HUMAN GENES AND GENE EXPRESSION PRODUCTS II

Field of the Invention

The present invention relates to novel polynucleotides, particularly to novel polynucleotides of human origin that are expressed in a selected cell type, are differentially expressed in one cell type relative to another cell type (*e.g.*, in cancerous cells, or in cells of a specific tissue origin) and/or share homology to polynucleotides encoding a gene product having an identified functional domain and/or activity.

Background of the Invention

Identification of novel polynucleotides, particularly those that encode an expressed gene product, is important in the advancement of drug discovery, diagnostic technologies, and the understanding of the progression and nature of complex diseases such as cancer. Identification of genes expressed in different cell types isolated from sources that differ in disease state or stage, developmental stage, exposure to various environmental factors, the tissue of origin, the species from which the tissue was isolated, and the like is key to identifying the genetic factors that are responsible for the phenotypes associated with these various differences

This invention provides novel human polynucleotides, the polypeptides encoded by these polynucleotides, and the genes and proteins corresponding to these novel polynucleotides.

Summary of the Invention

This invention relates to novel human polynucleotides and variants thereof, their encoded polypeptides and variants thereof, to genes corresponding to these polynucleotides and to proteins expressed by the genes. The invention also relates to diagnostic and therapeutic agents employing such novel human polynucleotides, their corresponding genes or gene products, *e.g.*, these genes and proteins, including probes, antisense constructs, and antibodies. The polynucleotides of the invention correspond to a polynucleotide comprising the sequence information of at least one of SEQ ID NOS: 1-3544, 3546-4510, 4512-4725, 4727-4748, and 4750-5252, which for convenience sake is referred to herein as "SEQ ID NOS:1-5252."

Accordingly, in one embodiment, the present invention features a library of polynucleotides, the library comprising the sequence information of at least one of "SEQ ID NOS:1-5252". In related aspects, the invention features a library provided on a nucleic acid array, or in a computer-readable format.

In one embodiment, the library is comprises a differentially expressed polynucleotide comprising a sequence selected from one of the differentially expressed polynucleotides disclosed herein. In specific related embodiments, the library comprises: 1) a polynucleotide that is differentially expressed in a human breast cancer cell, where the polynucleotide comprises a sequence selected from the group consisting of SEQ ID NOS:15, 36, 44, 45, 89, 146, 154, 159, 165, 172, 174, 183, 203, 261, 364, 366, 387, 419, 420, 496, 503, 510, 512, 529, 552, 560, 564, 570, 590, 606, 644, 646, 693, 707, 711, 726, 746, 754, 756, 875, 902, 921, 942, 990, 1095, 1104, 1122, 1131, 1142, 1170, 1184, 1205, 1286, 1289, 1354, 1387, 1435, 1535, 1751, 1764, 1777, 1795, 1860, 1869, 1882, 1890, 1915, 1933, 1934, 1979, 1980, 2007, 2023, 2040, 2059, 2223, 2245, 2300, 2325, 2409, 2462, 2488, 2486, and 2492; 2) a polynucleotide differentially expressed in a human colon cancer cell, where the polynucleotide comprises a sequence selected from the group consisting of SEQ ID NOS: , 33, 65, 228, 250, 252, 253, 280, 282, 355, 370, 387, 443, 460, 491, 545, 560, 581, 603, 680, 693, 703, 704, 716, 726, 746, 752, 753, 1095, 1104, 1205, 1241, 1264, 1354, 1387, 1401, 1442, 1514, 1734, 1742, 1780, 1851, 1899, 1915, 1954, 2024, 2066, 2262, and 2325; 3) a polynucleotide differentially expressed in a human lung cancer cell, where the polynucleotide comprises a sequence selected from the group consisting of SEQ ID NOS: 10, 54, 65, 171, 174, , 203, 252, 253, 254, , 285, 419, 420, 466, 491, 525, 526, 552, 571, 574, 590, 693, 700, 726, 742, 746, 861, 922, 990, 1088, 1288, 1355, 1417, 1422, 1444, 1454, 1570, 1597, 1979, 2007, 2024, 2034, 2038, 2126, and 2245; 4) a polynucleotide differentially expressed in growth factor-treated human microvascular endothelial cells (HMEC) relative to untreated HMEC, where the polynucleotide comprises a sequence selected from the group consisting of SEQ ID NOS:648, 1899, and 648; or 5) polynucleotides that are differentially expressed across multiple libraries, where the polynucleotide comprises a sequence selected from the group consisting of SEQ ID NOS: 65, 174, 203, 252, 253, 387, 419, 420, 491, 552, 560, 581, 590, 648, 693, 726, 746, 990, 1095, 1124, 1205, 1354, 1387, 1780, 1899, 1915, 1979, 2007, 2024, 2245, and 2325,

In another aspect, the invention features an isolated polynucleotide comprising a nucleotide sequence having at least 90% sequence identity to an identifying sequence of "SEQ ID NOS:1-5252" or a degenerate variant thereof. In related aspects, the invention features recombinant host cells and vectors comprising the polynucleotides of the invention, as well as isolated polypeptides encoded by the polynucleotides of the invention and antibodies that specifically bind such polypeptides.

In one embodiment, the invention features an isolated polynucleotide comprising a sequence encoding a polypeptide of a protein family or having a functional domain selected from the group consisting of: 4 transmembrane segments integral membrane proteins, 7 transmembrane receptors (rhodopsin family or secretin family), eukaryotic aspartyl proteases, ATPases associated with various cellular activities (AAA), Bcl-2, cyclins, DEAD box protein family, DEAD/H helicase protein family, MAP kinase kinase protein family, novel 3'5'-cyclic nucleotide phosphodiesterases, protein kinases, ras protein family, G-protein alpha subunit, phorbol esters/diacylglycerol binding proteins, protein kinase, trypsin, protein tyrosine phosphatase, wnt family of developmental signaling proteins, WW/rsp5/WWP domain containing proteins, Ank repeat, basic region plus leucine zipper domain, bromodomain, eukaryotic thiol (cysteine) protease active site, EF-hand, ETS domain, type II fibronectin collagen binding domain, thioredoxin, homeobox domain, TNFR/NGFR family cysteine-rich region, WD domain/G-beta repeats, zinc finger (C2H2 type), zinc finger (CCHC class), and zinc finger (C3HC4 type). In a specific related embodiment, the invention features a polynucleotide comprising a sequence of one of the SEQ ID NOS: listed in Table 3 or Table 20.

In another aspect, the invention features a method of detecting differentially expressed genes correlated with a cancerous state of a mammalian cell, where the method comprises the step of detecting at least one differentially expressed gene product in a test sample derived from a cell suspected of being cancerous, where the gene product is encoded by a gene corresponding to a sequence of at least one of the differentially expressed polynucleotides disclosed herein. Detection of the differentially expressed gene product is correlated with a cancerous state of the cell from which the test sample was derived. In one embodiment, the detecting is by hybridization of the test sample to a

reference array, wherein the reference array comprises an identifying sequence of at least one of the differentially expressed polynucleotides disclosed herein.

In one embodiment of the method of the invention, the cell is a breast tissue derived cell, and the differentially expressed gene product is encoded by a gene corresponding to a sequence of at least one of SEQ ID NOS:15, 36, 44, 45, 89, 146, 154, 159, 165, 172, 174, 183, 203, 261, 364, 366, 387, 419, 420, 496, 503, 510, 512, 529, 552, 560, 564, 570, 590, 606, 644, 646, 693, 707, 711, 726, 746, 754, 756, 875, 902, 921, 942, 990, 1095, 1104, 1122, 1131, 1142, 1170, 1184, 1205, 1286, 1289, 1354, 1387, 1435, 1535, 1751, 1764, 1777, 1795, 1860, 1869, 1882, 1890, 1915, 1933, 1934, 1979, 1980, 2007, 2023, 2040, 2059, 2223, 2245, 2300, 2325, 2409, 2462, 2486 2488, and 2492.

In another embodiment of the method of the invention, the cell is a colon tissue derived cell, and differentially expressed gene product is encoded by a gene corresponding to a sequence of at least one of SEQ ID NOS: 65, 228, 252, 253, 280, 355, 491, 581, 603, 680, 693, 716, 726, 746, 752, 753, 1241, 1264, 1401, 1442, 1514, 1851, 1915, 2024, 2066, 33, 250, 282, 370, 387, 443, 460, 545, 560, 703, 704, 1095, 1104, 1205, 1354, 1387, 1734, 1742, 1780, 1899, 1954, 2262, and 2325.

In yet another embodiment of the method of the invention, the cell is a lung tissue derived cell, and differentially expressed gene product is encoded by a gene corresponding to a sequence of at least one of SEQ ID NOS:10, 54, 65, 171, 174, 203, 252, 253, 254, 285, 419, 420, 466, 491, 525, 526, 552, 571, 574, 590, 693, 700, 726, 742, 746, 861, 922, 990, 1088, 1288, 1355, 1417, 1422, 1444, 1454, 1570, 1597, 1979, 2007, 2024, 2034, 2038, 2126, and 2245.

In another embodiment, the cell is any of a lung, breast, or colon cell and the differentially expressed gene product is encoded by a gene corresponding to a sequence of at least one of SEQ ID NOS:648 and 1899.

In still another embodiment, the cell is any of a breast, colon, or lung cell and the differentially expressed gene product is encoded by a gene corresponding to a sequence of at least one of SEQ ID NOS: 65, 174, 203, 252, 253, 387, 419, 420, 491, 552, 560, 581, 590, 648, 693, 726, 746, 990, 1095, 1124, 1205, 1354, 1387, , 1780, 1899, 1915, 1979, 2007, 2024, 2245, and 2325.

Other aspects and embodiments of the invention will be readily apparent to the ordinarily skilled artisan upon reading the description provided herein.

Detailed Description of the Invention

The invention relates to polynucleotides comprising the disclosed nucleotide sequences, to full length cDNA, mRNA and genes corresponding to these sequences, and to polypeptides and proteins encoded by these polynucleotides and genes.

Also included are polynucleotides that encode polypeptides and proteins encoded by the polynucleotides of the Sequence Listing. The various polynucleotides that can encode these polypeptides and proteins differ because of the degeneracy of the genetic code, in that most amino acids are encoded by more than one triplet codon. The identity of such codons is well-known in this art, and this information can be used for the construction of the polynucleotides within the scope of the invention.

Polynucleotides encoding polypeptides and proteins that are variants of the polypeptides and proteins encoded by the polynucleotides and related cDNA and genes are also within the scope of the invention. The variants differ from wild type protein in having one or more amino acid substitutions that either enhance, add, or diminish a biological activity of the wild type protein. Once the amino acid change is selected, a polynucleotide encoding that variant is constructed according to the invention.

The following detailed description describes the polynucleotide compositions encompassed by the invention, methods for obtaining cDNA or genomic DNA encoding a full-length gene product, expression of these polynucleotides and genes, identification of structural motifs of the polynucleotides and genes, identification of the function of a gene product encoded by a gene corresponding to a polynucleotide of the invention, use of the provided polynucleotides as probes and in mapping and in tissue profiling, use of the corresponding polypeptides and other gene products to raise antibodies, and use of the polynucleotides and their encoded gene products for therapeutic and diagnostic purposes.

I. Polynucleotide Compositions

The scope of the invention with respect to polynucleotide compositions includes, but is not necessarily limited to, polynucleotides having a sequence set forth in any one of

"SEQ ID NOS:1-5252"; polynucleotides obtained from the biological materials described herein or other biological sources (particularly human sources) by hybridization under stringent conditions (particularly conditions of high stringency); genes corresponding to the provided polynucleotides; variants of the provided polynucleotides and their corresponding genes, particularly those variants that retain a biological activity of the encoded gene product (*e.g.*, a biological activity ascribed to a gene product corresponding to the provided polynucleotides as a result of the assignment of the gene product to a protein family(ies) and/or identification of a functional domain present in the gene product). Other nucleic acid compositions contemplated by and within the scope of the present invention will be readily apparent to one of ordinary skill in the art when provided with the disclosure here.

The invention features polynucleotides that are expressed in cells of human tissue, specifically human colon, breast, and/or lung tissue. Novel nucleic acid compositions of the invention of particular interest comprise a sequence set forth in any one of "SEQ ID NOS:1-5252" or an identifying sequence thereof. An "identifying sequence" is a contiguous sequence of residues at least about 10 nt to about 20 nt in length, usually at least about 50 nt to about 100 nt in length, that uniquely identifies a polynucleotide sequence, *e.g.*, exhibits less than 90%, usually less than about 80% to about 85% sequence identity to any contiguous nucleotide sequence of more than about 20 nt. Thus, the subject novel nucleic acid compositions include full length cDNAs or mRNAs that encompass an identifying sequence of contiguous nucleotides from any one of "SEQ ID NOS:1-5252."

The polynucleotides of the invention also include polynucleotides having sequence similarity or sequence identity. Nucleic acids having sequence similarity are detected by hybridization under low stringency conditions, for example, at 50°C and 10XSSC (0.9 M saline/0.09 M sodium citrate) and remain bound when subjected to washing at 55°C in 1XSSC. Sequence identity can be determined by hybridization under stringent conditions, for example, at 50°C or higher and 0.1XSSC (9 mM saline/0.9 mM sodium citrate). Hybridization methods and conditions are well known in the art, see, *e.g.*, U.S. Patent No. 5,707,829. Nucleic acids that are substantially identical to the provided polynucleotide sequences, *e.g.* allelic variants, genetically altered versions of the gene, *etc.*, bind to the provided polynucleotide sequences ("SEQ ID NOS:1-5252") under stringent hybridization conditions. By using probes, particularly labeled probes of DNA sequences, one can

isolate homologous or related genes. The source of homologous genes can be any species, *e.g.* primate species, particularly human; rodents, such as rats and mice; canines, felines, bovines, ovines, equines, yeast, nematodes, *etc.*

Preferably, hybridization is performed using at least 15 contiguous nucleotides of at least one of "SEQ ID NOS:1-5252." That is, when at least 15 contiguous nucleotides of one of the disclosed SEQ ID NOs. is used as a probe, the probe will preferentially hybridize with a gene or mRNA (of the biological material) comprising the complementary sequence, allowing the identification and retrieval of the nucleic acids of the biological material that uniquely hybridize to the selected probe. Probes from more than one SEQ ID NO. will hybridize with the same gene or mRNA if the cDNA from which they were derived corresponds to one mRNA. Probes of more than 15 nucleotides can be used, but 15 nucleotides represents enough sequence for unique identification.

The polynucleotides of the invention also include naturally occurring variants of the nucleotide sequences (*e.g.*, degenerate variants, allelic variants, *etc.*). Variants of the polynucleotides of the invention are identified by hybridization of putative variants with nucleotide sequences disclosed herein, preferably by hybridization under stringent conditions For example, by using appropriate wash conditions, variants of the polynucleotides of the invention can be identified where the allelic variant exhibits at most about 25-30% base pair mismatches relative to the selected polynucleotide probe. In general, allelic variants contain 15-25% base pair mismatches, and can contain as little as even 5-15%, or 2-5%, or 1-2% base pair mismatches, as well as a single base-pair mismatch.

The invention also encompasses homologs corresponding to the polynucleotides of "SEQ ID NOS:1-5252", where the source of homologous genes can be any mammalian species, *e.g.*, primate species, particularly human; rodents, such as rats; canines, felines, bovines, ovines, equines, yeast, nematodes, etc. Between mammalian species, *e.g.*, human and mouse, homologs have substantial sequence similarity, *e.g.*, at least 75% sequence identity, usually at least 90%, more usually at least 95% between nucleotide sequences. Sequence similarity is calculated based on a reference sequence, which may be a subset of a larger sequence, such as a conserved motif, coding region, flanking region, *etc.* A reference sequence will usually be at least about 18 contiguous nt long, more usually at

least about 30 nt long, and may extend to the complete sequence that is being compared. Algorithms for sequence analysis are known in the art, such as BLAST, described in Altschul *et al.*, *J. Mol. Biol.* (1990) *215*:403-10.

In general, variants of the invention have a sequence identity greater than at least about 65%, preferably at least about 75%, more preferably at least about 85%, and can be greater than at least about 90% or more as determined by the Smith-Waterman homology search algorithm as implemented in MPSRCH program (Oxford Molecular). For the purposes of this invention, a preferred method of calculating percent identity is the Smith-Waterman algorithm, using the following. Global DNA sequence identity must be greater than 65% as determined by the Smith-Waterman homology search algorithm as implemented in MPSRCH program (Oxford Molecular) using an affine gap search with the following search parameters: gap open penalty, 12; and gap extension penalty, 1.

The subject nucleic acids can be cDNAs or genomic DNAs, as well as fragments thereof, particularly fragments that encode a biologically active gene product and/or are useful in the methods disclosed herein (*e.g.*, in diagnosis, as a unique identifier of a differentially expressed gene of interest, *etc.*). The term "cDNA" as used herein is intended to include all nucleic acids that share the arrangement of sequence elements found in native mature mRNA species, where sequence elements are exons and 3' and 5' non-coding regions. Normally mRNA species have contiguous exons, with the intervening introns, when present, being removed by nuclear RNA splicing, to create a continuous open reading frame encoding a polypeptide of the invention.

A genomic sequence of interest comprises the nucleic acid present between the initiation codon and the stop codon, as defined in the listed sequences, including all of the introns that are normally present in a native chromosome. It can further include the 3' and 5' untranslated regions found in the mature mRNA. It can further include specific transcriptional and translational regulatory sequences, such as promoters, enhancers, *etc.*, including about 1 kb, but possibly more, of flanking genomic DNA at either the 5' and 3' end of the transcribed region. The genomic DNA can be isolated as a fragment of 100 kbp or smaller; and substantially free of flanking chromosomal sequence. The genomic DNA flanking the coding region, either 3' and 5', or internal regulatory sequences as sometimes

found in introns, contains sequences required for proper tissue, stage-specific, or disease-state specific expression.

The nucleic acid compositions of the subject invention can encode all or a part of the subject polypeptides. Double or single stranded fragments can be obtained from the DNA sequence by chemically synthesizing oligonucleotides in accordance with conventional methods, by restriction enzyme digestion, by PCR amplification, *etc.* Isolated polynucleotides and polynucleotide fragments of the invention comprise at least about 10, about 15, about 20, about 35, about 50, about 100, about 150 to about 200, about 250 to about 300, or about 350 contiguous nucleotides selected from the polynucleotide sequences as shown in "SEQ ID NOS:1-5252." For the most part, fragments will be of at least 15 nt, usually at least 18 nt or 25 nt, and up to at least about 50 contiguous nt in length or more. In a preferred embodiment, the polynucleotide molecules comprise a contiguous sequence of at least twelve nucleotides selected from the group consisting of the polynucleotides shown in "SEQ ID NOS:1-5252."

Probes specific to the polynucleotides of the invention can be generated using the polynucleotide sequences disclosed in "SEQ ID NOS:1-5252." The probes are preferably at least about 12, 15, 16, 18, 20, 22, 24, or 25 nucleotide fragment of a corresponding contiguous sequence of "SEQ ID NOS:1-5252", and can be less than 2, 1, 0.5, 0.1, or 0.05 kb in length. The probes can be synthesized chemically or can be generated from longer polynucleotides using restriction enzymes. The probes can be labeled, for example, with a radioactive, biotinylated, or fluorescent tag. Preferably, probes are designed based upon an identifying sequence of a polynucleotide of one of "SEQ ID NOS:1-5252." More preferably, probes are designed based on a contiguous sequence of one of the subject polynucleotides that remain unmasked following application of a masking program for masking low complexity (*e.g.*, XBLAST) to the sequence., *i.e.*, one would select an unmasked region, as indicated by the polynucleotides outside the poly-n stretches of the masked sequence produced by the masking program.

The polynucleotides of the subject invention are isolated and obtained in substantial purity, generally as other than an intact chromosome. Usually, the polynucleotides, either as DNA or RNA, will be obtained substantially free of other naturally-occurring nucleic acid sequences, generally being at least about 50%, usually at least about 90% pure and are

typically "recombinant", *e.g.*, flanked by one or more nucleotides with which it is not normally associated on a naturally occurring chromosome.

The polynucleotides of the invention can be provided as a linear molecule or within a circular molecule. They can be provided within autonomously replicating molecules (vectors) or within molecules without replication sequences. They can be regulated by their own or by other regulatory sequences, as is known in the art. The polynucleotides of the invention can be introduced into suitable host cells using a variety of techniques which are available in the art, such as transferrin polycation-mediated DNA transfer, transfection with naked or encapsulated nucleic acids, liposome-mediated DNA transfer, intracellular transportation of DNA-coated latex beads, protoplast fusion, viral infection, electroporation, gene gun, calcium phosphate-mediated transfection, and the like.

The subject nucleic acid compositions can be used to, for example, produce polypeptides, as probes for the detection of mRNA of the invention in biological samples (*e.g.*, extracts of human cells) to generate additional copies of the polynucleotides, to generate ribozymes or antisense oligonucleotides, and as single stranded DNA probes or as triple-strand forming oligonucleotides. The probes described herein can be used to, for example, determine the presence or absence of the polynucleotide sequences as shown in "SEQ ID NOS:1-5252" or variants thereof in a sample. These and other uses are described in more detail below.

Use of Polynucleotides to Obtain Full-Length cDNA and Full-Length Human Gene and Promoter Region

Full-length cDNA molecules comprising the disclosed polynucleotides are obtained as follows. A polynucleotide having a sequence of one of "SEQ ID NOS:1-5252", or a portion thereof comprising at least 12, 15, 18, or 20 nucleotides, is used as a hybridization probe to detect hybridizing members of a cDNA library using probe design methods, cloning methods, and clone selection techniques such as those described in U.S. Patent No. 5,654,173. Libraries of cDNA are made from selected tissues, such as normal or tumor tissue, or from tissues of a mammal treated with, for example, a pharmaceutical agent. Preferably, the tissue is the same as the tissue from which the polynucleotides of the invention were isolated, as both the polynucleotides described herein and the cDNA

represent expressed genes. Most preferably, the cDNA library is made from the biological material described herein in the Examples. Alternatively, many cDNA libraries are available commercially. (Sambrook *et al.*, *Molecular Cloning: A Laboratory Manual, 2nd Ed.*, (1989) Cold Spring Harbor Press, Cold Spring Harbor, NY). The choice of cell type for library construction can be made after the identity of the protein encoded by the gene corresponding to the polynucleotide of the invention is known. This will indicate which tissue and cell types are likely to express the related gene, and thus represent a suitable source for the mRNA for generating the cDNA. Where the provided polynucleotides are isolated from cDNA libraries, the libraries are prepared from mRNA of human colon cells, more preferably, human colon cancer cells, even more preferably, from a highly metastatic colon cell, Km12L4-A.

Techniques for producing and probing nucleic acid sequence libraries are described, for example, in Sambrook *et al.*, *Molecular Cloning: A Laboratory Manual, 2nd Ed.*, (1989) Cold Spring Harbor Press, Cold Spring Harbor, NY. The cDNA can be prepared by using primers based on sequence from "SEQ ID NOS:1-5252." In one embodiment, the cDNA library can be made from only poly-adenylated mRNA. Thus, poly-T primers can be used to prepare cDNA from the mRNA.

Members of the library that are larger than the provided polynucleotides, and preferably that encompass the complete coding sequence of the native message, are obtained. In order to confirm that the entire cDNA has been obtained, RNA protection experiments are performed as follows. Hybridization of a full-length cDNA to an mRNA will protect the RNA from RNase degradation. If the cDNA is not full length, then the portions of the mRNA that are not hybridized will be subject to RNase degradation. This is assayed, as is known in the art, by changes in electrophoretic mobility on polyacrylamide gels, or by detection of released monoribonucleotides. Sambrook *et al.*, *Molecular Cloning: A Laboratory Manual, 2nd Ed.*, (1989) Cold Spring Harbor Press, Cold Spring Harbor, NY. In order to obtain additional sequences 5' to the end of a partial cDNA, 5' RACE (*PCR Protocols: A Guide to Methods and Applications*, (1990) Academic Press, Inc.) is performed.

Genomic DNA is isolated using the provided polynucleotides in a manner similar to the isolation of full-length cDNAs. Briefly, the provided polynucleotides, or portions

thereof, are used as probes to libraries of genomic DNA. Preferably, the library is obtained from the cell type that was used to generate the polynucleotides of the invention, but this is not essential. Most preferably, the genomic DNA is obtained from the biological material described herein in the Examples. Such libraries can be in vectors suitable for carrying large segments of a genome, such as P1 or YAC, as described in detail in Sambrook *et al.*, 9.4-9.30. In addition, genomic sequences can be isolated from human BAC libraries, which are commercially available from Research Genetics, Inc., Huntville, Alabama, USA, for example. In order to obtain additional 5' or 3' sequences, chromosome walking is performed, as described in Sambrook *et al.*, such that adjacent and overlapping fragments of genomic DNA are isolated. These are mapped and pieced together, as is known in the art, using restriction digestion enzymes and DNA ligase.

Using the polynucleotide sequences of the invention, corresponding full-length genes can be isolated using both classical and PCR methods to construct and probe cDNA libraries. Using either method, Northern blots, preferably, are performed on a number of cell types to determine which cell lines express the gene of interest at the highest level. Classical methods of constructing cDNA libraries are taught in Sambrook *et al.*, *supra*. With these methods, cDNA can be produced from mRNA and inserted into viral or expression vectors. Typically, libraries of mRNA comprising poly(A) tails can be produced with poly(T) primers. Similarly, cDNA libraries can be produced using the instant sequences as primers.

PCR methods are used to amplify the members of a cDNA library that comprise the desired insert. In this case, the desired insert will contain sequence from the full length cDNA that corresponds to the instant polynucleotides. Such PCR methods include gene trapping and RACE methods. Gene trapping entails inserting a member of a cDNA library into a vector. The vector then is denatured to produce single stranded molecules. Next, a substrate-bound probe, such a biotinylated oligo, is used to trap cDNA inserts of interest. Biotinylated probes can be linked to an avidin-bound solid substrate. PCR methods can be used to amplify the trapped cDNA. To trap sequences corresponding to the full length genes, the labeled probe sequence is based on the polynucleotide sequences of the invention. Random primers or primers specific to the library vector can be used to amplify the trapped cDNA. Such gene trapping techniques are described in Gruber *et al.*, WO

95/04745 and Gruber *et al.*, U.S. Pat. No. 5,500,356. Kits are commercially available to perform gene trapping experiments from, for example, Life Technologies, Gaithersburg, Maryland, USA.

"Rapid amplification of cDNA ends," or RACE, is a PCR method of amplifying cDNAs from a number of different RNAs. The cDNAs are ligated to an oligonucleotide linker, and amplified by PCR using two primers. One primer is based on sequence from the instant polynucleotides, for which full length sequence is desired, and a second primer comprises sequence that hybridizes to the oligonucleotide linker to amplify the cDNA. A description of this methods is reported in WO 97/19110. In preferred embodiments of RACE, a common primer is designed to anneal to an arbitrary adaptor sequence ligated to cDNA ends (Apte and Siebert, *Biotechniques* (1993) *15*:890-893; Edwards *et al.*, *Nuc. Acids Res.* (1991) *19*:5227-5232). When a single gene-specific RACE primer is paired with the common primer, preferential amplification of sequences between the single gene specific primer and the common primer occurs. Commercial cDNA pools modified for use in RACE are available.

Another PCR-based method generates full-length cDNA library with anchored ends without needing specific knowledge of the cDNA sequence. This method is described in WO 96/40998.

The promoter region of a gene generally is located 5' to the initiation site for RNA polymerase II. Hundreds of promoter regions contain the "TATA" box, a sequence such as TATTA or TATAA, which is sensitive to mutations. The promoter region can be obtained by performing 5' RACE using a primer from the coding region of the gene. Alternatively, the cDNA can be used as a probe for the genomic sequence, and the region 5' to the coding region is identified by "walking up." If the gene is highly expressed or differentially expressed, the promoter from the gene can be of use in a regulatory construct for a heterologous gene.

Once the full-length cDNA or gene is obtained, DNA encoding variants can be prepared by site-directed mutagenesis, described in detail in Sambrook *et al.*, 15.3-15.63. The choice of codon or nucleotide to be replaced can be based on disclosure herein on optional changes in amino acids to achieve altered protein structure and/or function.

As an alternative method to obtaining DNA or RNA from a biological material, nucleic acid comprising nucleotides having the sequence of one or more polynucleotides of the invention can be synthesized. Thus, the invention encompasses nucleic acid molecules ranging in length from 15 nucleotides (corresponding to at least 15 contiguous nucleotides of one of "SEQ ID NOS:1-5252") up to a maximum length suitable for one or more biological manipulations, including replication and expression, of the nucleic acid molecule. The invention includes but is not limited to (a) nucleic acid having the size of a full gene, and comprising at least one of "SEQ ID NOS:1-5252;"; (b) the nucleic acid of (a) also comprising at least one additional gene, operably linked to permit expression of a fusion protein; (c) an expression vector comprising (a) or (b); (d) a plasmid comprising (a) or (b) ; and (e) a recombinant viral particle comprising (a) or (b). Once provided with the polynucleotides disclosed herein, construction or preparation of (a) - (e) are well within the skill in the art.

The sequence of a nucleic acid comprising at least 15 contiguous nucleotides of at least any one of "SEQ ID NOS:1-5252,", preferably the entire sequence of at least any one of "SEQ ID NOS:1-5252," is not limited and can be any sequence of A, T, G, and/or C (for DNA) and A, U, G, and/or C (for RNA) or modified bases thereof, including inosine and pseudouridine. The choice of sequence will depend on the desired function and can be dictated by coding regions desired, the intron-like regions desired, and the regulatory regions desired. Where the entire sequence of any one of "SEQ ID NOS:1-5252" is within the nucleic acid, the nucleic acid obtained is referred to herein as a polynucleotide comprising the sequence of any one of "SEQ ID NOS:1-5252."

II. Expression of Polypeptide Encoded by Full-Length cDNA or Full-Length Gene

The provided polynucleotide (*e.g.*, a polynucleotide having a sequence of one of "SEQ ID NOS:1-5252"), the corresponding cDNA, or the full-length gene is used to express a partial or complete gene product. Constructs of polynucleotides having sequences of "SEQ ID NOS:1-5252" can be generated synthetically. Alternatively, single-step assembly of a gene and entire plasmid from large numbers of oligodeoxyribonucleotides is described by, *e.g.*, Stemmer *et al., Gene (Amsterdam)* (1995) *164(1)*:49-53. In this method, assembly PCR (the synthesis of long DNA sequences from

large numbers of oligodeoxyribonucleotides (oligos)) is described. The method is derived from DNA shuffling (Stemmer, *Nature* (1994) *370*:389-391), and does not rely on DNA ligase, but instead relies on DNA polymerase to build increasingly longer DNA fragments during the assembly process.

Appropriate polynucleotide constructs are purified using standard recombinant DNA techniques as described in, for example, Sambrook *et al.*, *Molecular Cloning: A Laboratory Manual, 2nd Ed.*, (1989) Cold Spring Harbor Press, Cold Spring Harbor, NY, and under current regulations described in United States Dept. of HHS, National Institute of Health (NIH) Guidelines for Recombinant DNA Research. The gene product encoded by a polynucleotide of the invention is expressed in any expression system, including, for example, bacterial, yeast, insect, amphibian and mammalian systems. Suitable vectors and host cells are described in U.S. Patent No. 5,654,173.

Bacteria. Expression systems in bacteria include those described in Chang *et al.*, *Nature* (1978) *275*:615; Goeddel *et al.*, *Nature* (1979) *281*:544; Goeddel *et al.*, *Nucleic Acids Res.* (1980) *8*:4057; EP 0 036,776; U.S. Patent No. 4,551,433; DeBoer *et al.*, *Proc. Natl. Acad. Sci. (USA)* (1983) *80*:21-25; and Siebenlist *et al.*, *Cell* (1980) *20*:269.

