCCUGC (SEQ ID NO: 46)	ORF	42.10526316
NM_005139_sRNA_827	827	GCCUUGAAGGGUAUUGGAA (SEQ ID NO: 47)	UUCCAAUAACCCUUAAGGC (SEQ ID NO: 48)	ORF	47.36842105

Gene Name:	APTX	GenBank Accession No.	NM_017692	GI:	28329424
Organism:	Homo sapiens	Length:	2016	ORF Region:	605-1111
Locus:	54840	Blast database:	Human	ORF GC%	47.93
Definition:	Homo sapiens aprataxin (APTX), transcript variant 4, mRNA.				
Name	Start	Sense RNA Sequence 5'-3'	Antisense RNA Sequence 5'-3'	Region	GC%
NM_017692_sRNA_956	956	GCUUGAUGCAGAGUAGUAC (SEQ ID NO: 49)	GUACCAUCUCGACUACACAGC (SEQ ID NO: 50)	ORF	52.63157895
NM_017692_sRNA_983	983	GGUAGAGUAACUUGCCGAG (SEQ ID NO: 51)	CUCGGACAGUUAUCUACUACC (SEQ ID NO: 52)	ORF	52.63157895
NM_017692_sRNA_1005	1005	GGAUGCCUGAGCUCUUGAA (SEQ ID NO: 53)	UUCAAGAGCUCAGGCAUCC (SEQ ID NO: 54)	ORF	52.63157895

Gene Name:	APTX	GenBank Accession No.	NM_175069	GI:	28329429
Organism:	Homo sapiens	Length:	2036	ORF Region:	25-945
Locus:	54840	Blast database:	Human	ORF GC%	48.0
Definition:	Homo sapiens aprataxin (APTX), transcript variant 2, mRNA.				
Name	Start	Sense RNA Sequence 5'-3'	Antisense RNA Sequence 5'-3'	Region	GC%
NM_175069_sRNA_105	105	GCACCAGCGAAUACAGACUU (SEQ ID NO: 55)	AAGUCUGAUUCGUGGUC (SEQ ID NO: 56)	ORF	52.63157895
NM_175069_sRNA_266	266	GCAUUGACUCAGUCGUAAU (SEQ ID NO: 57)	AUUACGACUGAGUCAAU (SEQ ID NO: 58)	ORF	42.10526316
NM_175069_sRNA_389	389	GCCUGGAAACACACAGGAA (SEQ ID NO: 59)	UUCUGUGUGUUUCCAGGC (SEQ ID NO: 60)	ORF	52.63157895
NM_175069_sRNA_652	652	CCAAAGGCCCGUUAACCAUU (SEQ ID NO: 61)	AUUGGUAACGGGCCUUUGG (SEQ ID NO: 62)	ORF	52.63157895
NM_175069_sRNA_720	720	GGAACACCUUGAACUCCUU (SEQ ID NO: 63)	AAGGAGUUCAAGGUGUUC (SEQ ID NO: 64)	ORF	47.36842105

Gene Name:	APTX	GenBank Accession No.	NM_175071	GI:	28329426
Organism:	Homo sapiens	Length:	1836	ORF Region:	425-931
Locus:	54840	Blast database:	Human	ORF GC%	47.93
Definition:	Homo sapiens aprataxin (APTX), transcript variant 5, mRNA.				
Name	Start	Sense RNA Sequence 5'-3'	Antisense RNA Sequence 5'-3'	Region	GC%
NM_175071_sRNA_799	799	GGCUGGUAAGAGUAACUGUC (SEQ ID NO: 65)	GACGUUACUCUACCGACC (SEQ ID NO: 66)	ORF	52.63157895
NM_175071_sRNA_803	803	GGUAGAGUAACUGUCCGAG (SEQ ID NO: 67)	CUCGGACAGUUACUCUACC (SEQ ID NO: 68)	ORF	52.63157895
NM_175071_sRNA_825	825	GGAUGCCUGAGCUCUUGAA (SEQ ID NO: 69)	UUCAAGAGCUCAGGCAUCC (SEQ ID NO: 70)	ORF	52.63157895

Gene Name:	APTX	GenBank Accession No.	NM_175072	GI:	28329432
Organism:	Homo sapiens	Length:	2041	ORF Region:	372-1136
Locus:	54840	Blast database:	Human	ORF GC%	47.98
Definition:	Homo sapiens aprataxin (APTX), transcript variant 3, mRNA.				

Name	Start	Sense RNA Sequence 5'-3'	Antisense RNA Sequence 5'-3'	Region	GC%
NM_175072_sirna_981	981	GCUGUGAUCGAGAGGUAC (SEQ ID NO: 71)	GUACCAUCUCGAUCACAGC (SEQ ID NO: 72)	ORF	52.63157895
NM_175072_sirna_1030	1030	GGAUGCCUGAGCUCUUGAA (SEQ ID NO: 73)	UUAAGAGCUCAGGCAUCC (SEQ ID NO: 74)	ORF	52.63157895
NM_175072_sirna_1094	1094	UCCUCAGCUGAAAGAACAU (SEQ ID NO: 75)	AUGUUCUUUCAGCUGAGGA (SEQ ID NO: 76)	ORF	42.10526316

Gene Name:	DNAJA1	GenBank Accession No.	NM_001539	GI:	49472820
Organism:	Homo sapiens	Length:	1538	ORF Region:	184-1377
Locus:	3301	Blast database:	Human	ORF GC%	43.22
Definition:	Homo sapiens DnaJ (Hsp40) homolog, subfamily A, member 1 (DNAJA1), mRNA.				

Name	Start	Sense RNA Sequence 5'-3'	Antisense RNA Sequence 5'-3'	Region	GC%
NM_001539_sirna_642	642	CCGAGGUACUGGAUUGCAA (SEQ ID NO: 77)	UUGCAUUCACAGUACCUCCG (SEQ ID NO: 78)	ORF	52.63157895
NM_001539_sirna_646	646	GGUACUGGAUUGCAAUAA (SEQ ID NO: 79)	UUAUUUGCAUUCACGUACC (SEQ ID NO: 80)	ORF	36.84210526
NM_001539_sirna_682	682	CCUGGAUUGGUUCAGCAAA (SEQ ID NO: 81)	UUUGCUGAACCAUUCUCCAGG (SEQ ID NO: 82)	ORF	47.36842105
NM_001539_sirna_779	779	GGAGAUAGUUCGAGAGAA (SEQ ID NO: 83)	UUCUCUCGAAACUAUCUCC (SEQ ID NO: 84)	ORF	42.10526316
NM_001539_sirna_840	840	CCAGAAGAUAAACAUUCCAU (SEQ ID NO: 85)	AUGGAUGUUUAUCUUCUGG (SEQ ID NO: 86)	ORF	36.84210526

Gene Name:	ATP6V0C	GenBank Accession No.	NM_001694	GI:	19913436
Organism:	Homo sapiens	Length:	1126	ORF Region:	153-620
Locus:	527	Blast database:	Human	ORF GC%	63.47
Definition:	Homo sapiens ATPase, H+ transporting, lysosomal 16kDa, V0 subunit c(ATP6V0C), mRNA.				

Name	Start	Sense RNA Sequence 5'-3'	Antisense RNA Sequence 5'-3'	Region	GC%
NM_001694_sirna_388	388	CCCUGAAUGACGACAUACAG (SEQ ID NO: 87)	CUGAUGUCGUCAUUCAGGG (SEQ ID NO: 88)	ORF	52.63157895
NM_001694_sirna_529	529	GACUUAUCGUGGGCAUGAU (SEQ ID NO: 89)	AUCAUGCCCCACGAUAGUC (SEQ ID NO: 90)	ORF	47.36842105
NM_001694_sirna_535	535	UCGUGGGCAUGAUCCUGAU (SEQ ID NO: 91)	AUCAGGAUCAUGCCCCACGA (SEQ ID NO: 92)	ORF	52.63157895

Gene Name:	BCL2L1	GenBank Accession No.	NM_001191	GI:	20336333
Organism:	Homo sapiens	Length:	2386	ORF Region:	367-879
Locus:	598	Blast database:	Human	ORF GC%	57.12
Definition:	Homo sapiens BCL2-like 1 (BCL2L1), nuclear gene encoding mitochondrial protein, transcript variant 2, mRNA.				
Name	Start	Sense RNA Sequence 5'-3'	Antisense RNA Sequence 5'-3'	Region	GC%
NM_001191_sRNA_753	753	GGAACUCUAUGGGAACAAU (SEQ ID NO : 93)	AUUGUCCCAUAGAGUUC (SEQ ID NO : 94)	ORF	42.10526316
NM_001191_sRNA_857	857	GCUCACUUCAGUCGGAA (SEQ ID NO : 95)	UUCGACUGAAGAGUGAGC (SEQ ID NO : 96)	ORF	52.63157895
NM_001191_sRNA_859	859	UCACUCUUCAGUCGGAAU (SEQ ID NO : 97)	AUUCCGACUGAAGAGUGA (SEQ ID NO : 98)	ORF	42.10526316

Gene Name:	BCL2L1	GenBank Accession No.	NM_138578	GI:	20336334
Organism:	Homo sapiens	Length:	2575	ORF Region:	367-1068
Locus:	598	Blast database:	Human	ORF GC%	56.84
Definition:	Homo sapiens BCL2-like 1 (BCL2L1), nuclear gene encoding mitochondrial protein, transcript variant 1, mRNA.				
Name	Start	Sense RNA Sequence 5'-3'	Antisense RNA Sequence 5'-3'	Region	GC%
NM_138578_sRNA_514	514	GCCAUCAAUGGCAACCCAU (SEQ ID NO : 99)	AUGGGUUGCCCAUUGAUGGC (SEQ ID NO : 100)	ORF	52.63157895
NM_138578_sRNA_676	676	GCAUUCAGUGACCUAGACAU (SEQ ID NO : 101)	AUGUCAGGUCACUGAAUGC (SEQ ID NO : 102)	ORF	47.36842105
NM_138578_sRNA_716	716	GGACAGCAUAUCAGAGCUU (SEQ ID NO : 103)	AAGCUCUGAUAUGCUGUCC (SEQ ID NO : 104)	ORF	47.36842105
NM_138578_sRNA_818	818	GGUGGAAAGCGUAGACAA (SEQ ID NO : 105)	UUGUCUACGCUUCCACGC (SEQ ID NO : 106)	ORF	52.63157895
NM_138578_sRNA_872	872	GGAUGGCCACUUAACUGAA (SEQ ID NO : 107)	UUCAGGUAAGUGGCCAUCC (SEQ ID NO : 108)	ORF	52.63157895

Gene Name:	BRD2	GenBank Accession No.	NM_005104	GI:	12408641
Organism:	Homo sapiens	Length:	4693	ORF Region:	1702-4107
Locus:	6046	Blast database:	Human	ORF GC%	49.26
Definition:	Homo sapiens bromodomain containing 2 (BRD2), mRNA.				
Name	Start	Sense RNA Sequence 5'-3'	Antisense RNA Sequence 5'-3'	Region	GC%
NM_005104_sirna_1851	1851	GGUGCCUGCUUUGCAACUU (SEQ ID NO : 109)	AAGUUGCAAAAGCAGGCACC (SEQ ID NO : 110)	ORF	52.63157895
NM_005104_sirna_2229	2229	GGUUGCAUCAAAUGCCACAA (SEQ ID NO : 111)	UUGUGGCAUUGAUGCAACC (SEQ ID NO : 112)	ORF	47.36842105
NM_005104_sirna_2694	2694	GCCUGACUCUCAGCAACAA (SEQ ID NO : 113)	UUGUUGCUGAGAGUCAGGC (SEQ ID NO : 114)	ORF	52.63157895
NM_005104_sirna_2944	2944	GCUGCUGAUGUACGGCUUA (SEQ ID NO : 115)	UAAGCCGUACAUCAGCAGC (SEQ ID NO : 116)	ORF	52.63157895
NM_005104_sirna_2969	2969	CCAACUGCUAUUAAGUACAA (SEQ ID NO : 117)	UUGUACUUAUAGCAGUUGG (SEQ ID NO : 118)	ORF	36.84210526

Gene Name:	BRD3	GenBank Accession No.	NM_007371	GI:	12408642
Organism:	Homo sapiens	Length:	3085	ORF Region:	140-2320
Locus:	8019	Blast database:	Human	ORF GC%	55.03
Definition:	Homo sapiens bromodomain containing 3 (BRD3), mRNA.				
Name	Start	Sense RNA Sequence 5'-3'	Antisense RNA Sequence 5'-3'	Region	GC%
NM_007371_sirna_1098	1098	GGGAGAUGCUAUCCAAGAA (SEQ ID NO : 119)	UUCUUGGAUAGCAUCUCCC (SEQ ID NO : 120)	ORF	47.36842105
NM_007371_sirna_1279	1279	CCGGCUGAUGUUCUCGAAU (SEQ ID NO : 121)	AUUCGAGAACAUCAGCCGG (SEQ ID NO : 122)	ORF	52.63157895
NM_007371_sirna_1921	1921	GGUAGUGCACAUCAUCCAA (SEQ ID NO : 123)	UUGGAUGAUGUGCAGCAGC (SEQ ID NO : 124)	ORF	47.36842105
NM_007371_sirna_2017	2017	GCGGGAACUGGAGAGAUAU (SEQ ID NO : 125)	AUAUCUCUCCAGUUCGCCG (SEQ ID NO : 126)	ORF	52.63157895

Gene Name:	WDR5	GenBank Accession No.	NM_017588	GI:	61744459
Organism:	Homo sapiens	Length:	3163	ORF Region:	172-1176
Locus:	11091	Blast database:	Human	ORF GC%	48.96
Definition:	Homo sapiens WD repeat domain 5 (WDR5), transcript variant 1, mRNA.				
Name	Start	Sense RNA Sequence 5'-3'	Antisense RNA Sequence 5'-3'	Region	GC%
NM_017588_sRNA_424	424	GGUCACAAAGCUGGGAUAU (SEQ ID NO : 127)	AUAUCCCCAGCUUGUGACC (SEQ ID NO : 128)	ORF	47.36842105
NM_017588_sRNA_452	452	CCUGGUCGUCAGAUUCUAA (SEQ ID NO : 129)	UUAGAAUUCUGACGACCAGG (SEQ ID NO : 130)	ORF	47.36842105
NM_017588_sRNA_1032	1032	CCUUCAGACGAAAGAGAUU (SEQ ID NO : 131)	AAUCUCUUUCGUCUGAAGG (SEQ ID NO : 132)	ORF	42.10526316
Gene Name:	C9orf119	GenBank Accession No.	XM_372143	GI:	51467631
Organism:	Homo sapiens	Length:	884	ORF Region:	1-636
Locus:	375757	Blast database:	Human	ORF GC%	59.12
Definition:	PREDICTED: Homo sapiens chromosome 9 open reading frame 119(C9orf119), mRNA.				
Name	Start	Sense RNA Sequence 5'-3'	Antisense RNA Sequence 5'-3'	Region	GC%
XM_372143_sRNA_501	501	GGACCACAUUACCCAGCUU (SEQ ID NO : 133)	AAGCUGGGUAAUGUGGUCC (SEQ ID NO : 134)	ORF	52.63157895
XM_372143_sRNA_512	512	CCCAGCUUCACGAGUACAA (SEQ ID NO : 135)	UUGUACUCUGGAAGCUGGG (SEQ ID NO : 136)	ORF	52.63157895
XM_372143_sRNA_513	513	CCAGCUUCACGAGUACAAU (SEQ ID NO : 137)	AUUGUACUCUGGAAGCUGG (SEQ ID NO : 138)	ORF	47.36842105
Gene Name:	GOLGA2	GenBank Accession No.	NM_004486	GI:	47078236
Organism:	Homo sapiens	Length:	4304	ORF Region:	50-3022
Locus:	2801	Blast database:	Human	ORF GC%	55.84
Definition:	Homo sapiens golgi autoantigen, golgin subfamily a, 2 (GOLGA2), mRNA.				