Yeast. Expression systems in yeast include those described in Hinnen *et al.*, *Proc. Natl. Acad. Sci. (USA)* (1978) *75*:1929; Ito *et al.*, *J. Bacteriol.* (1983) *153*:163; Kurtz *et al.*, *Mol. Cell. Biol.* (1986) *6*:142; Kunze *et al.*, *J. Basic Microbiol.* (1985) *25*:141; Gleeson *et al.*, *J. Gen. Microbiol.* (1986) *132*:3459; Roggenkamp *et al.*, *Mol. Gen. Genet.* (1986) *202*:302; Das *et al.*, *J. Bacteriol.* (1984) *158*:1165; De Louvencourt *et al.*, *J. Bacteriol.* (1983) *154*:737; Van den Berg *et al.*, *Bio/Technology* (1990) *8*:135; Kunze *et al.*, *J. Basic Microbiol.* (1985) *25*:141; Cregg *et al.*, *Mol. Cell. Biol.* (1985) *5*:3376; U.S. Patent Nos. 4,837,148 and 4,929,555; Beach and Nurse, *Nature* (1981) *300*:706; Davidow *et al.*, *Curr. Genet.* (1985) *10*:380; Gaillardin *et al.*, *Curr. Genet.* (1985) *10*:49; Ballance *et al.*, *Biochem. Biophys. Res. Commun.* (1983) *112*:284-289; Tilburn *et al.*, *Gene* (1983) *26*:205-221; Yelton *et al.*, *Proc. Natl. Acad. Sci. (USA)* (1984) *81*:1470-1474; Kelly and Hynes, *EMBO J.* (1985) *4*:475479; EP 0 244,234; and WO 91/00357.

Insect Cells. Expression of heterologous genes in insects is accomplished as described in U.S. Patent No. 4,745,051; Friesen *et al.*, "The Regulation of Baculovirus Gene Expression", in: *The Molecular Biology Of Baculoviruses* (1986) (W. Doerfler, ed.);

EP 0 127,839; EP 0 155,476; and Vlak *et al.*, *J. Gen. Virol.* (1988) *69*:765-776; Miller *et al.*, *Ann. Rev. Microbiol.* (1988) *42*:177; Carbonell *et al.*, *Gene* (1988) *73*:409; Maeda *et al.*, *Nature* (1985) *315*:592-594; Lebacq-Verheyden *et al.*, *Mol. Cell. Biol.* (1988) *8*:3129; Smith *et al.*, *Proc. Natl. Acad. Sci. (USA)* (1985) *82*:8844; Miyajima *et al.*, *Gene* (1987) *58*:273; and Martin *et al.*, *DNA* (1988) *7*:99. Numerous baculoviral strains and variants and corresponding permissive insect host cells from hosts are described in Luckow *et al.*, *Bio/Technology* (1988) *6*:47-55, Miller *et al.*, *Generic Engineering* (1986) *8*:277-279, and Maeda *et al.*, *Nature* (1985) *315*:592-594.

Mammalian Cells. Mammalian expression is accomplished as described in Dijkema *et al.*, *EMBO J.* (1985) *4*:761, Gorman *et al.*, *Proc. Natl. Acad. Sci. (USA)* (1982) *79*:6777, Boshart *et al.*, *Cell* (1985) *41*:521 and U.S. Patent No. 4,399,216. Other features of mammalian expression are facilitated as described in Ham and Wallace, *Meth. Enz.* (1979) *58*:44, Barnes and Sato, *Anal. Biochem.* (1980) *102*:255, U.S. Patent Nos. 4,767,704, 4,657,866, 4,927,762, 4,560,655, WO 90/103430, WO 87/00195, and U.S. RE 30,985.

Polynucleotide molecules comprising a polynucleotide sequence provided herein propagated by placing the molecule in a vector. Viral and non-viral vectors are used, including plasmids. The choice of plasmid will depend on the type of cell in which propagation is desired and the purpose of propagation. Certain vectors are useful for amplifying and making large amounts of the desired DNA sequence. Other vectors are suitable for expression in cells in culture. Still other vectors are suitable for transfer and expression in cells in a whole animal or person. The choice of appropriate vector is well within the skill of the art. Many such vectors are available commercially. The partial or full-length polynucleotide is inserted into a vector typically by means of DNA ligase attachment to a cleaved restriction enzyme site in the vector. Alternatively, the desired nucleotide sequence can be inserted by homologous recombination in vivo. Typically this is accomplished by attaching regions of homology to the vector on the flanks of the desired nucleotide sequence. Regions of homology are added by ligation of oligonucleotides, or by polymerase chain reaction using primers comprising both the region of homology and a portion of the desired nucleotide sequence, for example.

The polynucleotides set forth in "SEQ ID NOS:1-5252" or their corresponding full-length polynucleotides are linked to regulatory sequences as appropriate to obtain the desired expression properties. These can include promoters (attached either at the 5' end of the sense strand or at the 3' end of the antisense strand), enhancers, terminators, operators, repressors, and inducers. The promoters can be regulated or constitutive. In some situations it may be desirable to use conditionally active promoters, such as tissue-specific or developmental stage-specific promoters. These are linked to the desired nucleotide sequence using the techniques described above for linkage to vectors. Any techniques known in the art can be used.

When any of the above host cells, or other appropriate host cells or organisms, are used to replicate and/or express the polynucleotides or nucleic acids of the invention, the resulting replicated nucleic acid, RNA, expressed protein or polypeptide, is within the scope of the invention as a product of the host cell or organism. The product is recovered by any appropriate means known in the art.

Once the gene corresponding to a selected polynucleotide is identified, its expression can be regulated in the cell to which the gene is native. For example, an endogenous gene of a cell can be regulated by an exogenous regulatory sequence as disclosed in U.S. Patent No. 5,641,670.

III. Identification of Functional and Structural Motifs of Novel Genes

A. Screening Polynucleotide Sequences and Amino Acid Sequences Against Publicly Available Databases

Translations of the nucleotide sequence of the provided polynucleotides, cDNAs or full genes can be aligned with individual known sequences. Similarity with individual sequences can be used to determine the activity of the polypeptides encoded by the polynucleotides of the invention. For example, sequences that show similarity with a chemokine sequence can exhibit chemokine activities. Also, sequences exhibiting similarity with more than one individual sequence can exhibit activities that are characteristic of either or both individual sequences.

The full length sequences and fragments of the polynucleotide sequences of the nearest neighbors can be used as probes and primers to identify and isolate the full length

sequence corresponding to provided polynucleotides. The nearest neighbors can indicate a tissue or cell type to be used to construct a library for the full-length sequences corresponding to the provided polynucleotides..

Typically, a selected polynucleotide is translated in all six frames to determine the best alignment with the individual sequences. The sequences disclosed herein in the Sequence Listing are in a 5' to 3' orientation and translation in three frames can be sufficient (with a few specific exceptions as described in the Examples). These amino acid sequences are referred to, generally, as query sequences, which will be aligned with the individual sequences. Databases with individual sequences are described in "Computer Methods for Macromolecular Sequence Analysis" *Methods in Enzymology* (1996) *266*, Doolittle, Academic Press, Inc., a division of Harcourt Brace & Co., San Diego, California, USA. Databases include Genbank, EMBL, and DNA Database of Japan (DDBJ).

Query and individual sequences can be aligned using the methods and computer programs described above, and include BLAST, available over the world wide web at http://ww.ncbi.nlm.nih.gov/BLAST/. Another alignment algorithm is Fasta, available in the Genetics Computing Group (GCG) package, Madison, Wisconsin, USA, a wholly owned subsidiary of Oxford Molecular Group, Inc. Other techniques for alignment are described in Doolittle, *supra*. Preferably, an alignment program that permits gaps in the sequence is utilized to align the sequences. The Smith-Waterman is one type of algorithm that permits gaps in sequence alignments. See *Meth. Mol. Biol.* (1997) *70*: 173-187. Also, the GAP program using the Needleman and Wunsch alignment method can be utilized to align sequences. An alternative search strategy uses MPSRCH software, which runs on a MASPAR computer. MPSRCH uses a Smith-Waterman algorithm to score sequences on a massively parallel computer. This approach improves ability to identify sequences that are distantly related matches, and is especially tolerant of small gaps and nucleotide sequence errors. Amino acid sequences encoded by the provided polynucleotides can be used to search both protein and DNA databases.

Results of individual and query sequence alignments can be divided into three categories, high similarity, weak similarity, and no similarity. Individual alignment results ranging from high similarity to weak similarity provide a basis for determining polypeptide activity and/or structure. Parameters for categorizing individual results include: percentage

of the alignment region length where the strongest alignment is found, percent sequence identity, and p value.

The percentage of the alignment region length is calculated by counting the number of residues of the individual sequence found in the region of strongest alignment, *e.g.*, contiguous region of the individual sequence that contains the greatest number of residues that are identical to the residues of the corresponding region of the aligned query sequence. This number is divided by the total residue length of the query sequence to calculate a percentage. For example, a query sequence of 20 amino acid residues might be aligned with a 20 amino acid region of an individual sequence. The individual sequence might be identical to amino acid residues 5, 9-15, and 17-19 of the query sequence. The region of strongest alignment is thus the region stretching from residue 9-19, an 11 amino acid stretch. The percentage of the alignment region length is: 11 (length of the region of strongest alignment) divided by (query sequence length) 20 or 55%.

Percent sequence identity is calculated by counting the number of amino acid matches between the query and individual sequence and dividing total number of matches by the number of residues of the individual sequences found in the region of strongest alignment. Thus, the percent identity in the example above would be 10 matches divided by 11 amino acids, or approximately, 90.9%

P value is the probability that the alignment was produced by chance. For a single alignment, the p value can be calculated according to Karlin *et al.*, *Proc. Natl. Acad. Sci.* (1990) *87*:2264 and Karlin *et al.*, *Proc. Natl. Acad. Sci.* (1993) *90*. The p value of multiple alignments using the same query sequence can be calculated using an heuristic approach described in Altschul *et al.*, *Nat. Genet.* (1994) *6*:119. Alignment programs such as BLAST program can calculate the p value.

Another factor to consider for determining identity or similarity is the location of the similarity or identity. Strong local alignment can indicate similarity even if the length of alignment is short. Sequence identity scattered throughout the length of the query sequence also can indicate a similarity between the query and profile sequences. The boundaries of the region where the sequences align can be determined according to Doolittle, *supra*; BLAST or FAST programs; or by determining the area where sequence identity is highest.

High Similarity. In general, in alignment results considered to be of high similarity, the percent of the alignment region length is typically at least about 55% of total length query sequence; more typically, at least about 58%; even more typically; at least about 60% of the total residue length of the query sequence. Usually, percent length of the alignment region can be as much as about 62%; more usually, as much as about 64%; even more usually, as much as about 66%. Further, for high similarity, the region of alignment, typically, exhibits at least about 75% of sequence identity; more typically, at least about 78%; even more typically; at least about 80% sequence identity. Usually, percent sequence identity can be as much as about 82%; more usually, as much as about 84%; even more usually, as much as about 86%.

The p value is used in conjunction with these methods. If high similarity is found, the query sequence is considered to have high similarity with a profile sequence when the p value is less than or equal to about 10^{-2}; more usually; less than or equal to about 10^{-3}; even more usually; less than or equal to about 10^{-4}. More typically, the p value is no more than about 10^{-5}; more typically; no more than or equal to about 10^{-10}; even more typically; no more than or equal to about 10^{-15} for the query sequence to be considered high similarity.

Weak Similarity. In general, where alignment results considered to be of weak similarity, there is no minimum percent length of the alignment region nor minimum length of alignment. A better showing of weak similarity is considered when the region of alignment is, typically, at least about 15 amino acid residues in length; more typically, at least about 20; even more typically; at least about 25 amino acid residues in length. Usually, length of the alignment region can be as much as about 30 amino acid residues; more usually, as much as about 40; even more usually, as much as about 60 amino acid residues. Further, for weak similarity, the region of alignment, typically, exhibits at least about 35% of sequence identity; more typically, at least about 40%; even more typically; at least about 45% sequence identity. Usually, percent sequence identity can be as much as about 50%; more usually, as much as about 55%; even more usually, as much as about 60%.

If low similarity is found, the query sequence is considered to have weak similarity with a profile sequence when the p value is usually less than or equal to about 10^{-2}; more usually; less than or equal to about 10^{-3}; even more usually; less than or equal to about 10^{-4}. More

typically, the p value is no more than about 10^{-5}; more usually; no more than or equal to about 10^{-10}; even more usually; no more than or equal to about 10^{-15} for the query sequence to be considered weak similarity.

Similarity Determined by Sequence Identity Alone. Sequence identity alone can be used to determine similarity of a query sequence to an individual sequence and can indicate the activity of the sequence. Such an alignment, preferably, permits gaps to align sequences. Typically, the query sequence is related to the profile sequence if the sequence identity over the entire query sequence is at least about 15%; more typically, at least about 20%; even more typically, at least about 25%; even more typically, at least about 50%. Sequence identity alone as a measure of similarity is most useful when the query sequence is usually, at least 80 residues in length; more usually, 90 residues; even more usually, at least 95 amino acid residues in length. More typically, similarity can be concluded based on sequence identity alone when the query sequence is preferably 100 residues in length; more preferably, 120 residues in length; even more preferably, 150 amino acid residues in length.

Determining Activity from Alignments with Profile and Multiple Aligned Sequences. Translations of the provided polynucleotides can be aligned with amino acid profiles that define either protein families or common motifs. Also, translations of the provided polynucleotides can be aligned to multiple sequence alignments (MSA) comprising the polypeptide sequences of members of protein families or motifs. Similarity or identity with profile sequences or MSAs can be used to determine the activity of the gene products (*e.g.*, polypeptides) encoded by the provided polynucleotides or corresponding cDNA or genes. For example, sequences that show an identity or similarity with a chemokine profile or MSA can exhibit chemokine activities.

Profiles can designed manually by (1) creating an MSA, which is an alignment of the amino acid sequence of members that belong to the family and (2) constructing a statistical representation of the alignment. Such methods are described, for example, in Birney *et al.*, *Nucl. Acid Res.* (1996) *24(14)*: 2730-2739. MSAs of some protein families and motifs are publicly available. For example, http://genome.wustl.edu/Pfam/ includes MSAs of 547 different families and motifs. These MSAs are described also in Sonnhammer *et al.*, *Proteins* (1997) *28*: 405-420. Other sources over the world wide web

include the site at http://www.embl-heidelberg.de/argos/ali/ali.html; alternatively, a message can be sent to ALI@EMBL-HEIDELBERG.DE for the information. A brief description of these MSAs is reported in Pascarella *et al.*, *Prot. Eng.* (1996) *9(3)*:249-251. Techniques for building profiles from MSAs are described in Sonnhammer *et al.*, *supra*; Birney *et al.*, *supra*; and "Computer Methods for Macromolecular Sequence Analysis," *Methods in Enzymology* (1996) *266*, Doolittle, Academic Press, Inc., a division of Harcourt Brace & Co., San Diego, California, USA.

Similarity between a query sequence and a protein family or motif can be determined by (a) comparing the query sequence against the profile and/or (b) aligning the query sequence with the members of the family or motif. Typically, a program such as Searchwise is used to compare the query sequence to the statistical representation of the multiple alignment, also known as a profile. The program is described in Birney *et al.*, *supra*. Other techniques to compare the sequence and profile are described in Sonnhammer *et al.*, *supra* and Doolittle, *supra*.

Next, methods described by Feng *et al.*, *J. Mol. Evol.* (1987) *25*:351 and Higgins *et al.*, *CABIOS* (1989) *5*:151 can be used align the query sequence with the members of a family or motif, also known as a MSA. Computer programs, such as PILEUP, can be used. See Feng *et al.*, *infra*. In general, the following factors are used to determine if a similarity between a query sequence and a profile or MSA exists: (1) number of conserved residues found in the query sequence, (2) percentage of conserved residues found in the query sequence, (3) number of frameshifts, and (4) spacing between conserved residues.

Some alignment programs that both translate and align sequences can make any number of frameshifts when translating the nucleotide sequence to produce the best alignment. The fewer frameshifts needed to produce an alignment, the stronger the similarity or identity between the query and profile or MSAs. For example, a weak similarity resulting from no frameshifts can be a better indication of activity or structure of a query sequence, than a strong similarity resulting from two frameshifts. Preferably, three or fewer frameshifts are found in an alignment; more preferably two or fewer frameshifts; even more preferably, one or fewer frameshifts; even more preferably, no frameshifts are found in an alignment of query and profile or MSAs.

Conserved residues are those amino acids found at a particular position in all or some of the family or motif members. For example, most chemokines contain four conserved cysteines. Alternatively, a position is considered conserved if only a certain class of amino acids is found in a particular position in all or some of the family members. For example, the N-terminal position can contain a positively charged amino acid, such as lysine, arginine, or histidine.

Typically, a residue of a polypeptide is conserved when a class of amino acids or a single amino acid is found at a particular position in at least about 40% of all class members; more typically, at least about 50%; even more typically, at least about 60% of the members. Usually, a residue is conserved when a class or single amino acid is found in at least about 70% of the members of a family or motif; more usually, at least about 80%; even more usually, at least about 90%; even more usually, at least about 95%.

A residue is considered conserved when three unrelated amino acids are found at a particular position in the some or all of the members; more usually, two unrelated amino acids. These residues are conserved when the unrelated amino acids are found at particular positions in at least about 40% of all class member; more typically, at least about 50%; even more typically, at least about 60% of the members. Usually, a residue is conserved when a class or single amino acid is found in at least about 70% of the members of a family or motif; more usually, at least about 80%; even more usually, at least about 90%; even more usually, at least about 95%.

A query sequence has similarity to a profile or MSA when the query sequence comprises at least about 25% of the conserved residues of the profile or MSA; more usually, at least about 30%; even more usually; at least about 40%. Typically, the query sequence has a stronger similarity to a profile sequence or MSA when the query sequence comprises at least about 45% of the conserved residues of the profile or MSA; more typically, at least about 50%; even more typically; at least about 55%.

B. Screening Polynucleotide and Amino Acid Sequences Against Protein Profiles

The identify and function of the gene that correlates to a polynucleotide described herein can be determined by screening the polynucleotides or their corresponding amino acid sequences against profiles of protein families. Such profiles focus on common

structural motifs among proteins of each family. Publicly available profiles are described above in Section IVA. Additional or alternative profiles are described below.

In comparing a novel polynucleotide with known sequences, several alignment tools are available. Examples include PileUp, which creates a multiple sequence alignment, and is described in Feng *et al.*, *J. Mol. Evol.* (1987) *25*:351. Another method, GAP, uses the alignment method of Needleman *et al.*, *J. Mol. Biol.* (1970) *48*:443. GAP is best suited for global alignment of sequences. A third method, BestFit, functions by inserting gaps to maximize the number of matches using the local homology algorithm of Smith *et al.*, *Adv. Appl. Math.* (1981) *2*:482.

C. Identification of Secreted & Membrane-Bound Polypeptides

Both secreted and membrane-bound polypeptides of the present invention are of particular interest. For example, levels of secreted polypeptides can be assayed in body fluids that are convenient, such as blood, urine, prostatic fluid and semen. Membrane-bound polypeptides are useful for constructing vaccine antigens or inducing an immune response. Such antigens would comprise all or part of the extracellular region of the membrane-bound polypeptides. Because both secreted and membrane-bound polypeptides comprise a fragment of contiguous hydrophobic amino acids, hydrophobicity predicting algorithms can be used to identify such polypeptides.

A signal sequence is usually encoded by both secreted and membrane-bound polypeptide genes to direct a polypeptide to the surface of the cell. The signal sequence usually comprises a stretch of hydrophobic residues. Such signal sequences can fold into helical structures. Membrane-bound polypeptides typically comprise at least one transmembrane region that possesses a stretch of hydrophobic amino acids that can transverse the membrane. Some transmembrane regions also exhibit a helical structure. Hydrophobic fragments within a polypeptide can be identified by using computer algorithms. Such algorithms include Hopp & Woods, *Proc. Natl. Acad. Sci. USA* (1981) *78*:3824-3828; Kyte & Doolittle, *J. Mol. Biol.* (1982) *157*: 105-132; and RAOAR algorithm, Degli Esposti *et al.*, *Eur. J. Biochem.* (1990) *190*: 207-219.

Another method of identifying secreted and membrane-bound polypeptides is to translate the polynucleotides of the invention in all six frames and determine if at least 8

contiguous hydrophobic amino acids are present. Those translated polypeptides with at least 8; more typically, 10; even more typically, 12 contiguous hydrophobic amino acids are considered to be either a putative secreted or membrane bound polypeptide. Hydrophobic amino acids include alanine, glycine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, threonine, tryptophan, tyrosine, and valine.

IV. Identification of the Function of an Expression Product of a Full-Length Gene Corresponding to a Polynucleotide

Ribozymes, antisense constructs, and dominant negative mutants can be used to determine function of the expression product of a gene corresponding to a polynucleotide provided herein. These methods and compositions are particularly useful where the provided novel polynucleotide exhibits no significant or substantial homology to a sequence encoding a gene of known function. Antisense molecules and ribozymes can be constructed from synthetic polynucleotides. Typically, the phosphoramidite method of oligonucleotide synthesis is used. See Beaucage *et al.*, *Tet. Lett.* (1981) *22*:1859 and U.S. Patent No. 4,668,777. Automated devices for synthesis are available to create oligonucleotides using this chemistry. Examples of such devices include Biosearch 8600, Models 392 and 394 by Applied Biosystems, a division of Perkin-Elmer Corp., Foster City, California, USA; and Expedite by Perceptive Biosystems, Framingham, Massachusetts, USA. Synthetic RNA, phosphate analog oligonucleotides, and chemically derivatized oligonucleotides can also be produced, and can be covalently attached to other molecules. RNA oligonucleotides can be synthesized, for example, using RNA phosphoramidites. This method can be performed on an automated synthesizer, such as Applied Biosystems, Models 392 and 394, Foster City, California, USA. See Applied Biosystems User Bulletin 53 and Ogilvie *et al.*, *Pure & Applied Chem.* (1987) *59*:325.

Phosphorothioate oligonucleotides can also be synthesized for antisense construction. A sulfurizing reagent, such as tetraethylthiruam disulfide (TETD) in acetonitrile can be used to convert the internucleotide cyanoethyl phosphite to the phosphorothioate triester within 15 minutes at room temperature. TETD replaces the iodine reagent, while all other reagents used for standard phosphoramidite chemistry

remain the same. Such a synthesis method can be automated using Models 392 and 394 by Applied Biosystems, for example.

Oligonucleotides of up to 200 nucleotides can be synthesized, more typically, 100 nucleotides, more typically 50 nucleotides; even more typically 30 to 40 nucleotides. These synthetic fragments can be annealed and ligated together to construct larger fragments. See, for example, Sambrook *et al., supra.*

A. Ribozymes

Trans-cleaving catalytic RNAs (ribozymes) are RNA molecules possessing endoribonuclease activity. Ribozymes are specifically designed for a particular target, and the target message must contain a specific nucleotide sequence. They are engineered to cleave any RNA species site-specifically in the background of cellular RNA. The cleavage event renders the mRNA unstable and prevents protein expression. Importantly, ribozymes can be used to inhibit expression of a gene of unknown function for the purpose of determining its function in an in vitro or in vivo context, by detecting the phenotypic effect.

One commonly used ribozyme motif is the hammerhead, for which the substrate sequence requirements are minimal. Design of the hammerhead ribozyme is disclosed in Usman *et al., Current Opin. Struct. Biol.* (1996) *6*:527. Ribozymes can also be prepared and used as described in Long *et al., FASEB J.* (1993) *7*:25; Symons, *Ann. Rev. Biochem.* (1992) *61*:641; Perrotta *et al., Biochem.* (1992) *31*:16; Ojwang *et al., Proc. Natl. Acad. Sci. (USA)* (1992) *89*:10802; and U.S. Patent No. 5,254,678. Ribozyme cleavage of HIV-I RNA is described in U.S. Patent No. 5,144,019; methods of cleaving RNA using ribozymes is described in U.S. Patent No. 5,116,742; and methods for increasing the specificity of ribozymes are described in U.S. Patent No. 5,225,337 and Koizumi *et al., Nucleic Acid Res.* (1989) *17*:7059. Preparation and use of ribozyme fragments in a hammerhead structure are also described by Koizumi *et al., Nucleic Acids Res.* (1989) *17*:7059. Preparation and use of ribozyme fragments in a hairpin structure are described by Chowrira and Burke, *Nucleic Acids Res.* (1992) *20*:2835. Ribozymes can also be made by rolling transcription as described in Daubendiek and Kool, *Nat. Biotechnol.* (1997) *15(3)*:273.

The hybridizing region of the ribozyme can be modified or can be prepared as a branched structure as described in Horn and Urdea, *Nucleic Acids Res.* (1989) *17*:6959. The basic structure of the ribozymes can also be chemically altered in ways familiar to those skilled in the art, and chemically synthesized ribozymes can be administered as synthetic oligonucleotide derivatives modified by monomeric units. In a therapeutic context, liposome mediated delivery of ribozymes improves cellular uptake, as described in Birikh *et al., Eur. J. Biochem.* (1997) *245*:1.

Using the polynucleotide sequences of the invention and methods known in the art, ribozymes are designed to specifically bind and cut the corresponding mRNA species. Ribozymes thus provide a means to inhibit the expression of any of the proteins encoded by the disclosed polynucleotides or their full-length genes. The full-length gene need not be known in order to design and use specific inhibitory ribozymes. In the case of a polynucleotide or full-length cDNA of unknown function, ribozymes corresponding to that nucleotide sequence can be tested in vitro for efficacy in cleaving the target transcript. Those ribozymes that effect cleavage in vitro are further tested in vivo. The ribozyme can also be used to generate an animal model for a disease, as described in Birikh *et al., supra.* An effective ribozyme is used to determine the function of the gene of interest by blocking its transcription and detecting a change in the cell. Where the gene is found to be a mediator in a disease, an effective ribozyme is designed and delivered in a gene therapy for blocking transcription and expression of the gene.

Therapeutic and functional genomic applications of ribozymes proceed beginning with knowledge of a portion of the coding sequence of the gene to be inhibited. Thus, for many genes, a partial polynucleotide sequence provides adequate sequence for constructing an effective ribozyme. A target cleavage site is selected in the target sequence, and a ribozyme is constructed based on the 5' and 3' nucleotide sequences that flank the cleavage site. Retroviral vectors are engineered to express monomeric and multimeric hammerhead ribozymes targeting the mRNA of the target coding sequence. These monomeric and multimeric ribozymes are tested in vitro for an ability to cleave the target mRNA. A cell line is stably transduced with the retroviral vectors expressing the ribozymes, and the transduction is confirmed by Northern blot analysis and reverse-transcription polymerase chain reaction (RT-PCR). The cells are screened for inactivation of the target mRNA by

such indicators as reduction of expression of disease markers or reduction of the gene product of the target mRNA.

B. Antisense

Antisense nucleic acids are designed to specifically bind to RNA, resulting in the formation of RNA-DNA or RNA-RNA hybrids, with an arrest of DNA replication, reverse transcription or messenger RNA translation. Antisense polynucleotides based on a selected polynucleotide sequence can interfere with expression of the corresponding gene. Antisense polynucleotides are typically generated within the cell by expression from antisense constructs that contain the antisense strand as the transcribed strand. Antisense polynucleotides based on the disclosed polynucleotides will bind and/or interfere with the translation of mRNA comprising a sequence complementary to the antisense polynucleotide. The expression products of control cells and cells treated with the antisense construct are compared to detect the protein product of the gene corresponding to the polynucleotide upon which the antisense construct is based. The protein is isolated and identified using routine biochemical methods.

Given the extensive background literature and clinical experience in antisense therapy, one skilled in the art can use selected polynucleotides of the invention as additional potential therapeutics. The choice of polynucleotide can be narrowed by first testing them for binding to "hot spot" regions of the genome of cancerous cells. If a polynucleotide is identified as binding to a "hot spot", testing the polynucleotide as an antisense compound in the corresponding cancer cells clearly is warranted.

C. Dominant Negative Mutations

As an alternative method for identifying function of the gene corresponding to a polynucleotide disclosed herein, dominant negative mutations are readily generated for corresponding proteins that are active as homomultimers. A mutant polypeptide will interact with wild-type polypeptides (made from the other allele) and form a non-functional multimer. Thus, a mutation is in a substrate-binding domain, a catalytic domain, or a cellular localization domain. Preferably, the mutant polypeptide will be overproduced. Point mutations are made that have such an effect. In addition, fusion of different polypeptides of various lengths to the terminus of a protein can yield dominant negative mutants. General strategies are available for making dominant negative mutants (see, *e.g.*,

Herskowitz, *Nature* (1987) *329*:219). Such techniques can be used to create loss of function mutations, which are useful for determining protein function.

V. Construction of Polypeptides of the Invention and Variants Thereof

The polypeptides of the invention include those encoded by the disclosed polynucleotides. These polypeptides can also be encoded by nucleic acids that, by virtue of the degeneracy of the genetic code, are not identical in sequence to the disclosed polynucleotides. Thus, the invention includes within its scope a polypeptide encoded by a polynucleotide having the sequence of any one of "SEQ ID NOS:1-5252" or a variant thereof.

In general, the term "polypeptide" as used herein refers to both the full length polypeptide encoded by the recited polynucleotide, the polypeptide encoded by the gene represented by the recited polynucleotide, as well as portions or fragments thereof. "Polypeptides" also includes variants of the naturally occurring proteins, where such variants are homologous or substantially similar to the naturally occurring protein, and can be of an origin of the same or different species as the naturally occurring protein (*e.g.*, human, murine, or some other species that naturally expresses the recited polypeptide, usually a mammalian species). In general, variant polypeptides have a sequence that has at least about 80%, usually at least about 90%, and more usually at least about 98% sequence identity with a differentially expressed polypeptide of the invention, as measured by BLAST using the parameters described above. The variant polypeptides can be naturally or non-naturally glycosylated, *i.e.*, the polypeptide has a glycosylation pattern that differs from the glycosylation pattern found in the corresponding naturally occurring protein.

The invention also encompasses homologs of the disclosed polypeptides (or fragments thereof) where the homologs are isolated from other species, *i.e.* other animal or plant species, where such homologs, usually mammalian species, *e.g.* rodents, such as mice, rats; domestic animals, *e.g.*, horse, cow, dog, cat; and humans. By homolog is meant a polypeptide having at least about 35%, usually at least about 40% and more usually at least about 60% amino acid sequence identity a particular differentially expressed protein as identified above, where sequence identity is determined using the BLAST algorithm, with the parameters described *supra*.

In general, the polypeptides of the subject invention are provided in a non-naturally occurring environment, *e.g.* are separated from their naturally occurring environment. In certain embodiments, the subject protein is present in a composition that is enriched for the protein as compared to a control. As such, purified polypeptide is provided, where by purified is meant that the protein is present in a composition that is substantially free of non-differentially expressed polypeptides, where by substantially free is meant that less than 90%, usually less than 60% and more usually less than 50% of the composition is made up of non-differentially expressed polypeptides.

Also within the scope of the invention are variants; variants of polypeptides include mutants, fragments, and fusions. Mutants can include amino acid substitutions, additions or deletions. The amino acid substitutions can be conservative amino acid substitutions or substitutions to eliminate non-essential amino acids, such as to alter a glycosylation site, a phosphorylation site or an acetylation site, or to minimize misfolding by substitution or deletion of one or more cysteine residues that are not necessary for function. Conservative amino acid substitutions are those that preserve the general charge, hydrophobicity/hydrophilicity, and/or steric bulk of the amino acid substituted. For example, substitutions between the following groups are conservative: Gly/Ala, Val/Ile/Leu, Asp/Glu, Lys/Arg, Asn/Gln, Ser/Cys, Thr, and Phe/Trp/Tyr.

Variants can be designed so as to retain biological activity of a particular region of the protein (*e.g.*, a functional domain and/or, where the polypeptide is a member of a protein family, a region associated with a consensus sequence). In a non-limiting example, Osawa *et al., Biochem. Mol. Int.* (1994) *34*:1003, discusses the actin binding region of a protein from several different species. The actin binding regions of the these species are considered homologous based on the fact that they have amino acids that fall within "homologous residue groups." Homologous residues are judged according to the following groups (using single letter amino acid designations): STAG; ILVMF; HRK; DEQN; and FYW. For example, and S, a T, an A or a G can be in a position and the function (in this case actin binding) is retained.

Additional guidance on amino acid substitution is available from studies of protein evolution. Go *et al, Int. J. Peptide Protein Res.* (1980) *15*:211, classified amino acid residue sites as interior or exterior depending on their accessibility. More frequent

substitution on exterior sites was confirmed to be general in eight sets of homologous protein families regardless of their biological functions and the presence or absence of a prosthetic group. Virtually all types of amino acid residues had higher mutabilities on the exterior than in the interior. No correlation between mutability and polarity was observed of amino acid residues in the interior and exterior, respectively. Amino acid residues were classified into one of three groups depending on their polarity: polar (Arg, Lys, His, Gln, Asn, Asp, and Glu); weak polar (Ala, Pro, Gly, Thr, and Ser), and nonpolar (Cys, Val, Met, Ile, Leu, Phe, Tyr, and Trp). Amino acid replacements during protein evolution were very conservative: 88% and 76% of them in the interior or exterior, respectively, were within the same group of the three. Inter-group replacements are such that weak polar residues are replaced more often by nonpolar residues in the interior and more often by polar residues on the exterior.

Additional guidance for production of polypeptide variants is provided in Querol *et al.*, *Prot. Eng.* (1996) *9*:265, which provides general rules for amino acid substitutions to enhance protein thermostability. New glycosylation sites can be introduced as discussed in Olsen and Thomsen, *J. Gen. Microbiol.* (1991) *137*:579. An additional disulfide bridge can be introduced, as discussed by Perry and Wetzel, *Science* (1984) *226*:555; Pantoliano *et al.*, *Biochemistry* (1987) *26*:2077; Matsumura *et al.*, *Nature* (1989) *342*:291; Nishikawa *et al.*, *Protein Eng.* (1990) *3*:443; Takagi *et al.*, *J. Biol. Chem.* (1990) *265*:6874; Clarke *et al.*, *Biochemistry* (1993) *32*:4322; and Wakarchuk *et al.*, *Protein Eng.* (1994) *7*:1379. Metal binding sites can be introduced, according to Toma *et al.*, *Biochemistry* (1991) *30*:97, and Haezerbrouck *et al.*, *Protein Eng.* (1993) *6*:643. Substitutions with prolines in loops can be made according to Masul *et al.*, *Appl. Env. Microbiol.* (1994) *60*:3579; and Hardy *et al.*, *FEBS Lett. 317*:89.

Cysteine-depleted muteins are considered variants within the scope of the invention. These variants can be constructed according to methods disclosed in U.S. Patent No. 4,959,314, which discloses substitution of cysteines with other amino acids, and methods for assaying biological activity and effect of the substitution. Such methods are suitable for proteins according to this invention that have cysteine residues suitable for such substitutions, for example to eliminate disulfide bond formation.

Variants also include fragments of the polypeptides disclosed herein, particularly biologically active fragments and/or fragments corresponding to functional domains. Fragments of interest will typically be at least about 10 aa to at least about 15 aa in length, usually at least about 50 aa in length, and can be as long as 300 aa in length or longer, but will usually not exceed about 1000 aa in length, where the fragment will have a stretch of amino acids that is identical to a polypeptide encoded by a polynucleotide having a sequence of any "SEQ ID NOS:1-5252", or a homolog thereof.

The protein variants described herein are encoded by polynucleotides that are within the scope of the invention. The genetic code can be used to select the appropriate codons to construct the corresponding variants.

VI. Computer-Related Embodiments

In general, a library of polynucleotides is a collection of sequence information, which information is provided in either biochemical form (*e.g.*, as a collection of polynucleotide molecules), or in electronic form (*e.g.*, as a collection of polynucleotide sequences stored in a computer-readable form, as in a computer system and/or as part of a computer program). The sequence information of the polynucleotides can be used in a variety of ways, *e.g.*, as a resource for gene discovery, as a representation of sequences expressed in a selected cell type (*e.g.*, cell type markers), and/or as markers of a given disease or disease state. In general, a disease marker is a representation of a gene product that is present in all cells affected by disease either at an increased or decreased level relative to a normal cell (*e.g.*, a cell of the same or similar type that is not substantially affected by disease). For example, a polynucleotide sequence in a library can be a polynucleotide that represents an mRNA, polypeptide, or other gene product encoded by the polynucleotide, that is either overexpressed or underexpressed in a breast ductal cell affected by cancer relative to a normal (*i.e.*, substantially disease-free) breast cell.

The nucleotide sequence information of the library can be embodied in any suitable form, *e.g.*, electronic or biochemical forms. For example, a library of sequence information embodied in electronic form includes an accessible computer data file (or, in biochemical form, a collection of nucleic acid molecules) that contains the representative nucleotide sequences of genes that are differentially expressed (*e.g.*, overexpressed or underexpressed)

as between, for example, i) a cancerous cell and a normal cell; ii) a cancerous cell and a dysplastic cell; iii) a cancerous cell and a cell affected by a disease or condition other than cancer; iv) a metastatic cancerous cell and a normal cell and/or non-metastatic cancerous cell; v) a malignant cancerous cell and a non-malignant cancerous cell (or a normal cell) and/or vi) a dysplastic cell relative to a normal cell. Other combinations and comparisons of cells affected by various diseases or stages of disease will be readily apparent to the ordinarily skilled artisan. Biochemical embodiments of the library include a collection of nucleic acids that have the sequences of the genes in the library, where the nucleic acids can correspond to the entire gene in the library or to a fragment thereof, as described in greater detail below.

The polynucleotide libraries of the subject invention include sequence information of a plurality of polynucleotide sequences, where at least one of the polynucleotides has a sequence of any of "SEQ ID NOS:1-5252." By plurality is meant at least 2, usually at least 3 and can include up to all of "SEQ ID NOS:1-5252." The length and number of polynucleotides in the library will vary with the nature of the library, *e.g.*, if the library is an oligonucleotide array, a cDNA array, a computer database of the sequence information, etc.

Where the library is an electronic library, the nucleic acid sequence information can be present in a variety of media. "Media" refers to a manufacture, other than an isolated nucleic acid molecule, that contains the sequence information of the present invention. Such a manufacture provides the genome sequence or a subset thereof in a form that can be examined by means not directly applicable to the sequence as it exists in a nucleic acid. For example, the nucleotide sequence of the present invention, *e.g.* the nucleic acid sequences of any of the polynucleotides of "SEQ ID NOS:1-5252," can be recorded on computer readable media, *e.g.* any medium that can be read and accessed directly by a computer. Such media include, but are not limited to: magnetic storage media, such as a floppy disc, a hard disc storage medium, and a magnetic tape; optical storage media such as CD-ROM; electrical storage media such as RAM and ROM; and hybrids of these categories such as magnetic/optical storage media. One of skill in the art can readily appreciate how any of the presently known computer readable mediums can be used to create a manufacture comprising a recording of the present sequence information.

"Recorded" refers to a process for storing information on computer readable medium, using any such methods as known in the art. Any convenient data storage structure can be chosen, based on the means used to access the stored information. A variety of data processor programs and formats can be used for storage, *e.g.* word processing text file, database format, *etc.* In addition to the sequence information, electronic versions of the libraries of the invention can be provided in conjunction or connection with other computer-readable information and/or other types of computer-readable files (*e.g.*, searchable files, executable files, *etc*, including, but not limited to, for example, search program software, *etc.*.).

By providing the nucleotide sequence in computer readable form, the information can be accessed for a variety of purposes. Computer software to access sequence information is publicly available. For example, the BLAST (Altschul *et al.*, *supra.*) and BLAZE (Brutlag *et al. Comp. Chem.* (1993) 17:203) search algorithms on a Sybase system can be used to identify open reading frames (ORFs) within the genome that contain homology to ORFs from other organisms.

As used herein, "a computer-based system" refers to the hardware means, software means, and data storage means used to analyze the nucleotide sequence information of the present invention. The minimum hardware of the computer-based systems of the present invention comprises a central processing unit (CPU), input means, output means, and data storage means. A skilled artisan can readily appreciate that any one of the currently available computer-based system are suitable for use in the present invention. The data storage means can comprise any manufacture comprising a recording of the present sequence information as described above, or a memory access means that can access such a manufacture.

"Search means" refers to one or more programs implemented on the computer-based system, to compare a target sequence or target structural motif with the stored sequence information. Search means are used to identify fragments or regions of the genome that match a particular target sequence or target motif. A variety of known algorithms are publicly known and commercially available, *e.g.* MacPattern (EMBL), BLASTN and BLASTX (NCBI). A "target sequence" can be any DNA or amino acid

sequence of six or more nucleotides or two or more amino acids, preferably from about 10 to 100 amino acids or from about 30 to 300 nucleotide residues.

A "target structural motif," or "target motif," refers to any rationally selected sequence or combination of sequences in which the sequence(s) are chosen based on a three-dimensional configuration that is formed upon the folding of the target motif, or on consensus sequences of regulatory or active sites. There are a variety of target motifs known in the art. Protein target motifs include, but arc not limited to, enzyme active sites and signal sequences. Nucleic acid target motifs include, but are not limited to, hairpin structures, promoter sequences and other expression elements such as binding sites for transcription factors.

A variety of structural formats for the input and output means can be used to input and output the information in the computer-based systems of the present invention. One format for an output means ranks fragments of the genome possessing varying degrees of homology to a target sequence or target motif. Such presentation provides a skilled artisan with a ranking of sequences and identifies the degree of sequence similarity contained in the identified fragment.

A variety of comparing means can be used to compare a target sequence or target motif with the data storage means to identify sequence fragments of the genome. A skilled artisan can readily recognize that any one of the publicly available homology search programs can be used as the search means for the computer based systems of the present invention.

As discussed above, the "library" of the invention also encompasses biochemical libraries of the polynucleotides of "SEQ ID NOS:1-5252," *e.g.*, collections of nucleic acids representing the provided polynucleotides. The biochemical libraries can take a variety of forms, *e.g.*, a solution of cDNAs, a pattern of probe nucleic acids stably associated with a surface of a solid support (*i.e.*, an array) and the like. Of particular interest are nucleic acid arrays in which one or more of "SEQ ID NOS:1-5252"is represented on the array. By array is meant a an article of manufacture that has at least a substrate with at least two distinct nucleic acid targets on one of its surfaces, where the number of distinct nucleic acids can be considerably higher, typically being at least 10 nt, usually at least 20 nt and often at least 25 nt. A variety of different array formats have been developed and are known to those of

skill in the art, including those described in 5,242,974; 5,384,261; 5,405,783; 5,412,087; 5,424,186; 5,429,807; 5,436,327; 5,445,934; 5,472,672; 5,527,681; 5,529,756; 5,545,531; 5,554,501; 5,556,752; 5,561,071; 5,599,895; 5,624,711; 5,639,603; 5,658,734; WO 93/17126; WO 95/11995; WO 95/35505; EP 742287; and EP 799897. The arrays of the subject invention find use in a variety of applications, including gene expression analysis, drug screening, mutation analysis and the like, as disclosed in the above-listed exemplary patent documents.

In addition to the above nucleic acid libraries, analogous libraries of polypeptides are also provided, where the where the polypeptides of the library will represent at least a portion of the polypeptides encoded by "SEQ ID NOS:1-5252."

VII. Utilities

A. Use of Polynucleotide Probes in Mapping, and in Tissue Profiling

Polynucleotide probes, generally comprising at least 12 contiguous nucleotides of a polynucleotide as shown in the Sequence Listing, are used for a variety of purposes, such as chromosome mapping of the polynucleotide and detection of transcription levels. Additional disclosure about preferred regions of the disclosed polynucleotide sequences is found in the Examples. A probe that hybridizes specifically to a polynucleotide disclosed herein should provide a detection signal at least 5-, 10-, or 20-fold higher than the background hybridization provided with other unrelated sequences.

Probes in Detection of Expression Levels. Nucleotide probes are used to detect expression of a gene corresponding to the provided polynucleotide. In Northern blots, mRNA is separated electrophoretically and contacted with a probe. A probe is detected as hybridizing to an mRNA species of a particular size. The amount of hybridization is quantitated to determine relative amounts of expression, for example under a particular condition. Probes are used for in situ hybridization to cells to detect expression. Probes can also be used *in vivo* for diagnostic detection of hybridizing sequences. Probes are typically labeled with a radioactive isotope. Other types of detectable labels can be used such as chromophores, fluors, and enzymes. Other examples of nucleotide hybridization assays are described in WO92/02526 and U.S. Patent No. 5,124,246.

The Polymerase Chain Reaction (PCR) is another means for detecting small amounts of target nucleic acids (see, *e.g.*, Mullis *et al.*, *Meth. Enzymol.* (1987) *155*:335; U.S. Patent No. 4,683,195; and U.S. Patent No. 4,683,202). Two primer polynucleotides nucleotides hybridize with the target nucleic acids and are used to prime the reaction. The primers can be composed of sequence within or 3' and 5' to the polynucleotides of the Sequence Listing. Alternatively, if the primers are 3' and 5' to these polynucleotides, they need not hybridize to them or the complements. A thermostable polymerase creates copies of target nucleic acids from the primers using the original target nucleic acids as a template. After a large amount of target nucleic acids is generated by the polymerase, it is detected by methods such as Southern blots. When using the Southern blot method, the labeled probe will hybridize to a polynucleotide of the Sequence Listing or complement.

Furthermore, mRNA or cDNA can be detected by traditional blotting techniques described in Sambrook *et al.*, "Molecular Cloning: A Laboratory Manual" (New York, Cold Spring Harbor Laboratory, 1989). mRNA or cDNA generated from mRNA using a polymerase enzyme can be purified and separated using gel electrophoresis. The nucleic acids on the gel are then blotted onto a solid support, such as nitrocellulose. The solid support is exposed to a labeled probe and then washed to remove any unhybridized probe. Next, the duplexes containing the labeled probe are detected. Typically, the probe is labeled with radioactivity.

Mapping. Polynucleotides of the present invention are used to identify a chromosome on which the corresponding gene resides. Such mapping can be useful in identifying the function of the polynucleotide-related gene by its proximity to other genes with known function. Function can also be assigned to the polynucleotide-related gene when particular syndromes or diseases map to the same chromosome. For example, use of polynucleotide probes in identification and quantification of nucleic acid sequence aberrations is described in U.S. Patent No. 5,783,387.

For example, fluorescence in situ hybridization (FISH) on normal metaphase spreads facilitates comparative genomic hybridization to allow total genome assessment of changes in relative copy number of DNA sequences. See Schwartz and Samad, *Curr. Opin. Biotechnol.* (1994) *8*:70; Kallioniemi *et al.*, *Sem. Cancer Biol.* (1993) *4*:41; Valdes

et al., *Methods in Molecular Biology* (1997) *68*:1, Boultwood, ed., Human Press, Totowa, NJ.

Polynucleotides are mapped to particular chromosomes using, for example, radiation hybrids or chromosome-specific hybrid panels. See Leach *et al.*, *Advances in Genetics*, (1995) *33*:63-99; Walter *et al.*, *Nature Genetics* (1994) *7*:22; Walter and Goodfellow, *Trends in Genetics* (1992) *9*:352. Panels for radiation hybrid mapping are available from Research Genetics, Inc., Huntsville, Alabama, USA. Databases for markers using various panels are available via the world wide web at http:/F/shgc-www.stanford.edu; and http://www-genome.wi.mit.edu/cgi-bin/contig/rhmapper.pl. The statistical program RHMAP can be used to construct a map based on the data from radiation hybridization with a measure of the relative likelihood of one order versus another. RHMAP is available via the world wide web at http://www.sph.umich.edu/group/statgen/software.

In addition, commercial programs are available for identifying regions of chromosomes commonly associated with disease, such as cancer. Polynucleotides based on the polynucleotides of the invention can be used to probe these regions. For example, if through profile searching a provided polynucleotide is identified as corresponding to a gene encoding a kinase, its ability to bind to a cancer-related chromosomal region will suggest its role as a kinase in one or more stages of tumor cell development/growth. Although some experimentation would be required to elucidate the role, the polynucleotide constitutes a new material for isolating a specific protein that has potential for developing a cancer diagnostic or therapeutic.

Tissue Typing or Profiling. Expression of specific mRNA corresponding to the provided polynucleotides can vary in different cell types and can be tissue-specific. This variation of mRNA levels in different cell types can be exploited with nucleic acid probe assays to determine tissue types. For example, PCR, branched DNA probe assays, or blotting techniques utilizing nucleic acid probes substantially identical or complementary to polynucleotides listed in the Sequence Listing can determine the presence or absence of the corresponding cDNA or mRNA.

For example, a metastatic lesion is identified by its developmental organ or tissue source by identifying the expression of a particular marker of that organ or tissue. If a

polynucleotide is expressed only in a specific tissue type, and a metastatic lesion is found to express that polynucleotide, then the developmental source of the lesion has been identified. Expression of a particular polynucleotide is assayed by detection of either the corresponding mRNA or the protein product. Immunological methods, such as antibody staining, are used to detect a particular protein product. Hybridization methods can be used to detect particular mRNA species, including but not limited to in situ hybridization and Northern blotting.

Use of Polymorphisms. A polynucleotide of the invention will be useful in forensics, genetic analysis, mapping, and diagnostic applications if the corresponding region of a gene is polymorphic in the human population. Particular polymorphic forms of the provided polynucleotides can be used to either identify a sample as deriving from a suspect or rule out the possibility that the sample derives from the suspect. Any means for detecting a polymorphism in a gene are used, including but not limited to electrophoresis of protein polymorphic variants, differential sensitivity to restriction enzyme cleavage, and hybridization to allele-specific probes.

B. Antibody Production

Expression products of a polynucleotide of the invention, the corresponding mRNA or cDNA, or the corresponding complete gene are prepared and used for raising antibodies for experimental, diagnostic, and therapeutic purposes. For polynucleotides to which a corresponding gene has not been assigned, this provides an additional method of identifying the corresponding gene. The polynucleotide or related cDNA is expressed as described above, and antibodies are prepared. These antibodies are specific to an epitope on the polypeptide encoded by the polynucleotide, and can precipitate or bind to the corresponding native protein in a cell or tissue preparation or in a cell-free extract of an in vitro expression system.

Immunogens for raising antibodies are prepared by mixing the polypeptides encoded by the polynucleotides of the present invention with adjuvants. Alternatively, polypeptides are made as fusion proteins to larger immunogenic proteins. Polypeptides are also covalently linked to other larger immunogenic proteins, such as keyhole limpet hemocyanin. Immunogens are typically administered intradermally, subcutaneously, or intramuscularly. Immunogens are administered to experimental animals such as rabbits,

sheep, and mice, to generate antibodies. Optionally, the animal spleen cells are isolated and fused with myeloma cells to form hybridomas which secrete monoclonal antibodies. Such methods are well known in the art. According to another method known in the art, the selected polynucleotide is administered directly, such as by intramuscular injection, and expressed in vivo. The expressed protein generates a variety of protein-specific immune responses, including production of antibodies, comparable to administration of the protein.

Preparations of polyclonal and monoclonal antibodies specific for polypeptides encoded by a selected polynucleotide are made using standard methods known in the art. The antibodies specifically bind to epitopes present in the polypeptides encoded by polynucleotides disclosed in the Sequence Listing. Typically, at least 6, 8, 10, or 12 contiguous amino acids are required to form an epitope. However, epitopes which involve non-contiguous amino acids may require more, for example at least 15, 25, or 50 amino acids. A short sequence of a polynucleotide may then be unsuitable for use as an epitope to raise antibodies for identifying the corresponding novel protein, because of the potential for cross-reactivity with a known protein. However, the antibodies can be useful for other purposes, particularly if they identify common structural features of a known protein and a novel polypeptide encoded by a polynucleotide of the invention.

Antibodies that specifically bind to human polypeptides encoded by the provided polypeptides should provide a detection signal at least 5-, 10-, or 20-fold higher than a detection signal provided with other proteins when used in Western blots or other immunochemical assays. Preferably, antibodies that specifically polypeptides of the invention do not bind to other proteins in immunochemical assays at detectable levels and can immunoprecipitate the specific polypeptide from solution.

To test for the presence of serum antibodies to the polypeptide of the invention in a human population, human antibodies are purified by methods well known in the art. Preferably, the antibodies are affinity purified by passing antiserum over a column to which the corresponding selected polypeptide or fusion protein is bound. The bound antibodies can then be eluted from the column, for example using a buffer with a high salt concentration.

In addition to the antibodies discussed above, genetically engineered antibody derivatives are made, such as single chain antibodies, according to methods well known in the art.

C. Use of Polynucleotides to Construct Arrays for Diagnostics

Polynucleotide arrays provide a high throughput technique that can assay a large number of polynucleotide sequences in a sample. This technology can be used as a diagnostic and as a tool to test for differential expression to determine function of an encoded protein. Arrays can be created by spotting polynucleotide probes onto a substrate (*e.g.*, glass, nitrocelllose, *etc.*) in a two-dimensional matrix or array having bound probes. The probes can be bound to the substrate by either covalent bonds or by non-specific interactions, such as hydrophobic interactions. Samples of polynucleotides can be detectably labeled (*e.g.*, using radioactive or fluorescent labels) and then hybridized to the probes. Double stranded polynucleotides, comprising the labeled sample polynucleotides bound to probe polynucleotides, can be detected once the unbound portion of the sample is washed away. 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. No. 5,593,839; U.S. Pat. No. 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.

As discussed in some detail above, arrays can be used to examine differential expression of genes and can be used to determine gene function. For example, arrays of the instant polynucleotide sequences can be used to determine if any of the provided polynucleotides are differentially expressed between a test cell and control cell (*e.g.*, cancer cells and normal cells). For example, high expression of a particular message in a cancer cell, which is not observed in a corresponding normal cell, can indicate a cancer specific protein. Exemplary uses of arrays are further described in, for example, Pappalarado *et al.*, *Sem. Radiation Oncol.* (1998) *8*:217; and Ramsay *Nature Biotechnol.* (1998) *16*:40.

D. Differential Expression

The polynucleotides of the invention can also be used to detect differences in expression levels between two cells, *e.g.*, as a method to identify abnormal or diseased tissue in a human. For polynucleotides corresponding to profiles of protein families, the

choice of tissue can be selected according to the putative biological function. In general, the expression of a gene corresponding to a specific polynucleotide is compared between a first tissue that is suspected of being diseased and a second, normal tissue of the human. The tissue suspected of being abnormal or diseased can be derived from a different tissue type of the human, but preferably it is derived from the same tissue type; for example an intestinal polyp or other abnormal growth should be compared with normal intestinal tissue. The normal tissue can be the same tissue as that of the test sample, or any normal tissue of the patient, especially those that express the polynucleotide-related gene of interest (*e.g.*, brain, thymus, testis, heart, prostate, placenta, spleen, small intestine, skeletal muscle, pancreas, and the mucosal lining of the colon). A difference between the polynucleotide-related gene, mRNA, or protein in the two tissues which are compared, for example in molecular weight, amino acid or nucleotide sequence, or relative abundance, indicates a change in the gene, or a gene which regulates it, in the tissue of the human that was suspected of being diseased. Examples of detection of differential expression and its use in diagnosis of cancer are described in U.S. Patent Nos. 5,688,641 and 5,677,125.

The polynucleotide-related genes in the two tissues are compared by any means known in the art. For example, the two genes can be sequenced, and the sequence of the gene in the tissue suspected of being diseased compared with the gene sequence in the normal tissue. The genes corresponding to a provided polynucleotide, or portions thereof, in the two tissues are amplified, for example using nucleotide primers based on the nucleotide sequence shown in the Sequence Listing, using the polymerase chain reaction. The amplified genes or portions of genes are hybridized to detectably labeled nucleotide probes selected from a nucleotide sequence shown in the Sequence Listing. A difference in the nucleotide sequence of the isolated gene in the tissue suspected of being diseased compared with the normal nucleotide sequence suggests a role of the gene product encoded by the subject polynucleotide in the disease, and provides guidance for preparing a therapeutic agent.

Alternatively, mRNA corresponding to a provided polynucleotide in the two tissues is compared. PolyA$^+$RNA is isolated from the two tissues as is known in the art. For example, one of skill in the art can readily determine differences in the size or amount of mRNA transcripts between the two tissues using Northern blots and detectably labeled

nucleotide probes selected from the nucleotide sequence shown in the Sequence Listing. Increased or decreased expression of a given mRNA in a tissue sample suspected of being diseased, compared with the expression of the same mRNA in a normal tissue, suggests that the expressed protein has a role in the disease, and also provides a lead for preparing a therapeutic agent.

The comparison can also be accomplished by analyzing polypeptides between the matched samples. The sizes of the proteins in the two tissues are compared, for example, using antibodies of the present invention to detect polypeptides in Western blots of protein extracts from the two tissues. Other changes, such as expression levels and subcellular localization, can also be detected immunologically, using antibodies to the corresponding protein. A higher or lower level of expression of a given polypeptide in a tissue suspected of being diseased, compared with the same protein expression level in a normal tissue, is indicative that the expressed protein has a role in the disease, and provides guidance for preparing a therapeutic agent.

Similarly, comparison of polynucleotide sequences or of gene expression products, *e.g.*, mRNA and protein, between a human tissue that is suspected of being diseased and a normal tissue of a human, are used to follow disease progression or remission in the human. Such comparisons are made as described above. For example, increased or decreased expression of a gene corresponding to an inventive polynucleotide in the tissue suspected of being neoplastic can indicate the presence of neoplastic cells in the tissue. The degree of increased expression of a given gene in the neoplastic tissue relative to expression of the same gene in normal tissue, or differences in the amount of increased expression of a given gene in the neoplastic tissue over time, is used to assess the progression of the neoplasia in that tissue or to monitor the response of the neoplastic tissue to a therapeutic protocol over time.

The expression pattern of any two cell types can be compared, such as low and high metastatic tumor cell lines, malignant or non-malignant cells, or cells from tissue which have and have not been exposed to a therapeutic agent. A genetic predisposition to disease in a human is detected by comparing expression levels of an mRNA or protein corresponding to a polynucleotide of the invention in a fetal tissue with levels associated in normal fetal tissue. Fetal tissues that are used for this purpose include, but are not limited

to, amniotic fluid, chorionic villi, blood, and the blastomere of an in vitro-fertilized embryo. The comparable normal polynucleotide-related gene is obtained from any tissue. The mRNA or protein is obtained from a normal tissue of a human in which the polynucleotide-related gene is expressed. Differences such as alterations in the nucleotide sequence or size of the same product of the fetal polynucleotide-related gene or mRNA, or alterations in the molecular weight, amino acid sequence, or relative abundance of fetal protein, can indicate a germline mutation in the polynucleotide-related gene of the fetus, which indicates a genetic predisposition to disease. Particular diagnostic and prognostic uses of the disclosed polynucleotides are described in more detail below.

E. Diagnostic, Prognostic, and Other Uses Based On Differential Expression

In general, diagnostic methods of the invention for involve detection of a level or amount of a gene product, particularly a differentially expressed gene product, in a test sample obtained from a patient suspected of having or being susceptible to a disease (*e.g.*, breast cancer, lung cancer, colon cancer and/or metastatic forms thereof), and comparing the detected levels to those levels found in normal cells (*e.g.*, cells substantially unaffected by cancer) and/or other control cells (*e.g.*, to differentiate a cancerous cell from a cell affected by dysplasia). Furthermore, the severity of the disease can be assessed by comparing the detected levels of a differentially expressed gene product with those levels detected in samples representing the levels of differentially gene product associated with varying degrees of severity of disease.

The term "differentially expressed gene" is intended to encompass a polynucleotide that can, for example, include an open reading frame encoding a gene product (*e.g.*, a polypeptide), and/or introns of such genes and adjacent 5' and 3' non-coding nucleotide sequences involved in the regulation of expression, up to about 20 kb beyond the coding region, but possibly further in either direction. The gene can be introduced into an appropriate vector for extrachromosomal maintenance or for integration into a host genome. In general, a difference in expression level associated with a decrease in expression level of at least about 25%, usually at least about 50% to 75%, more usually at least about 90% or more is indicative of a differentially expressed gene of interest, *i.e.*, a gene that is underexpressed or down-regulated in the test sample relative to a control sample. Furthermore, a difference in expression level associated with an increase in

expression of at least about 25%, usually at least about 50% to 75%, more usually at least about 90% and can be at least about 1 ½-fold, usually at least about 2-fold to about 10-fold, and can be about 100-fold to about 1,000-fold increase relative to a control sample is indicative of a differentially expressed gene of interest, *i.e.*, an overexpressed or up-regulated gene.

"Differentially expressed polynucleotide" as used herein means a nucleic acid molecule (RNA or DNA) having a sequence that represents a differentially expressed gene, *e.g.*, the differentially expressed polynucleotide comprises a sequence (*e.g.*, an open reading frame encoding a gene product) that uniquely identifies a differentially expressed gene so that detection of the differentially expressed polynucleotide in a sample is correlated with the presence of a differentially expressed gene in a sample. "Differentially expressed polynucleotides" is also meant to encompass fragments of the disclosed polynucleotides, *e.g.*, fragments retaining biological activity, as well as nucleic acids homologous, substantially similar, or substantially identical (*e.g.*, having about 90% sequence identity) to the disclosed polynucleotides.

Methods of the subject invention useful in diagnosis or prognosis typically involve comparison of the abundance of a selected differentially expressed gene product in a sample of interest with that of a control to determine any relative differences in the expression of the gene product, where the difference can be measured qualitatively and/or quantitatively. Quantitation can be accomplished, for example, by comparing the level of expression product detected in the sample with the amounts of product present in a standard curve. A comparison can be made visually; by using a technique such as densitometry, with or without computerized assistance; by preparing a representative library of cDNA clones of mRNA isolated from a test sample, sequencing the clones in the library to determine that number of cDNA clones corresponding to the same gene product, and analyzing the number of clones corresponding to that same gene product relative to the number of clones of the same gene product in a control sample; or by using an array to detect relative levels of hybridization to a selected sequence or set of sequences, and comparing the hybridization pattern to that of a control. The differences in expression are then correlated with the presence or absence of an abnormal expression pattern. A variety of different methods for determining the nucleic acid abundance in a sample are known to

those of skill in the art, where particular methods of interest include those described in: Pietu *et al. Genome Res.* (1996) 6:492; Zhao *et al., Gene* (1995) *156*:207; Soares , *Curr. Opin. Biotechnol.* (1977) *8*: 542; Raval, *J. Pharmacol Toxicol Methods* (1994) *32*:125; Chalifour *et al., Anal. Biochem* (1994) *216*:299; Stolz *et al., Mol. Biotechnol.* (1996) *6*:225; Hong *et al., Biosci. Reports* (1982) *2*:907; and McGraw, *Anal. Biochem.* (1984) *143*:298. Also of interest are the methods disclosed in WO 97/27317, the disclosure of which is herein incorporated by reference.