Name	Start	Sense RNA Sequence 5'-3'	Antisense RNA Sequence 5'-3'	Region	GC%
NM_004486_sRNA_406	406	CCAACAGCUCAUUGGUCUU (SEQ ID NO : 139)	AAGACCAUUGAGCUGUUGG (SEQ ID NO : 140)	ORF	47.36842105
NM_004486_sRNA_528	528	CCAGCUAUGUAACAACAA (SEQ ID NO : 141)	UUUUUUUUUAUACUAGCUGG (SEQ ID NO : 142)	ORF	36.84210526
NM_004486_sRNA_655	655	GCAGUACAGGUUCACAUU (SEQ ID NO : 143)	AAUGUGAACCUUGUAAACUGC (SEQ ID NO : 144)	ORF	42.10526316
Gene Name:	C10orf3	GenBank Accession No.	NM_018131	GI:	34147683
Organism:	Homo sapiens	Length:	2635	ORF Region:	285-1679
Locus:	55165	Blast database:	Human	ORF GC%	40.72
Definition:	Homo sapiens chromosome 10 open reading frame 3 (C10orf3), mRNA.				
Name	Start	Sense RNA Sequence 5'-3'	Antisense RNA Sequence 5'-3'	Region	GC%
NM_018131_sRNA_292	292	CCAGAGUACCAAGAUUUU (SEQ ID NO : 145)	AAUUCUUUGGUACUUCUUGG (SEQ ID NO : 146)	ORF	36.84210526
NM_018131_sRNA_494	494	GGAGAAGAUUGCUUAUCAA (SEQ ID NO : 147)	UUGAUAGCAUUCUUCUCC (SEQ ID NO : 148)	ORF	36.84210526
NM_018131_sRNA_551	551	CCAACUGAAGGCCAGAUUU (SEQ ID NO : 149)	AUAUCUGGCCUUCAGUUGG (SEQ ID NO : 150)	ORF	47.36842105
NM_018131_sRNA_753	753	CCAAACUGCUUACACUCAU (SEQ ID NO : 151)	AUGAGUUGAAGCAGUUGG (SEQ ID NO : 152)	ORF	42.10526316
Gene Name:	CALD1	GenBank Accession No.	NM_033138	GI:	44680104
Organism:	Homo sapiens	Length:	5233	ORF Region:	460-2841
Locus:	800	Blast database:	Human	ORF GC%	37.41
Definition:	Homo sapiens caldesmon 1 (CALD1), transcript variant 1, mRNA.				
Name	Start	Sense RNA Sequence 5'-3'	Antisense RNA Sequence 5'-3'	Region	GC%
NM_033138_sRNA_695	695	CCAAGACAACCAACCAAAA	UUUGUGUGGUGGUUGUCUUGG	ORF	47.36842105
NM_033138_sRNA_826	826	CCAACAAUACAGAUAGCAA (SEQ ID NO : 153)	UUGCAUCUGUUAUUGUUGG (SEQ ID NO : 154)	ORF	36.84210526
NM_033138_sRNA_926	926	GCCAGAAAGAUACGAGAU (SEQ ID NO : 155)	AUCUCGUAUCUUUCUUGGC (SEQ ID NO : 156)	ORF	42.10526316
NM_033138_sRNA_2638	2638	GCAGCAGGCACACCAAAUA (SEQ ID NO : 157)	UAUUUGGUGUGCCUGCUGC (SEQ ID NO : 158)	ORF	52.63157895

Gene Name:	CALM2	GenBank Accession No.	NM_001743	GI:	20428653
Organism:	Homo sapiens	Length:	1128	ORF Region:	69-518
Locus:	805	Blast database:	Human	ORF GC%	39.12
Definition:	Homo sapiens calmodulin 2 (phosphorylase kinase, delta) (CALM2), mRNA.				
Name	Start	Sense RNA Sequence 5'-3'	Antisense RNA Sequence 5'-3'	Region	GC%
NM_001743_sRNA_138	138	GGUGAUGGAAACUAUAACAA (SEQ ID NO : 159)	UUGUUUAUAGUCCAUACACC (SEQ ID NO : 160)	ORF	36.84210526
NM_001743_sRNA_328	328	GAGAAAGCAUCCGUGUGUU (SEQ ID NO : 161)	AACACACGGAAUGCUUCUC (SEQ ID NO : 162)	ORF	47.36842105
NM_001743_sRNA_333	333	GCAUCCGUGUGUUUGAUA (SEQ ID NO : 163)	UAUCAAAACACACGGAAUGC (SEQ ID NO : 164)	ORF	42.10526316

Gene Name:	CELSR2	GenBank Accession No.	NM_001408	GI:	13325063
Organism:	Homo sapiens	Length:	10531	ORF Region:	63-8834
Locus:	1952	Blast database:	Human	ORF GC%	60.9
Definition:	Homo sapiens cadherin, EGF LAG seven-pass G-type receptor 2 (flamingo homolog, Drosophila) (CELSR2), mRNA.				
Name	Start	Sense RNA Sequence 5'-3'	Antisense RNA Sequence 5'-3'	Region	GC%
NM_001408_sRNA_1997	1997	CCAGAUACACGAGUGGCAAU (SEQ ID NO : 165)	AUUGCCACUGGUGAUCUGG (SEQ ID NO : 166)	ORF	52.63157895
NM_001408_sRNA_2011	2011	GCAUAUCUCGAAACCCGCUU (SEQ ID NO : 167)	AAGCGGUUUCGAGUAUUGC (SEQ ID NO : 168)	ORF	47.36842105
NM_001408_sRNA_2950	2950	GCAUAUCCUGAGGUCUU (SEQ ID NO : 169)	AAGACCUCACGGGAUUGUC (SEQ ID NO : 170)	ORF	52.63157895
NM_001408_sRNA_4427	4427	GCAGCUGAAAUACUACAAU (SEQ ID NO : 171)	AUUGUAGUAUUUCAGCUGC (SEQ ID NO : 172)	ORF	36.84210526
NM_001408_sRNA_5512	5512	GCAGCUGUGAUCCAGGUUA (SEQ ID NO : 173)	UAACCUGGAUCACAGCUGC (SEQ ID NO : 174)	ORF	52.63157895

Gene Name:	COPG2	GenBank Accession No.	NM_012133	GI:	66348036
Organism:	Homo sapiens	Length:	1703	ORF Region:	61-828
Locus:	26958	Blast database:	Human	ORF GC%	42.45
Definition:	Homo sapiens coatamer protein complex, subunit gamma 2 (COPG2), mRNA.				
Name	Start	Sense RNA Sequence 5'-3'	Antisense RNA Sequence 5'-3'	Region	GC%
NM_012133_sRNA_97	97	GGUAGUGGCUCCAAUCCUU (SEQ ID NO : 175)	AAGGAUUGGAGCCACUACC (SEQ ID NO : 176)	ORF	52.63157895
NM_012133_sRNA_147	147	GGAGCUCGUAUAUUAUCAAU (SEQ ID NO : 177)	AUUGAAUAUAACGAGCCUCC (SEQ ID NO : 178)	ORF	42.10526316
NM_012133_sRNA_232	232	GGUGAACACUUUGGAACAA (SEQ ID NO : 179)	UUUGUCCAAAGAGUUCUACC (SEQ ID NO : 180)	ORF	42.10526316
NM_012133_sRNA_380	380	GCAGUCUGACUAAGACAU (SEQ ID NO : 181)	AUGUCUUUAGUCAGACUGC (SEQ ID NO : 182)	ORF	42.10526316
NM_012133_sRNA_548	548	CCCUGCACAUAGAUGAAGAU (SEQ ID NO : 183)	AUCUUCAUCAUGUGCAGGG (SEQ ID NO : 184)	ORF	47.36842105
Gene Name:	TSGA13	GenBank Accession No.	NM_052933	GI:	31377632
Organism:	Homo sapiens	Length:	1700	ORF Region:	458-1285
Locus:	114960	Blast database:	Human	ORF GC%	46.02
Definition:	Homo sapiens testis specific, 13 (TSGA13), mRNA.				
Name	Start	Sense RNA Sequence 5'-3'	Antisense RNA Sequence 5'-3'	Region	GC%
NM_052933_sRNA_1130	1130	GCGAGUGAAAGGCCAAUUU (SEQ ID NO : 185)	AAAUUGGCCUUUUCACUCCG (SEQ ID NO : 186)	ORF	47.36842105
NM_052933_sRNA_1140	1140	GGCCAAUUUCCAAAGUGAU (SEQ ID NO : 187)	AUCACUUUUGGAAAUUGGCC (SEQ ID NO : 188)	ORF	42.10526316
NM_052933_sRNA_1141	1141	GCCAAUUUCCAAAGUGAUU (SEQ ID NO : 189)	AAUCACUUUUGGAAAUUGGC (SEQ ID NO : 190)	ORF	36.84210526

Gene Name:	CSTF2T	GenBank Accession No.	NM_015235	GI:	46094083
Organism:	Homo sapiens	Length:	4127	ORF Region:	47-1897
Locus:	23283	Blast database:	Human	ORF GC%	54.14
Definition:	Homo sapiens cleavage stimulation factor, 3' pre-RNA, subunit 2, 64kDa, tau variant (CSTF2T), mRNA.				
Name	Start	Sense RNA Sequence 5'-3'	Antisense RNA Sequence 5'-3'	Region	GC%
NM_015235_sirna_219	219	GCUAUGGCUUCUGCGAAUA (SEQ ID NO : 191)	UAUUCGCGAAGACCAUAGC (SEQ ID NO : 192)	ORF	47.36842105
NM_015235_sirna_340	340	GGAGGAGUUAAGAGCCUU (SEQ ID NO : 193)	AAGGCUCUUUAAUCUCCUC (SEQ ID NO : 194)	ORF	47.36842105
NM_015235_sirna_641	641	CCACUGAUCCAGGCAAAU (SEQ ID NO : 195)	AUUUGCCUGGGAUCAGUGG (SEQ ID NO : 196)	ORF	52.63157895
NM_015235_sirna_1138	1138	GCAUCAUGCCUCUGGUCAU (SEQ ID NO : 197)	AUGACCAGAGGCAUGAUGC (SEQ ID NO : 198)	ORF	52.63157895
NM_015235_sirna_1167	1167	GCCCUUCCUACAUGAGAU (SEQ ID NO : 199)	AUCUCAUGAGGAAGGCG (SEQ ID NO : 200)	ORF	52.63157895
Gene Name:	CSMD2	GenBank Accession No.	NM_052896	GI:	38045884
Organism:	Homo sapiens	Length:	13113	ORF Region:	30-10493
Locus:	114784	Blast database:	Human	ORF GC%	57.15
Definition:	Homo sapiens CUB and Sushi multiple domains 2 (CSMD2), mRNA.				
Name	Start	Sense RNA Sequence 5'-3'	Antisense RNA Sequence 5'-3'	Region	GC%
NM_052896_sirna_224	224	GCUUGUGUUCACAGUCCUUU (SEQ ID NO : 201)	AAAGGACUGGAACACAAGC (SEQ ID NO : 202)	ORF	47.36842105
NM_052896_sirna_520	520	GCUGCAACCUUGGCUUCUU (SEQ ID NO : 203)	AAGAAGCCAAAGGUUGCAGC (SEQ ID NO : 204)	ORF	52.63157895
NM_052896_sirna_797	797	GGAAGUCACUGGGACAGAA (SEQ ID NO : 205)	UUCUGUCCCGAGUGACUCC (SEQ ID NO : 206)	ORF	52.63157895
NM_052896_sirna_931	931	CCCAAUACCAAGUCAAGAA (SEQ ID NO : 207)	UUUCUUGACUUGGUUUGGG (SEQ ID NO : 208)	ORF	42.10526316
NM_052896_sirna_938	938	CCAAGUCAAGAAGCAAAUU (SEQ ID NO : 209)	AAUUUGCUUCUUGACUUGG (SEQ ID NO : 210)	ORF	36.84210526

Gene Name:	CTCF	GenBank Accession No.	NM_006565	GI:	62952500
Organism:	Homo sapiens	Length:	3797	ORF Region:	291-2474
Locus:	10664	Blast database:	Human	ORF GC%	48.81
Definition:	Homo sapiens CCCTC-binding factor (zinc finger protein) (CTCF), mRNA.				
Name	Start	Sense RNA Sequence 5'-3'	Antisense RNA Sequence 5'-3'	Region	GC%
NM_006565_sirNA_812	812	GGUGGAGACACUAGAACAA (SEQ ID NO: 211)	UUUUUUUAGUGUCCACC (SEQ ID NO: 212)	ORF	47.36842105
NM_006565_sirNA_1211	1211	CCUCCUGAGGAUACACCUU (SEQ ID NO: 213)	AAGGUGAUUCCUCAGGAGG (SEQ ID NO: 214)	ORF	52.63157895
NM_006565_sirNA_1540	1540	CCCAAAGUGGUACCAUGAA (SEQ ID NO: 215)	UUCAUGGUACCAUUUGGG (SEQ ID NO: 216)	ORF	47.36842105
NM_006565_sirNA_1667	1667	GCAUUCUUAUUAUGAGCAA (SEQ ID NO: 217)	UUGCUCAAUAUAGGAAUGC (SEQ ID NO: 218)	ORF	36.84210526
NM_006565_sirNA_2285	2285	CCAGCCAACAGCUAUCAUU (SEQ ID NO: 219)	AAUGAUAGCUUGUUGGCUUG (SEQ ID NO: 220)	ORF	47.36842105
Gene Name:	CUTL1	GenBank Accession No.	NM_001913	GI:	31652235
Organism:	Homo sapiens	Length:	2942	ORF Region:	20-2056
Locus:	1523	Blast database:	Human	ORF GC%	55.38
Definition:	Homo sapiens cut-like 1, CCAAT displacement protein (Drosophila)(CUTL1), transcript variant 2, mRNA.				
Name	Start	Sense RNA Sequence 5'-3'	Antisense RNA Sequence 5'-3'	Region	GC%
NM_001913_sirNA_418	418	GGAAGAAUACAACAAGGAA (SEQ ID NO: 221)	UUCCUUUGUUAUUCUCC (SEQ ID NO: 222)	ORF	36.84210526
NM_001913_sirNA_1357	1357	GCAGGACCUGAGCAUCAUU (SEQ ID NO: 223)	AAUGAUGCUCAGGUCCUGC (SEQ ID NO: 224)	ORF	52.63157895
NM_001913_sirNA_1507	1507	CCAGGUGGAUUCACUGCUU (SEQ ID NO: 225)	AAGCAGUGAAUCCACCUGG (SEQ ID NO: 226)	ORF	52.63157895
NM_001913_sirNA_1644	1644	CCGACACAUCUACGCUUU (SEQ ID NO: 227)	AAGAGCUUGAUGUUGUCGG (SEQ ID NO: 228)	ORF	47.36842105
NM_001913_sirNA_2002	2002	GCACAAGUUCACGAGAAU (SEQ ID NO: 229)	AUUCUCUGGGAACUUGUGC (SEQ ID NO: 230)	ORF	47.36842105

Gene Name:	MYLC2PL	GenBank Accession No.	NM_138403	GI:	40286635
Organism:	Homo sapiens	Length:	681	ORF Region:	1-681
Locus:	93408	Blast database:	Human	ORF GC%	54.78
Definition:	Homo sapiens myosin light chain 2, precursor lymphocyte-specific(MYLC2PL), mRNA.				
Name	Start	Sense RNA Sequence 5'-3'	Antisense RNA Sequence 5'-3'	Region	GC%
NM_138403_sRNA_321	321	GGACUUAGAGGACACCUUU (SEQ ID NO: 231)	AAAGGUGUCCCUCAAGUCC (SEQ ID NO: 232)	ORF	52.63157895
NM_138403_sRNA_350	350	GCCGCAUCAUUGUCAAGAA (SEQ ID NO: 233)	UUCUUGACAUUGAUGCGGC (SEQ ID NO: 234)	ORF	47.36842105
NM_138403_sRNA_473	473	CCAUUCUCCACGCCUUCAA (SEQ ID NO: 235)	UUGAAGGCGUGGAGAAUGG (SEQ ID NO: 236)	ORF	52.63157895
NM_138403_sRNA_588	588	GCAGAUUUUGCAGCGUUU (SEQ ID NO: 237)	AAACGCUGCAACAUCUGC (SEQ ID NO: 238)	ORF	47.36842105

Gene Name:	DLX2	GenBank Accession No.	NM_004405	GI:	6996003
Organism:	Homo sapiens	Length:	2091	ORF Region:	1-987
Locus:	1746	Blast database:	Human	ORF GC%	61.81
Definition:	Homo sapiens distal-less homeo box 2 (DLX2), mRNA.				
Name	Start	Sense RNA Sequence 5'-3'	Antisense RNA Sequence 5'-3'	Region	GC%
NM_004405_sRNA_676	676	GCUUCCACCUUGUGCUU (SEQ ID NO: 239)	AAGCACAAAGGUGGAGAAAGC (SEQ ID NO: 240)	ORF	52.63157895