In general, diagnostic assays of the invention involve detection of a gene product of a the polynucleotide sequence (*e.g.*, mRNA or polypeptide) that corresponds to a sequence of "SEQ ID NOS:1-5252." The patient from whom the sample is obtained can be apparently healthy, susceptible to disease (*e.g.*, as determined by family history or exposure to certain environmental factors), or can already be identified as having a condition in which altered expression of a gene product of the invention is implicated.

In the assays of the invention, the diagnosis can be determined based on detected gene product expression levels of a gene product encoded by at least one, preferably at least two or more, at least 3 or more, or at least 4 or more of the polynucleotides having a sequence set forth in "SEQ ID NOS:1-5252," and can involve detection of expression of genes corresponding to all of "SEQ ID NOS:1-5252" and/or additional sequences that can serve as additional diagnostic markers and/or reference sequences. Where the diagnostic method is designed to detect the presence or susceptibility of a patient to cancer, the assay preferably involves detection of a gene product encoded by a gene corresponding to a polynucleotide that is differentially expressed in cancer. For example, a higher level of expression of a polynucleotide corresponding to SEQ ID NO:2024 relative to a level associated with a normal sample can indicate the presence of cancer in the patient from whom the sample is derived. In another example, detection of a lower level of a polynucleotide corresponding to SEQ ID NO:590 relative to a normal level is indicative of the presence of cancer in the patient. Further examples of such differentially expressed polynucleotides are described in the Examples below. Given the provided polynucleotides and information regarding their relative expression levels provided herein, assays using such polynucleotides and detection of their expression levels in diagnosis and prognosis will be readily apparent to the ordinarily skilled artisan.

Any of a variety of detectable labels can be used in connection with the various embodiments of the diagnostic methods of the invention. Suitable detectable 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, 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, ^{3}H, *etc.*), and the like. The detectable label can involve a two stage systems (*e.g.*, biotin-avidin, hapten-anti-hapten antibody, *etc.*)

Reagents specific for the polynucleotides and polypeptides of the invention, such as antibodies and nucleotide probes, can be supplied in a kit for detecting the presence of an expression product in a biological sample. The kit can also contain buffers or labeling components, as well as instructions for using the reagents to detect and quantify expression products in the biological sample. Exemplary embodiments of the diagnostic methods of the invention are described below in more detail.

Polypeptide detection in diagnosis. In one embodiment, the test sample is assayed for the level of a differentially expressed polypeptide. Diagnosis can be accomplished using any of a number of methods to determine the absence or presence or altered amounts of the differentially expressed polypeptide in the test sample. For example, detection can utilize staining of cells or histological sections with labeled antibodies, performed in accordance with conventional methods. Cells can be permeabilized to stain cytoplasmic molecules. In general, antibodies that specifically bind a differentially expressed polypeptide of the invention are added to a sample, and incubated for a period of time sufficient to allow binding to the epitope, usually at least about 10 minutes. The antibody can be detectably labeled for direct detection (*e.g.*, using radioisotopes, enzymes, fluorescers, chemiluminescers, and the like), or can be used in conjunction with a second stage antibody or reagent to detect binding (*e.g.*, biotin with horseradish peroxidase-conjugated avidin, a secondary antibody conjugated to a fluorescent compound, *e.g.* fluorescein, rhodamine, Texas red, *etc.*). The absence or presence of antibody binding can be determined by various methods, including flow cytometry of dissociated cells, microscopy, radiography, scintillation counting, *etc.* Any suitable alternative methods can

of qualitative or quantitative detection of levels or amounts of differentially expressed polypeptide can be used, for example ELISA, western blot, immunoprecipitation, radioimmunoassay, etc.

In general, the detected level of differentially expressed polypeptide in the test sample is compared to a level of the differentially expressed gene product in a reference or control sample, *e.g.*, in a normal cell (negative control) or in a cell having a known disease state (positive control).

mRNA detection. The diagnostic methods of the invention can also or alternatively involve detection of mRNA encoded by a gene corresponding to a differentially expressed polynucleotides of the invention. Any suitable qualitative or quantitative methods known in the art for detecting specific mRNAs can be used. mRNA can be detected by, for example, *in situ* hybridization in tissue sections, by reverse transcriptase-PCR, or in Northern blots containing poly A+ mRNA. One of skill in the art can readily use these methods to determine differences in the size or amount of mRNA transcripts between two samples. For example, the level of mRNA of the invention in a tissue sample suspected of being cancerous or dysplastic is compared with the expression of the mRNA in a reference sample, *e.g.*, a positive or negative control sample (*e.g.*, normal tissue, cancerous tissue, *etc.*).

Any suitable method for detecting and comparing mRNA expression levels in a sample can be used in connection with the diagnostic methods of the invention (see, *e.g.*, U.S. 5,804,382). For example, mRNA expression levels in a sample can be determined by generation of a library of expressed sequence tags (ESTs) from the sample, where the EST library is representative of sequences present in the sample (Adams, et al., (1991) *Science* 252:1651). Enumeration of the relative representation of ESTs within the library can be used to approximate the relative representation of the gene transcript within the starting sample. The results of EST analysis of a test sample can then be compared to EST analysis of a reference sample to determine the relative expression levels of a selected polynucleotide, particularly a polynucleotide corresponding to one or more of the differentially expressed genes described herein.

Alternatively, gene expression in a test sample can be performed using serial analysis of gene expression (SAGE) methodology (Velculescu et al., *Science* (1995)

270:484). In short, SAGE involves the isolation of short unique sequence tags from a specific location within each transcript. The sequence tags are concatenated, cloned, and sequenced. The frequency of particular transcripts within the starting sample is reflected by the number of times the associated sequence tag is encountered with the sequence population.

Gene expression in a test sample can also be analyzed using differential display (DD) methodology. In DD, fragments defined by specific sequence delimiters (*e.g.*, restriction enzyme sites) are used as unique identifiers of genes, coupled with information about fragment length or fragment location within the expressed gene. The relative representation of an expressed gene with a sample can then be estimated based on the relative representation of the fragment associated with that gene within the pool of all possible fragments. Methods and compositions for carrying out DD are well known in the art, see, *e.g.*, U.S. 5,776,683; and U.S. 5,807,680.

Alternatively, gene expression in a sample using hybridization analysis, which is based on the specificity of nucleotide interactions. Oligonucleotides or cDNA can be used to selectively identify or capture DNA or RNA of specific sequence composition, and the amount of RNA or cDNA hybridized to a known capture sequence determined qualitatively or quantitatively, to provide information about the relative representation of a particular message within the pool of cellular messages in a sample. Hybridization analysis can be designed to allow for concurrent screening of the relative expression of hundreds to thousands of genes by using, for example, array-based technologies having high density formats, including filters, microscope slides, or microchips, or solution-based technologies that use spectroscopic analysis (*e.g.*, mass spectrometry). One exemplary use of arrays in the diagnostic methods of the invention is described below in more detail.

Use of a single gene in diagnostic applications. The diagnostic methods of the invention can focus on the expression of a single differentially expressed gene. For example, the diagnostic method can involve detecting a differentially expressed gene, or a polymorphism of such a gene (*e.g.*, a polymorphism in an coding region or control region), that is associated with disease. Disease-associated polymorphisms can include deletion or truncation of the gene, mutations that alter expression level and/or affect activity of the encoded protein, *etc.*

Changes in the promoter or enhancer sequence that affect expression levels of an differentially gene can be compared to expression levels of the normal allele by various methods known in the art. Methods for determining promoter or enhancer strength include quantitation of the expressed natural protein; insertion of the variant control element into a vector with a reporter gene such as β-galactosidase, luciferase, chloramphenicol acetyltransferase, *etc.* that provides for convenient quantitation; and the like.

A number of methods are available for analyzing nucleic acids for the presence of a specific sequence, *e.g.* a disease associated polymorphism. Where large amounts of DNA are available, genomic DNA is used directly. Alternatively, the region of interest is cloned into a suitable vector and grown in sufficient quantity for analysis. Cells that express a differentially expressed gene can be used as a source of mRNA, which can be assayed directly or reverse transcribed into cDNA for analysis. The nucleic acid can be amplified by conventional techniques, such as the polymerase chain reaction (PCR), to provide sufficient amounts for analysis, and a detectable label can be included in the amplification reaction (*e.g.*, using a detectably labeled primer or detectably labeled oligonucleotides) to facilitate detection. The use of the polymerase chain reaction is described in Saiki, *et al.*, *Science* (1985) *239*:487, and a review of techniques can be found in Sambrook, *et al.*, *Molecular Cloning: A Laboratory Manual*, (1989) pp. 14.2. Alternatively, various methods are known in the art that utilize oligonucleotide ligation as a means of detecting polymorphisms, for examples see Riley *et al.*, *Nucl. Acids Res.* (1990) *18*:2887; and Delahunty *et al.*, *Am. J. Hum. Genet.* (1996) *58*:1239.

The sample nucleic acid, *e.g.* amplified or cloned fragment, is analyzed by one of a number of methods known in the art. The nucleic acid can be sequenced by dideoxy or other methods, and the sequence of bases compared to a selected sequence, *e.g.*, to a wild-

type sequence. Hybridization with the polymorphic or variant sequence can also be used to determine its presence in a sample (*e.g.*, by Southern blot, dot blot, *etc.)*. The hybridization pattern of a polymorphic or variant sequence and a control sequence to an array of oligonucleotide probes immobilized on a solid support, as described in US 5,445,934, or in WO 95/35505, can also be used as a means of identifying polymorphic or variant sequences associated with disease. Single strand conformational polymorphism (SSCP) analysis, denaturing gradient gel electrophoresis (DGGE), and heteroduplex analysis in gel matrices are used to detect conformational changes created by DNA sequence variation as alterations in electrophoretic mobility. Alternatively, where a polymorphism creates or destroys a recognition site for a restriction endonuclease, the sample is digested with that endonuclease, and the products size fractionated to determine whether the fragment was digested. Fractionation is performed by gel or capillary electrophoresis, particularly acrylamide or agarose gels.

Screening for mutations in an differentially expressed gene can be based on the functional or antigenic characteristics of the protein. Protein truncation assays are useful in detecting deletions that can affect the biological activity of the protein. Various immunoassays designed to detect polymorphisms in proteins can be used in screening. Where many diverse genetic mutations lead to a particular disease phenotype, functional protein assays have proven to be effective screening tools. The activity of the encoded protein can be determined by comparison with the wild-type protein.

Pattern matching in diagnosis using arrays. In another embodiment, the diagnostic and/or prognostic methods of the invention involve detection of expression of a selected set of genes in a test sample to produce a test expression pattern (TEP). The TEP is compared to a reference expression pattern (REP), which is generated by detection of expression of the selected set of genes in a reference sample (*e.g.*, a positive or negative control sample). The selected set of genes includes at least one of the genes of the invention, which genes correspond to the polynucleotide sequences of "SEQ ID NOS:1-5252." Of particular interest is a selected set of genes that includes gene differentially expressed in the disease for which the test sample is to be screened.

"Reference sequences" or "reference polynucleotides" as used herein in the context of differential gene expression analysis and diagnosis/prognosis refers to a selected set of

polynucleotides, which selected set includes at least one or more of the differentially expressed polynucleotides described herein. A plurality of reference sequences, preferably comprising positive and negative control sequences, can be included as reference sequences. Additional suitable reference sequences are found in Genbank, Unigene, and other nucleotide sequence databases (including, *e.g.*, expressed sequence tag (EST), partial, and full-length sequences).

"Reference array" means an array having reference sequences for use in hybridization with a sample, where the reference sequences include all, at least one of, or any subset of the differentially expressed polynucleotides described herein. Usually such an array will include at least 3 different reference sequences, and can include any one or all of the provided differentially expressed sequences. Arrays of interest can further comprise sequences, including polymorphisms, of other genetic sequences, particularly other sequences of interest for screening for a disease or disorder (*e.g.*, cancer, dysplasia, or other related or unrelated diseases, disorders, or conditions). The oligonucleotide sequence on the array will usually be at least about 12 nt in length, and can be of about the length of the provided sequences, or can extend into the flanking regions to generate fragments of 100 nt to 200 nt in length or more.

A "reference expression pattern" or "REP" as used herein refers to the relative levels of expression of a selected set of genes, particularly of differentially expressed genes, that is associated with a selected cell type, *e.g.*, a normal cell, a cancerous cell, a cell exposed to an environmental stimulus, and the like. A "test expression pattern" or "TEP" refers to relative levels of expression of a selected set of genes, particularly of differentially expressed genes, in a test sample (*e.g.*, a cell of unknown or suspected disease state, from which mRNA is isolated).

"Diagnosis" as used herein generally includes determination of a subject's susceptibility to a disease or disorder, determination as to whether a subject is presently affected by a disease or disorder, as well as to the prognosis of a subject affected by a disease or disorder (*e.g.*, identification of pre-metastatic or metastatic cancerous states, stages of cancer, or responsiveness of cancer to therapy). The present invention particularly encompasses diagnosis of subjects in the context of breast cancer (*e.g.*, carcinoma in situ (*e.g.*, ductal carcinoma in situ), estrogen receptor (ER)-positive breast

cancer, ER-negative breast cancer, or other forms and/or stages of breast cancer), lung cancer (*e.g.*, small cell carcinoma, non-small cell carcinoma, mesothelioma, and other forms and/or stages of lung cancer), and colon cancer (*e.g.*, adenomatous polyp, colorectal carcinoma, and other forms and/or stages of colon cancer).

"Sample" or "biological sample" as used throughout here are generally meant to refer to samples of biological fluids or tissues, particularly samples obtained from tissues, especially from cells of the type associated with the disease for which the diagnostic application is designed (*e.g.*, ductal adenocarcinoma), and the like. "Samples" is also meant to encompass derivatives and fractions of such samples (*e.g.*, cell lysates). Where the sample is solid tissue, the cells of the tissue can be dissociated or tissue sections can be analyzed.

REPs can be generated in a variety of ways according to methods well known in the art. For example, REPs can be generated by hybridizing a control sample to an array having a selected set of polynucleotides (particularly a selected set of differentially expressed polynucleotides), acquiring the hybridization data from the array, and storing the data in a format that allows for ready comparison of the REP with a TEP. Alternatively, all expressed sequences in a control sample can be isolated and sequenced, *e.g.*, by isolating mRNA from a control sample, converting the mRNA into cDNA, and sequencing the cDNA. The resulting sequence information roughly or precisely reflects the identity and relative number of expressed sequences in the sample. The sequence information can then be stored in a format (*e.g.*, a computer-readable format) that allows for ready comparison of the REP with a TEP. The REP can be normalized prior to or after data storage, and/or can be processed to selectively remove sequences of expressed genes that are of less interest or that might complicate analysis (*e.g.*, some or all of the sequences associated with housekeeping genes can be eliminated from REP data).

TEPs can be generated in a manner similar to REPs, *e.g.*, by hybridizing a test sample to an array having a selected set of polynucleotides, particularly a selected set of differentially expressed polynucleotides, acquiring the hybridization data from the array, and storing the data in a format that allows for ready comparison of the TEP with a REP. The REP and TEP to be used in a comparison can be generated simultaneously, or the TEP can be compared to previously generated and stored REPs.

In one embodiment of the invention, comparison of a TEP with a REP involves hybridizing a test sample with a reference array, where the reference array has one or more reference sequences for use in hybridization with a sample. The reference sequences include all, at least one of, or any subset of the differentially expressed polynucleotides described herein. Hybridization data for the test sample is acquired, the data normalized, and the produced TEP compared with a REP generated using an array having the same or similar selected set of differentially expressed polynucleotides. Probes that correspond to sequences differentially expressed between the two samples will show decreased or increased hybridization efficiency for one of the samples relative to the other.

Reference arrays can be produced according to any suitable methods known in the art. For example, methods of producing large arrays of oligonucleotides are described in U.S. 5,134,854, and U.S. 5,445,934 using light-directed synthesis techniques. Using a computer controlled system, a heterogeneous array of monomers is converted, through simultaneous coupling at a number of reaction sites, into a heterogeneous array of polymers. Alternatively, microarrays are generated by deposition of pre-synthesized oligonucleotides onto a solid substrate, for example as described in PCT published application no. WO 95/35505.

Methods for collection of data from hybridization of samples with a reference arrays are also well known in the art. For example, the polynucleotides of the reference and test samples can be generated using a detectable fluorescent label, and hybridization of the polynucleotides in the samples detected by scanning the microarrays for the presence of the detectable label. Methods and devices for detecting fluorescently marked targets on devices are known in the art. Generally, such detection devices include a microscope and light source for directing light at a substrate. A photon counter detects fluorescence from the substrate, while an x-y translation stage varies the location of the substrate. A confocal detection device that can be used in the subject methods is described in U.S. Patent no. 5,631,734. A scanning laser microscope is described in Shalon et al., *Genome Res.* (1996) *6*:639. A scan, using the appropriate excitation line, is performed for each fluorophore used. The digital images generated from the scan are then combined for subsequent analysis. For any particular array element, the ratio of the fluorescent signal from one

sample (*e.g.*, a test sample) is compared to the fluorescent signal from another sample (*e.g.*, a reference sample), and the relative signal intensity determined.

Methods for analyzing the data collected from hybridization to arrays are well known in the art. For example, where detection of hybridization involves a fluorescent label, data analysis can include the steps of determining fluorescent intensity as a function of substrate position from the data collected, removing outliers, *i.e.* data deviating from a predetermined statistical distribution, and calculating the relative binding affinity of the targets from the remaining data. The resulting data can be displayed as an image with the intensity in each region varying according to the binding affinity between targets and probes.

In general, the test sample is classified as having a gene expression profile corresponding to that associated with a disease or non-disease state by comparing the TEP generated from the test sample to one or more REPs generated from reference samples (*e.g.*, from samples associated with cancer or specific stages of cancer, dysplasia, samples affected by a disease other than cancer, normal samples, *etc.*). The criteria for a match or a substantial match between a TEP and a REP include expression of the same or substantially the same set of reference genes, as well as expression of these reference genes at substantially the same levels (*e.g.*, no significant difference between the samples for a signal associated with a selected reference sequence after normalization of the samples, or at least no greater than about 25% to about 40% difference in signal strength for a given reference sequence. In general, a pattern match between a TEP and a REP includes a match in expression, preferably a match in qualitative or quantitative expression level, of at least one of, all or any subset of the differentially expressed genes of the invention.

Pattern matching can be performed manually, or can be performed using a computer program. Methods for preparation of substrate matrices (*e.g.*, arrays), design of oligonucleotides for use with such matrices, labeling of probes, hybridization conditions, scanning of hybridized matrices, and analysis of patterns generated, including comparison analysis, are described in, for example, U.S. 5,800,992.

F. Use of the Polynucleotides of the Invention in Cancer

Oncogenesis involves the unbridled growth, dedifferentiation and abnormal migration of cells. Cancerous cells can have the ability to compress, invade, and destroy

normal tissue. Cancerous cells may also metastasize to other parts of the body via the bloodstream or the lymph system and colonize in these other areas. Different cancers are classified by the cell from which the cancerous cell is derived and from its cellular morphology and/or state of differentiation.

Somatic genetic abnormalities cause cancer initiation and progression. Cancer generally is clonally formed, *i.e.* gain of function of oncogenes and loss of function of tumor suppressor genes within a single cell transform the cell to be cancerous, and that single cell grows and divides to form a cancerous lesion. The genes known to be involved in cancer initiation and progression are involved in numerous cellular functions, including developmental differentiation, cell cycle regulation, cell signaling, immunological response, DNA replication, and DNA repair.

The identification and characterization of genetic or biochemical markers in blood or tissues that will detect the earliest changes along the carcinogenesis pathway and monitor the efficacy of various therapies and preventive interventions is a major goal of cancer research. Scientists have identified genetic changes in stool specimens that indicate the stages of colon cancer, and other biomarkers such as gene mutations, hormone receptors, proteins that inhibit metastasis, and enzymes that metabolize drugs are all being used to determine the severity and predict the course of breast, prostate, lung, and other cancers.

Recent advances in the pathogenesis of certain cancers has been helpful in determining patient treatment. The level of expression of certain polynucleotides can be indicative of a poorer prognosis, and therefore warrant more aggressive chemo- or radio-therapy for a patient. The correlation of novel surrogate tumor specific features with response to treatment and outcome in patients has defined certain prognostic indicators that allow the design of tailored therapy based on the molecular profile of the tumor. These therapies include antibody targeting and gene therapy. Moreover, a promising level of one or more marker polynucleotides can provide impetus for not aggressively treating a particular patient, thus sparing the patient the deleterious side effects of aggressive therapy. Determining expression of certain polynucleotides and comparison of a patients profile with known expression in normal tissue and variants of the disease allows

a determination of the best possible treatment for a patient, both in terms of specificity of treatment and in terms of comfort level of the patient.

Surrogate tumor markers, such as polynucleotide expression, can also be used to better classify, and thus diagnose and treat, different forms and disease states of cancer. Two classifications widely used in oncology that can benefit from identification of the expression levels of the polynucleotides of the invention are staging of the cancerous disorder, and grading the nature of the cancerous tissue.

Staging. Staging is a process used by physicians to describe how advanced the cancerous state is in a patient. Staging assists the physician in determining a prognosis, planning treatment and evaluating the results of such treatment. Different staging systems are used for different types of cancer, but each generally involves the following determinations: the type of tumor, indicated by T; whether the cancer has metastasized to nearby lymph nodes, indicated by N; and whether the cancer has metastasized to more distant parts of the body, indicated by M. This system of staging is called the TNM system. Generally, if a cancer is only detectable in the area of the primary lesion without having spread to any lymph nodes it is called Stage I. If it has spread only to the closest lymph nodes, it is called Stage II. In Stage III, the cancer has generally spread to the lymph nodes in near proximity to the site of the primary lesion. Cancers that have spread to a distant part of the body, such as the liver, bone, brain or another site, are called Stage IV, the most advanced stage.

Currently, the determination of staging is done using pathological techniques and is based more on the presence or absence of malignant tissue rather than the characteristics of the tumor type. Presence or absence of malignant tissue is based primarily on the gross morphology of the cells in the areas biopsied. The polynucleotides of the invention can facilitate fine-tuning of the staging process by identifying markers for the aggresivity of a cancer, *e.g.* the metastatic potential, as well as the presence in different areas of the body. Thus, a Stage II cancer with a polynucleotide signifying a high metastatic potential cancer can be used to change a borderline Stage II tumor to a Stage III tumor, justifying more aggressive therapy. Conversely, the presence of a polynucleotide signifying a lower metastatic potential allows more conservative staging of a tumor.

Grading of cancers. Grade is a term used to describe how closely a tumor resembles normal tissue of its same type. Based on the microscopic appearance of a tumor, pathologists will identify the grade of a tumor based on parameters such as cell morphology, cellular organization, and other markers of differentiation. As a general rule, the grade of a tumor corresponds to its rate of growth or aggressiveness. That is, undifferentiated or high-grade tumors grow more quickly than well differentiated or low-grade tumors. Information about tumor grade is useful in planning treatment and predicting prognosis.

The American Joint Commission on Cancer has recommended the following guidelines for grading tumors: 1) GX Grade cannot be assessed; 2) G1 Well differentiated; G2 Moderately well differentiated; 3) G3 Poorly differentiated; 4) G4 Undifferentiated. Although grading is used by pathologists to describe most cancers, it plays a more important role in treatment planning for certain types than for others. An example is the Gleason system that is specific for prostate cancer, which uses grade numbers to describe the degree of differentiation. Lower Gleason scores indicate well-differentiated cells. Intermediate scores denote tumors with moderately differentiated cells. Higher scores describe poorly differentiated cells. Grade is also important in some types of brain tumors and soft tissue sarcomas.

The polynucleotides of the invention can be especially valuable in determining the grade of the tumor, as they not only can aid in determining the differentiation status of the cells of a tumor, they can also identify factors other than differentiation that are valuable in determining the aggressivity of a tumor, such as metastatic potential.

Familial Cancer Genes. A number of cancer syndromes are linked to Mendelian inheritance of a predisposition to develop particular cancers. The following table contains a list of cancer types that can be inherited, and for which the gene or genes responsible have been identified. Most of the cancer types listed can occur as part of several different genetic conditions, each caused by alterations in a different gene.

Cancer Type	Genetic Condition	Gene
Brain	Li-Fraumeni syndrome	TP53
Brain	Neurofibromatosis 1	NF1
	Neurofibromatosis 2	NF2
	von Hippel-Lindau syndrome	VHL

Cancer Type	Genetic Condition	Gene
	Tuberous sclerosis 2	TSC2
Breast	Hereditary breast/ovarian cancer 1	BRCA1
	Hereditary breast/ovarian cancer 2	BRCA2
	Li-Fraumeni syndrome	TP53
	Ataxia telangiectasia	ATM
Colon	Familial adenomatous polyposis (FAP)	APC
	Hereditary non-polyposis colon cancer (HNPCC) 1	HMSH2
	Hereditary non-polyposis colon cancer (HNPCC) 2	hMLH1
	Hereditary non-polyposis colon cancer (HNPCC) 3	hPMS1
	Hereditary non-polyposis colon cancer (HNPCC) 4	hPMS2
Endocrine (parathyroid, pituitary, GI endocrine)	Multiple endocrine neoplasia 1 (MEN1)	MEN1
Endocrine (pheochromacytoma, medullary thyroid)	Multiple endocrine neoplasia 2 (MEN2)	RET
Endometrial	Hereditary non-polyposis colon cancer (HNPCC) 1	hMSH2
	Hereditary non-polyposis colon cancer (HNPCC) 2	hMLH1
	Hereditary non-polyposis colon cancer (HNPCC) 3	hPMS1
	Hereditary non-polyposis colon cancer (HNPCC) 4	hPMS2
Eye	Hereditary retinoblastoma	RB1
Hematologic (lymphomas and leukemia)	Li-Fraumeni syndrome	TP53
	Ataxia telangiectasia	ATM
Kidney	Hereditary Wilms' tumor	WT1
	von Hippel-Lindau syndrome	VHL
	Tuberous sclerosis 2	TSC2
Ovary	Hereditary breast/ovarian cancer 1	BRCA1
	Hereditary breast/ovarian cancer 2	BRCA2
Sarcoma	Hereditary retinoblastoma	RB1
	Li-Fraumeni syndrome	TP53
	Neurofibromatosis 1	NF1
Skin	Hereditary melanoma 1	CDKN2
	Hereditary melanoma 2	CDK4
	Basal cell naevus (Gorlin) syndrome	PTCH
Stomach	Hereditary non-polyposis colon cancer (HNPCC) 1	hMSH2
	Hereditary non-polyposis colon cancer (HNPCC) 2	hMLH1
	Hereditary non-polyposis colon cancer (HNPCC) 3	hPMS1
	Hereditary non-polyposis colon cancer (HNPCC) 4	hPMS2

The polynucleotides of the invention can be especially useful to monitor patients having any of the above syndromes to detect potentially malignant events at a molecular level before they are detectable at a gross morphological level. As can be seen from the table, a number of genes are involved in multiple forms of cancer. Thus, a polynucleotide of the invention identified as important for metastatic colon cancer can also have clinical implications for a patient diagnosed with stomach cancer or endometrial cancer.

Lung Cancer. Lung cancer is one of the most common cancers in the United States, accounting for about 15 percent of all cancer cases, or 170,000 new cases each year. At this time, over half of the lung cancer cases in the United States are in men, but the number found in women is increasing and will soon equal that in men. Today more women die of lung cancer than of breast cancer. Lung cancer is especially difficult to diagnose and treat because of the large size of the lungs, which allows cancer to develop for years undetected. In fact, lung cancer can spread outside the lungs without causing any symptoms. Adding to the confusion, the most common symptom of lung cancer, a persistent cough, can often be mistaken for a cold or bronchitis.

Although there are more than a dozen different kinds of lung cancer, the two main types of lung cancer are small cell and nonsmall cell, which encompass about 90% of all lung cancer cases. Small cell carcinoma (also called oat cell carcinoma), which usually starts in one of the larger bronchial tubes, grows fairly rapidly, and is likely to be large by the time of diagnosis. Nonsmall cell lung cancer (NSCLC) is made up of three general subtypes of lung cancer. Epidermoid carcinoma (also called squamous cell carcinoma) usually starts in one of the larger bronchial tubes and grows relatively slowly. The size of these tumors can range from very small to quite large. Adenocarcinoma starts growing near the outside surface of the lung and can vary in both size and growth rate. Some slowly growing adenocarcinomas are described as alveolar cell cancer. Large cell carcinoma starts near the surface of the lung, grows rapidly, and the growth is usually fairly large when diagnosed. Other less common forms of lung cancer are carcinoid, cylindroma, mucoepidermoid, and malignant mesothelioma.

Currently, CT scans, MRIs, X-rays, sputum cytology, and biopsies are used to diagnose nonsmall cell lung cancer. The form and cellular origin of the lung cancer is diagnosed primarily through biopsy from either a surgical biopsy or a needle aspiration of lung tissue, and usually the biopsy is prompted from an abnormality identified on an X-ray. In some cases, sputum cytology can reveal lung cancers in patients with normal X-rays or can determine the type of lung cancer, but because it cannot pinpoint the tumor's location, a positive sputum cytology test is usually followed by further tests. Since these tests are based in large part on gross morphology of the tissue, the diagnosis of a particular kind of tumor is largely subjective, and the diagnosis can vary significantly between clinicians.

The polynucleotides of the invention can be used to distinguish types of lung cancer as well as identifying traits specific to a certain patient's cancer. For example, if the patient's biopsy expresses a polynucleotide that is associated with a low metastatic potential, it may justify leaving a larger portion of the patient's lung in surgery to remove the lesion. Alternatively, a smaller lesion with expression of a polynucleotide that is associated with high metastatic potential may justify a more radical removal of lung tissue and/or the surrounding lymph nodes, even if no metastasis can be identified through pathological examination.

Similarly, the expression of polynucleotides of the invention can be used in the diagnosis, prognosis and management of colorectal cancer. The differential expression of a polynucleotide in hyperplasia can be used as a diagnostic marker for metastatic lung cancer. The polynucleotides of the invention that would be especially useful for this purpose are those that exhibit differential expression between high metastatic versus low metastatic lung cancer , *i.e.* SEQ ID NOS: 174, 254, 466, 571, 574, 590, 922, 1355, 1422, 2007, 2038, 2245, 10, 54, 65, 171, 203, 252, 253, 285, 419, 420, 491, 525, 526, 552, 693, 700, 726, 742, 746, 861, 990, 1088, 1288, 1417, 1444, 1454, 1570, 1597, 1979, 2024, 2034, and 2126. Detection of malignant lung cancer with a higher metastatic potential can be determined using expression levels of any of these sequences alone or in combination with the levels of expression of other known genes.

Breast Cancer. The National Cancer Institute (NCI) estimates that about 1 in 8 women in the United States will develop breast cancer during her lifetime. Clinical breast examination and mammography are recommended as combined modalities for breast cancer screening, and the nature of the cancer will often depend upon the location of the tumor and the cell type from which the tumor is derived. The majority of breast cancers are adenocarcinomas subtypes, which can be summarized as follows:

Ductal carcinoma in situ (DCIS): Ductal carcinoma in situ is the most common type of noninvasive breast cancer. In DCIS, the malignant cells have not metastasized through the walls of the ducts into the fatty tissue of the breast. Comedocarcinoma is a type of DCIS that is more likely than other types of DCIS to come back in the same area after lumpectomy. It is more closely linked to eventual development of invasive ductal carcinoma than other forms of DCIS.

Infiltrating (or invasive) ductal carcinoma (IDC): this type of cancer has metastasized through the wall of the duct and invaded the fatty tissue of the breast. At this point, it has the potential to use the lymphatic system and bloodstream for metastasis to more distant parts of the body. Infiltrating ductal carcinoma accounts for about 80% of breast cancers.

Lobular carcinoma in situ (LCIS): While not a true cancer, LCIS (also called lobular neoplasia) is sometimes classified as a type of noninvasive breast cancer. It does not penetrate through the wall of the lobules. Although it does not itself usually become an invasive cancer, women with this condition have a higher risk of developing an invasive breast cancer in the same breast, or in the opposite breast.

Infiltrating (or invasive) lobular carcinoma (ILC): ILC is similar to IDC, in that it has the potential metastasize elsewhere in the body. About 10% to 15% of invasive breast cancers are invasive lobular carcinomas. ILC can be more difficult to detect by mammogram than IDC.

Inflammatory breast cancer: This rare type of invasive breast cancer accounts for about 1% of all breast cancers and is extremely aggressive. Multiple skin symptoms associated with this cancer are caused by cancer cells blocking lymph vessels or channels in the skin over the breast.

Medullary carcinoma: This special type of infiltrating breast cancer has a relatively well defined, distinct boundary between tumor tissue and normal tissue. It accounts for about 5% of breast cancers. The prognosis for this kind of breast cancer is better than for other types of invasive breast cancer.

Mucinous carcinoma: This rare type of invasive breast cancer originates from mucus-producing cells. The prognosis for mucinous carcinoma is better than for the more common types of invasive breast cancer.

Paget's disease of the nipple: This type of breast cancer starts in the ducts and spreads to the skin of the nipple and the areola. It is a rare type of breast cancer, occurring in only 1% of all cases. Paget's disease can be associated with in situ carcinoma, or with infiltrating breast carcinoma. If no lump can be felt in the breast tissue, and the biopsy shows DCIS but no invasive cancer, the prognosis is excellent.

Phyllodes tumor: This very rare type of breast tumor forms from the stroma of the breast, in contrast to carcinomas which develop in the ducts or lobules. Phyllodes (also spelled phylloides) tumors are usually benign, but are malignant on rare occasions. Nevertheless, malignant phyllodes tumors are very rare and less than 10 women per year in the US die of this disease. Benign phyllodes tumors are successfully treated by removing the mass and a narrow margin of normal breast tissue.

Tubular carcinoma: Accounting for about 2% of all breast cancers, tubular carcinomas are a special type of infiltrating breast carcinoma. They have a better prognosis than usual infiltrating ductal or lobularcarcinomas.

High-quality mammography combined with clinical breast exam remains the only screening method clearly tied to reduction in breast cancer mortality. Lower dose x-rays, digitized computer rather than film images, and the use of computer programs to assist diagnosis, are almost ready for widespread dissemination. Other technologies also are being developed, including magnetic resonance imaging and ultrasound. In addition, a very low radiation exposure technique, positron emission tomography has the potential for detecting early breast cancer.

It is also possible to differentiate between non-cancerous breast tissue and malignant breast tissue by analyzing differential gene expression between tissues. In addition, there may be several possible alterations that lead to the various possible types of breast cancer. The different types of breast tumors (*e.g.*, invasive vs. non-invasive, ductal vs. axillary lymph node) can be differentiable from one another by the identification of the differences in genes expressed by different types of breast tumor tissues (Porter-Jordan *et al.*, *Hematol Oncol Clin North Am* (1994) *8:*73). Breast cancer can thus be generally diagnosed by detection of expression of a gene or genes associated with breast tumors. Where enough information is available about the differential gene expression between various types of breast tumor tissues, the specific type of breast tumor can also be diagnosed.

For example, increased estrogen receptor (ER) expression in normal breast epithileum, while not itself indicative of malignant tissue, is a known risk marker for development of breast cancer. Khan SA *et al.*, *Cancer Res* (1994) *54:*993. Malignant breast cancer is often divided into two groups, ER-positive and ER-negative, based on the

estrogen receptor status of the tissue. The ER status represents different survival length and response to hormone therapy, and is thought to represent either: 1) an indicator of different stages of the disease, or 2) an indicator that allows differentiation between two similar but distinct diseases. K. Zhu *et al.*, *Med. Hypoth.* (1997) *49*:69. A number of other genes are known to vary expression between either different stages of cancer or different types of similar breast cancer.

Similarly, the expression of polynucleotides of the invention can be used in the diagnosis and management of breast cancer. The differential expression of a polynucleotide in human breast tumor tissue can be used as a diagnostic marker for human breast cancer. The polynucleotides of the invention that would be especially useful for this purpose are those that exhibit differential expression between breast cancer tissue with a high metastatic potential and a low metastatic potential, *i.e.* SEQ ID NOS:15, 36, 44, 89, 172, 203, 261, 419, 420, 503, 552, 564, 570, 590, 693, 707, 711, 726, 746, 756, 990, 1122, 1142, 1286, 1289, 1435, 1860, 1933, 1934, 1979, 1980, 2007, 2023, 2409, 2486, 45, 146, 154, 159, 165, 174, 183, 364, 366, 387, 496, 510, 512, 529, 560, 606, 644, 646, 754, 875, 902, 921, 942, 1095, 1104, 1131, 1170, 1184, 1205, 1354, 1387, 1535, 1751, 1764, 1777, 1795, 1869, 1882, 1890, 1915, 2040, 2059, 2223, 2245, 2300, 2325, 2462, 2488, 2492; Detection of breast cancer can be determined using expression levels of any of these sequences alone or in combination. Determination of the aggressive nature and/or the metastatic potential of a breast cancer can also be determined by comparing levels of one or more polynucleotides of the invention and comparing levels of another sequence known to vary in cancerous tissue, *e.g.* ER expression. In addition, development of breast cancer can be detected by examining the ratio of SEQ ID NO: to the levels of steroid hormones (*e.g.*, testosterone or estrogen) or to other hormones (*e.g.*, growth hormone, insulin). Thus expression of specific marker polynucleotides can be used to discriminate between normal and cancerous breast tissue, to discriminate between breast cancers with different cells of origin, to discriminate between breast cancers with different potential metastatic rates, etc.

Diagnosis of breast cancer can also involve comparing the expression of a polynucleotide of the invention with the expression of other sequences in non-malignant breast tissue samples in comparison to one or more forms of the diseased tissue. A comparison of expression of one or more polynucleotides of the invention between the

samples provides information on relative levels of these polynucleotides as well as the ratio of these polynucleotides to the expression of other sequences in the tissue of interest compared to normal.

This risk of breast cancer is elevated significantly by the presence of an inherited risk for breast cancer, such as a mutation in BRCA-1 or BRCA-2. New diagnostic tools are being developed to address the needs of higher risk patients to complement mammography and physical examinations for early detection of breast cancer, particularly among younger women. The presence of antigen or expression markers in nipple aspirate fluid (NAF) samples collected from one or both breasts can be useful for useful for risk assessment or early cancer detection. Breast cytology and biomarkers obtained by random fine needle aspiration have been used to identify hyperplasia with atypia and overexpression of p53 and EGFR. The polynucleotides of the invention can be used in multivariate analysis with expression studies with genes such as p53 and EGFR as risk predictors and as surrogate endpoint biomarkers for breast cancer.

As well as being used for diagnosis and risk assessment, the expression of certain genes can also correlated to prognosis of a disease state. The expression of particular gene have been used as prognostic indicators for breast cancer including increased expression of *c-erbB-2*, pS2, ER, progesterone receptor, epidermal growth factor receptor (EGFR), *neu*, *myc*, *bcl-2*, *int2*, cytosolic tyrosine kinase, cyclin E, *prad-1*, *hst*, uPA, PAI-1, PAI-2, cathepsin D, as well as the presence of a number of cancer-specific antigens, *e.g.* CEA, CA M26, CA M29 and CA 15.3. Davis, *Br. J. Biomed Sci.* (1996) *53*:157. Poor prognosis has also been linked to a decrease in expression of certain genes, such as *p53, Rb, nm23.* The expression of the polynucleotides of the invention can be of prognostic value for determining the metastatic potential of a malignant breast cancer, as this molecules are differentially expressed between high and low metastatic potential tissues tumors. The levels of these polynucleotides in patients with malignant breast cancer can compared to normal tissue, malignant tissue with a known high potential metastatic level, and malignant tissue with a known lower level of metastatic potential to provide a prognosis for a particular patient. Such a prognosis is predictive of the extent and nature of the cancer. The determined prognosis is useful in determining the prognosis of a patient with breast cancer, both for initial treatment of the disease and for longer-term monitoring of the same

patient. If samples are taken from the same individual over a period of time, differences in polynucleotide expression that are specific to that patient can be identified and closely watched.

Colon Cancer. Colorectal cancer is one of the most common neoplasms in humans and perhaps the most frequent form of hereditary neoplasia. Prevention and early detection are key factors in controlling and curing colorectal cancer. Indeed, colorectal cancer is the second most preventable cancer, after lung cancer. Colorectal cancer begins as polyps, which are small, benign growths of cells that form on the inner lining of the colon. Over a period of several years, some of these polyps accumulate additional mutations and become cancerous. About 20 percent of all cases of colon cancer are thought to be related to heredity. Currently, multiple familial colorectal cancer disorders have been identified, which are summarized as follows:

Familial adenomatous polyposis (FAP): This condition results in a person having hundreds or even thousands of polyps in the colon and rectum that usually first appear during the teenage years. Cancer nearly always develops in one or more of these polyps between the ages of 30 and 50.

Gardner's syndrome: Like FAP, Gardner's syndrome results in polyps and colorectal cancers that develop at a young age. It can also cause benign tumors of the skin, soft connective tissue and bones.

Hereditary nonpolyposis colon cancer (HNPCC): People with this condition tend to develop colorectal cancer at a young age, without first having many polyps. HNPCC has an autosomal dominant pattern of inheritance with variable but high penetrance estimated to be about 90%. HNPCC underlies 0.5%-10% of all cases of colorectal cancer. An understanding of the mechanisms behind the development of HNPCC is emerging, and genetic presymptomatic testing, now being conducted in research settings, soon will be available on a widespread basis for individuals identified at risk for this disease.

Familial colorectal cancer in Ashkenazi Jews: Recent research has found an inherited tendency to developing colorectal cancer among some Jews of Eastern European descent. Like people with FAP, Gardner's syndrome, and HNPCC, their increased risk is due to an inherited mutation present in about 6% of American Jews.

Several tests are currently used to screen for colorectal cancer, including digital rectal examination, fecal occult blood test, sigmoidoscopy, colonoscopy, virtual colonoscopy and MRI. Each of these tests identifies potential colorectal cancer lesions, or a risk of development of these lesions, at a fairly gross morphological level.

The sequential alteration of a number of genes is associated with malignant adenocarcinoma, including the genes DCC, p53, ras, and FAP. For a review, see *e.g.* Fearon ER, *et al.*, *Cell* (1990) *61(5)*:759; Hamilton SR *et al.*, *Cancer* (1993) *72*:957; Bodmer W, *et al.*, *Nat Genet.* (1994) *4(3)*:217; Fearon ER, *Ann N Y Acad Sci.* (1995) *768*:101. Molecular genetic alterations are thus promising as potential diagnostic and prognostic indicators in colorectal carcinoma and molecular genetics of colorectal carcinoma since it is possible to differentiate between different types of colorectal neoplasias using molecular markers. Colorectal cancer can thus be generally diagnosed by detection of expression of a gene or genes associated with colorectal tumors.

Similarly, the expression of polynucleotides of the invention can be used in the diagnosis, prognosis and management of colorectal cancer. The differential expression of a polynucleotide in hyperplasia can be used as a diagnostic marker for colon cancer. The polynucleotides of the invention that would be especially useful for this purpose are those that exhibit differential expression between malignant metastatic colon cancer and normal patient tissue , *i.e.* SEQ ID NOS:228, 280, 355, 491, 603, 680, 752, 753, 1241, 1264, 1401, 1442, 1514, 1851, 1915, 2024, 2066, 33, 250, 282, 370, 387, 443, 460, 545, 560, 703, 704, 1095, 1104, 1205, 1354, 1387, 1734, 1742, 1954, 2262, 2325, 1899, 252, 253, 491, 581, 693, 726, 746, 1780, 1899, 65, 252, 253, 581, 693, 716, 726, 746, 1780, 1899, and 1780. Detection of malignant colon cancer can be determined using expression levels of any of these sequences alone or in combination with the levels of expression.

Determination of the aggressive nature and/or the metastatic potential of a colon cancer can also be determined by comparing levels of one or more polynucleotides of the invention and comparing total levels of another sequence known to vary in cancerous tissue, *e.g.* p53 expression. In addition, development of colon cancer can be detected by examining the ratio of any of the polynucleotides of the invention to the levels of oncogenes (*e.g.* ras) or tumor suppressor genes (*e.g.* FAP or p53). Thus expression of specific marker polynucleotides can be used to discriminate between normal and cancerous

breast tissue, to discriminate between breast cancers with different cells of origin, to discriminate between breast cancers with different potential metastatic rates, etc.

G. Use of Polynucleotides to Screen for Peptide Analogs and Antagonists

Polypeptides encoded by the instant polynucleotides and corresponding full length genes can be used to screen peptide libraries to identify binding partners, such as receptors, from among the encoded polypeptides.

A library of peptides can be synthesized following the methods disclosed in U.S. Pat. No. 5,010,175 ('175), and in WO 91/17823. As described below in brief, one prepares a mixture of peptides, which is then screened to identify the peptides exhibiting the desired signal transduction and receptor binding activity. In the '175 method, a suitable peptide synthesis support (*e.g.*, a resin) is coupled to a mixture of appropriately protected, activated amino acids. The concentration of each amino acid in the reaction mixture is balanced or adjusted in inverse proportion to its coupling reaction rate so that the product is an equimolar mixture of amino acids coupled to the starting resin. The bound amino acids are then deprotected, and reacted with another balanced amino acid mixture to form an equimolar mixture of all possible dipeptides. This process is repeated until a mixture of peptides of the desired length (*e.g.*, hexamers) is formed. Note that one need not include all amino acids in each step: one can include only one or two amino acids in some steps (*e.g.*, where it is known that a particular amino acid is essential in a given position), thus reducing the complexity of the mixture. After the synthesis of the peptide library is completed, the mixture of peptides is screened for binding to the selected polypeptide. The peptides are then tested for their ability to inhibit or enhance activity. Peptides exhibiting the desired activity are then isolated and sequenced.

The method described in WO 91/17823 is similar. However, instead of reacting the synthesis resin with a mixture of activated amino acids, the resin is divided into twenty equal portions (or into a number of portions corresponding to the number of different amino acids to be added in that step), and each amino acid is coupled individually to its portion of resin. The resin portions are then combined, mixed, and again divided into a number of equal portions for reaction with the second amino acid. In this manner, each reaction can be easily driven to completion. Additionally, one can maintain separate "subpools" by treating portions in parallel, rather than combining all resins at each step.

This simplifies the process of determining which peptides are responsible for any observed receptor binding or signal transduction activity.

In such cases, the subpools containing, *e.g.*, 1-2,000 candidates each are exposed to one or more polypeptides of the invention. Each subpool that produces a positive result is then resynthesized as a group of smaller subpools (sub-subpools) containing, *e.g.*, 20-100 candidates, and reassayed. Positive sub-subpools can be resynthesized as individual compounds, and assayed finally to determine the peptides that exhibit a high binding constant. These peptides can be tested for their ability to inhibit or enhance the native activity. The methods described in WO 91/7823 and U.S. Patent No. 5,194,392 (herein incorporated by reference) enable the preparation of such pools and subpools by automated techniques in parallel, such that all synthesis and resynthesis can be performed in a matter of days.

Peptide agonists or antagonists are screened using any available method, such as signal transduction, antibody binding, receptor binding, mitogenic assays, chemotaxis assays, etc. The methods described herein are presently preferred. The assay conditions ideally should resemble the conditions under which the native activity is exhibited *in vivo*, that is, under physiologic pH, temperature, and ionic strength. Suitable agonists or antagonists will exhibit strong inhibition or enhancement of the native activity at concentrations that do not cause toxic side effects in the subject. Agonists or antagonists that compete for binding to the native polypeptide can require concentrations equal to or greater than the native concentration, while inhibitors capable of binding irreversibly to the polypeptide can be added in concentrations on the order of the native concentration.

The end results of such screening and experimentation will be at least one novel polypeptide binding partner, such as a receptor, encoded by a gene or a cDNA corresponding to a polynucleotide of the invention, and at least one peptide agonist or antagonist of the novel binding partner. Such agonists and antagonists can be used to modulate, enhance, or inhibit receptor function in cells to which the receptor is native, or in cells that possess the receptor as a result of genetic engineering. Further, if the novel receptor shares biologically important characteristics with a known receptor, information about agonist/antagonist binding can facilitate development of improved agonists/antagonists of the known receptor.

H. Pharmaceutical Compositions and Therapeutic Uses

Pharmaceutical compositions can comprise polypeptides, antibodies, or polynucleotides of the claimed invention. The pharmaceutical compositions will comprise a therapeutically effective amount of either polypeptides, antibodies, or polynucleotides of the claimed invention.

The term "therapeutically effective amount" as used herein refers to an amount of a therapeutic agent to treat, ameliorate, or prevent a desired disease or condition, or to exhibit a detectable therapeutic or preventative effect. The effect can be detected by, for example, chemical markers or antigen levels. Therapeutic effects also include reduction in physical symptoms, such as decreased body temperature. The precise effective amount for a subject will depend upon the subject's size and health, the nature and extent of the condition, and the therapeutics or combination of therapeutics selected for administration. Thus, it is not useful to specify an exact effective amount in advance. However, the effective amount for a given situation is determined by routine experimentation and is within the judgment of the clinician. For purposes of the present invention, an effective dose will generally be from about 0.01 mg/ kg to 50 mg/kg or 0.05 mg/kg to about 10 mg/kg of the DNA constructs in the individual to which it is administered.

A pharmaceutical composition can also contain a pharmaceutically acceptable carrier. The term "pharmaceutically acceptable carrier" refers to a carrier for administration of a therapeutic agent, such as antibodies or a polypeptide, genes, and other therapeutic agents. The term refers to any pharmaceutical carrier that does not itself induce the production of antibodies harmful to the individual receiving the composition, and which can be administered without undue toxicity. Suitable carriers can be large, slowly metabolized macromolecules such as proteins, polysaccharides, polylactic acids, polyglycolic acids, polymeric amino acids, amino acid copolymers, and inactive virus particles. Such carriers are well known to those of ordinary skill in the art.

Pharmaceutically acceptable salts can be used therein, for example, mineral acid salts such as hydrochlorides, hydrobromides, phosphates, sulfates, and the like; and the salts of organic acids such as acetates, propionates, malonates, benzoates, and the like. A thorough discussion of pharmaceutically acceptable excipients is available in *Remington's Pharmaceutical Sciences* (Mack Pub. Co., N.J. 1991).

Pharmaceutically acceptable carriers in therapeutic compositions can include liquids such as water, saline, glycerol and ethanol. Auxiliary substances, such as wetting or emulsifying agents, pH buffering substances, and the like, can also be present in such vehicles. Typically, the therapeutic compositions are prepared as injectables, either as liquid solutions or suspensions; solid forms suitable for solution in, or suspension in, liquid vehicles prior to injection can also be prepared. Liposomes are included within the definition of a pharmaceutically acceptable carrier.

Delivery Methods. Once formulated, the compositions of the invention can be (1) administered directly to the subject (*e.g.*, as polynucleotide or polypeptides); (2) delivered ex vivo, to cells derived from the subject (*e.g.*, as in *ex vivo* gene therapy); or (3) delivered *in vitro* for expression of recombinant proteins (*e.g.*, polynucleotides). Direct delivery of the compositions will generally be accomplished by injection, either subcutaneously, intraperitoneally, intravenously or intramuscularly, or delivered to the interstitial space of a tissue. The compositions can also be administered into a tumor or lesion. Other modes of administration include oral and pulmonary administration, suppositories, and transdermal applications, needles, and gene guns or hyposprays. Dosage treatment can be a single dose schedule or a multiple dose schedule.

Methods for the ex vivo delivery and reimplantation of transformed cells into a subject are known in the art and described in *e.g.*, International Publication No. WO 93/14778. Examples of cells useful in ex vivo applications include, for example, stem cells, particularly hematopoetic, lymph cells, macrophages, dendritic cells, or tumor cells. Generally, delivery of nucleic acids for both ex vivo and in vitro applications can be accomplished by, for example, dextran-mediated transfection, calcium phosphate precipitation, polybrene mediated transfection, protoplast fusion, electroporation, encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the DNA into nuclei, all well known in the art.

Once a gene corresponding to a polynucleotide of the invention has been found to correlate with a proliferative disorder, such as neoplasia, dysplasia, and hyperplasia, the disorder can be amenable to treatment by administration of a therapeutic agent based on the provided polynucleotide or corresponding polypeptide.

Preparation of antisense polynucleotides is discussed above. Neoplasias that are treated with the antisense composition include, but are not limited to, cervical cancers, melanomas, colorectal adenocarcinomas, Wilms' tumor, retinoblastoma, sarcomas, myosarcomas, lung carcinomas, leukemias, such as chronic myelogenous leukemia, promyelocytic leukemia, monocytic leukemia, and myeloid leukemia, and lymphomas, such as histiocytic lymphoma. Proliferative disorders that are treated with the therapeutic composition include disorders such as anhydric hereditary ectodermal dysplasia, congenital alveolar dysplasia, epithelial dysplasia of the cervix, fibrous dysplasia of bone, and mammary dysplasia. Hyperplasias, for example, endometrial, adrenal, breast, prostate, or thyroid hyperplasias or pseudoepitheliomatous hyperplasia of the skin, are treated with antisense therapeutic compositions based upon a polynucleotide of the invention. Even in disorders in which mutations in the corresponding gene are not implicated, downregulation or inhibition of expression of a gene corresponding to a polynucleotide of the invention can have therapeutic application. For example, decreasing gene expression can help to suppress tumors in which enhanced expression of the gene is implicated.

Both the dose of the antisense composition and the means of administration are determined based on the specific qualities of the therapeutic composition, the condition, age, and weight of the patient, the progression of the disease, and other relevant factors. Administration of the therapeutic antisense agents of the invention includes local or systemic administration, including injection, oral administration, particle gun or catheterized administration, and topical administration. Preferably, the therapeutic antisense composition contains an expression construct comprising a promoter and a polynucleotide segment of at least 12, 22, 25, 30, or 35 contiguous nucleotides of the antisense strand of a polynucleotide disclosed herein. Within the expression construct, the polynucleotide segment is located downstream from the promoter, and transcription of the polynucleotide segment initiates at the promoter.

Various methods are used to administer the therapeutic composition directly to a specific site in the body. For example, a small metastatic lesion is located and the therapeutic composition injected several times in several different locations within the body of tumor. Alternatively, arteries which serve a tumor are identified, and the therapeutic composition injected into such an artery, in order to deliver the composition directly into

the tumor. A tumor that has a necrotic center is aspirated and the composition injected directly into the now empty center of the tumor. The antisense composition is directly administered to the surface of the tumor, for example, by topical application of the composition. X-ray imaging is used to assist in certain of the above delivery methods.

Receptor-mediated targeted delivery of therapeutic compositions containing an antisense polynucleotide, subgenomic polynucleotides, or antibodies to specific tissues is also used. Receptor-mediated DNA delivery techniques are described in, for example, Findeis *et al.*, *Trends Biotechnol.* (1993) *11*:202; Chiou *et al.*, *Gene Therapeutics: Methods And Applications Of Direct Gene Transfer* (J.A. Wolff, ed.) (1994); Wu *et al.*, *J. Biol. Chem.* (1988) *263*:621; Wu *et al.*, *J. Biol. Chem.* (1994) *269*:542; Zenke *et al.*, *Proc. Natl. Acad. Sci. (USA)* (1990) *87*:3655; Wu *et al.*, *J. Biol. Chem.* (1991) *266*:338. Preferably, receptor-mediated targeted delivery of therapeutic compositions containing antibodies of the invention is used to deliver the antibodies to specific tissue.

Therapeutic compositions containing antisense subgenomic polynucleotides are administered in a range of about 100 ng to about 200 mg of DNA for local administration in a gene therapy protocol. Concentration ranges of about 500 ng to about 50 mg, about 1 μg to about 2 mg, about 5 μg to about 500 μg, and about 20 μg to about 100 μg of DNA can also be used during a gene therapy protocol. Factors such as method of action and efficacy of transformation and expression are considerations which will affect the dosage required for ultimate efficacy of the antisense subgenomic polynucleotides. Where greater expression is desired over a larger area of tissue, larger amounts of antisense subgenomic polynucleotides or the same amounts readministered in a successive protocol of administrations, or several administrations to different adjacent or close tissue portions of, for example, a tumor site, may be required to effect a positive therapeutic outcome. In all cases, routine experimentation in clinical trials will determine specific ranges for optimal therapeutic effect. A more complete description of gene therapy vectors, especially retroviral vectors, is contained in U.S. Serial No. 08/869,309, which is expressly incorporated herein, and in section G below.

For polynucleotide-related genes encoding polypeptides or proteins with anti-inflammatory activity, suitable use, doses, and administration are described in U.S. Patent No. 5,654,173. Therapeutic agents also include antibodies to proteins and polypeptides

encoded by the polynucleotides of the invention and related genes, as described in U.S. Patent No. 5,654,173.

I. Gene Therapy

The therapeutic polynucleotides and polypeptides of the present invention can be utilized in gene delivery vehicles. The gene delivery vehicle can be of viral or non-viral origin (see generally, Jolly, *Cancer Gene Therapy* (1994) *1*:51; Kimura, *Human Gene Therapy* (1994) *5*:845; Connelly, *Human Gene Therapy* (1995) *1*:185; and Kaplitt, *Nature Genetics* (1994) *6*:148). Gene therapy vehicles for delivery of constructs including a coding sequence of a therapeutic of the invention can be administered either locally or systemically. These constructs can utilize viral or non-viral vector approaches. Expression of such coding sequences can be induced using endogenous mammalian or heterologous promoters. Expression of the coding sequence can be either constitutive or regulated.

The present invention can employ recombinant retroviruses which are constructed to carry or express a selected nucleic acid molecule of interest. Retrovirus vectors that can be employed include those described in EP 0 415 731; WO 90/07936; WO 94/03622; WO 93/25698; WO 93/25234; U.S. Patent No. 5, 219,740; WO 93/11230; WO 93/10218; Vile and Hart, *Cancer Res.* (1993) *53*:3860; Vile *et al.*, *Cancer Res.* (1993) *53*:962; Ram et al., *Cancer Res.* (1993) *53*:83; Takamiya *et al.*, J. *Neurosci. Res.* (1992) *33*:493; Baba et al., *J. Neurosurg.* (1993) *79*:729; U.S. Patent No. 4,777,127; GB Patent No. 2,200,651; and EP 0 345 242. Preferred recombinant retroviruses include those described in WO 91/02805.

Packaging cell lines suitable for use with the above-described retroviral vector constructs can be readily prepared (see, *e.g.*, WO 95/30763 and WO 92/05266), and used to create producer cell lines (also termed vector cell lines) for the production of recombinant vector particles. Within particularly preferred embodiments of the invention, packaging cell lines are made from human (such as HT1080 cells) or mink parent cell lines, thereby allowing production of recombinant retroviruses that can survive inactivation in human serum.

The present invention also employs alphavirus-based vectors that can function as gene delivery vehicles. Such vectors can be constructed from a wide variety of alphaviruses, including, for example, Sindbis virus vectors, Semliki forest virus (ATCC VR-67; ATCC VR-1247), Ross River virus (ATCC VR-373; ATCC VR-1246) and

Venezuelan equine encephalitis virus (ATCC VR-923; ATCC VR-1250; ATCC VR 1249; ATCC VR-532). Representative examples of such vector systems include those described in U.S. Patent Nos. 5,091,309; 5,217,879; and 5,185,440; WO 92/10578; WO 94/21792; WO 95/27069; WO 95/27044; and WO 95/07994. Gene delivery vehicles of the present invention can also employ parvovirus such as adeno-associated virus (AAV) vectors. Representative examples include the AAV vectors disclosed by Srivastava in WO 93/09239, Samulski et al., *J. Virol.* (1989) *63*:3822; Mendelson et al., *Virol.* (1988) *166*:154; and Flotte *et al.*, *PNAS* (1993) *90*:10613.

Representative examples of adenoviral vectors include those described by Berkner, *Biotechniques* (1988) *6*:616; Rosenfeld *et al.*, *Science* (1991) *252*:431; WO 93/19191; Kolls *et al.*, *PNAS* (1994) *91*:215; Kass-Eisler *et al.*, *PNAS* (1993) *90*:11498; Guzman *et al.*, *Circulation* (1993) *88*:2838; Guzman *et al.*., *Cir. Res.* (1993) *73*:1202; Zabner *et al.*, *Cell* (1993) *75*:207; Li *et al.*, *Hum. Gene Ther.* (1993) *4*:403; Cailaud *et al.*, *Eur. J. Neurosci.* (1993) *5*:1287; Vincent *et al.*, *Nat. Genet.* (1993) *5*:130; Jaffe *et al.*, *Nat. Genet.* (1992) *1*:372; and Levrero *et al.*, *Gene* (1991) *101*:195. Exemplary adenoviral gene therapy vectors employable in this invention also include those described in WO 94/12649, WO 93/03769; WO 93/19191; WO 94/28938; WO 95/11984 and WO 95/00655. Administration of DNA linked to killed adenovirus as described in Curiel, *Hum. Gene Ther.* (1992) *3*:147 can be employed.

Other gene delivery vehicles and methods can be employed, including polycationic condensed DNA linked or unlinked to killed adenovirus alone, for example Curiel, *Hum. Gene Ther.* (1992) *3*:147; ligand linked DNA, for example see Wu, *J. Biol. Chem.* (1989) *264*:16985; eukaryotic cell delivery vehicles cells, for example see U.S. Pat. No. 5,814,482; WO 95/07994; WO 96/17072; WO 95/30763; and WO 97/42338; deposition of photopolymerized hydrogel materials; hand-held gene transfer particle gun, as described in U.S. Patent No. 5,149,655; ionizing radiation as described in U.S. Patent No. 5,206,152 and in WO92/11033; nucleic charge neutralization or fusion with cell membranes. Additional approaches are described in Philip, *Mol. Cell Biol.* (1994) *14*:2411, and in Woffendin, *Proc. Natl. Acad. Sci.* (1994) *91*:1581.

Naked DNA can also be employed. Exemplary naked DNA introduction methods are described in WO 90/11092 and U.S. Patent No. 5,580,859. Liposomes that can act as

gene delivery vehicles are described in U.S. Patent No. 5,422,120; WO 95/13796; WO 94/23697; WO 91/14445; and EP 0524968.

Further non-viral delivery suitable for use includes mechanical delivery systems such as the approach described in Woffendin *et al., Proc. Natl. Acad. Sci. USA* (1994) *91*(24):11581. Moreover, the coding sequence and the product of expression of such can be delivered through deposition of photopolymerized hydrogel materials. Other conventional methods for gene delivery that can be used for delivery of the coding sequence include, for example, use of hand-held gene transfer particle gun, as described in U.S. Patent No. 5,149,655; use of ionizing radiation for activating transferred gene, as described in U.S. Patent No. 5,206,152 and WO 92/11033.

The present invention will now be illustrated by reference to the following examples which set forth particularly advantageous embodiments. However, it should be noted that these embodiments are illustrative and are not to be construed as restricting the invention in any way.