Gene Name:	KLHL24	GenBank Accession No.	NM_017644	GI:	62865888
Organism:	Homo sapiens	Length:	7331	ORF Region:	296-2098
Locus:	54800	Blast database:	Human	ORF GC%	42.55
Definition:	Homo sapiens kelch-like 24 (Drosophila) (KLHL24), mRNA.				
Name	Start	Sense RNA Sequence 5'-3'	Antisense RNA Sequence 5'-3'	Region	GC%
NM_017644_sirNA_558	558	GCAGCUACUUCAGAGCUAU (SEQ ID NO: 241)	AUAGCUCUGAAGUAGCUGC (SEQ ID NO: 242)	ORF	47.36842105
NM_017644_sirNA_594	594	GGGAAAGCCGAGAAUGUU (SEQ ID NO: 243)	AACAUUUCUCGGCUUCCCC (SEQ ID NO: 244)	ORF	47.36842105
NM_017644_sirNA_778	778	GCAACUUGAUCCUUGUAAU (SEQ ID NO: 245)	AUUACAAGGAUCAAGUUGC (SEQ ID NO: 246)	ORF	36.84210526
NM_017644_sirNA_811	811	GCGCUUUGCUGAUACCAU (SEQ ID NO: 247)	AUGGGUAUCAGCAAAAGCGC (SEQ ID NO: 248)	ORF	52.63157895
NM_017644_sirNA_913	913	GCUUGACAAAGAUGAACUU (SEQ ID NO: 249)	AAGUUCAUCUUUGUCAAGC (SEQ ID NO: 250)	ORF	36.84210526
NM_017644_sirNA_1679	1679	GGACCUGAUGAAUAUACUU (SEQ ID NO: 251)	AAGUAUUUAUCAAGGUCC (SEQ ID NO: 252)	ORF	36.84210526
Gene Name:	CHCHD8 aka E2IG2	GenBank Accession No.	NM_016565	GI:	46198303
Organism:	Homo sapiens	Length:	833	ORF Region:	106-369
Locus:	51287	Blast database:	Human	ORF GC%	60.99
Definition:	Homo sapiens coiled-coil-helix-coiled-coil-helix domain containing8 (CHCHD8), mRNA.				
Name	Start	Sense RNA Sequence 5'-3'	Antisense RNA Sequence 5'-3'	Region	GC%
NM_016565_sirNA_115	115	UCAGUCCCUCAAGGCCAU (SEQ ID NO: 256)	UAUGGCCUUGAGGGACUGA (SEQ ID NO: 254)	ORF	52.63157895
NM_016565_sirNA_138	138	GACCAACGCGGUGAAGAAA (SEQ ID NO: 255)	UUUCUACACCCGUUGGGUC (SEQ ID NO: 256)	ORF	52.63157895
NM_016565_sirNA_140	140	CCCAACGGGUGAAGAAAGA (SEQ ID NO: 257)	UCUUUCUUCACCCGUUGGG (SEQ ID NO: 258)	ORF	52.63157895
Gene Name:	EIF3S10	GenBank Accession No.	NM_003750	GI:	4503508
Organism:	Homo sapiens	Length:	5256	ORF Region:	114-4262
Locus:	8661	Blast database:	Human	ORF GC%	46.81
Definition:	Homo sapiens eukaryotic translation initiation factor 3, subunit 10theta, 150/170kDa (EIF3S10), mRNA.				
Name	Start	Sense RNA Sequence 5'-3'	Antisense RNA Sequence 5'-3'	Region	GC%
NM_003750_sirNA_298	298	GCAAGAGCCACUUGGCAAA (SEQ ID NO: 259)	UUUGCCAAAGUGGCUUCC (SEQ ID NO: 260)	ORF	52.63157895
NM_003750_sirNA_440	440	GCAGAUGGUCUAGAUAAU (SEQ ID NO: 261)	UAUAUCUAAGACCAUCUGC (SEQ ID NO: 262)	ORF	36.84210526

NM_003750_sirna_626	626	GGCCUGUACCAUGAUUU (SEQ ID NO: 263)	AAUAUUGGUACAGGCGC (SEQ ID NO: 264)	ORF	47.36842105
NM_003750_sirna_635	635	CCAUGAUUUGCCAGCAA (SEQ ID NO: 265)	UUGUGGGCAUAUUAUGG (SEQ ID NO: 266)	ORF	47.36842105
NM_003750_sirna_1328	1328	GGGAGUCACAAAGGUUCUA (SEQ ID NO: 267)	UAGAACCUUUGUGACUCGC (SEQ ID NO: 268)	ORF	47.36842105

Gene Name:	ERBB2IP	GenBank Accession No.	NM_018695	GI:	56237019
Organism:	Homo sapiens	Length:	6916	ORF Region:	309-4424
Locus:	55914	Blast database:	Human	ORF GC%	38.63
Definition:	Homo sapiens erbb2 interacting protein (ERBB2IP), transcript variant 2, mRNA.				

Name	Start	Sense RNA Sequence 5'-3'	Antisense RNA Sequence 5'-3'	Region	GC%
NM_018695_sirna_899	899	GGAAGUGCCUGAAGUACUU (SEQ ID NO: 269)	AAGUACUUCAGGCACUUC (SEQ ID NO: 270)	ORF	47.36842105
NM_018695_sirna_920	920	GCAACUAAUGGAGUUGAAA (SEQ ID NO: 271)	UUUCAUCCACUUAUUGC (SEQ ID NO: 272)	ORF	36.84210526
NM_018695_sirna_1106	1106	GCAGUCCUGAGACUAAU (SEQ ID NO: 273)	AAUAGUCUACAGGAGCUGC (SEQ ID NO: 274)	ORF	47.36842105
NM_018695_sirna_1598	1598	GCCAGGACUGAGGAGUUGU (SEQ ID NO: 275)	AACAUCUCAGUCCUUGGC (SEQ ID NO: 276)	ORF	52.63157895
NM_018695_sirna_2568	2568	GCUGAUGACACUCACAAU (SEQ ID NO: 277)	AUUUGAGUGUCACAGC (SEQ ID NO: 278)	ORF	42.10526316
NM_018695_sirna_3434	3434	CCAUUUACAUCAGAGACUU (SEQ ID NO: 279)	AAGUCUCUGAUGUAAUUGG (SEQ ID NO: 280)	ORF	36.84210526

Gene Name:	FER1L3	GenBank Accession No.	NM_013451	GI:	19718757
Organism:	Homo sapiens	Length:	6829	ORF Region:	89-6274
Locus:	26509	Blast database:	Human	ORF GC%	47.63
Definition:	Homo sapiens fer-1-like 3, myoferlin (C. elegans) (FER1L3), transcript variant 1, mRNA.				

Name	Start	Sense RNA Sequence 5'-3'	Antisense RNA Sequence 5'-3'	Region	GC%
NM_013451_sirna_1529	1529	GCUGCAUCAUAUACAGUAA (SEQ ID NO: 281)	UUACUGUAUAUGAUGCAGC (SEQ ID NO: 282)	ORF	36.84210526
NM_013451_sirna_1589	1589	CCUUGUUAUCCUGAAUUCUU (SEQ ID NO: 283)	AAAGAUUCAGGUACAAGG (SEQ ID NO: 284)	ORF	36.84210526
NM_013451_sirna_1747	1747	GCUUGAGCCCAUUAUCAAU (SEQ ID NO: 285)	AUUUGAAAUGGCGCUAAGC (SEQ ID NO: 286)	ORF	42.10526316
NM_013451_sirna_3081	3081	CCAUUCCUCCUGAUAUAA (SEQ ID NO: 287)	UUUAUGAUCAGGAGGAAUUGG (SEQ ID NO: 288)	ORF	42.10526316
NM_013451_sirna_5017	5017	CCGAUUCUUUCCCGCUUU (SEQ ID NO: 289)	AAAGCGGAAAGGAUUCGG (SEQ ID NO: 290)	ORF	52.63157895

Gene Name:	FER1L3	GenBank Accession No.	NM_133337	GI:	19718758
Organism:	Homo sapiens	Length:	6790	ORF Region:	89-6235

Locus:	26509	Blast database:		Human	ORF GC%	47.64
Definition:	Homo sapiens fer-1-like 3, myoferlin (C. elegans) (FER1L3),transcript variant 2, mRNA.					
Name	Start	Sense RNA Sequence 5'-3'		Antisense RNA Sequence 5'-3'		Region
NM_133337_sirna_1501	1501	GGAAGUAAACACAGAGAA (SEQ ID NO: 291)		UUCUCCUGUGUUUACUCC (SEQ ID NO: 292)		ORF
NM_133337_sirna_1550	1550	CCUUGUUUACUGAAUCUUU (SEQ ID NO: 293)		AAAGAUUCAGGUAAACAAGG (SEQ ID NO: 294)		ORF
NM_133337_sirna_1708	1708	GCUUGAGCCCAUUUCAAUU (SEQ ID NO: 295)		AUUUGAAAUGGGCUCUAAAGC (SEQ ID NO: 296)		ORF
NM_133337_sirna_3042	3042	CCAUUCCUCCUGAUCAUAA (SEQ ID NO: 297)		UUAUGAUCAGGAGGAAUGG (SEQ ID NO: 298)		ORF
Gene Name:	FKBP8	GenBank Accession No.		NM_012181	GI:	52630439
Organism:	Homo sapiens	Length:		1787	ORF Region:	114-1355
Locus:	23770	Blast database:		Human	ORF GC%	62.08
Definition:	Homo sapiens FK506 binding protein 8, 38kDa (FKBP8), mRNA.					
Name	Start	Sense RNA Sequence 5'-3'		Antisense RNA Sequence 5'-3'		Region
NM_012181_sirna_855	855	GCCAUCAAGGCUAUCACCU (SEQ ID NO: 299)		AGGUGAUGCCUUGAUGGC (SEQ ID NO: 300)		ORF
NM_012181_sirna_916	916	UCCUGCAGUUGAAGGUGAA (SEQ ID NO: 301)		UUCACCUUCAACUGCAGGA (SEQ ID NO: 302)		ORF
NM_012181_sirna_1019	1019	CCAGCCAGACAAUCAUAG (SEQ ID NO: 303)		CUUGAUGUUGUCUGGCGUGG (SEQ ID NO: 304)		ORF
NM_012181_sirna_1022	1022	GCCAGACAAUCAAGGCU (SEQ ID NO: 305)		AGCCUUGAUGUUGUCUGGC (SEQ ID NO: 306)		ORF
NM_012181_sirna_1141	1141	UCCACGCAGAGCUCUCAAA (SEQ ID NO: 307)		UUUGAGAGCUCUGCGUGGA (SEQ ID NO: 308)		ORF
Gene Name:	FUSIP1	GenBank Accession No.		NM_006625	GI:	16905515
Organism:	Homo sapiens	Length:		1842	ORF Region:	77-628
Locus:	10772	Blast database:		Human	ORF GC%	45.66
Definition:	Homo sapiens FUS interacting protein (serine/arginine-rich) 1(FUSIP1), transcript variant 1, mRNA.					
Name	Start	Sense RNA Sequence 5'-3'		Antisense RNA Sequence 5'-3'		Region
NM_006625_sirna_157	157	GCGUGAAUUGGUGUUAU (SEQ ID NO: 309)		AUAACGACCAAUUCACGC (SEQ ID NO: 310)		ORF
NM_006625_sirna_567	567	GACCAACUGCAGCUGGAA (SEQ ID NO: 311)		UUCACGUCAGUUGGUC (SEQ ID NO: 312)		ORF
NM_006625_sirna_569	569	CCAAACUGCAGCUGGAAUA (SEQ ID NO: 313)		UAUUCACGUCGAGUUUGG (SEQ ID NO: 314)		ORF

Gene Name:	FUSIP1	GenBank Accession No.	NM_054016	GI:	16905516
Organism:	Homo sapiens	Length:	2924	ORF Region:	77-865
Locus:	10772	Blast database:	Human	ORF GC%	43.98
Definition:	Homo sapiens FUS interacting protein (serine/arginine-rich) 1(FUSIP1), transcript variant 2, mRNA.				
Sequence:	NM_054016				

Name	Start	Sense RNA Sequence 5'-3'	Antisense RNA Sequence 5'-3'	Region	GC%
NM_054016_sRNA_157	157	GCGUGAAUUUGGUCGUUUAU (SEQ ID NO: 315)	AUAACGACCAAAUUCACGC (SEQ ID NO: 316)	ORF	42.10526316
NM_054016_sRNA_169	169	UCGUUAUGGUCCUAUAGUU (SEQ ID NO: 317)	AACUAUAGGACCAUAACGA (SEQ ID NO: 318)	ORF	36.84210526
NM_054016_sRNA_220	220	CCGUCCAAGAGGAUUUGCU (SEQ ID NO: 319)	AGCAAAUCCUUGGACGG (SEQ ID NO: 320)	ORF	52.63157895

Gene Name:		GenBank Accession No.	AK025846	GI:	10438485
Organism:	Homo sapiens	Length:	2388	ORF Region:	
Locus:		Blast database:	Human	ORF GC%	
Definition:	Homo sapiens cDNA: FLJ22193 fis, clone HRC01108, gas5 mRNA				

Name	Start	Sense RNA Sequence 5'-3'	Antisense RNA Sequence 5'-3'	Region	GC%
AK025846_sRNA_246	246	GCAGAUUGUCUUAUGCAU (SEQ ID NO: 321)	AUGCAUGAAGCACAUUCG (SEQ ID NO: 322)		47.36842105
AK025846_sRNA_1968	1968	GCUAUACCUUUGCUUCUUU (SEQ ID NO: 323)	AAAGAAGCAAGGUUAUAGC (SEQ ID NO: 324)		36.84210526
AK025846_sRNA_2088	2088	CCCAACUACUGUUUCAGUU (SEQ ID NO: 325)	AACUGAAACAGUAGUUGGG (SEQ ID NO: 326)		42.10526316
AK025846_sRNA_2287	2287	CCAGGAGCUGGAUAUACAA (SEQ ID NO: 327)	UUUGUAUUCAGCUCUCCUG (SEQ ID NO: 328)		47.36842105
AK025846_sRNA_2296	2296	GGAUACAAUAGAGGACUU (SEQ ID NO: 329)	AAGUCCUAAUUUGUAUUC (SEQ ID NO: 330)		36.84210526

Gene Name:	GATA4	GenBank Accession No.	NM_002052	GI:	33188460
Organism:	Homo sapiens	Length:	3372	ORF Region:	519-1847
Locus:	2626	Blast database:	Human	ORF GC%	68.78
Definition:	Homo sapiens GATA binding protein 4 (GATA4), mRNA.				