EXAMPLES

Example 1: Source of Biological Materials and Overview of Novel Polynucleotides Expressed by the Biological Materials

Human colon cancer cell line Km12L4-A (Morika, W. A. K. et al., *Cancer Research* (1988) *48*:6863) was used to construct a cDNA library from mRNA isolated from the cells. As described in the above overview, a total of 4,693 sequences expressed by the Km12L4-A cell line were isolated and analyzed; most sequences were about 275-300 nucleotides in length. The KM12L4-A cell line is derived from the KM12C cell line. The KM12C cell line, which is poorly metastatic (low metastatic) was established in culture from a Dukes' stage B_2 surgical specimen (Morikawa *et al. Cancer Res.* (1988) *48*:6863). The KML4-A is a highly metastatic subline derived from KM12C (Yeatman *et al. Nucl. Acids. Res.* (1995) *23*:4007; Bao-Ling *et al. Proc. Annu. Meet. Am. Assoc. Cancer. Res.* (1995) *21*:3269). The KM12C and KM12C-derived cell lines (*e.g.*, KM12L4, KM12L4-A, *etc.*) are well-recognized in the art as a model cell line for the study of colon cancer (see, *e.g.*, Moriakawa *et al.*, *supra*; Radinsky *et al. Clin. Cancer Res.* (1995) *1*:19; Yeatman *et al.*, (1995) *supra*; Yeatman *et al. Clin. Exp. Metastasis* (1996) *14*:246).

The sequences were first masked to eliminate low complexity sequences using the XBLAST masking program (Claverie "Effective Large-Scale Sequence Similarity Searches," In: Computer Methods for Macromolecular Sequence Analysis, Doolittle, ed., *Meth. Enzymol.* 266:212-227 Academic Press, NY, NY (1996); see particularly Claverie, in "Automated DNA Sequencing and Analysis Techniques" Adams *et al.*, eds., Chap. 36, p. 267 Academic Press, San Diego, 1994 and Claverie *et al. Comput. Chem.* (1993) 17:191). Generally, masking does not influence the final search results, except to eliminate sequences of relative little interest due to their low complexity, and to eliminate multiple "hits" based on similarity to repetitive regions common to multiple sequences, e.g., Alu repeats. Masking resulted in the elimination of 43 sequences. The remaining sequences were then used in a BLASTN vs. Genbank search with search parameters of greater than 70% overlap, 99% identity, and a p value of less than 1×10^{-40}, which search resulted in the discarding of 1,432 sequences. Sequences from this search also were discarded if the inclusive parameters were met, but the sequence was ribosomal or vector-derived.

The resulting sequences from the previous search were classified into three groups (1, 2 and 3 below) and searched in a BLASTX vs. NRP (non-redundant proteins) database

search: (1) unknown (no hits in the Genbank search), (2) weak similarity (greater than 45% identity and p value of less than 1 x 10^{-5}), and (3) high similarity (greater than 60% overlap, greater than 80% identity, and p value less than 1 x 10^{-5}). This search resulted in discard of 98 sequences as having greater than 70% overlap, greater than 99% identity, and p value of less than 1 x 10^{-40}.

The remaining sequences were classified as unknown (no hits), weak similarity, and high similarity (parameters as above). Two searches were performed on these sequences. First, a BLAST vs. EST database search resulted in discard of 1771 sequences (sequences with greater than 99% overlap, greater than 99% similarity and a p value of less than 1 x 10^{-40}; sequences with a p value of less than 1 x 10^{-65} when compared to a database sequence of human origin were also excluded). Second, a BLASTN vs. Patent GeneSeq database resulted in discard of 15 sequences (greater than 99% identity; p value less than 1 x 10^{-40}; greater than 99% overlap).

The remaining sequences were subjected to screening using other rules and redundancies in the dataset. Sequences with a p value of less than 1 x 10^{-111} in relation to a database sequence of human origin were specifically excluded. The final result provided the 2502 sequences listed in the accompanying Sequence Listing. The Sequence Listing is arranged beginning with sequences with no similarity to any sequence in a database searched, and ending with sequences with the greatest similarity. Each identified polynucleotide represents sequence from at least a partial mRNA transcript. Polynucleotides that were determined to be novel were assigned a sequence identification number.

The novel polynucleotides were assigned sequence identification numbers SEQ ID NOS:1-2502. The DNA sequences corresponding to the novel polynucleotides are provided in the Sequence Listing. The majority of the sequences are presented in the Sequence Listing in the 5' to 3' direction. A small number of sequences are listed in the Sequence Listing in the 5' to 3' direction but the sequence as written is actually 3' to 5'. These sequences are readily identified with the designation "AR" in the Sequence Name in Table 1 (inserted before the claims). The sequences correctly listed in the 5' to 3' direction in the Sequence Listing are designated "AF." Table 1 provides: 1) the SEQ ID NO assigned to each sequence for use in the present specification; 2) the filing date of the U.S. priority application in which the sequence was first filed; 3) the SEQ ID NO assigned to the sequence in the priority application; 4) the sequence name used as an internal identifier of

the sequence; 5) the name assigned to the clone from which the sequence was isolated; and 6) the number of the cluster to which the sequence is assigned (Cluster ID; where the cluster ID is 0, the sequence was not assigned to any cluster

Because the provided polynucleotides represent partial mRNA transcripts, two or more polynucleotides of the invention may represent different regions of the same mRNA transcript and the same gene. Thus, if two or more SEQ ID NOS: are identified as belonging to the same clone, then either sequence can be used to obtain the full-length mRNA or gene. In addition, some sequences are identified with multiple SEQ ID NOS, since these sequences were present in more than one filing. For example, SEQ ID NO:87 and SEQ ID NO:1000 represent the same sequence.

In order to confirm the sequences of SEQ ID NOS:1-2502, inserts of the clones corresponding to these polynucleotides were re-sequenced. These "validation" sequences are provided in SEQ ID NOS:2503-5106. Of these validation sequences, SEQ ID NOS:3040, 3545, 3863, 4511, 4726, and 4749 are not true validation sequences. Instead, SEQ ID NOS:3545, 4511, 4726, and 4749 represent "placeholder" sequences, *i.e.*, sequences that were inserted into the Sequence Listing only to prevent renumbering of the subsequent sequences during generation of the Sequence Listing. Thus, reference to "SEQ ID NOS:1-5252," "SEQ ID NOS:1-5106," or other ranges of SEQ ID NOS that include these placeholder sequences should be read to exclude SEQ ID NOS:3545, 4511, 4726, and 4749.

The validation sequences were often longer than the original polynucleotide sequences they validate, and thus often provide additional sequence information. Validation sequences can be correlated with the original sequences they validate by referring to Table 1. For example, validation sequences of SEQ ID NOS:2503-3039, 3041-3544, 3546-3862 3864-4510, and 4512-4725 share the clone name of the sequence of SEQ ID NOS:1-2502 that they validate.

Example 2: Results of Public Database Search to Identify Function of Gene Products

SEQ ID NOS:1-2502, as well as the validation sequences SEQ ID NOS:2503-3039, 3041-3544, 3546-3862 3864-4510, and 4512-4725 xx:clf were translated in all three reading frames to determine the best alignment with the individual sequences. These amino acid sequences and nucleotide sequences are referred, generally, as query sequences, which are aligned with the individual sequences. Query and individual sequences were

aligned using the BLAST programs, available over the world wide web at http://ww.ncbi.nlm.nih.gov/BLAST/. Again the sequences were masked to various extents to prevent searching of repetitive sequences or poly-A sequences, using the XBLAST program for masking low complexity as described above in Example 1.

Table 2 (inserted before the claims) shows the results of the alignments. Table 2 refers to each sequence by its SEQ ID NO:, the accession numbers and descriptions of nearest neighbors from the Genbank and Non-Redundant Protein searches, and the p values of the search results.

For each of "SEQ ID NOS:1-5106," the best alignment to a protein or DNA sequence is included in Table 2. The activity of the polypeptide encoded by "SEQ ID NOS:1-5106" is the same or similar to the nearest neighbor reported in Table 2. The accession number of the nearest neighbor is reported, providing a reference to the activities exhibited by the nearest neighbor. The search program and database used for the alignment also are indicated as well as a calculation of the p value.

Full length sequences or fragments of the polynucleotide sequences of the nearest neighbors can be used as probes and primers to identify and isolate the full length sequence of "SEQ ID NOS:1-5106." The nearest neighbors can indicate a tissue or cell type to be used to construct a library for the full-length sequences of "SEQ ID NOS:1-5106."

"SEQ ID NOS:1-5106" and the translations thereof may be human homologs of known genes of other species or novel allelic variants of known human genes. In such cases, these new human sequences are suitable as diagnostics or therapeutics. As diagnostics, the human sequences "SEQ ID NOS:1-5106" exhibit greater specificity in detecting and differentiating human cell lines and types than homologs of other species. The human polypeptides encoded by "SEQ ID NOS1-5106" are likely to be less immunogenic when administered to humans than homologs from other species. Further, on administration to humans, the polypeptides encoded by "SEQ ID NOS:1-5106" can show greater specificity or can be better regulated by other human proteins than are homologs from other species.

Example 3: Members of Protein Families

The validation sequences ("SEQ ID NOS:2503-5106") were used to conduct a profile search as described in the specification above. Several of the polynucleotides of the invention were found to encode polypeptides having characteristics of a polypeptide

belonging to a known protein families (and thus represent new members of these protein families) and/or comprising a known functional domain (Table 3, inserted prior to claims). Thus the invention encompasses fragments, fusions, and variants of such polynucleotides that retain biological activity associated with the protein family and/or functional domain identified herein.

Start and stop indicate the position within the individual sequences that align with the query sequence having the indicated SEQ ID NO. The direction (Dir) indicates the orientation of the query sequence with respect to the individual sequence, where forward (for) indicates that the alignment is in the same direction (left to right) as the sequence provided in the Sequence Listing and reverse (rev) indicates that the alignment is with a sequence complementary to the sequence provided in the Sequence Listing.

Some polynucleotides exhibited multiple profile hits because, for example, the particular sequence contains overlapping profile regions, and/or the sequence contains two different functional domains. These profile hits are described in more detail below. The acronyms used in Table 3 are provided in parentheses following the full name of the protein family or functional domain to which they refer.

a) Seven Transmembrane Integral Membrane Proteins -- Rhodopsin Family (7tm_1). Several of the validation sequences, and thus their corresponding sequence within SEQ ID NOS:1-2502, correspond to a sequence encoding a polypeptide that is a member of the seven transmembrane receptor rhodopsin family. G-protein coupled receptors of the seven transmembrane rhodopsin family (also called R7G) are an extensive group of hormones, neurotransmitters, and light receptors which transduce extracellular signals by interaction with guanine nucleotide-binding (G) proteins (Strosberg A.D. *Eur. J. Biochem.* (1991) *196*:1, Kerlavage A.R. *Curr. Opin. Struct. Biol.* (1991) *1*:394, Probst, et al., *DNA Cell Biol.* (1992) *11*:1, Savarese, et al., Biochem. J. (1992) *283*:1, http://www.gcrdb.uthscsa.edu/, http://swift.embl-heidelberg.de/7tm/. The receptors that are currently known to belong to this family are: 1) 5-hydroxytryptamine (serotonin) 1A to 1F, 2A to 2C, 4, 5A, 5B, 6 and 7 (Branchek T., *Curr. Biol.* (1993) *3*:315); 2) acetylcholine, muscarinic-type, M1 to M5; 3) adenosine A1, A2A, A2B and A3 (Stiles G.L. *J. Biol. Chem.* (1992) *267*:6451; 4) adrenergic alpha-1A to -1C; alpha-2A to -2D; beta-1 to -3 (Friell T. et al., *Trends Neurosci.* (1988) *11*:321); 5) angiotensin II types I and II; 6) bombesin subtypes 3 and 4; 7) bradykinin B1 and B2; 8) c3a and C5a anaphylatoxin; 9) cannabinoid CB1 and CB2; 10) chemokines C-C CC-CKR-1 to CC-CKR-8; 11)

Chemokines C-X-C CXC-CKR-1 to CXC-CKR-4; 12) Cholecystokinin-A and cholecystokinin-B/gastrin Dopamine D1 to D5 (Stevens C.F., *Curr. Biol.* (1991) *1*:20); 13) Endothelin ET-a and ET-b (Sakurai T. et al., *Trends Pharmacol. Sci.* (1992) *13*:103-107); 14) fMet-Leu-Phe (fMLP) (Nformyl peptide); 15) Follicle stimulating hormone (FSH-R); 16) Galanin; 17) Gastrin-releasing peptide (GRP-R); 18) Gonadotropin-releasing hormone (GNRH-R); 19) Histamine H1 and H2 (gastric receptor I); 20) Lutropin-choriogonadotropic hormone (LSH-R) (Salesse R., et al., *Biochimie* (1991) *73*:109); 21) Melanocortin MC1R to MC5R; 22) Melatonin; 23) Neuromedin B (NMB-R); 24) Neuromedin K (NK-3R); 25) Neuropeptide Y types 1 to 6; 26) Neurotensin (NT-R); 27) Octopamine (tyramine), from insects; 28) Odorants (Lancet D., et al., *Curr. Biol.* (1993)*3*:668; 29) Opioids delta-, kappa- and mu-types (Uhl G.R., et al., *Trends Neurosci.* (1994) *17*:89; 30) Oxytocin (OT-R); 31) Platelet activating factor (PAF-R); 32) Prostacyclin; 33) Prostaglandin D2; 34) Prostaglandin E2, EP1 to EP4 subtypes; 35) Prostaglandin F2; 36) Purinoreceptors (ATP) (Barnard E.A., et al., *Trends Pharmacol. Sci.* (1994)*15*:67; 37); Somatostatin types 1 to 5; 38) Substance-K (NK-2R); Substance-P (NK-1R); 39) Thrombin; 40) Thromboxane A2; 41) Thyrotropin (TSH-R) (Salesse R., et al., *Biochimie* (1991) *73*:109); 42) Thyrotropin releasing factor (TRH-R); 42) Vasopressin V1a, V1b and V2; 43) Visual pigments (opsins and rhodopsin) (Applebury M.L., et al., *Vision Res.* (1986) *26*:1881; 44) Proto-oncogene mas; 45) A number of orphan receptors (whose ligand is not known) from mammals and birds; 46) Caenorhabditis elegans putative receptors C06G4.5, C38C10.1, C43C3.2; 47) T27D1.3 and ZC84.4; 48) Three putative receptors encoded in the genome of cytomegalovirus: US27, US28, and UL33; and 49) ECRF3, a putative receptor encoded in the genome of herpesvirus saimiri.

The structure of these receptors is thought to be identical. They have seven hydrophobic regions, each of which most probably spans the membrane. The N-terminus is located on the extracellular side of the membrane and is often glycosylated, while the C-terminus is cytoplasmic and generally phosphorylated. Three extracellular loops alternate with three intracellular loops to link the seven transmembrane regions. Most, but not all of these receptors, lack a signal peptide. The most conserved parts of these proteins are the transmembrane regions and the first two cytoplasmic loops. A conserved acidic-Arg-aromatic triplet is present in the N-terminal extremity of the second cytoplasmic loop (Attwood T.K., Eliopoulos E.E., Findlay J.B.C. *Gene* (1991) *98*:153-159) and could be implicated in the interaction with G proteins.

A consensus pattern that contains the conserved triplet and that also spans the major part of the third transmembrane helix is used to detect this widespread family of proteins: [GSTALIVMFYWC]-[GSTANCPDE]-{EDPKRH}-x(2)-[LIVMNQGA]-x(2)- [LIVMFT]-[GSTANC]-[LIVMFYWSTAC]-[DENH]-R-[FYWCSH]-x(2)- [LIVM].

b) Seven Transmembrane Integral Membrane Proteins -- Secretin Family (7tm_2). Several of the validation sequences, and thus their corresponding sequence within SEQ ID NOS:1-2502, correspond to a sequence encoding a polypeptide that is a member of the seven transmembrane receptor secretin family. A number of peptide hormones bind to G-protein coupled receptors that, while structurally similar to the majority of G-protein coupled receptors (R7G) (see profile for 7 transmembrane receptors (rhodopsin family), do not show any similarity at the level of their sequence, thus new family whose current known members (Jueppner et al. *Science* (1991) *254*:1024; Hamann et al. *Genomics* (1996) *32*:144).are: 1) calcitonin receptor, 2) calcitonin gene-related peptide receptor; 3) corticotropin releasing factor receptor types 1 and 2; 4) gastric inhibitory polypeptide receptor; 5) glucagon receptor; 6) glucagon-like peptide 1 receptor; 7) growth hormone-releasing hormone receptor; 7) parathyroid hormone / parathyroid hormone-related peptide types 1 and 2; 8) pituitary adenylate cyclase activating polypeptide receptor; 9) secretin receptor; 10) vasoactive intestinal peptide receptor types 1 and 2; 10) insects diuretic hormone receptor; 11) Caenorhabditis elegans putative receptor C13B9.4; 12) Caenorhabditis elegans putative receptor ZK643.3; 13) human leucocyte CD97 (which contains 3 EGF-like domains in its N-terminal section); 14) human cell surface glycoprotein EMR1 (which contains 6 EGF-like domains in it N-terminal section); and 15) mouse cell surface glycoprotein F4/80 (which contains 7 EGF-like domains in its N-terminal section). All of 1) through 10) are coupled to G-proteins which activate both adenylyl cyclase and the phosphatidylinositol-calcium pathway.

Like classical R7G the secretin family of 7 transmembrane proteins contain seven transmembrane regions. Their N-terminus is located on the extracellular side of the membrane and potentially glycosylated, while their C-terminus is cytoplasmic. But apart from these topological similarities they do not share any region of sequence similarity and are therefore probably not evolutionary related.

Every receptor in the 7 transmember secretin family is encoded on multiple exons, and several of these functionally distinct products. The N-terminal extracellular domain of these receptors contains five conserved cysteines residues that may be involved in disulfide

bonds, with a consensus pattern in the region that spans the first three cysteines. One of the most highly conserved regions spans the C-terminal part of the last transmembrane region and the beginning of the adjacent intracellular region. This second region is used as a second signature pattern. The two consensus patterns are:

1) C-x(3)-[FYWLIV]-D-x(3,4)-C-[FW]-x(2)-[STAGV]-x(8,9)-C-[PF]

2) Q-G-[LMFCA]-[LIVMFT]-[LIV]-x-[LIVFST]-[LIF]-[VFYH]-C- [LFY]-x-N-x(2)-V

c) Ank Repeats (ANK). SEQ IS NO:2656, and thus its corresponding sequence within SEQ ID NOS:1-2502, represents a polynucleotide encoding an Ank repeat-containing protein. The ankyrin motif is a 33 amino acid sequence named after the protein ankyrin which has 24 tandem 33-amino-acid motifs. Ank repeats were originally identified in the cell-cycle-control protein cdc10 (Breeden *et al., Nature* (1987) *329*:651). Proteins containing ankyrin repeats include ankyrin, myotropin, I-kappaB proteins, cell cycle protein cdc10, the Notch receptor (Matsuno *et al., Development* (1997) *124(21)*:4265); G9a (or BAT8) of the class III region of the major histocompatibility complex (Biochem J. 290:811-818, 1993), FABP, GABP, 53BP2, Lin12, glp-1, SW14, and SW16. The functions of the ankyrin repeats are compatible with a role in protein-protein interactions (Bork, *Proteins* (1993) *17(4)*:363; Lambert and Bennet, *Eur. J. Biochem.* (1993) *211*:1; Kerr *et al., Current Op. Cell Biol.* (1992) *4*:496; Bennet *et al., J. Biol. Chem.* (1980) *255*:6424).

The 90 kD N-terminal domain of ankyrin contains a series of 24 33-amino-acid ank repeats. (Lux *et al., Nature* (1990) *344*:36-42, Lambert *et al., PNAS USA* (1990) *87*:1730.) The 24 ank repeats form four folded subdomains of 6 repeats each. These four repeat subdomains mediate interactions with at least 7 different families of membrane proteins. Ankyrin contains two separate binding sites for anion exchanger dimers. One site utilizes repeat subdomain two (repeats 7-12) and the other requires both repeat subdomains 3 and 4 (repeats 13-24). Since the anion exchangers exist in dimers, ankyrin binds 4 anion exchangers at the same time (Michaely and Bennett, *J. Biol. Chem.* (1995) *270(37)*:22050). The repeat motifs are involved in ankyrin interaction with tubulin, spectrin, and other membrane proteins. (Lux *et al., Nature* (1990) *344*:36.)

The Rel/NF-kappaB/Dorsal family of transcription factors have activity that is controlled by sequestration in the cytoplasm in association with inhibitory proteins referred to as I-kappaB. (Gilmore, *Cell* (1990) *62*:841; Nolan and Baltimore, *Curr Opin Genet Dev.* (1992) *2*:211; Baeuerle, *Biochim Biophys Acta* (1991) *1072*:63; Schmitz *et al., Trends Cell*

Biol. (1991) *1*:130.) I-kappaB proteins contain 5 to 8 copies of 33 amino acid ankyrin repeats and certain NF-kappaB/rel proteins are also regulated by cis-acting ankyrin repeat containing domains including p105NF-kappaB which contains a series of ankyrin repeats (Diehl and Hannink, *J. Virol.* (1993) *67(12)*:7161). The I-kappaBs and Cactus (also containing ankyrin repeats) inhibit activators through differential interactions with the Rel-homology domain. The gene family includes proto-oncogenes, thus broadly implicating I-kappaB in the control of both normal gene expression and the aberrant gene expression that makes cells cancerous. (Nolan and Baltimore, *Curr Opin Genet Dev.* (1992) *2(2)*:211-220). In the case of rel/NF-kappaB and pp40/I-kappaB(, both the ankyrin repeats and the carboxy-terminal domain are required for inhibiting DNA-binding activity and direct association of pp40/I-kappaB(with rel/NF-kappaB protein. The ankyrin repeats and the carboxy-terminal of pp40/I-kappaB(form a structure that associates with the rel homology domain to inhibit DNA binding activity (Inoue *et al.*, *PNAS USA* (1992) *89*:4333).

The 4 ankyrin repeats in the amino terminus of the transcription factor subunit GABP are required for its interaction with the GABP subunit to form a functional high affinity DNA-binding protein. These repeats can be crosslinked to DNA when GABP is bound to its target sequence. (Thompson *et al.*, *Science* (1991) *253*:762; LaMarco *et al.*, *Science* (1991) *253*:789). Myotrophin, a 12.5 kDa protein having a key role in the initiation of cardiac hypertrophy, comprises ankyrin repeats. The ankyrin repeats are characteristic of a hairpin-like protruding tip followed by a helix-turn-helix motif. The V-shaped helix-turn-helix of the repeats stack sequentially in bundles and are stabilized by compact hydrophobic cores, whereas the protruding tips are less ordered.

d) Eukaryotic Aspartyl Proteases (asp). Several of the validation sequences, and thus their corresponding sequence within SEQ ID NOS:1-2502, correspond to a sequence encoding a novel eukaryotic aspartyl protease. Aspartyl proteases, known as acid proteases, (EC 3.4.23.-) are a widely distributed family of proteolytic enzymes (Foltmann B., *Essays Biochem.* (1981) *17*:52; Davies D.R., *Annu. Rev. Biophys. Chem.* (1990) *19*:189; Rao J.K.M., *et al.*, *Biochemistry* (1991) *30*:4663) known to exist in vertebrates, fungi, plants, retroviruses and some plant viruses. Aspartate proteases of eukaryotes are monomeric enzymes which consist of two domains. Each domain contains an active site centered on a catalytic aspartyl residue. The two domains most probably evolved from the duplication of an ancestral gene encoding a primordial domain. Currently known eukaryotic aspartyl proteases include: 1) Vertebrate gastric pepsins A and C (also known as

gastricsin); 2) Vertebrate chymosin (rennin), involved in digestion and used for making cheese; 3) Vertebrate lysosomal cathepsins D (EC 3.4.23.5) and E (EC 3.4.23.34); 4) Mammalian renin (EC 3.4.23.15) whose function is to generate angiotensin I from angiotensinogen in the plasma; 5) Fungal proteases such as aspergillopepsin A (EC 3.4.23.18), candidapepsin (EC 3.4.23.24), mucoropepsin (EC 3.4.23.23) (mucor rennin), endothiapepsin (EC 3.4.23.22), polyporopepsin (EC 3.4.23.29), and rhizopuspepsin (EC 3.4.23.21); and 6) Yeast saccharopepsin (EC 3.4.23.25) (proteinase A) (gene PEP4). PEP4 is implicated in posttranslational regulation of vacuolar hydrolases; 7) Yeast barrierpepsin (EC 3.4.23.35) (gene BAR1); a protease that cleaves alpha-factor and thus acts as an antagonist of the mating pheromone; and 8) Fission yeast sxa1 which is involved in degrading or processing the mating pheromones.

Most retroviruses and some plant viruses, such as badnaviruses, encode for an aspartyl protease which is an homodimer of a chain of about 95 to 125 amino acids. In most retroviruses, the protease is encoded as a segment of a polyprotein which is cleaved during the maturation process of the virus. It is generally part of the pol polyprotein and, more rarely, of the gag polyprotein. Because the sequence around the two aspartates of eukaryotic aspartyl proteases and around the single active site of the viral proteases is conserved, a single signature pattern can be used to identify members of both groups of proteases. The consensus pattern is: [LIVMFGAC]-[LIVMTADN]-[LIVFSA]-D-[ST]-G-[STAV]-[STAPDENQ]- x-[LIVMFSTNC]-x-[LIVMFGTA], where D is the active site residue.

e) ATPases Associated with Various Cellular Activities (ATPases). Several of the validation sequences, and thus their corresponding sequence within SEQ ID NOS:1-2502, correspond to a sequence that encodes a novel member of the "ATPases Associated with diverse cellular Activities" (AAA) protein family. The AAA protein family is composed of a large number of ATPases that share a conserved region of about 220 amino acids that contains an ATP-binding site (Froehlich *et al., J. Cell Biol.* (1991) *114*:443; Erdmann *et al. Cell* (1991) *64*:499; Peters *et al., EMBO J.* (1990) *9*:1757; Kunau *et al., Biochimie* (1993) *75*:209-224; Confalonieri *et al., BioEssays* (1995) *17*:639; http://yeamob.pci.chemie.uni-tuebingen.de/AAA/Description.html). The proteins that belong to this family either contain one or two AAA domains.

Proteins containing two AAA domains include: 1) Mammalian and drosophila NSF (N-ethylmaleimide-sensitive fusion protein) and the fungal homolog, SEC18, which are

involved in intracellular transport between the endoplasmic reticulum and Golgi, as well as between different Golgi cisternae; 2) Mammalian transitional endoplasmic reticulum ATPase (previously known as p97 or VCP), which is involved in the transfer of membranes from the endoplasmic reticulum to the golgi apparatus. This ATPase forms a ring-shaped homooligomer composed of six subunits. The yeast homolog, CDC48, plays a role in spindle pole proliferation; 3) Yeast protein PAS1 essential for peroxisome assembly and the related protein PAS1 from Pichia pastoris; 4) Yeast protein AFG2; 5) Sulfolobus acidocaldarius protein SAV and Halobacterium salinarium cdcH, which may be part of a transduction pathway connecting light to cell division.

Proteins containing a single AAA domain include: 1) Escherichia coli and other bacteria ftsH (or hflB) protein. FtsH is an ATP-dependent zinc metallopeptidase that degrades the heat-shock sigma-32 factor, and is an integral membrane protein with a large cytoplasmic C-terminal domain that contain both the AAA and the protease domains; 2) Yeast protein YME1, a protein important for maintaining the integrity of the mitochondrial compartment. YME1 is also a zinc-dependent protease; 3) Yeast protein AFG3 (or YTA10). This protein also contains an AAA domain followed by a zinc-dependent protease domain; 4) Subunits from regulatory complex of the 26S proteasome (Hilt *et al., Trends Biochem. Sci.* (1996) *21*:96), which is involved in the ATP-dependent degradation of ubiquitinated proteins, which subunits include: a) Mammalian 4 and homologs in other higher eukaryotes, in yeast (gene YTA5) and fission yeast (gene mts2); b) Mammalian 6 (TBP7) and homologs in other higher eukaryotes and in yeast (gene YTA2); c) Mammalian subunit 7 (MSS1) and homologs in other higher eukaryotes and in yeast (gene CIM5 or YTA3); d) Mammalian subunit 8 (P45) and homologs in other higher eukaryotes and in yeast (SUG1 or CIM3 or TBY1) and fission yeast (gene let1); e) Other probable subunits include human TBP1, which influences HIV gene expression by interacting with the virus tat transactivator protein, and yeast YTA1 and YTA6; 5) Yeast protein BCS1, a mitochondrial protein essential for the expression of the Rieske iron-sulfur protein; 6) Yeast protein MSP1, a protein involved in intramitochondrial sorting of proteins; 7) Yeast protein PAS8, and the corresponding proteins PAS5 from Pichia pastoris and PAY4 from Yarrowia lipolytica; 8) Mouse protein SKD1 and its fission yeast homolog (SpAC2G11.06); 9) Caenorhabditis elegans meiotic spindle formation protein mei-1; 10) Yeast protein SAP1' 11) Yeast protein YTA7; and 12) Mycobacterium leprae hypothetical protein A2126A.

In general, the AAA domains in these proteins act as ATP-dependent protein clamps(Confalonieri *et al.* (1995) *BioEssays 17*:639). In addition to the ATP-binding 'A' and 'B' motifs, which are located in the N-terminal half of this domain, thereis a highly conserved region located in the central part of the domain which was used in the development of the signature pattern. The consensus pattern is: [LIVMT]-x-[LIVMT]-[LIVMF]-x-[GATMC]-[ST]-[NS]-x(4)-[LIVM]- D-x-A-[LIFA]-x-R.

f) Bcl-2 family (Bcl-2). SEQ ID NO:3404, and thus the corresponding sequence it validates, represents a polynucleotide encoding an apoptosis regulator protein of the Bcl-2 family. Active cell suicide (apoptosis) is induced by events such as growth factor withdrawal and toxins. It is controlled by regulators, which have either an inhibitory effect on programmed cell death (anti-apoptotic) or block the protective effect of inhibitors (pro-apoptotic) (Vaux, 1993, Curr. Biol. 3:877-878, and White, 1996, Genes Dev. 10:2859-2869). Many viruses have found a way of countering defensive apoptosis by encoding their own anti-apoptosis genes, preventing their target cells from dying prematurely.

All proteins belonging to the Bcl-2 family (Reed et al., 1996, Adv. Exp. Med. Biol. 406:99-112) contain either a BH1, BH2, BH3, or BH4 domain. All anti-apoptotic proteins contain BH1 and BH2 domains; some of them contain an additional N-terminal BH4 domain (Bcl-2, Bcl-x(L), Bcl-w), which is never seen in pro-apoptotic proteins, except for Bcl-x(S). On the other hand, all pro-apoptotic proteins contain a BH3 domain (except for Bad) necessary for dimerization with other proteins of Bcl-2 family and crucial for their killing activity; some of them also contain BH1 and BH2 domains (Bax, Bak). The BH3 domain is also present in some anti-apoptotic protein, such as Bcl-2 or Bcl-x(L). Proteins that are known to contain these domains are listed below.

1. Vertebrate protein Bcl-2. Bcl-2 blocks apoptosis; it prolongs the survival of hematopoietic cells in the absence of required growth factors and also in the presence of various stimuli inducing cellular death. Two isoforms of bcl-2 (alpha and beta) are generated by alternative splicing. Bcl-2 is expressed in a wide range of tissues at various times during development. It forms heterodimers with the Bax proteins.

2. Vertebrate protein Bcl-x. Two isoforms of Bcl-x (Bcl-x(L) and Bcl-x(S)) are generated by alternative splicing. While the longer product (Bcl-x(L)) can protect a growth-factor-dependent cell line from apoptosis, the shorter form blocks the protective effect of Bcl-2 and Bcl-x(L) and acts as an anti-anti-apoptosis protein.

3. Mammalian protein Bax. Bax blocks the anti-apoptosis ability of Bcl-2 with which

it forms heterodimers. There is no evidence that Bax has any activity in the absence of Bcl-2. Three isoforms of bax (alpha, beta and gamma) are generated by alternative splicing.

4. Mammalian protein Bak, which promotes cell death and counteracts the protection from apoptosis provided by Bcl-2.

5. Mammalian protein Bcl-w, which promotes cell survival.

6. Mammalian protein bad, which promotes cell death, and counteracts the protection from apoptosis provided by Bcl-x(L), but not that of Bcl-2.

7. Human protein Bik, which promotes cell death, but cannot counteract the protection from apoptosis provided by Bcl-2.

8. Mouse protein Bid, which induces caspases and apoptosis, and counteracts the protection from apoptosis provided by Bcl-2.

9. Human induced myeloid leukemia cell differentiation protein MCL1. MCL1 is probably involved in programming of differentiation and concomitant maintenance of viability but not proliferation. Its expression increases early during phorbol ester induced differentiation in myeloid leukemia cell line ML-1.

10. Mouse hemopoietic-specific early response protein A1.

11. Mammalian activator of apoptosis Harakiri (Inohara et al., 1997, EMBO J. 16:1686-1694) (also known as neuronal death protein Dp5). This is a small protein of 92 residues that activates apoptosis. It contains a BH3 domain, but no BH1, BH2 or BH4 domains.

The following consensus patterns have been developed for the four BH domains:

1) [LVME]-[FT]-x-[GSD]-[GL]-x(1,2)-[NS]-[YW]-G-R-[LIV]- [LIVC]-[GAT]-[LIVMF](2)-x-F-[GSAE]-[GSARY]

2) W-[LIM]-x(3)-[GR]-G-[WQ]-[DENSAV]-x-[FLGA]-[LIVFTC]

3) [LIVAT]-x(3)-L-[KARQ]-x-[IVAL]-G-D-[DESG]-[LIMFV]-[DENSHQ]-[LVSHRQ]-[NSR]

4) [DS]-[NT]-R-[AE]-[LI]-V-x-[KD]-[FY]-[LIV]-[GHS]-Y-K-L- [SR]-Q-[RK]-G-[HY]-x-[CW].

g) Bromodomain (bromodomain). SEQ ID NOS:4036 and 4489, and thus the corresponding sequences they validate, represent polynucleotides encoding a polypeptide having a bromodomain region (Haynes et al., 1992, Nucleic Acids Res. 20:2693-2603, Tamkun et al., 1992, Cell 68:561-572, and Tamkun, 1995, Curr. Opin. Genet. Dev. 5:473-

477), which is a conserved region of about 70 amino acids found in the following proteins: 1) Higher eukaryotes transcription initiation factor TFIID 250 Kd subunit (TBP-associated factor p250) (gene CCG1); P250 is associated with the TFIID TATA-box binding protein and seems essential for progression of the G1 phase of the cell cycle. 2) Human RING3, a protein of unknown function encoded in the MHC class II locus; 3) Mammalian CREB-binding protein (CBP), which mediates cAMP-gene regulation by binding specifically to phosphorylated CREB protein; 4) Mammalian homologs of brahma, including three brahma-like human: SNF2a(hBRM), SNF2b, and BRG1; 5) Human BS69, a protein that binds to adenovirus E1A and inhibits E1A transactivation; 6) Human peregrin (or Br140).

The bromodomain is thought to be involved in protein-protein interactions and may be important for the assembly or activity of multicomponent complexes involved in transcriptional activation. The consensus pattern, which spans a major part of the bromodomain, is: [STANVF]-x(2)-F-x(4)-[DNS]-x(5,7)-[DENQTF]-Y-[HFY]-x(2)-[LIVMFY]-x(3)-[LIVM]-x(4)-[LIVM]-x(6,8)-Y-x(12,13)-[LIVM]-x(2)-N-[SACF]-x(2)-[FY].

h) Basic Region Plus Leucine Zipper Transcription Factors (BZIP). SEQ ID NO:3408, 2951, and 4850, and thus the corresponding sequences these sequences validate, represent polynucleotides encoding a novel member of the family of basic region plus leucine zipper transcription factors. The bZIP superfamily (Hurst, *Protein Prof.* (1995) *2*:105; and Ellenberger, *Curr. Opin. Struct. Biol.* (1994) *4*:12) of eukaryotic DNA-binding transcription factors encompasses proteins that contain a basic region mediating sequence-specific DNA-binding followed by a leucine zipper required for dimerization. Members of the family include transcription factor AP-1, which binds selectively to enhancer elements in the cis control regions of SV40 and metallothionein IIA. AP-1, also known as c-jun, is the cellular homolog of the avian sarcoma virus 17 (ASV17) oncogene v-jun.
Other members of this protein family include jun-B and jun-D, probable transcription factors that are highly similar to jun/AP-1; the fos protein, a proto-oncogene that forms a non-covalent dimer with c-jun; the fos-related proteins fra-1, and fos B; and mammalian cAMP response element (CRE) binding proteins CREB, CREM, ATF-1, ATF-3, ATF-4, ATF-5, ATF-6 and LRF-1. The consensus pattern for this protein family is: [KR]-x(1,3)-[RKSAQ]-N-x(2)-[SAQ](2)-x-[RKTAENQ]-x-R-x-[RK].

i) Cyclins (cyclin). SEQ ID NOS:3618, 3895, and 4536, and thus the corresponding sequences these sequences validate, represent polynucleotides encoding

cyclins, and SEQ ID NO:55 and 56, respectively, show the corresponding full-length polynucleotides. SEQ ID NO:57 and 58 show, respectively, the translations of SEQ ID NO:55 and 56. Cyclins (Nurse, 1990, Nature 344:503-508; Norbury et al., 1991, Curr. Biol. 1:23-24; and Lew et al., 1992, Trends Cell Biol. 2:77-81) are eukaryotic proteins that play an active role in controlling nuclear cell division cycles. There are two main groups of cyclins. G2/M cyclins are essential for the control of the cell cycle at the G2/M (mitosis) transition. G2/M cyclins accumulate steadily during G2 and are abruptly destroyed as cells exit from mitosis (at the end of the M-phase). G1/S cyclins are essential for the control of the cell cycle at the G1/S (start) transition.

The best conserved region is in the central part of the cyclins' sequences, known as the "cyclin-box," from which a 32 residue consensus pattern was derived: R-x(2)-[LIVMSA]-x(2)-[FYWS]-[LIVM]-x(8)-[LIVMFC]-x(4)-[LIVMFYA]-x(2)-[STAGC]-[LIVMFYQ]-x-[LIVMFYC]-[LIVMFY]-D-[RKH]-[LIVMFYW].

j) Eukaryotic thiol (cysteine) proteases active sites (Cys-protease). SEQ ID NOS:3344, 3684, 3688, and 4801, and thus also the sequences they validate, repreasent polynucleotides encoding proteins having a eukaryotic thiol (cysteine) protease active site. Eukaryotic thiol proteases (Dufour E., *Biochimie* (1988) *70*:1335); are a family of proteolytic enzymes which contain an active site cysteine. Catalysis proceeds through a thioester intermediate and is facilitated by a nearby histidine side chain; an asparagine completes the essential catalytic triad. The proteases that belong to this family are: 1) vertebrate lysosomal cathepsins B (Kirschke H., et al., *Protein Prof.* (1995) *2*:1587-1643); 2) vertebrate lysosomal dipeptidyl peptidase I (also known as cathepsin C) (Kirschke H., et al., *supra*); 3) vertebrate calpains (Calpains are intracellular calcium-activated thiol protease that contain both an N-terminal catalytic domain and a C-terminal calcium-binding domain); 4) mammalian cathepsin K, which seems involved in osteoclastic bone resorption (Shi G.-P., et al., *FEBS Lett.* (1995) *357*:129); 5) human cathepsin O ([4] Velasco G., Ferrando A.A., Puente X.S., Sanchez L.M., Lopez-Otin C. *J. Biol. Chem.* (1994) *269*:27136); 6) bleomycin hydrolase (which catalyzes the inactivation of the antitumor drug BLM (a glycopeptide)); 7) Plant enzymes such as: barley aleurain, EP-B1/B4; kidney bean EP-C1, rice bean SH-EP; kiwi fruit actinidin; papaya latex papin, chymopapain, caricain, and proteinase IV; pea turgor-responsive protein 15A; pineapple stem bromelain; rape COT44; rice oryzain alpha, beta, and gamma; tomato low-temperature induced, Arabidopsis thaliana A494, RD19A and RD21A; 8) - House-dust

mites allergens DerP1 and EurM1; 9) cathepsin B-like proteinases from the worms Caenorhabditis elegans (genes gcp-1, cpr-3, cpr-4, cpr-5 and cpr-6), Schistosoma mansoni (antigen SM31) and Japonica (antigen SJ31), Haemonchus contortus (genes AC-1 and AC-2), and Ostertagia ostertagi (CP-1 and CP-3); 10) slime mold cysteine proteinases CP1 and CP2; 11) cruzipain from Trypanosoma cruzi and brucei; 12) throphozoite cysteine proteinase (TCP) from various Plasmodium species; 13) proteases from Leishmania mexicana, Theileria annulata and Theileria parva; 14) Baculoviruses cathepsin-like enzyme (v-cath); 15) Drosophila small optic lobes protein (gene sol), a neuronal protein that contains a calpain-like domain; 16) yeast thiol protease BLH1/YCP1/LAP3; 17) Caenorhabditis elegans hypothetical protein C06G4.2, a calpain-like protein.

In addition, two bacterial peptidases are also part of this family: 1) aminopeptidase C from Lactococcus lactis (gene pepC) (Chapot-Chartier M.P., et al., *Appl. Environ. Microbiol.* (1993) *59*:330); and 2) thiol protease tpr from Porphyromonas gingivalis. Three other proteins are structurally related to this family, but may have lost their proteolytic activity. These include: 1) soybean oil body protein P34 (which has its active site cysteine replaced by a glycine); 2) rat testin (which is a sertoli cell secretory protein highly similar to cathepsin L but with the active site cysteine is replaced by a serine); and 3) Plasmodium falciparum serine-repeat protein (SERA) (which is the major blood stage antigen and possesses a C-terminal thiol-protease-like domain (Higgins D.G., et al., *Nature* (1989) *340*:604), with the active site cysteine is replaced by a serine).

The sequences around the three active site residues are well conserved and can be used as signature patterns:

Consensus pattern #1: Q-x(3)-[GE]-x-C-[YW]-x(2)-[STAGC]-[STAGCV] (where C is the active site residue)

Consensus pattern #2: [LIVMGSTAN]-x-H-[GSACE]-[LIVM]-x-[LIVMAT](2)-G-x-[GSADNH] (where H is the active site residue);

Consensus patern #3: [FYCH]-[WI]-[LIVT]-x-[KRQAG]-N-[ST]-W-x(3)-[FYW]-G-x(2)-G- [LFYW]-[LIVMFYG]-x-[LIVMF] (where N is the active site residue).

k) Phorbol Esters/Diacylglycerol Binding (DAG_PE_bind). SEQ ID NO:4659, and thus the sequence it validates, represents a polynucleotide encoding a protein belonging to the family including phorbol esters/diacylglycerol binding proteins. Diacylglycerol (DAG) is an important second messenger. Phorbol esters (PE) are analogues of DAG and potent tumor promoters that cause a variety of physiological changes when administered to both

cells and tissues. DAG activates a family of serine/threonine protein kinases, collectively known as protein kinase C (PKC) (Azzi *et al.*, *Eur. J. Biochem.* (1992) *208*:547). Phorbol esters can directly stimulate PKC. The N-terminal region of PKC, known as C1, has been shown (Ono *et al.*, *Proc. Natl. Acad. Sci. USA* (1989) *86*:4868) to bind PE and DAG in a phospholipid and zinc-dependent fashion. The C1 region contains one or two copies (depending on the isozyme of PKC) of a cysteine-rich domain about 50 amino-acid residues long and essential for DAG/PE-binding. Such a domain has also been found in, for example, the following proteins.

(1) Diacylglycerol kinase (EC 2.7.1.107) (DGK) (Sakane *et al.*, *Nature* (1990) *344*:345), the enzyme that converts DAG into phosphatidate. It contains two copies of the DAG/PE-binding domain in its N-terminal section. At least five different forms of DGK are known in mammals; and

(2) N-chimaerin, a brain specific protein which shows sequence similarities with the BCR protein at its C-terminal part and contains a single copy of the DAG/PE-binding domain at its N-terminal part. It has been shown (Ahmed *et al.*, *Biochem. J.* (1990) *272*:767, and Ahmed *et al.*, *Biochem. J.* (1991) *280*:233) to be able to bind phorbol esters.

The DAG/PE-binding domain binds two zinc ions; the ligands of these metal ions are probably the six cysteines and two histidines that are conserved in this domain. The signature pattern completely spans the DAG/PE domain. The consensus pattern is: H-x-[LIVMFYW]-x(8,11)-C-x(2)-C-x(3)-[LIVMFC]-x(5,10)-C-x(2)-C-x(4)-[HD]-x(2)-C-x(5,9)-C. All the C and H are probably involved in binding zinc.

l) <u>DEAD and DEAH box families ATP-dependent helicases signatures (Dead_box_helic).</u> SEQ ID NOS:4821 and 5083, and thus the sequences they validate, represent polynucleotides encoding a novel member of the DEAD box family. A number of eukaryotic and prokaryotic proteins have been characterized (Schmid S.R., et al., *Mol. Microbiol.* (1992) *6*:283; Linder P., et al., *Nature* (1989) *337*:121; Wassarman D.A., et al., *Nature* (1991) *349*:463) on the basis of their structural similarity. All are involved in ATP-dependent, nucleic-acid unwinding. Proteins currently known to belong to this family are:

1) Initiation factor eIF-4A. Found in eukaryotes, this protein is a subunit of a high molecular weight complex involved in 5'cap recognition and the binding of mRNA to ribosomes. It is an ATP-dependent RNA-helicase.

2) PRP5 and PRP28. These yeast proteins are involved in various ATP-requiring steps of the pre-mRNA splicing process.

3) Pl10, a mouse protein expressed specifically during spermatogenesis.

4) An3, a Xenopus putative RNA helicase, closely related to Pl10.

5) SPP81/DED1 and DBP1, two yeast proteins involved in pre-mRNA splicing and related to Pl10.

6) Caenorhabditis elegans helicase glh-1.

7) MSS116, a yeast protein required for mitochondrial splicing.

8) SPB4, a yeast protein involved in the maturation of 25S ribosomal RNA.

9) p68, a human nuclear antigen. p68 has ATPase and DNA-helicase activities in vitro. It is involved in cell growth and division.

10) Rm62 (p62), a Drosophila putative RNA helicase related to p68.

11) DBP2, a yeast protein related to p68.

12) DHH1, a yeast protein.

13) DRS1, a yeast protein involved in ribosome assembly.

14) MAK5, a yeast protein involved in maintenance of dsRNA killer plasmid.

15) ROK1, a yeast protein.

16) ste13, a fission yeast protein.

17) Vasa, a Drosophila protein important for oocyte formation and specification of embryonic posterior structures.

18) Me31B, a Drosophila maternally expressed protein of unknown function.

19) dbpA, an Escherichia coli putative RNA helicase.

20) deaD, an Escherichia coli putative RNA helicase which can suppress a mutation in the rpsB gene for ribosomal protein S2.

21) rhlB, an Escherichia coli putative RNA helicase.

22) rhlE, an Escherichia coli putative RNA helicase.

23) rmB, an Escherichia coli protein that shows RNA-dependent ATPase activity, which interacts with 23S ribosomal RNA.

24) Caenorhabditis elegans hypothetical proteins T26G10.1, ZK512.2 and ZK686.2.

25) Yeast hypothetical protein YHR065c.

26) Yeast hypothetical protein YHR169w.

27) Fission yeast hypothetical protein SpAC31A2.07c.

28) Bacillus subtilis hypothetical protein yxiN.

All of the above proteins share a number of conserved sequence motifs. Some of them are specific to this family while others are shared by other ATP-binding proteins or by proteins belonging to the helicases 'superfamily' (Hodgman T.C., *Nature* (1988) *333*:22 and *Nature* (1988) *333*:578 (Errata); http://www.expasy.ch/www/linder/HELICASES_TEXT.html). One of these motifs, called the 'D-E-A-D-box', represents a special version of the B motif of ATP-binding proteins. Some other proteins belong to a subfamily which have His instead of the second Asp and are thus said to be 'D-E-A-H-box' proteins (Wassarman D.A., et al., *Nature* (1991) *349*:463; Harosh I., et al., *Nucleic Acids Res.* (1991) *19*:6331; Koonin E.V., et al., *J. Gen. Virol.* (1992) *73*:989; http://www.expasy.ch/www/linder/HELICASES_TEXT.html). Proteins currently known to belong to this DEAH subfamily are:

1) PRP2, PRP16, PRP22 and PRP43. These yeast proteins are all involved in various ATP-requiring steps of the pre-mRNA splicing process. 2) Fission yeast prh1, which my be involved in pre-mRNA splicing. 3) Male-less (mle), a Drosophila protein required in males, for dosage compensation of X chromosome linked genes. 4) RAD3 from yeast. RAD3 is a DNA helicase involved in excision repair of DNA damaged by UV light, bulky adducts or cross-linking agents. Fission yeast rad15 (rhp3) and mammalian DNA excision repair protein XPD (ERCC-2) are the homologs of RAD3. 5) Yeast CHL1 (or CTF1), which is important for chromosome transmission and normal cell cycle progression in G(2)/M. 6) Yeast TPS1. 7) Yeast hypothetical protein YKL078w. 8) Caenorhabditis elegans hypothetical proteins C06E1.10 and K03H1.2. 9) Poxviruses' early transcription factor 70 Kd subunit which acts with RNA polymerase to initiate transcription from early gene promoters. 10) I8, a putative vaccinia virus helicase. 11) hrpA, an Escherichia coli putative RNA helicase.

The following signature patterns are used to identify member for both subfamilies:

Consensus pattern: [LIVMF](2)-D-E-A-D-[RKEN]-x-[LIVMFYGSTN]

Consensus pattern: [GSAH]-x-[LIVMF](3)-D-E-[ALIV]-H-[NECR].

m) EF Hand (EFhand). Several of the validation sequences, and thus the sequences they validate, correspond to polynucleotides encoding a novel protein in the family of EF-hand proteins. Many calcium-binding proteins belong to the same evolutionary family and share a type of calcium-binding domain known as the EF-hand (Kawasaki *et al.*, *Protein. Prof.* (1995) *2*:305-490). This type of domain consists of a twelve residue loop flanked on both sides by a twelve residue alpha-helical domain. In an EF-hand loop the calcium ion is

coordinated in a pentagonal bipyramidal configuration. The six residues involved in the binding are in positions 1, 3, 5, 7, 9 and 12; these residues are denoted by X, Y, Z, -Y, -X and -Z. The invariant Glu or Asp at position 12 provides two oxygens for liganding Ca (bidentate ligand).

Proteins known to contain EF-hand regions include: Calmodulin (Ca=4, except in yeast where Ca=3) ("Ca=" indicates approximate number of EF-hand regions); diacylglycerol kinase (EC 2.7.1.107) (DGK) (Ca=2); 2) FAD-dependent glycerol-3-phosphate dehydrogenase (EC 1.1.99.5) from mammals (Ca=1); guanylate cyclase activating protein (GCAP) (Ca=3); MIF related proteins 8 (MRP-8 or CFAG) and 14 (MRP-14) (Ca=2); myosin regulatory light chains (Ca=1); oncomodulin (Ca=2); osteonectin (basement membrane protein BM-40) (SPARC); and proteins that contain an "osteonectin" domain (QR1, matrix glycoprotein SC1).

The consensus pattern includes the complete EF-hand loop as well as the first residue which follows the loop and which seem to always be hydrophobic: D-x-[DNS]-{ILVFYW}-[DENSTG]-[DNQGHRK]-{GP}-[LIVMC]-[DENQSTAGC]-x(2)-[DE]-[LIVMFYW].

n) Ets Domain (Ets_Nterm). SEQ ID NO:2849, and thus the sequence it validates, represents a polynucleotide encoding a polypeptide with N-terminal homology in ETS domain. Proteins of this family contain a conserved domain, the "ETS-domain," that is involved in DNA binding. The domain appears to recognize purine-rich sequences; it is about 85 to 90 amino acids in length, and is rich in aromatic and positively charged residues (Wasylyk, et al., , *Eur. J. Biochem.* (1993) *211*:718).

The *ets* gene family encodes a novel class of DNA-binding proteins, each of which binds a specific DNA sequence. These proteins comprise an *ets* domain that specifically interacts with sequences containing the common core tri-nucleotide sequence GGA. In addition to an *ets* domain, native *ets* proteins comprise other sequences which can modulate the biological specificity of the protein. *Ets* genes and proteins are involved in a variety of essential biological processes including cell growth, differentiation and development, and three members are implicated in oncogenic process.

o) Type II fibronectin collagen-binding domain (FntypeII). A few of the validation sequences, and thus the sequences they validate, represent polynucleotides encoding a polypeptide having a type II fibronectin collagen binding domain. Fibronectin is a plasma protein that binds cell surfaces and various compounds including collagen, fibrin, heparin,

DNA, and actin. The major part of the sequence of fibronectin consists of the repetition of three types of domains, which are called type I, II, and III (Skorstengaard K., et al., *Eur. J. Biochem.* (1986) *161*:441). Type II domain is approximately forty residues long, contains four conserved cysteines involved in disulfide bonds and is part of the collagen-binding region of fibronectin. In fibronectin the type II domain is duplicated. Type II domains have also been found in the following proteins: 1) blood coagulation factor XII (Hageman factor) (1 copy); 2) bovine seminal plasma proteins PDC-109 (BSP-A1/A2) and BSP-A3 (Seidah N.G., et al., *Biochem. J.* (1987) *243*:195. (twice); 3) cation-independent mannose-6-phosphate receptor (which is also the insulin-like growth factor II receptor) Kornfeld S., *Annu. Rev. Biochem.* (1992) *61*:307) (1 copy); 4) Mannose receptor of macrophages (Taylor M.E., et al., *J. Biol. Chem.* (1990) *265*:12156) (1 copy); 5) 180 Kd secretory phospholipase A2 receptor (1 copy) Lambeau G., et al., *J. Biol. Chem.* (1994) *269*:1575; 6) DEC-205 receptor (1 copy); 6) Jiang W., et al., *Nature* (1995) *375*:151); 7) 72 Kd type IV collagenase (EC 3.4.24.24) (MMP-2) (Collier I.E., et al., *J. Biol. Chem.* (1988) *263*:6579) (3 copies); 7) 92 Kd type IV collagenase (EC 3.4.24.24) (MMP-9) (3 copies); 8) Hepatocyte growth factor activator (Miyazawa K., et al., *J. Biol. Chem.* (1993) *268*:10024) (1 copy).

A schematic representation of the position of the invariant residues and the topology of the disulfide bonds in fibronectin type II domain is shown below:

xxCxxPFx#xxxxxxxCxxxxxxxxWCxxxxx#xxx#x#Cxx

where 'C' represents the conserved cysteine involved in a disulfide bond and '#' represents a large hydrophobic residue. The consensus pattern for identifying members of this family, which pattern spans this entire domain, is: C-x(2)-P-F-x-[FYWI]-x(7)-C-x(8,10)-W-C-x(4)-[DNSR]-[FYW]- x(3,5)-[FYW]-x-[FYWI]-C (where the four C's are involved in disulfide bonds).

p) G-Protein Alpha Subunit (G-alpha). Several of the validation sequences, and thus the sequences they validate, correspond to a gene encoding a novel polypeptide of the G-protein alpha subunit family. Guanine nucleotide binding proteins (G-proteins) are a family of membrane-associated proteins that couple extracellularly-activated integral-membrane receptors to intracellular effectors, such as ion channels and enzymes that vary the concentration of second messenger molecules. G-proteins are composed of 3 subunits (alpha, beta and gamma) which, in the resting state, associate as a trimer at the inner face of

the plasma membrane. The alpha subunit has a molecule of guanosine diphosphate (GDP) bound to it. Stimulation of the G-protein by an activated receptor leads to its exchange for GTP (guanosine triphosphate). This results in the separation of the alpha from the beta and gamma subunits, which always remain tightly associated as a dimer. Both the alpha and beta-gamma subunits are then able to interact with effectors, either individually or in a cooperative manner. The intrinsic GTPase activity of the alpha subunit hydrolyses the bound GTP to GDP. This returns the alpha subunit to its inactive conformation and allows it to reassociate with the beta-gamma subunit, thus restoring the system to its resting state.

G-protein alpha subunits are 350-400 amino acids in length and have molecular weights in the range 40-45 kDa. Seventeen distinct types of alpha subunit have been identified in mammals. These fall into 4 main groups on the basis of both sequence similarity and function: alpha-s, alpha-q, alpha-i and alpha-12 (Simon *et al.*, *Science* (1993) *252*:802). Many alpha subunits are substrates for ADP-ribosylation by cholera or pertussis toxins. They are often N-terminally acylated, usually with myristate and/or palmitoylate, and these fatty acid modifications are probably important for membrane association and high- affinity interactions with other proteins. The atomic structure of the alpha subunit of the G-protein involved in mammalian vision, transducin, has been elucidated in both GTP- and GDB-bound forms, and shows considerable similarity in both primary and tertiary structure in the nucleotide-binding regions to other guanine nucleotide binding proteins, such as p21-ras and EF-Tu.

q) Helicases conserved C-terminal domain (helicase_C). SEQ ID NOS:2503, 4469, and 5020, and thus the sequences they validate, represent polynucleotides encoding novel members of the DEAD/H helicase family. The DEAD and DEAH families are described above.

r) Homeobox domain (homeobox). SEQ ID NO:4241, and thus the sequence it validates, represents a polynucleotide encoding a protein having a homeobox domain. The 'homeobox' is a protein domain of 60 amino acids (Gehring In: Guidebook to the Homebox Genes, Duboule D., Ed., pp1-10, Oxford University Press, Oxford, (1994); Buerglin In: Guidebook to the Homebox Genes, pp25-72, Oxford University Press, Oxford, (1994); Gehring *Trends Biochem. Sci.* (1992) *17*:277-280; Gehring *et alAnnu. Rev. Genet.* (1986) *20*:147-173; Schofield *Trends Neurosci.* (1987) *10*:3-6; http://copan.bioz.unibas.ch/homeo.html) first identified in number of Drosophila homeotic and segmentation proteins. It is extremely well conserved in many other animals, including vertebrates. This domain

binds DNA through a helix-turn-helix type of structure. Several proteins that contain a homeobox domain play an important role in development. Most of these proteins are sequence-specific DNA-binding transcription factors. The homeobox domain is also very similar to a region of the yeast mating type proteins. These are sequence-specific DNA-binding proteins that act as master switches in yeast differentiation by controlling gene expression in a cell type-specific fashion.