Name	Start	Sense RNA Sequence 5'-3'	Antisense RNA Sequence 5'-3'	Region	GC%
NM_002052_sirna_1158	1158	GGCAGAGAGUGUGUCAAACU (SEQ ID NO: 331)	AGUUGACACACUCUCUGCC (SEQ ID NO: 332)	ORF	52.63157895
NM_002052_sirna_1243	1243	GCCUCUACCACAAAGAUCAA (SEQ ID NO: 333)	UUCAUCUUUGUGGAGAGGC (SEQ ID NO: 334)	ORF	47.36842105
NM_002052_sirna_1477	1477	GGAAAGCCCAAGAACCCUGAA (SEQ ID NO: 335)	UUCAGGUUUCUUGGGCUUCC (SEQ ID NO: 336)	ORF	52.63157895
NM_002052_sirna_1482	1482	CCCAAGAACCCUGAAUAAU (SEQ ID NO: 337)	AUUUAUUCAGGUUCUUGGG (SEQ ID NO: 338)	ORF	36.84210526
Gene Name:	GRB2	GenBank Accession No.	NM_002086	GI:	45359857
Organism:	Homo sapiens	Length:	3317	ORF Region:	358-1011
Locus:	2885	Blast database:	Human	ORF GC%	50.77
Definition:	Homo sapiens growth factor receptor-bound protein 2 (GRB2), transcript variant 1, mRNA.				
Name	Start	Sense RNA Sequence 5'-3'	Antisense RNA Sequence 5'-3'	Region	GC%
NM_002086_sirna_365	365	CCAUCGCCCAAAUUAUGACUU (SEQ ID NO: 339)	AAGUCAUUUUGGCGGAUGG (SEQ ID NO: 340)	ORF	42.10526316
NM_002086_sirna_464	464	GGUACAAGGCAGAGCUUAA (SEQ ID NO: 341)	UUAAGCUCUGCCUUGUACC (SEQ ID NO: 342)	ORF	47.36842105
NM_002086_sirna_494	494	GCUUCAUUCGCCAAGAACUA (SEQ ID NO: 343)	UAGUUCUUGGGGAAUGAAGC (SEQ ID NO: 344)	ORF	42.10526316
NM_002086_sirna_779	779	CCAGAAACCCAGCAGAUUU (SEQ ID NO: 345)	AAUAUCUGCUGGUUUCUGG (SEQ ID NO: 346)	ORF	42.10526316
NM_002086_sirna_840	840	CCAGGCCCUUCUUUGACUUU (SEQ ID NO: 347)	AAAGUCAAAAGAGGCCUUGG (SEQ ID NO: 348)	ORF	52.63157895

Gene Name:	GTF2E1	GenBank Accession No.	NM_005513	GI:	5031726
Organism:	Homo sapiens	Length:	2969	ORF Region:	55-1374
Locus:	2960	Blast database:	Human	ORF GC%	47.88
Definition:	Homo sapiens general transcription factor IIE, polypeptide 1 (alphasubunit, 56kD) (GTF2E1), mRNA.				
Name	Start	Sense RNA Sequence 5'-3'	Antisense RNA Sequence 5'-3'	Region	GC%
NM_005513_sirNA_198	198	GCUGGAGCUGCUCAAGUUU (SEQ ID NO: 349)	AAACUUGAGCAGCUCCAGC (SEQ ID NO: 350)	ORF	52.63157895
NM_005513_sirNA_378	378	CCACAUGAGAGAAGAAUU (SEQ ID NO: 351)	AAUUCUUCUUCUACUUGUGG (SEQ ID NO: 352)	ORF	36.84210526
NM_005513_sirNA_885	885	GCCUAUUUGGUUGAGAGAA (SEQ ID NO: 353)	UUCUCUCAACCAAAUAGGC (SEQ ID NO: 354)	ORF	42.10526316
NM_005513_sirNA_950	950	GCAUAGAUAUGGACGCAUU (SEQ ID NO: 355)	AAUGCGUCCAUACUUAUGC (SEQ ID NO: 356)	ORF	42.10526316
NM_005513_sirNA_1349	1349	GCAUGUUUGAGGACCUCUU (SEQ ID NO: 357)	AAGAGGUCCUCAACCAUGC (SEQ ID NO: 358)	ORF	47.36842105
Gene Name:	RABL3	GenBank Accession No.	NM_173825	GI:	62751416
Organism:	Homo sapiens	Length:	3449	ORF Region:	31-741
Locus:	285282	Blast database:	Human	ORF GC%	43.75
Definition:	Homo sapiens RAB, member of RAS oncogene family-like 3 (RABL3), mRNA.				
Name	Start	Sense RNA Sequence 5'-3'	Antisense RNA Sequence 5'-3'	Region	GC%
NM_173825_sirNA_47	47	GGGUGAAGGUACUGGUGUU (SEQ ID NO: 359)	AACACCAGUACCUACACCC (SEQ ID NO: 360)	ORF	52.63157895
NM_173825_sirNA_266	266	GCACAAGAGCAGUAUUCUA (SEQ ID NO: 361)	UAGAAUACUGCUCUUGUGC (SEQ ID NO: 362)	ORF	42.10526316
NM_173825_sirNA_467	467	GGACUAAACUGGACCAGAU (SEQ ID NO: 363)	AUCUGGUCCAGUUUAGUCC (SEQ ID NO: 364)	ORF	47.36842105
NM_173825_sirNA_528	528	CCUGGCUGAGGAUUUCAAU (SEQ ID NO: 365)	AUUGAAAUCCUCAGCCAGG (SEQ ID NO: 366)	ORF	47.36842105

Gene Name:	HM13	GenBank Accession No.	NM_030789	GI:	30581114
Organism:	Homo sapiens	Length:	1604	ORF Region:	115-1248
Locus:	81502	Blast database:	Human	ORF GC%	54.77
Definition:	Homo sapiens histocompatibility (minor) 13 (HM13), transcript variant 1, mRNA.				
Name	Start	Sense RNA Sequence 5'-3'	Antisense RNA Sequence 5'-3'	Region	GC%
NM_030789_sirna_293	293	GCAAGAAUGCUUCAGACAU (SEQ ID NO: 367)	AUGUCUGAAGCAUUCUUGC (SEQ ID NO: 368)	ORF	42.10526316
NM_030789_sirna_420	420	CCUCCUGCUGUCCAUGUAU (SEQ ID NO: 369)	AUACAUGGACAGCAGGAGG (SEQ ID NO: 370)	ORF	52.63157895
NM_030789_sirna_645	645	GCUGAGGAAGCACUGGAUU (SEQ ID NO: 371)	AAUCCAGUGCUUCUUCAGC (SEQ ID NO: 372)	ORF	52.63157895
NM_030789_sirna_870	870	CCUCGAAGCAAAACACUUU (SEQ ID NO: 373)	AAAGUUUGUUUGCUUCGAGG (SEQ ID NO: 374)	ORF	42.10526316
NM_030789_sirna_1155	1155	GGAGUCAAUCCUAAGGAU (SEQ ID NO: 375)	AUCCUUAGGAUUUGACUCC (SEQ ID NO: 376)	ORF	42.10526316

Gene Name:	HNRP1	GenBank Accession No.	NM_001533	GI:	52632382
Organism:	Homo sapiens	Length:	2129	ORF Region:	12-1781
Locus:	3191	Blast database:	Human	ORF GC%	51.53
Definition:	Homo sapiens heterogeneous nuclear ribonucleoprotein L (HNRP1), transcript variant 1, mRNA.				
Name	Start	Sense RNA Sequence 5'-3'	Antisense RNA Sequence 5'-3'	Region	GC%
NM_001533_sirna_480	480	GCAGCCGACAAACCAAUUAU (SEQ ID NO: 377)	AUAUUUGGUUGCGGCGUC (SEQ ID NO: 378)	ORF	47.36842105
NM_001533_sirna_716	716	GGUGGAAUUUGACUCAGUU (SEQ ID NO: 379)	AACUGAGUCAAAUUCACC (SEQ ID NO: 380)	ORF	42.10526316
NM_001533_sirna_719	719	GGAAUUUGACUCAGUUCUA (SEQ ID NO: 381)	UUGAACUGAGUCAAUUUC (SEQ ID NO: 382)	ORF	36.84210526
NM_001533_sirna_793	793	GCACUCUGAAGAUGCAUAU (SEQ ID NO: 383)	UAUUCGAUCUUCAGAGUGC (SEQ ID NO: 384)	ORF	42.10526316

Gene Name:	HOXC13	GenBank Accession No.	NM_017410	GI:	24497535
Organism:	Homo sapiens	Length:	2435	ORF Region:	116-1108
Locus:	3229	Blast database:	Human	ORF GC%	62.34
Definition:	Homo sapiens homeo box C13 (HOXC13), mRNA.				
Name	Start	Sense RNA Sequence 5'-3'	Antisense RNA Sequence 5'-3'	Region	GC%
NM_017410_sirna_154	154	GAGCCUUAUGUACGUCUAU (SEQ ID NO: 385)	AUAGACGUACAUAAGGCGUC (SEQ ID NO: 386)	ORF	42.10526316
NM_017410_sirna_912	912	CCUACACUAAGGUCAGCU (SEQ ID NO: 387)	AGCUGCACCUUAGUGUAGG (SEQ ID NO: 388)	ORF	52.63157895

NM_017410_sRNA_1066	1066	GGUGGUCAGCAAAUCGAAA (SEQ ID NO: 389)	UUUCGAUUUGCUGACCACC (SEQ ID NO: 390)	ORF	47.36842105
NM_017410_sRNA_1074	1074	GCAAAUCGAAAGCGCCUCA (SEQ ID NO: 391)	UGAGGCGCUUUCGAUUUGC (SEQ ID NO: 392)	ORF	52.63157895

Gene Name:	HP1BP3	GenBank Accession No.	NM_016287	GI:	56676329
Organism:	Homo sapiens	Length:	1855	ORF	101-1762
Locus:	50809	Blast database:	Human	ORF GC%	47.24
Definition:	Homo sapiens heterochromatin protein 1, binding protein 3 (HP1BP3), mRNA also known as HP1-BP74				
Name	Start	Sense RNA Sequence 5'-3'	Antisense RNA Sequence 5'-3'	Region	GC%
NM_016287_sRNA_576	576	CCAAGAUGGAUGCAAUCUU (SEQ ID NO: 393)	AAGAUUGCAUCCAUUCUGG (SEQ ID NO: 394)	ORF	42.10526316
NM_016287_sRNA_990	990	GGCCUCAGCUGUUGAAGAA (SEQ ID NO: 395)	UUCUUAACAGCUGAGGCC (SEQ ID NO: 396)	ORF	52.63157895
NM_016287_sRNA_1112	1112	GGUGGAAGCCUGAUGGAAU (SEQ ID NO: 397)	AUCCAUCAAGGCUUCCACC (SEQ ID NO: 398)	ORF	52.63157895

Gene Name:	HSPC135	GenBank Accession No.	NM_014170	GI:	56549684
Organism:	Homo sapiens	Length:	1364	ORF	48-902
Locus:	29083	Blast database:	Human	ORF GC%	46.91
Definition:	Homo sapiens HSPC135 protein (HSPC135), transcript variant 1, mRNA.				
Name	Start	Sense RNA Sequence 5'-3'	Antisense RNA Sequence 5'-3'	Region	GC%
NM_014170_sRNA_533	533	GGUGGACAUGCCAGGUUAU (SEQ ID NO: 399)	AUAACCGGCAUGUCCACC (SEQ ID NO: 400)	ORF	52.63157895
NM_014170_sRNA_638	638	GGAUAGCGUUGUUGGAAU (SEQ ID NO: 401)	AAUCCAAACAACGCUAUC (SEQ ID NO: 402)	ORF	42.10526316
NM_014170_sRNA_849	849	GGAUCCACCUGUUGAGAU (SEQ ID NO: 403)	AUCUCAACAGGUGGAUUC (SEQ ID NO: 404)	ORF	47.36842105
NM_014170_sRNA_854	854	CCACCUGUUGAGAUUCUUU (SEQ ID NO: 405)	AAAGCAUCUCAACAGGUGG (SEQ ID NO: 406)	ORF	47.36842105

Gene Name:	CD200R1	GenBank Accession No.	NM_138806	GI:	41327722
Organism:	Homo sapiens	Length:	2272	ORF Region:	234-1280
Locus:	131450	Blast database:	Human	ORF GC%	43.18
Definition:	Homo sapiens CD200 receptor 1 (CD200R1), transcript variant 1, mRNA.				
Name	Start	Sense RNA Sequence 5'-3'	Antisense RNA Sequence 5'-3'	Region	GC%
NM_138806_sRNA_341	341	GCAAAUCUAGCAAGGAGAAU (SEQ ID NO: 407)	AUUCUCCUUGCUAGUUUGC (SEQ ID NO: 408)	ORF	42.10526316
NM_138806_sRNA_429	429	GCAGAAGUUAAACACUUAU (SEQ ID NO: 409)	AUGAAGUGUUAAACUUCUGC (SEQ ID NO: 410)	ORF	36.84210526
NM_138806_sRNA_462	462	GUACAAAUGCUGUGCUUU (SEQ ID NO: 411)	AAAGCACAGCAUUUUGUAGC (SEQ ID NO: 412)	ORF	42.10526316
NM_138806_sRNA_590	590	GGAACCAACUCUGUACUGAU (SEQ ID NO: 413)	AUCAGUACAGUUGGUUUCUCC (SEQ ID NO: 414)	ORF	42.10526316
NM_138806_sRNA_869	869	GCAAGAAUACUGGGAGCAAU (SEQ ID NO: 415)	AUUGCUCCAGUAUUUCUUGC (SEQ ID NO: 416)	ORF	42.10526316
NM_138806_sRNA_1230	1230	GCAUCUGAGGCAUUUACAAA (SEQ ID NO: 417)	UUUGUAAUGCCUUCAGAUCC (SEQ ID NO: 418)	ORF	42.10526316
Gene Name:	ID3	GenBank Accession No.	NM_002167	GI:	32171181
Organism:	Homo sapiens	Length:	1203	ORF Region:	368-727
Locus:	3399	Blast database:	Human	ORF GC%	64.17
Definition:	Homo sapiens inhibitor of DNA binding 3, dominant negative helix-loop-helix protein (ID3), mRNA.				
Name	Start	Sense RNA Sequence 5'-3'	Antisense RNA Sequence 5'-3'	Region	GC%
NM_002167_sRNA_561	561	GCAGGUGGAAAUCCUACA (SEQ ID NO: 419)	UGUAGGAUUUCCACCUGGC (SEQ ID NO: 420)	ORF	52.63157895
NM_002167_sRNA_580	580	GCAGGUCUACGACUACAUU (SEQ ID NO: 421)	AUUGUAGUCGAGUACGCGC (SEQ ID NO: 422)	ORF	52.63157895
NM_002167_sRNA_680	680	GCUCCGGAACUUGUCAUCU (SEQ ID NO: 423)	AGAUGACAAGUUCGCGAGC (SEQ ID NO: 424)	ORF	52.63157895
Gene Name:	IGF2R	GenBank Accession No.	NM_000876	GI:	4504610
Organism:	Homo sapiens	Length:	9090	ORF Region:	148-7623
Locus:	3482	Blast database:	Human	ORF GC%	52.23
Definition:	Homo sapiens insulin-like growth factor 2 receptor (IGF2R), mRNA.				

Name	Start	Sense RNA Sequence 5'-3'	Antisense RNA Sequence 5'-3'	Region	GC%
NM_000876_sirna_461	461	CCAGAUUCUCCUGGAAUU (SEQ ID NO: 425)	AAUUCAGGAGAGAUUCUGG (SEQ ID NO: 426)	ORF	47.36842105
NM_000876_sirna_558	558	CCUGGGAACUCCUGAAUUU (SEQ ID NO: 427)	AAUUCAGGAGAUUCUCCAGG (SEQ ID NO: 428)	ORF	47.36842105
NM_000876_sirna_649	649	GCAAAUAAAGGAGGUGCCAU (SEQ ID NO: 429)	AUGGCACCUCCUUAUUUGC (SEQ ID NO: 430)	ORF	47.36842105
NM_000876_sirna_1146	1146	GCAGCAGGAUGUCUCAUA (SEQ ID NO: 431)	UAUGGAGACAUCCUGCUGC (SEQ ID NO: 432)	ORF	52.63157895
NM_000876_sirna_1927	1927	GCACGAGUGUGAGAAU (SEQ ID NO: 433)	AAGUUCUCAACACUGGUGC (SEQ ID NO: 434)	ORF	47.36842105
NM_000876_sirna_2092	2092	GCCUAUAAAGUUGAGACAA (SEQ ID NO: 435)	UUUGUCUACAUUUUAUAGGC (SEQ ID NO: 436)	ORF	36.84210526
NM_000876_sirna_2735	2735	GCAGCCUCCUUCUGGAAUA (SEQ ID NO: 437)	UAUCCAGAGAGGAGGUGC (SEQ ID NO: 438)	ORF	52.63157895
NM_000876_sirna_3901	3901	GCUGGCGAAUACACUUAUU (SEQ ID NO: 439)	AAUAGUGUAUUCGCCAGC (SEQ ID NO: 440)	ORF	42.10526316
NM_000876_sirna_6587	6587	GCUUCAGCCUCCUGGAGAUU (SEQ ID NO: 441)	AUAUCUCCGAGGUGGAGAGC (SEQ ID NO: 442)	ORF	52.63157895
NM_000876_sirna_6849	6849	GGAAUAGACCAAGUCUGUU (SEQ ID NO: 443)	AACAGACUUGGUCUUAUCC (SEQ ID NO: 444)	ORF	42.10526316

Gene Name:	JAK1	GenBank Accession No.	NM_002227	GI:	4504802
Organism:	Homo sapiens	Length:	3541	ORF Region:	76-3504
Locus:	3716	Blast database:	Human	ORF GC%	47.54
Definition:	Homo sapiens Janus kinase 1 (a protein tyrosine kinase) (JAK1), mRNA.				

Name	Start	Sense RNA Sequence 5'-3'	Antisense RNA Sequence 5'-3'	Region	GC%
NM_002227_sirna_297	297	GCUCUGGUAUGCUCCAAU (SEQ ID NO: 445)	AUUUGGAGCAUACCAGAGC (SEQ ID NO: 446)	ORF	47.36842105
NM_002227_sirna_320	320	CCAUCACCGUUGAUGACAA (SEQ ID NO: 447)	UUUGUCAACACGGUGAUGG (SEQ ID NO: 448)	ORF	47.36842105
NM_002227_sirna_380	380	CCAAUUGGCAUGGAACCAA (SEQ ID NO: 449)	UUGGUUCCAUUGCCAAUUGG (SEQ ID NO: 450)	ORF	47.36842105
NM_002227_sirna_387	387	GCAUGGAACCAACGACAAU (SEQ ID NO: 451)	AUUGUCGUUGGUUCCAU (SEQ ID NO: 452)	ORF	47.36842105
NM_002227_sirna_621	621	CCUGGCCAUUCACACUAU (SEQ ID NO: 453)	AUAGUGAGAGUCCCGAGG (SEQ ID NO: 454)	ORF	52.63157895
NM_002227_sirna_626	626	CCAUCACACAUUGCCAU (SEQ ID NO: 455)	AUGGCAUAGUGUGAUGG (SEQ ID NO: 456)	ORF	47.36842105
NM_002227_sirna_1511	1511	CCCAGAGCAGUUAAGAA (SEQ ID NO: 457)	UUUUUUAACUUGUUCUGG (SEQ ID NO: 458)	ORF	47.36842105
NM_002227_sirna_1701	1701	GCUGGUGGCUACUAAAGAA (SEQ ID NO: 459)	UUUUUUAAGUAGCCACAGC (SEQ ID NO: 460)	ORF	47.36842105
NM_002227_sirna_1814	1814	GCACGAGAACACACAUUA (SEQ ID NO: 461)	UAGAUGUGUGUUCUGGUGC (SEQ ID NO: 462)	ORF	47.36842105
NM_002227_sirna_2022	2022	GGAGAAUUAUUGGUGGAA (SEQ ID NO: 463)	UUUCCACCAUGAUUUCUCC (SEQ ID NO: 464)	ORF	42.10526316

Gene Name:	KIF13B	GenBank Accession No.	NM_015254	GI:	46852171
Organism:	Homo sapiens	Length:	8796	ORF Region:	91-5571
Locus:	23303	Blast database:	Human	ORF GC%	52.64
Definition:	Homo sapiens kinesin family member 13B (KIF13B), mRNA.				
Name	Start	Antisense RNA Sequence 5'-3'			
NM_015254_sRNA_141	141	GCGAGAGACUGACUUGCAU (SEQ ID NO: 465)	AUGCAAGUCAGUCUCUCGC (SEQ ID NO: 466)	ORF	52.63157895
NM_015254_sRNA_631	631	CCUUAUGUCGACGGACUUU (SEQ ID NO: 467)	AAAGUCCGUCGACAUAGG (SEQ ID NO: 468)	ORF	47.36842105
NM_015254_sRNA_1374	1374	GCUUGAGAGUCUUGGAAUA (SEQ ID NO: 469)	UUAUCCAAGACUCUCAAGC (SEQ ID NO: 470)	ORF	42.10526316
NM_015254_sRNA_1473	1473	GCUUCUGGUGUACUUAUUUA (SEQ ID NO: 471)	UAAUAGUACACCAGAAGC (SEQ ID NO: 472)	ORF	36.84210526
NM_015254_sRNA_4479	4479	GCUCUCAAGUCUCUCUUU (SEQ ID NO: 473)	AAAGAGAGACUUGAGGAGC (SEQ ID NO: 474)	ORF	47.36842105
Gene Name:	MK167	GenBank Accession No.	NM_002417	GI:	19923216
Organism:	Homo sapiens	Length:	12515	ORF Region:	197-9967
Locus:	4288	Blast database:	Human	ORF GC%	47.35
Definition:	Homo sapiens antigen identified by monoclonal antibody Ki-67(MK167), mRNA.				
Name	Start	Antisense RNA Sequence 5'-3'			
NM_002417_sRNA_727	727	GGGAACAACUAAUGUUCU (SEQ ID NO: 475)	AUGAACAUUAGUUGUUCU (SEQ ID NO: 476)	ORF	36.84210526
NM_002417_sRNA_1913	1913	GCACAAAGCUUGGUUUAUA (SEQ ID NO: 477)	UUUAUACCAAGCUUUGUGC (SEQ ID NO: 478)	ORF	36.84210526
NM_002417_sRNA_3621	3621	GCACAAAGCAUUGGCCUAA (SEQ ID NO: 479)	UUAGGCCAUUGCUUUGUGC (SEQ ID NO: 480)	ORF	47.36842105
NM_002417_sRNA_6317	6317	GCGUUUAGGAAUCUGCAA (SEQ ID NO: 481)	UUGCAGAUUCCUUAACGC (SEQ ID NO: 482)	ORF	42.10526316
NM_002417_sRNA_8846	8846	GCAUUUAAAGCAACCGCAA (SEQ ID NO: 483)	UUGCAGGUUGCUUAAUUGC (SEQ ID NO: 484)	ORF	42.10526316
NM_002417_sRNA_9505	9505	GCAAUUAACUGAGGUCUUU (SEQ ID NO: 485)	AAAGACCUUACAGUUAUUGC (SEQ ID NO: 486)	ORF	36.84210526

Gene Name:	LIPC	GenBank Accession No.	NM_000236	GI:	4557722
Organism:	Homo sapiens	Length:	1603	ORF Region:	58-1557
Locus:	3990	Blast database:	Human	ORF GC%	52.34
Definition:	Homo sapiens lipase, hepatic (LIPC), mRNA.				
Name	Start	Sense RNA Sequence 5'-3'		Antisense RNA Sequence 5'-3'	
NM_000236_sirna_122	122	CCCUUGGACAAAGCCUGAA (SEQ ID NO: 487)		UUCAGGCUUUGUCCAAGG (SEQ ID NO: 488)	ORF 52.63157895
NM_000236_sirna_646	646	GGACCUUUGUUGAGGGAA (SEQ ID NO: 489)		UUCCCUCAAAAGAGGUCC (SEQ ID NO: 490)	ORF 47.36842105
NM_000236_sirna_767	767	CCAAGGACACUAUAGACUU (SEQ ID NO: 491)		AAGUCAUAGUGUCCUAGG (SEQ ID NO: 492)	ORF 42.10526316
NM_000236_sirna_1058	1058	GCAAGAGCAAGAGGCUCUU (SEQ ID NO: 493)		AAGAGCCUUCUUGCUCUUGC (SEQ ID NO: 494)	ORF 52.63157895
NM_000236_sirna_1229	1229	GCAAAGGAAUUGCUAGUAA (SEQ ID NO: 495)		UUACUAGCAAUUCCUUGC (SEQ ID NO: 496)	ORF 36.84210526

Gene Name:	NFKBIZ	GenBank Accession No.	NM_031419	GI:	53832022
Organism:	Homo sapiens	Length:	3938	ORF Region:	116-2272
Locus:	64332	Blast database:	Human	ORF GC%	53.0
Definition:	Homo sapiens nuclear factor of kappa light polypeptide geneenhancer in B-cells inhibitor, zeta (NFKBIZ), transcript variant 1, mRNA (MAIL)				
Name	Start	Sense RNA Sequence 5'-3'		Antisense RNA Sequence 5'-3'	
NM_031419_sirna_490	490	GCACUCCGGAAGUCAUAAA (SEQ ID NO: 497)		UUUAUGACUUCGGAUGUGC (SEQ ID NO: 498)	ORF 42.10526316
NM_031419_sirna_616	616	GCCGUAUUCGUUGUCUGAU (SEQ ID NO: 499)		AUCAGACAACGAUUGGGC (SEQ ID NO: 500)	ORF 52.63157895
NM_031419_sirna_965	965	GCUCCGUGUACGAGUAAU (SEQ ID NO: 501)		AAUACUGGUACAGGGAAGC (SEQ ID NO: 502)	ORF 47.36842105
NM_031419_sirna_1175	1175	GCUAUCCCAUGCAGACUU (SEQ ID NO: 503)		AAGUCUGAUGGGAUAGC (SEQ ID NO: 504)	ORF 47.36842105
NM_031419_sirna_1494	1494	CCUAUGUUCUUGCAAGAAA (SEQ ID NO: 505)		UUUCUUGCAAGAAACAUAGG (SEQ ID NO: 506)	ORF 36.84210526
NM_031419_sirna_1520	1520	GCACUUCACAUUGCUGGAUA (SEQ ID NO: 507)		UAUCCAGCAUGUGAAGUGC (SEQ ID NO: 508)	ORF 47.36842105
NM_031419_sirna_1801	1801	CCACAUGCUGUGGUCCAU (SEQ ID NO: 509)		AUGGACCACAGCAUUGUGG (SEQ ID NO: 510)	ORF 52.63157895
NM_031419_sirna_1816	1816	CCAUGAACUCCAGAGAAAU (SEQ ID NO: 511)		AUUUCUCUGGAGUUAUGG (SEQ ID NO: 512)	ORF 42.10526316
NM_031419_sirna_1840	1840	GCCUCAUUCACCUAGAAGUU (SEQ ID NO: 513)		AACUUCAGGUAAUGAGGC (SEQ ID NO: 514)	ORF 47.36842105
NM_031419_sirna_2092	2092	GCAGUAUCGGUUGACACAA (SEQ ID NO: 515)		UUGUGUCAACCGAUACUGC (SEQ ID NO: 516)	ORF 47.36842105

Gene Name:	NFKBIZ	GenBank Accession No.	NM_001006474	GI:	53832023
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Organism:	Homo sapiens	Length:	3782	ORF Region:	260-2116
Locus:	64332	Blast database:	Human	ORF GC%	49.49
Definition:	Homo sapiens nuclear factor of kappa light polypeptide geneenhancer in B-cells inhibitor, zeta (NFKBIZ), transcript variant 2, mRNA.				
Name	Start	Sense RNA Sequence 5'-3'	Antisense RNA Sequence 5'-3'	Region	GC%
NM_001005474_sirna_334	334	GCACAUCCGAAGUCAUAAA (SEQ ID NO: 517)	UUUAUGACUUCGGAUGUC (SEQ ID NO: 518)	ORF	42.10526316
NM_001005474_sirna_460	460	GCCCGAUUCGUUGUCUGAU (SEQ ID NO: 519)	AUCAGACAACGAUCCGGC (SEQ ID NO: 520)	ORF	52.63157895
NM_001005474_sirna_809	809	GCUIUCCUGUACCAUAUU (SEQ ID NO: 521)	AAUACUGGUACAGGGAGC (SEQ ID NO: 522)	ORF	47.36842105
NM_001005474_sirna_1019	1019	GCUAUCCCAUGCAGACUU (SEQ ID NO: 523)	AAGUCUGCAUGGGGAUAGC (SEQ ID NO: 524)	ORF	47.36842105
NM_001005474_sirna_1338	1338	CCUAUGUUCUUGCAAGAAA (SEQ ID NO: 525)	UUUCUUGCAAGAAUAGG (SEQ ID NO: 526)	ORF	36.84210526
NM_001005474_sirna_1364	1364	GCACUUCACAUUGCUGGAU (SEQ ID NO: 527)	UAUCCAGCAUGAAGUAGC (SEQ ID NO: 528)	ORF	47.36842105
NM_001005474_sirna_1645	1645	CCACAAUGCUGUGGUCCAU (SEQ ID NO: 529)	AUGACCACACGAUUGUGG (SEQ ID NO: 530)	ORF	52.63157895
NM_001005474_sirna_1660	1660	CCAUGAACUCCAGAGAAU (SEQ ID NO: 531)	AUUUCUCUGGAGUUAUAGG (SEQ ID NO: 532)	ORF	42.10526316
NM_001005474_sirna_1684	1684	GCCUAUUCACCUAGAGUU (SEQ ID NO: 533)	AACUUCAGGUAAUAGAGC (SEQ ID NO: 534)	ORF	47.36842105
NM_001005474_sirna_1936	1936	GCAGUAUCGGUUGACACAA (SEQ ID NO: 535)	UUGUGUACACGAUACUCC (SEQ ID NO: 536)	ORF	47.36842105

Gene Name:	MAP3K7IP1	GenBank Accession No.	NM_006116	GI:	47717114
Organism:	Homo sapiens	Length:	3240	ORF Region:	50-1564
Locus:	10454	Blast database:	Human	ORF GC%	60.73
Definition:	Homo sapiens mitogen-activated protein kinase kinase 7 interacting protein 1 (MAP3K7IP1), transcript variant alpha, mRNA.				
Sequence:	NM_006116				

Name	Start	Sense RNA Sequence 5'-3'	Antisense RNA Sequence 5'-3'	Region	GC%
NM_006116_sirna_219	219	GGAGUGAGAAACAACUGCUU (SEQ ID NO: 537)	AAGCAGUUGUUCACUACUCC (SEQ ID NO: 538)	ORF	47.36842105
NM_006116_sirna_267	267	GCAACCGAGUGACCAACUU (SEQ ID NO: 539)	AAGUUGGUACUCGGUUGC (SEQ ID NO: 540)	ORF	52.63157895
NM_006116_sirna_685	685	GGAUGAGCUUCUCCGUCUU (SEQ ID NO: 541)	AAGACGGAAGAGCUCUACUCC (SEQ ID NO: 542)	ORF	52.63157895
NM_006116_sirna_831	831	CCAAGUCCAAACCAAUCAU (SEQ ID NO: 543)	AUGAUUGGUUGGACUUGG (SEQ ID NO: 544)	ORF	42.10526316

Gene Name:	MAP3K7IP1	GenBank Accession No.	NM_153497	GI:	47717113
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Organism:	Homo sapiens	Length:	ORF Region:	ORF GC%	ORF GC%
Locus:	10454	Blast database:	Human	ORF GC%	50-1438
Definition:	Homo sapiens mitogen-activated protein kinase kinase 7 interacting protein 1 (MAP3K7IP1), transcript variant beta, mRNA.			ORF GC%	60.12
Name	Start	Sense RNA Sequence 5'-3'	Antisense RNA Sequence 5'-3'	Region	GC%
NM_153497_sRNA_219	219	GGAGUGAGAGAACACUGCUU (SEQ ID NO: 545)	AAGCAGUUGUUCUCACUCC (SEQ ID NO: 546)	ORF	47.36842105
NM_153497_sRNA_267	267	GCAACCGAGUGACCAACU (SEQ ID NO: 547)	AAGUUGGUCACUGGUUGC (SEQ ID NO: 548)	ORF	52.63157895
NM_153497_sRNA_685	685	GGAUGAGCUCUCCGUCUU (SEQ ID NO: 549)	AAGACGGAAGAGCUCAUCC (SEQ ID NO: 550)	ORF	52.63157895
NM_153497_sRNA_831	831	CCAAGUCCAAACCAUCAU (SEQ ID NO: 551)	AUGAUUGGUUGGACUUGG (SEQ ID NO: 552)	ORF	42.10526316

Gene Name:	MAPT	GenBank Accession No.	GI:	ORF Region:	ORF GC%
Organism:	Homo sapiens		2796	ORF	237-1562
Locus:	4137	Blast database:	Human	ORF GC%	58.68
Definition:	Homo sapiens microtubule-associated protein tau (MAPT), transcript variant 2, mRNA.				
Name	Start	Sense RNA Sequence 5'-3'	Antisense RNA Sequence 5'-3'	Region	GC%
NM_005910_sRNA_1054	1054	GGAAGGUGCAGAUUUUA (SEQ ID NO: 553)	UUAAUUUUCUGCACCUCUCC (SEQ ID NO: 554)	ORF	36.84210526
NM_005910_sRNA_1147	1147	GCAGUGUGCAAAUAGUCUA (SEQ ID NO: 555)	UAGACUUAUUUGCACACUGC (SEQ ID NO: 556)	ORF	42.10526316
NM_005910_sRNA_1192	1192	CCUCCAAGUGUGGCUCAUU (SEQ ID NO: 557)	AAUGAGCCACACUUGGAGG (SEQ ID NO: 558)	ORF	52.63157895

Gene Name:	MAPT	GenBank Accession No.	GI:	ORF Region:	ORF GC%
Organism:	Homo sapiens		2622	ORF	237-1388
Locus:	4137	Blast database:	Human	ORF GC%	58.43
Definition:	Homo sapiens microtubule-associated protein tau (MAPT), transcript variant 3, mRNA.				
Name	Start	Sense RNA Sequence 5'-3'	Antisense RNA Sequence 5'-3'	Region	GC%
NM_005910_sRNA_1054	1054	GGAAGGUGCAGAUUUUA (SEQ ID NO: 553)	UUAAUUUUCUGCACCUCUCC (SEQ ID NO: 554)	ORF	36.84210526
NM_005910_sRNA_1147	1147	GCAGUGUGCAAAUAGUCUA (SEQ ID NO: 555)	UAGACUUAUUUGCACACUGC (SEQ ID NO: 556)	ORF	42.10526316
NM_005910_sRNA_1192	1192	CCUCCAAGUGUGGCUCAUU (SEQ ID NO: 557)	AAUGAGCCACACUUGGAGG (SEQ ID NO: 558)	ORF	52.63157895

Name	Start	Sense RNA Sequence 5'-3'	Antisense RNA Sequence 5'-3'	Region	GC%
NM_016834_sRNA_877	877	GCGGAAGGUGCAGAUAAU (SEQ ID NO: 559)	AUUAUCUGCACCUUCCCGC (SEQ ID NO: 560)	ORF	52.63157895
NM_016834_sRNA_973	973	GCAGUGUGCAAAUAGUCUA (SEQ ID NO: 561)	UAGACUAAUUGCACACUGC (SEQ ID NO: 562)	ORF	42.10526316
NM_016834_sRNA_1018	1018	CCUCCAAGUGUGGCUCUU (SEQ ID NO: 563)	AAUGAGCCACACUUGGAGG (SEQ ID NO: 564)	ORF	52.63157895

Gene Name:	MAPT	GenBank Accession No.	NM_016835	GI:	8400712
Organism:	Homo sapiens	Length:	3747	ORF Region:	237-2513
Locus:	4137	Blast database:	Human	ORF GC%	60.52
Definition:	Homo sapiens microtubule-associated protein tau (MAPT), transcript variant 1, mRNA.				

Name	Start	Sense RNA Sequence 5'-3'	Antisense RNA Sequence 5'-3'	Region	GC%
NM_016835_sRNA_250	250	GCCAGGAGUUCGAAAGUGAU (SEQ ID NO: 565)	AUCACUUGCAACUCCUGGC (SEQ ID NO: 566)	ORF	52.63157895
NM_016835_sRNA_797	797	GCUCAAGCACCAAGCUUCUA (SEQ ID NO: 567)	UAGAAGCUGGUGUCUUGAGC (SEQ ID NO: 568)	ORF	52.63157895
NM_016835_sRNA_1413	1413	GCCAAGACAUCACACGCUU (SEQ ID NO: 569)	AACGUGUGGAUGUCUUGGC (SEQ ID NO: 570)	ORF	52.63157895
NM_016835_sRNA_2098	2098	GCAGUGUGCAAAUAGUCUA (SEQ ID NO: 571)	UAGACUAAUUGCACACUGC (SEQ ID NO: 572)	ORF	42.10526316

Gene Name:	MGAT1	GenBank Accession No.	NM_002406	GI:	6031182
Organism:	Homo sapiens	Length:	2937	ORF Region:	497-1834
Locus:	4245	Blast database:	Human	ORF GC%	65.1
Definition:	Homo sapiens mannosyl (alpha-1,3-)-glycoprotein beta-1,2-N-acetylglucosaminyltransferase (MGAT1), mRNA.				

Name	Start	Sense RNA Sequence 5'-3'	Antisense RNA Sequence 5'-3'	Region	GC%
NM_002406_sRNA_541	541	CCUCUUUGUGGCCUGGAU (SEQ ID NO: 573)	AUUCAGGCCACAAAAGAGG (SEQ ID NO: 574)	ORF	52.63157895
NM_002406_sRNA_1026	1026	GCAAGUCCAGGGCUACUA (SEQ ID NO: 575)	UAGUAGCCCUUGGAACUUGC (SEQ ID NO: 576)	ORF	52.63157895
NM_002406_sRNA_1668	1668	GGGACAGCUCAAGGCUUU (SEQ ID NO: 577)	AAAGCCUUGAAGCUGUCC (SEQ ID NO: 578)	ORF	52.63157895

Gene Name:	MICAL2	GenBank Accession No.	NM_014632	GI:	41281417
Organism:	Homo sapiens	Length:	3934	ORF Region:	289-3663
Locus:	9645	Blast database:	Human	ORF GC%	53.75
Definition:	Homo sapiens microtubule associated monoxigenase, calponin and LIM domain containing 2 (MICAL2), mRNA.				
Name	Start	Sense RNA Sequence 5'-3'	Antisense RNA Sequence 5'-3'	Region	GC%
NM_014632_sirna_372	372	CCUCCAGGCCUUAACAUAU (SEQ ID NO: 579)	AUGUUGAAGCCUGGAGG (SEQ ID NO: 580)	ORF	52.63157895
NM_014632_sirna_473	473	CCAAAGCCCUUGUGGUACAA (SEQ ID NO: 581)	UUGUACCACAGGGCUUUGG (SEQ ID NO: 582)	ORF	52.63157895
NM_014632_sirna_585	585	GCACACUGCCAUUGAACUU (SEQ ID NO: 583)	AAGUUCAAUGGCGAGUGCGC (SEQ ID NO: 584)	ORF	52.63157895
NM_014632_sirna_746	746	CCAUCGACCAUAUCAGUAU (SEQ ID NO: 585)	AUACUGAUUUGGUGCAUGG (SEQ ID NO: 586)	ORF	42.10526316
NM_014632_sirna_753	753	CCAUAUCAGUAUUCGCCAA (SEQ ID NO: 587)	UUGCGAAUACUGAUUUGG (SEQ ID NO: 588)	ORF	42.10526316
NM_014632_sirna_912	912	CCAUUCUCUGCGGAGUUU (SEQ ID NO: 589)	AAACUCCGACAGAGAAUGG (SEQ ID NO: 590)	ORF	47.36842105
NM_014632_sirna_1136	1136	GCAUAGAUCUUGAGAGACAU (SEQ ID NO: 591)	AUGUUCUCAAGAUCAUUGC (SEQ ID NO: 592)	ORF	36.84210526
NM_014632_sirna_1338	1338	GCUGCCAUCUUGAGACUUU (SEQ ID NO: 593)	AAAGUCUAAAGGAGGCGAGC (SEQ ID NO: 594)	ORF	47.36842105
NM_014632_sirna_2402	2402	GCAGUAGGAAGGUGGAAA (SEQ ID NO: 595)	UUUCCACCUUCCUACUGC (SEQ ID NO: 596)	ORF	47.36842105
NM_014632_sirna_3111	3111	CCAUUUGAGAGAGUGCAU (SEQ ID NO: 597)	AUGCACUGUUCUCAAAUGG (SEQ ID NO: 598)	ORF	42.10526316

Gene Name:	CLEC2D	GenBank Accession No.	NM_001004419	GI:	52426781
Organism:	Homo sapiens	Length:	1821	ORF Region:	23-607
Locus:	29121	Blast database:	Human	ORF GC%	41.71
Definition:	Homo sapiens C-type lectin domain family 2, member D (CLEC2D), transcript variant 2, mRNA. (OCIL)				
Name	Start	Sense RNA Sequence 5'-3'	Antisense RNA Sequence 5'-3'	Region	GC%
NM_001004419_sirna_506	506	GCCAACUUGUAUGUUGCAA (SEQ ID NO: 599)	UUGCAACAUAACAAGUUGGC (SEQ ID NO: 600)	ORF	42.10526316
NM_001004419_sirna_507	507	CCAACUUGUAUGUUGCAA (SEQ ID NO: 601)	UUUGCAACAUAACAAGUUGG (SEQ ID NO: 602)	ORF	36.84210526
NM_001004419_sirna_551	551	CCAAGACCUGUAGUUGUUU (SEQ ID NO: 603)	AAACCAUGACAGGUCUUGG (SEQ ID NO: 604)	ORF	47.36842105
NM_001004419_sirna_582	582	GCAGGAGAGUGGCCUAUU (SEQ ID NO: 605)	AUAGGCACACUCUCCUGC (SEQ ID NO: 606)	ORF	52.63157895
Gene Name:	CLEC2D	GenBank Accession No.	NM_001004420	GI:	52426783

Organism:	Homo sapiens	Length:	1814	ORF	23-391
Locus:	29121	Blast database:	Human	ORF GC%	40.11
Definition:	Homo sapiens C-type lectin domain family 2, member D (CLEC2D), transcript variant 3, mRNA. (OCIL)				

Name	Start	Sense RNA Sequence 5'-3'	Antisense RNA Sequence 5'-3'	Region	GC%
NM_001004420_sRNA_59	59	CCAUCUGAAUUGCCUGCAA (SEQ ID NO: 607)	UUGCAGGCAAUUCAGAUAGG (SEQ ID NO: 608)	ORF	47.36842105
NM_001004420_sRNA_182	182	GCUGCUUUAAGCGCAUAA (SEQ ID NO: 609)	UUUUUGCGCUUAAAGCAGC (SEQ ID NO: 610)	ORF	42.10526316
NM_001004420_sRNA_220	220	GCCAUCAGUAGUGUCUCAA (SEQ ID NO: 611)	UUGAAGACAUACUGAUGGC (SEQ ID NO: 612)	ORF	42.10526316

Gene Name:	CLEC2D	GenBank Accession No.	NM_013269	GI:	52426785
Organism:	Homo sapiens	Length:	1739	ORF	23-598
Locus:	29121	Blast database:	Human	ORF GC%	42.19
Definition:	Homo sapiens C-type lectin domain family 2, member D (CLEC2D), transcript variant 1, mRNA. (OCIL)				

Name	Start	Sense RNA Sequence 5'-3'	Antisense RNA Sequence 5'-3'	Region	GC%
NM_013269_sRNA_402	402	GCCCAUCUGAUCACUGGAU (SEQ ID NO: 613)	AUCCAGUGAUCAGAUAGG (SEQ ID NO: 614)	ORF	52.63157895
NM_013269_sRNA_441	441	GCCCAACCAUGGAAUGGAU (SEQ ID NO: 615)	AUCCAUUUCCAUUGGUUGGC (SEQ ID NO: 616)	ORF	47.36842105
NM_013269_sRNA_500	500	GCAGGAGAGUGUGCCUAUU (SEQ ID NO: 617)	AUAGGCACACUCUCCUGC (SEQ ID NO: 618)	ORF	52.63157895
NM_013269_sRNA_561	561	GGAAGUGGAUUUGUCCAA (SEQ ID NO: 619)	UUGGAACAAAUCCACUCC (SEQ ID NO: 620)	ORF	42.10526316

Gene Name:	ASAM	GenBank Accession No.	NM_024769	GI:	41393588
Organism:	Homo sapiens	Length:	2645	ORF	360-1481
Locus:	79827	Blast database:	Human	ORF GC%	51.61
Definition:	Homo sapiens adipocyte-specific adhesion molecule (ASAM), mRNA.				

Name	Start	Sense RNA Sequence 5'-3'	Antisense RNA Sequence 5'-3'	Region	GC%
NM_024769_sRNA_391	391	CCUACUAUGUUGGAACCUU (SEQ ID NO: 621)	AAGGUUCCAAACAAGUAGG (SEQ ID NO: 622)	ORF	42.10526316
NM_024769_sRNA_682	682	GGUACACCUUGAAGGUUAA (SEQ ID NO: 623)	UUAAACCUUACAGGUUAGC (SEQ ID NO: 624)	ORF	42.10526316
NM_024769_sRNA_780	780	GGAGAGCUGACAGAGGAA (SEQ ID NO: 625)	UUCCUUCUGACAGCUCUCC (SEQ ID NO: 626)	ORF	52.63157895
NM_024769_sRNA_1022	1022	GCGAGUAACUGUACAGUAU (SEQ ID NO: 627)	AUACUGUACAGUACUCGC (SEQ ID NO: 628)	ORF	42.10526316
NM_024769_sRNA_1406	1406	CCAUGCUAAUCUGACCAAAA (SEQ ID NO: 629)	UUUGGUACAGAUUAGCAUGG (SEQ ID NO: 630)	ORF	42.10526316

Gene Name:	NUMB	GenBank Accession No.	NM 003744	GI:	54144623
Organism:	Homo sapiens	Length:	3614	ORF Region:	321-2243
Locus:	8650	Blast database:	Human	ORF GC%	52.06
Definition:	Homo sapiens numb homolog (Drosophila) (NUMB), transcript variant3, mRNA.				
Name	Start	Sense RNA Sequence 5'-3'	Antisense RNA Sequence 5'-3'	Region	GC%
NM_003744_sirNA_700	700	GCUGGAUCUGUCACUGCUU (SEQ ID NO: 631)	AAGCAGUGACAGAUCCAGC (SEQ ID NO: 632)	ORF	52.63157895
NM_003744_sirNA_864	864	GGAUCAUUCGUGUCACAA (SEQ ID NO: 633)	UUGUGACACGGAAUGAUCC (SEQ ID NO: 634)	ORF	47.36842105
NM_003744_sirNA_1139	1139	CCAGAAGAUGUCACCCUUU (SEQ ID NO: 635)	AAAGGUGACAUUCUUCUGG (SEQ ID NO: 636)	ORF	47.36842105
NM_003744_sirNA_1402	1402	CCUCCAUGUGCUUUCUAA (SEQ ID NO: 637)	UUAGCAAGCACAUGGAAGG (SEQ ID NO: 638)	ORF	47.36842105
NM_003744_sirNA_1615	1615	GGUUAGAAGAGGUGUCUAA (SEQ ID NO: 639)	UUAGACACCUCUUCUAACC (SEQ ID NO: 640)	ORF	42.10526316
NM_003744_sirNA_1999	1999	CCACCAGUCCUUCUUUAA (SEQ ID NO: 641)	UUAAAGAAGGGACUGGUGG (SEQ ID NO:642)	ORF	47.36842105

Gene Name:	PDE4B	GenBank Accession No.	NM_002600	GI:	32171240
Organism:	Homo sapiens	Length:	3186	ORF Region:	139-2349
Locus:	5142	Blast database:	Human	ORF GC%	46.32
Definition:	Homo sapiens phosphodiesterase 4B, cAMP-specific (phosphodiesteraseE4 dunce homolog, Drosophila) (PDE4B), mRNA.				
Name	Start	Sense RNA Sequence 5'-3'	Antisense RNA Sequence 5'-3'	Region	GC%
NM_002600_sirna_218	218	CCUACAGUUCUCCAGUAA (SEQ ID NO: 643)	UUACUGGAAGAACUCUGAGG (SEQ ID NO: 644)	ORF	42.10526316
NM_002600_sirna_527	527	GCAGAGAGUCAUUCUCUA (SEQ ID NO:645)	UAGAGAAUAGACUCUCUGC (SEQ ID NO: 646)	ORF	42.10526316
NM_002600_sirna_945	945	CCAGGUGUCUGAAUACAUU (SEQ ID NO:647)	AAUGUAUUCAGACACCCUGG (SEQ ID NO: 648)	ORF	42.10526316
NM_002600_sirna_1499	1499	CCAAUCAGUUCUCUCAUAA (SEQ ID NO: 649)	UUGAUGAGAAACUCUGAUUGG (SEQ ID NO: 650)	ORF	36.84210526
NM_002600_sirna_1763	1763	GCGUUCUUCUCCUAGACAA (SEQ ID NO: 651)	UUUGUCUAGGAGAGAAACGC (SEQ ID NO: 652)	ORF	47.36842105
NM_002600_sirna_2050	2050	CCUACAGGACAUUCUCCGUA (SEQ ID NO: 653)	UAUCGAGAAUUGUCCUGAGC (SEQ ID NO: 654)	ORF	47.36842105

Gene Name:	ABCB1	GenBank Accession No.	GI:	42741658
Organism:	Homo sapiens		ORF Region:	419-4261
Locus:	5243		ORF GC%	43.69
Definition:	Homo sapiens ATP-binding cassette, sub-family B (MDR/TAP), member 1(ABCB1), mRNA.			

Name	Start	Sense RNA Sequence 5'-3'	Antisense RNA Sequence 5'-3'	Region	GC%
NM_000927_sirna_761	761	GCCUAAUUUACAGUGGAA (SEQ ID NO: 655)	UCCACUGUAAUAAUAGGC (SEQ ID NO: 656)	ORF	36.84210526
NM_000927_sirna_1330	1330	GCUGAUCUAUGCAUCUUUAU (SEQ ID NO: 657)	AUAAGAUCAUAGAUCAAGC (SEQ ID NO: 658)	ORF	36.84210526
NM_000927_sirna_1470	1470	GCAUUGAAGCAUUUGCAA (SEQ ID NO: 659)	UUUGCAAUAGCUUCAUAGC (SEQ ID NO: 660)	ORF	36.84210526
NM_000927_sirna_1732	1732	GCUGAUGCAGAGGCUCUAU (SEQ ID NO: 661)	AUAGAGCCUCUGCAUCAGC (SEQ ID NO: 662)	ORF	52.63157895
NM_000927_sirna_2309	2309	GCAGAAUUGAAGUUGAAU (SEQ ID NO: 663)	AUUCACUUAUUAUCCUGC (SEQ ID NO: 664)	ORF	36.84210526
NM_000927_sirna_2815	2815	GGAUGUGAGUUGGUUUGAU (SEQ ID NO: 665)	AUCAAACCAACUCACAUC (SEQ ID NO: 666)	ORF	42.10526316
NM_000927_sirna_3915	3915	GCACUAAAGUAGGAGACAA (SEQ ID NO: 667)	UUUGUCUCCUACUUAUAGUGC (SEQ ID NO: 668)	ORF	42.10526316

Gene Name:	HTRA1	GenBank Accession No.	NM_002775	GI:	73747816
Organism:	Homo sapiens	Length:	2133	ORF Region:	113-1555
Locus:	5654	Blast database:	Human	ORF GC%	59.26
Definition:	Homo sapiens HtrA serine peptidase 1 (HTRA1), mRNA. (PRSS11)				

Name	Start	Sense RNA Sequence 5'-3'	Antisense RNA Sequence 5'-3'	Region	GC%
NM_002775_sirna_597	597	CCAAAGUUUUGCGCCAUAA (SEQ ID NO: 669)	UUUAGGCGCAAAACUGUUGG (SEQ ID NO: 670)	ORF	47.36842105
NM_002775_sirna_716	716	GCUAGUGGUCUGGGUUUA (SEQ ID NO: 671)	UAAACCCAGACCCCUAGC (SEQ ID NO: 672)	ORF	52.63157895
NM_002775_sirna_1073	1073	GCCAUCAUCAACUAGGAA (SEQ ID NO: 673)	UUCCAUAGUUGAUGAUGGC (SEQ ID NO: 674)	ORF	42.10526316
NM_002775_sirna_1114	1114	CCUGAGCGGUGAAGUGAUU (SEQ ID NO: 675)	AAUCACUUCACCGUCCAGG (SEQ ID NO: 676)	ORF	52.63157895
NM_002775_sirna_1535	1535	CCCGAAGAAAUUGACCCAU (SEQ ID NO: 677)	AUGGGUCAUUUUCUUGGGG (SEQ ID NO: 678)	ORF	47.36842105

Gene Name:	NPEPPS	GenBank Accession No.	NM_006310	GI:	15451906
Organism:	Homo sapiens	Length:	4177	ORF Region:	196-2823
Locus:	9520	Blast database:	Human	ORF GC%	44.79
Definition:	Homo sapiens aminopeptidase puromycin sensitive (NPEPPS), mRNA.				
Sequence:	NM_006310				

Name	Start	Sense RNA Sequence 5'-3'	Antisense RNA Sequence 5'-3'	Region	GC%
NM_006310_sirna_1939	1939	GCUCGAGCUGGAAUUAUUA (SEQ ID NO: 679)	UAAUGAUUCCAGCUCGAGC (SEQ ID NO: 680)	ORF	47.36842105
NM_006310_sirna_2539	2539	GCUCGCUUGGAAUUAUUA (SEQ ID NO: 681)	UUAUGAAUUUCCAGCAGC (SEQ ID NO: 682)	ORF	36.84210526
NM_006310_sirna_2622	2622	GCUAUCAGUUUGAGGGGAUUU (SEQ ID NO: 683)	AAAUCCCUCAACUGAUAGC (SEQ ID NO: 684)	ORF	42.10526316

Gene Name:	PSMA7	GenBank Accession No.	NM_002792	GI:	23110945
Organism:	Homo sapiens	Length:	984	ORF Region:	116-862
Locus:	5688	Blast database:	Human	ORF GC%	50.47
Definition:	Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 7 (PSMA7), transcript variant 1, mRNA.				

Name	Start	Sense RNA Sequence 5'-3'	Antisense RNA Sequence 5'-3'	Region	GC%
NM_002792_sirna_266	266	GCCAAACUGCAGGAUGAAA (SEQ ID NO: 685)	UUUCAUCCUGCAGUUUGGC (SEQ ID NO: 686)	ORF	47.36842105
NM_002792_sirna_300	300	UCUGUGCUUUGGAUGACAA (SEQ ID NO: 687)	UUGUCAUCCAAAGCACAGA (SEQ ID NO: 688)	ORF	42.10526316
NM_002792_sirna_348	348	CCGAUGCAAGGAUAGUCAU (SEQ ID NO: 689)	AUGACUAUCCUUGCAUCGG (SEQ ID NO: 690)	ORF	47.36842105

Gene Name:	PTS	GenBank Accession No.	NM_000317	GI:	4506330
Organism:	Homo sapiens	Length:	921	ORF Region:	69-506
Locus:	5805	Blast database:	Human	ORF GC%	43.16
Definition:	Homo sapiens 6-pyruvoyltetrahydropterin synthase (PTS), mRNA.				

Name	Start	Sense RNA Sequence 5'-3'	Antisense RNA Sequence 5'-3'	Region	GC%
NM_000317_sirna_137	137	CCACCGAUUGUACAGUAAA (SEQ ID NO: 691)	UUUACUGUACAAUCGGUGG (SEQ ID NO: 692)	ORF	42.10526316
NM_000317_sirna_275	275	GGUUAUGAAUCUGGCUGAU (SEQ ID NO: 693)	AUCAGCCAGAUUCAUAACC (SEQ ID NO: 694)	ORF	42.10526316
NM_000317_sirna_413	413	GGACAACCUCCAGAAAGUU (SEQ ID NO: 695)	AACUUUCUGGAGGUUGUCC (SEQ ID NO: 696)	ORF	47.36842105

Gene Name:	RIN2	GenBank Accession No.	NM_018993	GI:	35493905
Organism:	Homo sapiens	Length:	4259	Region:	37-2724
Locus:	54453	Blast database:	Human	ORF GC%	55.92
Definition:	Homo sapiens Ras and Rab interactor 2 (RIN2), mRNA.				

Name	Start	Sense RNA Sequence 5'-3'	Antisense RNA Sequence 5'-3'	Region	GC%
NM_018993_sirna_471	471	GGAAUUUGCCAUAAAGGAA (SEQ ID NO: 697)	UUCUUUAUGGCAAAUUC (SEQ ID NO: 698)	ORF	36.84210526
NM_018993_sirna_569	569	GCAGGGAUGUUCUACCAU (SEQ ID NO: 699)	AAUGGUAAGAACAUCCUGC (SEQ ID NO: 700)	ORF	47.36842105
NM_018993_sirna_1034	1034	GCAUGCCAGAAACAGUCAA (SEQ ID NO: 701)	UUGACUUGUUUCUGGCAUC (SEQ ID NO: 702)	ORF	47.36842105
NM_018993_sirna_1376	1376	GCAUGCCUCUGUUGGCUA (SEQ ID NO: 703)	UAGCCAAACAGAGGCAUC (SEQ ID NO: 704)	ORF	52.63157895
NM_018993_sirna_2236	2236	GGAGGCUAUUACUUGACAA (SEQ ID NO: 705)	UUGUCAAGUAAUAGCCUCC (SEQ ID NO: 706)	ORF	42.10526316

Gene Name:	ROR1	GenBank Accession No.	NM_005012	GI:	4826867
Organism:	Homo sapiens	Length:	3358	Region:	376-3189
Locus:	4919	Blast database:	Human	ORF GC%	47.45
Definition:	Homo sapiens receptor tyrosine kinase-like orphan receptor 1 (ROR1), mRNA.				

Name	Start	Sense RNA Sequence 5'-3'	Antisense RNA Sequence 5'-3'	Region	GC%
NM_005012_sirna_932	932	CCGUCUAUUGGAGUCUUU (SEQ ID NO: 707)	AAAGACUCCAUUAGACGG (SEQ ID NO: 708)	ORF	42.10526316
NM_005012_sirna_1543	1543	GCUUGCGAUUCAAAGGAU (SEQ ID NO: 709)	AAUCCUUUGAAUCGCAAGC (SEQ ID NO: 710)	ORF	42.10526316
NM_005012_sirna_1920	1920	GCAUUGGAUGGAUUUCAA (SEQ ID NO: 711)	UUGAAAUUUCCAUCCAUUGC (SEQ ID NO: 712)	ORF	36.84210526
NM_005012_sirna_2817	2817	GCGAUUCAUCCCAUCAAU (SEQ ID NO: 713)	AUUGAUGGGAUUGAAUCCG (SEQ ID NO: 714)	ORF	42.10526316
NM_005012_sirna_3031	3031	CCACACAUGUCAUUUCCAA (SEQ ID NO: 715)	UUUGAAUUUGACAUUGUGUGG (SEQ ID NO: 716)	ORF	42.10526316

Organism:	Homo sapiens	Length:	1657	ORF	287-1228
Locus:	10670	Blast database:	Human	ORF GC%	51.39
Definition:	Homo sapiens Ras-related GTP binding A (PRAGA), mRNA.				
Name	Start	Sense RNA Sequence 5'-3'	Antisense RNA Sequence 5'-3'	Region	GC%
NM_006570_sirna_351	351	GCAUGAGGUCGAUAUUCUU (SEQ ID NO: 717)	AAGAUUAUCGACCUCUAGC (SEQ ID NO: 718)	ORF	42.10526316
NM_006570_sirna_510	510	CCAGCCAGCGAGACAUAU (SEQ ID NO: 719)	AUAUUGUCUCGCGGCGUUG (SEQ ID NO: 720)	ORF	52.63157895
NM_006570_sirna_673	673	GGAUCUGGUUCAGGAGGGAU (SEQ ID NO: 721)	AUCCUCCUGAACCAAGAUCC (SEQ ID NO: 722)	ORF	52.63157895
NM_006570_sirna_1056	1056	CCAACUUCGCGCUUUCU (SEQ ID NO: 723)	AUGAAAGCAGCGAAGUUGG (SEQ ID NO: 724)	ORF	47.36842105

Gene Name:	RYK	GenBank Accession No.	NM_002958	GI:	54607017
Organism:	Homo sapiens	Length:	2951	ORF	91-1914
Locus:	6259	Blast database:	Human	ORF GC%	42.38
Definition:	Homo sapiens RYK receptor-like tyrosine kinase (RYK), transcript variant 2, mRNA.				

Name	Start	Sense RNA Sequence 5'-3'	Antisense RNA Sequence 5'-3'	Region	GC%
NM_002958_sirna_558	558	GCUUUCUGUACUGGCAAA (SEQ ID NO: 725)	UUUCCAGUACAGGAAAGC (SEQ ID NO: 726)	ORF	47.36842105
NM_002958_sirna_748	748	GCAGCUCCAACCAUUCUA (SEQ ID NO: 727)	UAGAGUGGUUGAGCUGC (SEQ ID NO: 728)	ORF	52.63157895
NM_002958_sirna_1367	1367	GCAAGUUAGUAGAGGCCAA (SEQ ID NO: 729)	UUGGCCUCUACUAAUUGC (SEQ ID NO: 730)	ORF	47.36842105
NM_002958_sirna_1413	1413	CCUGGUACACAUUGGCUAUU (SEQ ID NO: 731)	AAUAGCAUGUGUACCAGG (SEQ ID NO: 732)	ORF	47.36842105
NM_002958_sirna_1779	1779	GCCAAUCAACUGUCCUGAU (SEQ ID NO: 733)	AUCAGGACAGUUGAUUGGC (SEQ ID NO: 734)	ORF	47.36842105

Gene Name:	S100A6	GenBank Accession No.	NM_014624	GI:	52352807
Organism:	Homo sapiens	Length:	683	ORF	315-587
Locus:	6277	Blast database:	Human	ORF GC%	56.05
Definition:	Homo sapiens S100 calcium binding protein A6 (calyculin) (S100A6), mRNA.				
Name	Start	Sense RNA Sequence 5'-3'	Antisense RNA Sequence 5'-3'	Region	GC%
NM_014624_sirna_455	455	GCUGCAGGAUGCUGAAAUU (SEQ ID NO: 735)	AAUUUCAGCAUCCUGCAGC (SEQ ID NO: 736)	ORF	47.36842105
NM_014624_sirna_474	474	GCAAGGCUUGAUGGAAGACU (SEQ ID NO: 737)	AGUCUCCAUCCAGCCUUGC (SEQ ID NO: 738)	ORF	52.63157895
NM_014624_sirna_479	479	GCUGAUGGAAGACUUGGAC (SEQ ID NO: 739)	GUCCAAGUCUCCAUCCAGC (SEQ ID NO: 740)	ORF	52.63157895

Gene Name:	S100A1	GenBank Accession No.	NM_006271	GI:	5454031
Organism:	Homo sapiens	Length:	607	ORF Region:	114-398
Locus:	6271	Blast database:	Human	ORF GC%	55.44
Definition:	Homo sapiens S100 calcium binding protein A1 (S100A1), mRNA.				
Name	Start	Sense RNA Sequence 5'-3'	Antisense RNA Sequence 5'-3'	Region	GC%
NM_006271_sRNA_136	136	CGAUGGAGACCCUCAUCAA (SEQ ID NO: 741)	UUGAUGAGGGGUCUCAUCG (SEQ ID NO: 742)	ORF	52.63157895
NM_006271_sRNA_137	137	GAUGGAGACCCUCAUCAA (SEQ ID NO: 743)	GUUGAUGAGGGGUCUCAUC (SEQ ID NO: 744)	ORF	52.63157895
Gene Name:	SCMH1	GenBank Accession No.	NM_012236	GI:	6912641
Organism:	Homo sapiens	Length:	3250	ORF Region:	485-2260
Locus:	22955	Blast database:	Human	ORF GC%	54.79
Definition:	Homo sapiens sex comb on midleg homolog 1 (Drosophila) (SCMH1), transcript variant 2, mRNA.				
Name	Start	Sense RNA Sequence 5'-3'	Antisense RNA Sequence 5'-3'	Region	GC%
NM_012236_sRNA_876	876	GGAAGAAACCCUCAUUUCAU (SEQ ID NO: 745)	AUGAAUAGAGGGUUCUCC (SEQ ID NO: 746)	ORF	42.10526316
NM_012236_sRNA_1632	1632	GGGAACAGCAUACCCUCAU (SEQ ID NO: 747)	UUAGAGGUAGUGUGUCC (SEQ ID NO: 748)	ORF	52.63157895
NM_012236_sRNA_1743	1743	CCUUUACACAGACUCACUU (SEQ ID NO: 749)	AAGUGAGUCUGUGUAAAGG (SEQ ID NO: 750)	ORF	42.10526316
NM_012236_sRNA_1804	1804	CCUACAGGUGAAACCUUU (SEQ ID NO: 751)	AAAGGUUUCACCCUGGUAGG (SEQ ID NO: 752)	ORF	47.36842105

Gene Name:	SERP1	GenBank Accession No.	NM_014445	GI:	19923408
Organism:	Homo sapiens	Length:	2488	ORF Region:	316-516
Locus:	27230	Blast database:	Human	ORF GC%:	50.25
Definition:	Homo sapiens stress-associated endoplasmic reticulum protein 1 (SERP1), mRNA.				
Name	Start	Sense RNA Sequence 5'-3'	Antisense RNA Sequence 5'-3'	Region	GC%
NM_014445_sRNA_323	323	CCAGCAAAGGAUCCGUU (SEQ ID NO: 753)	AUACGGAUCCUUUGCUUGG (SEQ ID NO: 754)	ORF	47.36842105
NM_014445_sRNA_434	434	CCUGGUUUUUUGGCUCUCUU (SEQ ID NO: 755)	AAGAGAGCCAAUAACCAGG (SEQ ID NO: 756)	ORF	47.36842105
NM_014445_sRNA_437	437	GGUUUUUUGGCUCUCUCUUAU (SEQ ID NO: 757)	AUGAAGAGAGCCAAUAACC (SEQ ID NO: 758)	ORF	42.10526316

Gene Name:	SRP19	GenBank Accession No.	NM_003135	GI:	4507212
Organism:	Homo sapiens	Length:	894	ORF Region:	82-516
Locus:	6728	Blast database:	Human	ORF GC%:	41.38
Definition:	Homo sapiens signal recognition particle 19kDa (SRP19), mRNA.				
Name	Start	Sense RNA Sequence 5'-3'	Antisense RNA Sequence 5'-3'	Region	GC%
NM_003135_sRNA_110	110	CCGACCAGGACAGGUUUU (SEQ ID NO: 759)	AUAAACCUUGUCUGGUCGG (SEQ ID NO: 760)	ORF	52.63157895
NM_003135_sRNA_244	244	GCAGUUGGACUUUACGUU (SEQ ID NO: 761)	AUACGUUAAAGUCCAAUCUGC (SEQ ID NO: 762)	ORF	42.10526316
NM_003135_sRNA_454	454	GCUGACCAAGAGUCUUAAC (SEQ ID NO: 763)	GUUGAAGAGUUUGGUCAGC (SEQ ID NO: 764)	ORF	47.36842105

Gene Name:	TPM1	GenBank Accession No.	NM_000366	GI:	63252894
Organism:	Homo sapiens	Length:	1294	ORF Region:	192-1046
Locus:	7168	Blast database:	Human	ORF GC%:	50.77
Definition:	Homo sapiens tropomyosin 1 (alpha) (TPM1), transcript variant 5, mRNA.				
Name	Start	Sense RNA Sequence 5'-3'	Antisense RNA Sequence 5'-3'	Region	GC%
NM_000366_sRNA_688	688	CCCGUAAAGCUGGUCAU (SEQ ID NO: 765)	AUGAUGACCAGCUUACGGG (SEQ ID NO: 766)	ORF	52.63157895
NM_000366_sRNA_915	915	GCGGAGAGGUCAGUAACUA (SEQ ID NO: 767)	UAGUUACUGACCUUCUCCGC (SEQ ID NO: 768)	ORF	52.63157895
NM_000366_sRNA_1020	1020	GCUCUCAAGGAUAGACUU (SEQ ID NO: 769)	AAGUCAUAUCCGUUGAGAGC (SEQ ID NO: 770)	ORF	42.10526316

Gene Name:	TRIM52	GenBank Accession No.	NM_032765	GI:	34147443
Organism:	Homo sapiens	Length:	2244	ORF Region:	306-1199
Locus:	84851	Blast database:	Human	ORF GC%	48.77
Definition:	Homo sapiens tripartite motif-containing 52 (TRIM52), mRNA.				
Name	Start	Sense RNA Sequence 5'-3'	Antisense RNA Sequence 5'-3'	Region	GC%
NM_032765_sRNA_1115	1115	CCAGAAUAAGUUGGAA (SEQ ID NO: 771)	UUCCAACUUUUUUUCCUGG (SEQ ID NO: 772)	ORF	36.84210526
NM_032765_sRNA_1142	1142	GGUGGAAUACUUCAGAU (SEQ ID NO: 773)	UAUCUGAAGUAUCCACC (SEQ ID NO: 774)	ORF	42.10526316
NM_032765_sRNA_1145	1145	GGAAUACUUCAGAUAGAG (SEQ ID NO: 775)	CUCUAUCUGAAGUAUCCC (SEQ ID NO: 776)	ORF	42.10526316
NM_032765_sRNA_1171	1171	GCAUUCACAGCAAGGCCUA (SEQ ID NO: 777)	UAGGCCUUUGCUGUGAAUGC (SEQ ID NO: 778)	ORF	52.63157895

Gene Name:	MTHFD1	GenBank Accession No.	NM_005956	GI:	13699867
Organism:	Homo sapiens	Length:	3110	ORF Region:	54-2861
Locus:	4522	Blast database:	Human	ORF GC%	49.11
Definition:					
Sequence:	NM_005956				

Name	Start	Sense RNA Sequence 5'-3'	Antisense RNA Sequence 5'-3'	Region	GC%
NM_005956_sRNA_184	184	GCAACAGAGAUAUCCAA (SEQ ID NO: 779)	UUGGAAUCAUCUCUGUUGC (SEQ ID NO: 780)	ORF	42.10526316
NM_005956_sRNA_696	696	GCAACUGGUCAGCCUGAAA (SEQ ID NO: 781)	UUUCAGGCUGACCAGUUGC (SEQ ID NO: 782)	ORF	52.63157895
NM_005956_sRNA_1429	1429	CCAUUGAUGCUCGGAUUAU (SEQ ID NO: 783)	AUAUCCGAGCAUCAUUGG (SEQ ID NO: 784)	ORF	42.10526316
NM_005956_sRNA_1780	1780	CCACUUCUCUAGAAGACAU (SEQ ID NO: 785)	AUGUCUUCUAGAGAAGUGG (SEQ ID NO: 786)	ORF	42.10526316
NM_005956_sRNA_2482	2482	GCAGCUUCCAGCUCCUUUA (SEQ ID NO: 787)	UAAAGGAGCUGGAAGCUGC (SEQ ID NO: 788)	ORF	52.63157895

Gene Name:	UBE1C	GenBank Accession No.	NM_003968	GI:	38045941
Organism:	Homo sapiens	Length:	2136	ORF Region:	21-1412
Locus:	9039	Blast database:	Human	ORF GC%	42.25
Definition:					

Sequence:	NM_003968
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Name	Start	Sense RNA Sequence 5'-3'	Antisense RNA Sequence 5'-3'	Region	GC%
NM_003968_sRNA_133	133	GGAACCAUGUAAAGAGUU (SEQ ID NO: 789)	AACUUCUUUACAUGGUUCC (SEQ ID NO: 790)	ORF	36.84210526
NM_003968_sRNA_393	393	GCUGAAGUUGCUGCAGAAU (SEQ ID NO: 791)	AUUCUGCAGCAACUUCAGC (SEQ ID NO: 792)	ORF	47.36842105
NM_003968_sRNA_594	594	CCAAGCUCCAUUGUCCCUU (SEQ ID NO: 793)	AAGGACAAUUGGAGCUUGG (SEQ ID NO: 794)	ORF	52.63157895
NM_003968_sRNA_1023	1023	GCAUACAUUCCUUGAAUA (SEQ ID NO: 795)	UAUUCAGGGAAGUUAUGC (SEQ ID NO: 796)	ORF	36.84210526
NM_003968_sRNA_1197	1197	GCUUCUCUGCAAAUGAAU (SEQ ID NO: 797)	AUUCAUUUGCAGAGAAGC (SEQ ID NO: 798)	ORF	36.84210526

Gene Name:	UBE1C	GenBank Accession No.	NM_198195	GI:	38045943
Organism:	Homo sapiens	Length:	2094	Region:	ORF 21-1370
Locus:	9039	Blast database:	Human	ORF GC%	42.08
Definition:					
Sequence:	NM_198195				

Name	Start	Sense RNA Sequence 5'-3'	Antisense RNA Sequence 5'-3'	Region	GC%
NM_198195_sRNA_35	35	GGAGCCAAUGGCGUUGAU (SEQ ID NO: 799)	AUCAACAGCCAUUGGCUCC (SEQ ID NO: 800)	ORF	52.63157895
NM_198195_sRNA_91	91	GGAACCAUGUAAAGAGUU (SEQ ID NO: 801)	AACUUCUUUACAUGGUUCC (SEQ ID NO: 802)	ORF	36.84210526
NM_198195_sRNA_351	351	GCUGAAGUUGCUGCAGAAU (SEQ ID NO: 803)	AUUCUGCAGCAACUUCAGC (SEQ ID NO: 804)	ORF	47.36842105
NM_198195_sRNA_552	552	CCAAGCUCCAUUGUCCCUU (SEQ ID NO: 805)	AAGGACAAUUGGAGCUUGG (SEQ ID NO: 806)	ORF	52.63157895
NM_198195_sRNA_981	981	GCAUACAUUCCUUGAAUA (SEQ ID NO: 807)	UAUUCAGGGAAGUUAUGC (SEQ ID NO: 808)	ORF	36.84210526
NM_198195_sRNA_1155	1155	GCUUCUCUGCAAAUGAAU	AUUUCAUUUUGCAGAGAAGC	ORF	36.84210526

Gene Name:	UBE1C	GenBank Accession No.	NM_198197	GI:	38045945
Organism:	Homo sapiens	Length:	2015	Region:	ORF 200-1291
Locus:	9039	Blast database:	Human	ORF GC%	40.39
Definition:					
Sequence:	NM_198197				

Name	Start	Sense RNA Sequence 5'-3'	Antisense RNA Sequence 5'-3'	Region	GC%
NM_198197_sirNA_272	272	GCUGAAGUUGCUGCAGAAU (SEQ ID NO: 809)	AUUCUGCAGCAACUUCAGC (SEQ ID NO: 810)	ORF	47.36842105
NM_198197_sirNA_473	473	CCAAGCUCCAUUGUCCUU (SEQ ID NO: 811)	AAGGGACAAUGGAGCUUGG (SEQ ID NO: 812)	ORF	52.63157895
NM_198197_sirNA_902	902	GCAUACAUUCCCUUGAAUA (SEQ ID NO: 813)	UAUCAAAGGGAUUGUAUGC (SEQ ID NO: 814)	ORF	36.84210526
NM_198197_sirNA_1076	1076	GCUUCUCUGCAAAUUGAAAU (SEQ ID NO: 815)	AUUUCAUUUGCAGAGAAGC (SEQ ID NO: 816)	ORF	36.84210526

Gene Name:	ZNF207	GenBank Accession No.	NM_003457	GI:	75750493
Organism:	Homo sapiens	Length:	2348	ORF Region:	204-1640
Locus:	7756	Blast database:	Human	ORF GC%	48.3
Definition:					
Sequence:	NM_003457				

Name	Start	Sense RNA Sequence 5'-3'	Antisense RNA Sequence 5'-3'	Region	GC%
NM_003457_sirNA_747	747	CCACUGGAAUGAUGCCAA (SEQ ID NO: 817)	UUUGCAUCAAUCCAGGUGG (SEQ ID NO: 818)	ORF	52.63157895
NM_003457_sirNA_888	888	GCGCCAGGUUUUUUAUA (SEQ ID NO: 819)	UAUUAGAAUACCUUGGCGC (SEQ ID NO: 820)	ORF	42.10526316
NM_003457_sirNA_1014	1014	GCUUCAUCCAAUUCAGAAA (SEQ ID NO: 821)	UUUCUGAAUUGGAUGAAGC (SEQ ID NO: 822)	ORF	36.84210526
NM_003457_sirNA_1230	1230	CCAGCGCUUCAAUAACAA (SEQ ID NO: 823)	UUGUUUUUGAAGCCGUGG (SEQ ID NO: 824)	ORF	47.36842105
NM_003457_sirNA_1257	1257	GCUACACUUAACAACAUA (SEQ ID NO: 825)	UAGUUUUUGUAAGUGUAGC (SEQ ID NO: 826)	ORF	36.84210526

Gene Name:	ZNF7	GenBank Accession No.	NM_003416	GI:	4508034
Organism:	Homo sapiens	Length:	2351	ORF Region:	239-2299
Locus:	7553	Blast database:	Human	ORF GC%	48.62
Definition:					
Sequence:	NM_003416				

Name	Start	Sense RNA Sequence 5'-3'	Antisense RNA Sequence 5'-3'	Region	GC%
NM_003416_stealth_1839	1839	UCAGUAGAGCACACAGCUUACAAU (SEQ ID NO: 827)	AUUGAAGCUGUGUGUCUACUACA (SEQ ID NO: 828)	ORF	40
NM_003416_stealth_1843	1843	UAUGAGCACACAGCUUACAAUACAU (SEQ ID NO: 829)	AUGUAUUGUAAGCUGUGUCUCAUA (SEQ ID NO: 830)	ORF	36
NM_003416_stealth_1848	1848	GCACACAGCUUACAAUACAUAAG (SEQ ID NO: 831)	CUUUGAUGUAUUGAAGCUGUGUGC (SEQ ID NO: 832)	ORF	40

			NO: 831)	832)		
NM_003416_stealth_2089	2089	AGGGUCCACCUUUUGUGAGCCGUAAA (SEQ ID NO: 833)	UUUACGGCUCACAAAGGUGGACCCU (SEQ ID NO: 834)	ORF	52	
NM_003416_stealth_2163	2163	UAUUUAGGUGGGCGUUCACACCUAAU (SEQ ID NO: 835)	AUUAGGUGUGAACGCCACCUAAUA (SEQ ID NO: 836)	ORF	40	

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What is claimed is:

1. A method of identifying an antiviral agent comprising:
 - a) administering the agent to a cell containing a cellular gene listed in Table 1; and
 - b) detecting the level and/or activity of the gene product produced by the cellular gene, a decrease or elimination of the gene product and/or gene product activity indicating a compound with antiviral activity.
2. A method of identifying an antiviral agent comprising:
 - a) administering the agent to a cell containing a cellular gene listed in Table 1;
 - b) contacting the cell with a virus;
 - c) detecting the level of viral infection; and
 - d) associating the level of viral infection with the level of expression of the gene from Table 1 or the activity of the protein encoded by the gene from Table 1, a decrease or elimination of viral infection associated with a decrease or elimination of gene expression and/or activity indicating that the agent is an antiviral agent.
3. A method of identifying an antiviral agent comprising:
 - a) administering the agent to a cell containing a cellular gene listed in Table 1;
 - b) contacting the cell with a virus;
 - c) detecting the level of viral infection; and
 - d) associating the level of viral infection with the level of expression of the gene from Table 1 or the activity of the protein encoded by the gene from Table 1, a decrease or elimination of viral infection associated with a decrease or elimination of gene expression and/or activity indicating that the agent is an antiviral agent.
4. A non-human transgenic mammal comprising a functional deletion of one or more genes listed in Table 1, wherein the mammal has decreased susceptibility to infection by a pathogen.
5. The transgenic mammal of claim 4, wherein the pathogen is a virus.

6. The transgenic mammal of claim 4, wherein the pathogen is a bacteria.
7. The transgenic mammal of claim 4, wherein the pathogen is a fungi.
8. A cell including an altered or disrupted gene listed in Table 1 that has decreased susceptibility to infection by a pathogen.
9. The cell of claim 8, wherein the pathogen is a virus.
10. The cell of claim 8, wherein the pathogen is a bacteria.
11. The cell of claim 8, wherein the pathogen is a fungi.
12. The cell of claim 8, wherein the cell is a hematopoietic cell.
13. A population of cells including an altered or disrupted gene listed in Table 1 that has decreased susceptibility to infection by a pathogen.
14. A method of inhibiting infection in a cell comprising inhibiting expression or activity of a gene or a gene product listed in Table 1.
15. The method of claim 14, wherein the infection is a viral infection.
16. The method of claim 14, wherein the infection is a bacterial infection.
17. The method of claim 14, wherein the infection is a fungal infection.
18. A method of reducing or inhibiting a viral infection in a subject comprising administering to the subject an amount of a composition that inhibits expression or activity of a gene or a gene product in Table 1.
19. The method of claim 18, wherein the infection is a viral infection.
20. The method of claim 18, wherein the infection is a bacterial infection.
21. The method of claim 18, wherein the infection is a fungal infection.
22. A population of non-human animals possessing a variant form of one or more genes listed in Table 1, wherein the population is less susceptible to infection.
23. The population of claim 22, wherein the non-human animals are from an avian species.
24. The population of claim 23, wherein population is a flock of chickens.
25. The population of claim 23, wherein the flock of chickens is less susceptible to avian flu.
26. The antiviral agent identified by the method of claim 1.
27. The antiviral agent identified by the method of claim 1.
28. The method of claim 14, wherein expression or activity of a gene or a gene product listed in Table 1 is inhibited by contacting the cell with a chemical, a small molecule, a drug, a protein, a cDNA, an antibody, a

morpholino, a triple helix molecule, an siRNA, an shRNAs, an antisense RNA or a ribozyme.

29. The method of claim 18, wherein the composition is a chemical, a small molecule, a drug, a protein, a cDNA, an antibody, a morpholino, a triple helix molecule, an siRNA, an shRNAs, an antisense RNA or a ribozyme.