A schematic representation of the homeobox domain is shown below. The helix-turn-helix region is shown by the symbols 'H' (for helix), and 't' (for turn).

```
xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxHHHHHHHHHtttHHHHHHHHHHxxxxxxxxxx
1                                                              60
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The pattern detects homeobox sequences 24 residues long and spans positions 34 to 57 of the homeobox domain. The consensus pattern is as follows: [LIVMFYG]-[ASLVR]-x(2)-[LIVMSTACN]-x-[LIVM]-x(4)-[LIV]-[RKNQESTAIY]-[LIVFSTNKH]-W-[FYVC]-x-[NDQTAH]-x(5)-[RKNAIMW].

x) MAP kinase kinase (mkk). Several validation sequences, and thus the sequences they validate, represent novel members of the MAP kinase kinase family. MAP kinases (MAPK) are involved in signal transduction, and are important in cell cycle and cell growth controls. The MAP kinase kinases (MAPKK) are dual-specificity protein kinases which phosphorylate and activate MAP kinases. MAPKK homologues have been found in yeast, invertebrates, amphibians, and mammals. Moreover, the MAPKK/MAPK phosphorylation switch constitutes a basic module activated in distinct pathways in yeast and in vertebrates. MAPKK regulation studies have led to the discovery of at least four MAPKK convergent pathways in higher organisms. One of these is similar to the yeast pheromone response pathway which includes the ste11 protein kinase. Two other pathways require the activation of either one or both of the serine/threonine kinase-encoded oncogenes c-Raf-1 and c-Mos. Additionally, several studies suggest a possible effect of the cell cycle control regulator cyclin-dependent kinase 1 (cdc2) on MAPKK activity. Finally, MAPKKs are apparently essential transducers through which signals must pass before reaching the nucleus. For review, see, *e.g.*, Biologique *Biol Cell* (1993) *79*:193-207; Nishida *et al.*, *Trends Biochem Sci* (1993) *18*:128-31; Ruderman *Curr Opin Cell Biol* (1993) *5*:207-13; Dhanasekaran *et al.*, *Oncogene* (1998) *17*:1447-55; Kiefer *et al.*, *Biochem Soc Trans* (1997) *25*:491-8; and Hill, *Cell Signal* (1996) *8*:533-44.

y) 3'5'-cyclic nucleotide phosphodiesterases signature (PDEase). SEQ ID NO:4482, and thus the sequence it validates, represents a polynucleotide encoding a novel 3'5'-cyclic nucleotide phosphodiesterases (PDEases). PDEases catalyze the hydrolysis of cAMP or cGMP to the corresponding nucleoside 5' monophosphates (Charbonneau H., et al, *Proc. Natl. Acad. Sci. U.S.A.* (1986) *83*:9308). There are at least seven different subfamilies of PDEases (Beavo J.A., et al., *Trends Pharmacol. Sci.* (1990) *11*:150; http://weber.u.washington.edu/~pde/: 1) Type 1, calmodulin/calcium-dependent PDEases; 2) Type 2, cGMP-stimulated PDEases; 3) Type 3, cGMP-inhibited PDEases; 4) Type 4, cAMP-specific PDEases.; 5) Type 5, cGMP-specific PDEases; 6) Type 6, rhodopsin-sensitive cGMP-specific PDEases; and 7) Type 7, High affinity cAMP-specific PDEases.

All PDEase forms share a conserved domain of about 270 residues. The signature pattern is determined from a stretch of 12 residues that contains two conserved histidines: H-D-[LIVMFY]-x-H-x-[AG]-x(2)-[NQ]-x-[LIVMFY].

z) Protein Kinase (protkinase). Several validation sequences, and thus the sequences they validate, represent polynucleotides encoding protein kinases. Protein kinases catalyze phosphorylation of proteins in a variety of pathways, and are implicated in cancer. Eukaryotic protein kinases (Hanks S.K., *et al.*, *FASEB J.* (1995) *9*:576; Hunter T., *Meth. Enzymol.* (1991) *200*:3; Hanks S.K., *et al.*, *Meth. Enzymol.* (1991) *200*:38; Hanks S.K., *Curr. Opin. Struct. Biol.* (1991) *1*:369; Hanks S.K., *et al.*, *Science* (1988) *241*:42) are enzymes that belong to a very extensive family of proteins which share a conserved catalytic core common to both serine/threonine and tyrosine protein kinases. There are a number of conserved regions in the catalytic domain of protein kinases. Two of the conserved regions are the basis for the signature pattern in the protein kinase profile. The first region, which is located in the N-terminal extremity of the catalytic domain, is a glycine-rich stretch of residues in the vicinity of a lysine residue, which has been shown to be involved in ATP binding. The second region, which is located in the central part of the catalytic domain, contains a conserved aspartic acid residue which is important for the catalytic activity of the enzyme (Knighton D.R., *et al.*, *Science* (1991) *253*:407). The protein kinase profile includes two signature patterns for this second region: one specific for serine/threonine kinases and the other for tyrosine kinases. A third profile is based on the alignment in (Hanks S.K., *et al.*, *FASEB J.* (1995) *9*:576) and covers the entire catalytic domain. The consensus patterns are as follows:

1) Consensus pattern: [LIV]-G-{P}-G-{P}-[FYWMGSTNH]-[SGA]-{PW}-[LIVCAT]-{PD}-x-[GSTACLIVMFY]-x(5,18)-[LIVMFYWCSTAR]-[AIVP]-[LIVMFAGCKR]-K, where K binds ATP. The majority of known protein kinases are detected by this pattern. Proteins kinases that are not detected by this consensus include viral kinases, which are quite divergent in this region and are completely missed bythis pattern.

2) Consensus pattern: [LIVMFYC]-x-[HY]-x-D-[LIVMFY]-K-x(2)-N-[LIVMFYCT](3), where D is an active site residue. This consensus sequence identifies most serine/threonine-specific protein kinases with only 10 exceptions. Half of the exceptions are viral kinases, while the other exceptions include Epstein-Barr virus BGLF4 and Drosophila ninaC, which have Ser and Arg, respectively, instead of the conserved Lys. These latter two protein kinases are detected by the tyrosine kinase specific pattern described below.

3) Consensus pattern: [LIVMFYC]-x-[HY]-x-D-[LIVMFY]-[RSTAC]-x(2)-N-[LIVMFYC], where D is an active site residue. All tyrosine-specific protein kinases are detected by this consensus pattern, with the exception of human ERBB3 and mouse blk. This pattern also detects most bacterial aminoglycoside phosphotransferases (Benner S., *Nature* (1987) *329*:21; Kirby R., *J. Mol. Evol.* (1992) *30*:489) and herpesviruses ganciclovir kinases (Littler E., *et al.*, *Nature* (1992) *358*:160), which are structurally and evolutionary related to protein kinases.

The protein kinase profile also detects receptor guanylate cyclases and 2-5A-dependent ribonucleases. Sequence similarities between these two families and the eukaryotic protein kinase family have been noticed previously. The profile also detects Arabidopsis thaliana kinase-like protein TMKL1 which seems to have lost its catalytic activity.

If a protein analyzed includes the two of the above protein kinase signatures, the probability of it being a protein kinase is close to 100%. Eukaryotic-type protein kinases have also been found in prokaryotes such as Myxococcus xanthus (Munoz-Dorado J., *et al.*, *Cell* (1991) *67*:995) and Yersinia pseudotuberculosis. The patterns shown above has been updated since their publication in (Bairoch A., *et al.*, *Nature* (1988) *331*:22).

aa) Ras family proteins (ras). SEQ IDNO:3671, and thus the sequence it validates, represent polynucleotides encoding the ras family of small GTP/GDP-binding proteins (Valencia et al., 1991, Biochemistry 30:4637-4648). Ras family members generally require

a specific guanine nucleotide exchange factor (GEF) and a specific GTPase activating protein (GAP) as stimulators of overall GTPase activity. Among ras-related proteins, the highest degree of sequence conservation is found in four regions that are directly involved in guanine nucleotide binding. The first two constitute most of the phosphate and Mg2+ binding site (PM site) and are located in the first half of the G-domain. The other two regions are involved in guanosine binding and are located in the C-terminal half of the molecule. Motifs and conserved structural features of the ras-related proteins are described in Valencia et al., 1991, Biochemistry 30:4637-4648.

A major consensus pattern of ras proteins is: D-T-A-G-Q-E-K-[LF]-G-G-L-R-[DE]-G-Y-Y.

bb) Thioredoxin family active site (Thioredox). SEQ ID NO:3936, and thus the sequence it validates, represent a polynucleotide encoding a protein having a thioredoxin family active site. Thioredoxins (Holmgren A., *Annu. Rev. Biochem.* (1985) *54*:237; Gleason F.K., et al., *FEMS Microbiol. Rev.* (1988) *54*:271; Holmgren A. *J. Biol. Chem.* (1989) *264*:13963; Eklund H., et al. *Proteins* (1991) *11*:13) are small proteins of approximately one hundred amino- acid residues which participate in various redox reactions via the reversible oxidation of an active center disulfide bond. They exist in either a reduced form or an oxidized form where the two cysteine residues are linked in an intramolecular disulfide bond. Thioredoxin is present in prokaryotes and eukaryotes and the sequence around the redox-active disulfide bond is well conserved.

A number of eukaryotic proteins contain domains evolutionary related to thioredoxin, and all of them are protein disulphide isomerases (PDI). PDI (Freedman R.B., et al., *Biochem. Soc. Trans.* (1988) *16*:96; Kivirikko K.I., et al., *FASEB J.* (1989) *3*:1609; Freedman R.B., et al. *Trends Biochem. Sci.* (1994) *19*:331) is an endoplasmic reticulum enzyme that catalyzes the rearrangement of disulfide bonds in various proteins. The various forms of PDI which are currently known are: 1) PDI major isozyme; a multifunctional protein that also function as the beta subunit of prolyl 4-hydroxylase (EC 1.14.11.2), as a component of oligosaccharyl transferase (EC 2.4.1.119), as thyroxine deiodinase, as glutathione-insulin transhydrogenase, and as a thyroid hormone-binding protein; 2) ERp60 (ER-60; 58 Kd microsomal protein), which is a protease; 3) ERp72; and 4) P5.

All PDI contains two or three (ERp72) copies of the thioredoxin domain. The consensus pattern is: [LIVMF]-[LIVMSTA]-x-[LIVMFYC]-[FYWSTHE]-x(2)-

[FYWGTN]-C- [GATPLVE]-[PHYWSTA]-C-x(6)-[LIVMFYWT] (where the two C's form the redox-active bond.

cc) TNFR/NGFR family cysteine-rich region (TNFR_c6). SEQ ID NO:3927, and thus the sequence it validates, represent a polynucleotide encoding a protein having a TNFR/NGFR family cysteine-rich region. A number of proteins, some of which are known to be receptors for growth factors, have been found to contain a cysteine-rich domain of about 110 to 160 amino acids in their N-terminal part, that can be subdivided into four (or in some cases, three) modules of about 40 residues containing 6 conserved cysteines. Proteins known to belong to this family (Mallet S., et al., *Immunol. Today* (1991) 12:220; Sprang S.R., *Trends Biochem. Sci.* (1990) 15:366; Krammer P.H., et al., *Curr. Biol.* (1992) 2:383; Bazan J.F., *Curr. Biol.* (1993) *3*:603) are: 1) Tumor Necrosis Factor type I and type II receptors (TNFR) (Both receptors bind TNF-alpha and TNF-beta, but are only similar in the cysteine-rich region.); 2) Shope fibroma virus soluble TNF receptor (protein T2); 3) Lymphotoxin alpha/beta receptor; 4) Low-affinity nerve growth factor receptor (LA-NGFR); 5) CD40 (Bp50), the receptor for the CD40L (or TRAP) cytokine; 6) CD27, the receptor for the CD27L cytokine; 8) CD30, the receptor for the CD30L cytokine; 9) T-cell protein 4-1BB, the receptor for the 4-1BBL putative cytokine; 10) FAS antigen (or APO-1), the receptor for FASL, a protein involved in apoptosis (programmed cell death); 11) T-cell antigen OX40, the receptor for the OX40L cytokine; 12) Wsl-1, a receptor (for a yet undefined ligand) that mediates apoptosis; 13) Vaccinia virus protein A53 (SalF19R).

The six cysteines all involved in intrachain disulfide bonds (Banner D.W., et al, *Cell* (1993) *73*:431). A schematic representation of the structure of the 40 residue module of these receptors is shown below:

xCxxxxxxxxxxxxxCxCxxCxxxxxxxxxCxxxxCxx

where 'C' represents the conserved cysteine involved in a disulfide bond. The signature pattern for the cysteine-rich region is based mainly on the position of the six conserved cysteines in each of the repeats: Consensus pattern: C-x(4,6)-[FYH]-x(5,10)-C-x(0,2)-C-x(2,3)-C-x(7,11)-C-x(4,6)-[DNEQSKP]-x(2)-C (where the six C's are involved in disulfide bonds).

dd) Four Transmembrane Integral Membrane Proteins (transmembrane4). Several of the validation sequences, and thus the sequences they validate, correspond to a sequence encoding a polypeptide that is a member of the 4 transmembrane segments integral

membrane protein family (transmembrane 4 family). The transmembrane 4 family of proteins includes a number of evolutionarily-related eukaryotic cell surface antigens (Levy *et al.*, *J. Biol. Chem.*, (1991) *266*:14597; Tomlinson *et al.*, *Eur. J. Immunol.* (1993) *23*:136; Barclay *et al.* The leucocyte antigen factbooks. (1993) Academic Press, London/San Diego). The proteins belonging to this family include: 1) Mammalian antigen CD9 (MIC3), which is involved in platelet activation and aggregation; 2) Mammalian leukocyte antigen CD37, expressed on B lymphocytes; 3) Mammalian leukocyte antigen CD53 (OX-44), which is implicated in growth regulation in hematopoietic cells; 4) Mammalian lysosomal membrane protein CD63 (melanoma-associated antigen ME491; antigen AD1); 5) Mammalian antigen CD81 (cell surface protein TAPA-1), which is implicated in regulation of lymphoma cell growth; 6) Mammalian antigen CD82 (protein R2; antigen C33; Kangai 1 (KAI1)), which associates with CD4 or CD8 and delivers costimulatory signals for the TCR/CD3 pathway; 7) Mammalian antigen CD151 (SFA-1; platelet-endothelial tetraspan antigen 3 (PETA-3)); 8) Mammalian cell surface glycoprotein A15 (TALLA-1; MXS1); 9) Mammalian novel antigen 2 (NAG-2); 10) Human tumor-associated antigen CO-029; 11) Schistosoma mansoni and japonicum 23 Kd surface antigen (SM23 / SJ23).

The members of the 4 transmembrane family share several characteristics. First, they all are apparently type III membrane proteins, which are integral membrane proteins containing an N-terminal membrane-anchoring domain which is not cleaved during biosynthesis and which functions both as a translocation signal and as a membrane anchor. The family members also contain three additional transmembrane regions, at least seven conserved cysteines residues, and are of approximately the same size (218 to 284 residues). These proteins are collectively know as the "transmembrane 4 superfamily" (TM4) because they span plasma membrane four times.

A schematic diagram of the domain structure of these proteins is as follows:

```
+-+-----+-------+----+-----+-----+-------------------------+-----+----+
| | TMa | Extra | TM2| Cyt | TM3 | Extracellular           | TM4 | Cyt|
+-+-----+-------+----C-----C-----+-------CC---------C-----C---+-----C----+
                    *********
```

where Cyt is the cytoplasmic domain, TMa is the transmembrane anchor; TM2 to TM4 represents transmembrane regions 2 to 4, 'C' are conserved cysteines, and '*'indicates the position of the consensus pattern. The consensus pattern spans a conserved region including two cysteines located in a short cytoplasmic loop between two transmembrane domains: Consensus pattern: G-x(3)-[LIVMF]-x(2)-[GSA]-[LIVMF](2)-G-C-x-[GA]-[STA]- x(2)-[EG]-x(2)-[CWN]-[LIVM](2).

ee) Trypsin (trypsin). SEQ ID NOS:3381, 4684, and 4688, and thus the sequences they validate, correspond to novel serine proteases of the trypsin family. The catalytic activity of the serine proteases from the trypsin family is provided by a charge relay system involving an aspartic acid residue hydrogen-bonded to a histidine, which itself is hydrogen-bonded to a serine. The sequences in the vicinity of the active site serine and histidine residues are well conserved in this family of proteases (Brenner S., *Nature* (1988) *334*:528). Proteases known to belong to the trypsin family include: 1) Acrosin; 2) Blood coagulation factors VII, IX, X, XI and XII, thrombin, plasminogen, and protein C; 3) Cathepsin G; 4) Chymotrypsins; 5) Complement components C1r, C1s, C2, and complement factors B, D and I; 6) Complement-activating component of RA-reactive factor; 7) Cytotoxic cell proteases (granzymes A to H); 8) Duodenase I; 9) Elastases 1, 2, 3A, 3B (protease E), leukocyte (medullasin).; 10) Enterokinase (EC 3.4.21.9) (enteropeptidase); 11) Hepatocyte growth factor activator; 12) Hepsin; 13) Glandular (tissue) kallikreins (including EGF-binding protein types A, B, and C, NGF-gamma chain, gamma-renin, prostate specific antigen (PSA) and tonin); 14) Plasma kallikrein; 15) Mast cell proteases (MCP) 1 (chymase) to 8; 16) Myeloblastin (proteinase 3) (Wegener's autoantigen); 17) Plasminogen activators (urokinase-type, and tissue-type); 18) Trypsins I, II, III, and IV; 19) Tryptases; 20) Snake venom proteases such as ancrod, batroxobin, cerastobin, flavoxobin, and protein C activator; 21) Collagenase from common cattle grub and collagenolytic protease from Atlantic sand fiddler crab; 22) Apolipoprotein(a); 23) Blood fluke cercarial protease; 24) Drosophila trypsin like proteases: alpha, easter, snake-locus; 25) Drosophila protease stubble (gene sb); and 26) Major mite fecal allergen Der p

III. All the above proteins belong to family S1 in the classification of peptidases (Rawlings N.D., *et al.*, *Meth. Enzymol.* (1994) *244*:19; http://www.expasy.ch/cgi-bin/lists?peptidas.txt) and originate from eukaryotic species. It should be noted that bacterial proteases that belong to family S2A are similar enough in the regions of the active site residues that they can be picked up by the same patterns.

The consensus patterns for this trypsin protein family are: 1) [LIVM]-[ST]-A-[STAG]-H-C, where H is the active site residue. All sequences known to belong to this class detected by the pattern, except for complement components C1r and C1s, pig plasminogen, bovine protein C, rodent urokinase, ancrod, gyroxin and two insect trypsins; 2) [DNSTAGC]-[GSTAPIMVQH]-x(2)-G-[DE]-S-G-[GS]-[SAPHV]- [LIVMFYWH]-[LIVMFYSTANQH], where S is the active site residue. All sequences known to belong to this family are detected by the above consensus sequences, except for 18 different proteases which have lost the first conserved glycine. If a protein includes both the serine and the histidine active site signatures, the probability of it being a trypsin family serine protease is 100%.

ff) WD Domain, G-Beta Repeats (WD domain). A few of the validation sequences, and the sequences they validate, represent novel members of the WD domain/G-beta repeat family. Beta-transducin (G-beta) is one of the three subunits (alpha, beta, and gamma) of the guanine nucleotide-binding proteins (G proteins) which act as intermediaries in the transduction of signals generated by transmembrane receptors (Gilman, *Annu. Rev. Biochem.* (1987) *56*:615). The alpha subunit binds to and hydrolyzes GTP; the functions of the beta and gamma subunits are less clear but they seem to be required for the replacement of GDP by GTP as well as for membrane anchoring and receptor recognition.

In higher eukaryotes, G-beta exists as a small multigene family of highly conserved proteins of about 340 amino acid residues. Structurally, G-beta consists of eight tandem repeats of about 40 residues, each containing a central Trp-Asp motif (this type of repeat is sometimes called a WD-40 repeat). Such a repetitive segment has been shown to exist in a number of other proteins including: human LIS1, a neuronal protein involved in type-1 lissencephaly; and mammalian coatomer beta' subunit (beta'-COP), a component of a cytosolic protein complex that reversibly associates with Golgi membranes to form vesicles that mediate biosynthetic protein transport.

The consensus pattern for the WD domain/G-Beta repeat family is: [LIVMSTAC]-

[LIVMFYWSTAGC]-[LIMSTAG]-[LIVMSTAGC]-x(2)-[DN]-x(2)-[LIVMWSTAC]-x-[LIVMFSTAG]-W-[DEN]-[LIVMFSTAGCN].

gg) wnt Family of Developmental Signaling Proteins (Wnt_dev_sign). Several of the validation sequences, and thus the sequences they validate, correspond to novel members of the wnt family of developmental signaling proteins. Wnt-1 (previously known as int-1), the seminal member of this family, (Nusse R., *Trends Genet.* (1988) *4*:291) is a proto-oncogene induced by the integration of the mouse mammary tumor virus. It is thought to play a role in intercellular communication and seems to be a signalling molecule important in the development of the central nervous system (CNS). The sequence of wnt-1 is highly conserved in mammals, fish, and amphibians. Wnt-1 was found to be a member of a large family of related proteins (Nusse R., *et al.*, *Cell* (1992) *69*:1073; McMahon A.P., *Trends Genet.* (1992) *8*:1; Moon R.T., *BioEssays* (1993) *15*:91) that are all thought to be developmental regulators. These proteins are known as wnt-2 (also known as irp), wnt-3, -3A, -4, -5A, -5B, -6, -7A, -7B, -8, -8B, -9 and -10. At least four members of this family are present in Drosophila; one of them, wingless (wg), is implicated in segmentation polarity.

All these proteins share the following features characteristics of secretory proteins: a signal peptide, several potential N-glycosylation sites and 22 conserved cysteines that are probably involved in disulfide bonds. The Wnt proteins seem to adhere to the plasma membrane of the secreting cells and are therefore likely to signal over only few cell diameters. The consensus pattern, which is based upon a highly conserved region including three cysteines, is as follows: C-K-C-H-G-[LIVMT]-S-G-x-C. All sequences known to belong to this family are detected by the provided consensus pattern.

hh) Protein Tyrosine Phosphatase (Y_phosphatase). Several of the validation sequences, and thus the sequences they validate, represent a polynucleotide encoding a protein tyrosine kinase. Tyrosine specific protein phosphatases (EC 3.1.3.48) (PTPase) (Fischer *et al.*, *Science* (1991) *253*:401; Charbonneau *et al.*, *Annu. Rev. Cell Biol.* (1992) *8*:463; Trowbridge, *J. Biol. Chem.* (1991) *266*:23517; Tonks *et al.*, *Trends Biochem. Sci.* (1989) *14*:497; and Hunter, *Cell* (1989) *58*:1013) catalyze the removal of a phosphate group attached to a tyrosine residue. These enzymes are very important in the control of cell growth, proliferation, differentiation and transformation. Multiple forms of PTPase have been characterized and can be classified into two categories: soluble PTPases and transmembrane receptor proteins that contain PTPase domain(s).

Soluble PTPases include PTPN3 (H1) and PTPN4 (MEG), enzymes that contain an N-terminal band 4.1-like domain and could act at junctions between the membrane and cytoskeleton; PTPN6 (PTP-1C; HCP; SHP) and PTPN11 (PTP-2C; SH-PTP3; Syp), enzymes that contain two copies of the SH2 domain at its N-terminal extremity.

Dual specificity PTPases include DUSP1 (PTPN10; MAP kinase phosphatase-1; MKP-1) which dephosphorylates MAP kinase on both Thr-183 and Tyr-185; and DUSP2 (PAC-1), a nuclear enzyme that dephosphorylates MAP kinases ERK1 and ERK2 on both Thr and Tyr residues.

Structurally, all known receptor PTPases are made up of a variable length extracellular domain, followed by a transmembrane region and a C-terminal catalytic cytoplasmic domain. Some of the receptor PTPases contain fibronectin type III (FN-III) repeats, immunoglobulin-like domains, MAM domains or carbonic anhydrase-like domains in their extracellular region. The cytoplasmic region generally contains two copies of the PTPAse domain. The first seems to have enzymatic activity, while the second is inactive but seems to affect substrate specificity of the first. In these domains, the catalytic cysteine is generally conserved but some other, presumably important, residues are not.

PTPase domains consist of about 300 amino acids. There are two conserved cysteines and the second one has been shown to be absolutely required for activity. Furthermore, a number of conserved residues in its immediate vicinity have also been shown to be important. The consensus pattern for PTPases is: [LIVMF]-H-C-x(2)-G-x(3)-[STC]-[STAGP]-x-[LIVMFY]; C is the active site residue.

ii)Zinc Finger, C2H2 Type (Zincfing_C2H2). Several of the validation sequences, and thus the sequences they validate, correspond to polynucleotides encoding novel members of the of the C2H2 type zinc finger protein family. Zinc finger domains (Klug *et al.*, *Trends Biochem. Sci.* (1987) *12*:464; Evans *et al.*, *Cell* (1988) *52*:1; Payre *et al.*, *FEBS Lett.* (1988) *234*:245; Miller *et al.*, *EMBO J.* (1985) *4*:1609; and Berg, *Proc. Natl. Acad. Sci. USA* (1988) *85*:99) are nucleic acid-binding protein structures first identified in the Xenopus transcription factor TFIIIA. These domains have since been found in numerous nucleic acid-binding proteins. A zinc finger domain is composed of 25 to 30 amino acid residues. Two cysteine or histidine residues are positioned at both extremities of the domain, which are involved in the tetrahedral coordination of a zinc atom. It has been proposed that such a domain interacts with about five nucleotides.

Many classes of zinc fingers are characterized according to the number and

positions of the histidine and cysteine residues involved in the zinc atom coordination. In the first class to be characterized, called C2H2, the first pair of zinc coordinating residues are cysteines, while the second pair are histidines. A number of experimental reports have demonstrated the zinc-dependent DNA or RNA binding property of some members of this class.

Mammalian proteins having a C2H2 zipper include (number in parenthesis indicates number of zinc finger regions in the protein): basonuclin (6), BCL-6/LAZ-3 (6), erythroid krueppel-like transcription factor (3), transcription factors Sp1 (3), Sp2 (3), Sp3 (3) and Sp(4) 3, transcriptional repressor YY1 (4), Wilms' tumor protein (4), EGR1/Krox24 (3), EGR2/Krox20 (3), EGR3/Pilot (3), EGR4/AT133 (4), Evi-1 (10), GLI1 (5), GLI2 (4+), GLI3 (3+), HIV-EP1/ZNF40 (4), HIV-EP2 (2), KR1 (9+), KR2 (9), KR3 (15+), KR4 (14+), KR5 (11+), HF.12 (6+), REX-1 (4), ZfX (13), ZfY (13), Zfp-35 (18), ZNF7 (15), ZNF8 (7), ZNF35 (10), ZNF42/MZF-1 (13), ZNF43 (22), ZNF46/Kup (2), ZNF76 (7), ZNF91 (36), ZNF133 (3).

In addition to the conserved zinc ligand residues, it has been shown that a number of other positions are also important for the structural integrity of the C2H2 zinc fingers. (Rosenfeld *et al., J. Biomol. Struct. Dyn.* (1993) *11*:557) The best conserved position is found four residues after the second cysteine; it is generally an aromatic or aliphatic residue. The consensus pattern for C2H2 zinc fingers is: C-x(2,4)-C-x(3)-[LIVMFYWC]-x(8)-H-x(3,5)-H. The two C's and two H's are zinc ligands.

jj) Zinc finger, C3HC4 type (RING finger), signature (Zincfing_C3H4). SEQ ID NOS:3774 and 4477, and thus the sequences they validate, represent polynucleotides encoding a polypeptide having a C3HC4 type zinc finger signature. A number of eukaryotic and viral proteins contain this signature, which is primarily a conserved cysteine-rich domain of 40 to 60 residues (Borden K.L.B., et al., *Curr. Opin. Struct. Biol.* (1996) *6*:395) that binds two atoms of zinc, and is probably involved in mediating protein-protein interactions. The 3D structure of the zinc ligation system is uniqueto the RING domain and is refered to as the "cross-brace" motif. The spacing of the cysteines in such a domain is C-x(2)-C-x(9 to 39)-C-x(1 to 3)-H-x(2 to 3)-C-x(2)-C-x(4 to 48)-C-x(2)-C. Proteins that include the C3HC4 domain include:

1) Mammalian V(D)J recombination activating protein (RAG1). RAG1 activates the rearrangement of immunoglobulin and T-cell receptor genes.

2) Mouse rpt-1. Rpt-1 is a trans-acting factor that regulates gene expression directed

by the promoter region of the interleukin-2 receptor alpha chainor the LTR promoter region of HIV-1.

3) Human rfp. Rfp is a developmentally regulated protein that may function in male germ cell development. Recombination of the N-terminal section of rfp with a protein tyrosine kinase produces the ret transforming protein.

4) Human 52 Kd Ro/SS-A protein. A protein of unknown function from the Ro/SS-A ribonucleoprotein complex. Sera from patients with systemic lupus erythematosus or primary Sjogren's syndrome often contain antibodies that react with the Ro proteins.

5) Human histocompatibility locus protein RING1.

6) Human PML, a probable transcription factor. Chromosomal translocation ofPML with retinoic receptor alpha creates a fusion protein which is thecause of acute promyelocytic leukemia (APL).

7) Mammalian breast cancer type 1 susceptibility protein (BRCA1) ([E1] http://bioinformatics.weizmann.ac.il/hotmolecbase/entries/brca1.htm).

8) Mammalian cbl proto-oncogene.

9) Mammalian bmi-1 proto-oncogene.

10) Vertebrate CDK-activating kinase (CAK) assembly factor MAT1, a protein that stabilizes the complex between the CDK7 kinase and cyclin H (MAT1 stands for 'Menage A Trois').

11) Mammalian mel-18 protein. Mel-18 which is expressed in a variety of tumorcells is a transcriptional repressor that recognizes and bind a specific DNA sequence.

12) Mammalian peroxisome assembly factor-1 (PAF-1) (PMP35), which is somewhat involved in the biogenesis of peroxisomes. In humans, defects in PAF-1 are responsible for a form of Zellweger syndrome, an autosomal recessivedisorder associated with peroxisomal deficiencies.

13) Human MAT1 protein, which interacts with the CDK7-cyclin H complex.

14) Human RING1 protein.

15) Xenopus XNF7 protein, a probable transcription factor.

16) Trypanosoma protein ESAG-8 (T-LR), which may be involved in the postranscriptional regulation of genes in VSG expression sites or may interact with adenylate cyclase to regulate its activity.

17) Drosophila proteins Posterior Sex Combs (Psc) and Suppressor two of zeste

(Su(z)2). The two proteins belong to the Polycomb group of genes needed to maintain the segment-specific repression of homeotic selector genes.

18) Drosophila protein male-specific msl-2, a DNA-binding protein which is involved in X chromosome dosage compensation (the elevation of transcription of the male single X chromosome).

19) Arabidopsis thaliana protein COP1 which is involved in the regulation ofphotomorphogenesis.

20) Fungal DNA repair proteins RAD5, RAD16, RAD18 and rad8.

21) Herpesviruses trans-acting transcriptional protein ICP0/IE110. This protein which has been characterized in many different herpesviruses is a trans-activator and/or -repressor of the expression of many viral and cellular promoters.

22) Baculoviruses protein CG30.

23) Baculoviruses major immediate early protein (PE-38).

24) Baculoviruses immediate-early regulatory protein IE-N/IE-2.

25) Caenorhabditis elegans hypothetical proteins F54G8.4, R05D3.4 and T02C1.1.

26) Yeast hypothetical proteins YER116c and YKR017c.

The signature pattern for the C3HC4 finger is based on the central region of the domain:

Consensus pattern: C-x-H-x-[LIVMFY]-C-x(2)-C-[LIVMYA].

Example 4: Differential Expression of Polynucleotides of the Invention: Description of Libraries and Detection of Differential Expression

The relative expression levels of the polynucleotides of the invention was assessed in several libraries prepared from various sources, including cell lines and patient tissue samples. Table 4 provides a summary of these libraries, including the shortened library name (used hereafter), the mRNA source used to prepared the cDNA library, the "nickname" of the library that is used in the tables below (in quotes), and the approximate number of clones in the library.

Table 4 Description of cDNA Libraries

Library (lib #)	Description	Number of Clones in this Clustering
1	Km12 L4	

Library (lib #)	Description	Number of Clones in this Clustering
	Human Colon Cell Line, High Metastatic Potential (derived from Km12C) "High Colon"	307133
2	Km12C Human Colon Cell Line, Low Metastatic Potential "Low Colon"	284755
3	MDA-MB-231 Human Breast Cancer Cell Line, High Metastatic Potential; micro-metastases in lung "High Breast"	326937
4	MCF7 Human Breast Cancer Cell, Non Metastatic "Low Breast"	318979
8	MV-522 Human Lung Cancer Cell Line, High Metastatic Potential "High Lung"	223620
9	UCP-3 Human Lung Cancer Cell Line, Low Metastatic Potential "Low Lung"	312503
12	Human microvascular endothelial cells (HMEC) – Untreated PCR (OligodT) cDNA library	41938
13	Human microvascular endothelial cells (HMEC) – **Basic fibroblast growth factor** (bFGF) treated PCR (OligodT) cDNA library	42100
14	Human microvascular endothelial cells (HMEC) – Vascular endothelial growth factor (VEGF) treated PCR (OligodT) cDNA library	42825
15	Normal Colon – UC#2 Patient PCR (OligodT) cDNA library "Normal Colon Tumor Tissue"	34285
16	Colon Tumor – UC#2 Patient PCR (OligodT) cDNA library "Normal Colon Tumor Tissue"	35625
17	Liver Metastasis from Colon Tumor of UC#2 Patient PCR (OligodT) cDNA library "High Colon Metastasis Tissue"	36984
18	Normal Colon – UC#3 Patient PCR (OligodT) cDNA library "Normal Colon Tumor Tissue"	36216
19	Colon Tumor – UC#3 Patient PCR (OligodT) cDNA library "High Colon Tumor Tissue"	41388
20	Liver Metastasis from Colon Tumor of UC#3 Patient PCR (OligodT) cDNA library "High Colon Metastasis Tissue"	30956

The KM12L4 and KM12C cell lines are described in Example 1 above. The MDA-MB-231 cell line was originally isolated from pleural effusions (Cailleau, *J. Natl. Cancer. Inst.* (1974) *53*:661), is of high metastatic potential, and forms poorly differentiated

adenocarcinoma grade II in nude mice consistent with breast carcinoma. The MCF7 cell line was derived from a pleural effusion of a breast adenocarcinoma and is non-metastatic. The MV-522 cell line is derived from a human lung carcinoma and is of high metastatic potential. The UCP-3 cell line is a low metastatic human lung carcinoma cell line; the MV-522 is a high metastatic variant of UCP-3. These cell lines are well-recognized in the art as models for the study of human breast and lung cancer (see, *e.g.*, Chandrasekaran *et al.*, *Cancer Res.* (1979) *39*:870 (MDA-MB-231 and MCF-7); Gastpar *et al.*, *J Med Chem* (1998) *41*:4965 (MDA-MB-231 and MCF-7); Ranson *et al.*, *Br J Cancer* (1998) *77*:1586 (MDA-MB-231 and MCF-7); Kuang *et al.*, *Nucleic Acids Res* (1998) *26*:1116 (MDA-MB-231 and MCF-7); Varki *et al.*, *Int J Cancer* (1987) *40*:46 (UCP-3); Varki *et al.*, *Tumour Biol.* (1990) *11*:327; (MV-522 and UCP-3); Varki *et al.*, *Anticancer Res.* (1990) *10*:637; (MV-522); Kelner *et al.*, *Anticancer Res* (1995) *15*:867 (MV-522); and Zhang *et al.*, *Anticancer Drugs* (1997) *8*:696 (MV522)). The samples of libraries 15-20 are derived from two different patients (UC#2, and UC#3). The bFGF-treated HMEC were prepared by incubation with bFGF at 10ng/ml for 2 hrs; the VEGF-treated HMEC were prepared by incubation with 20ng/ml BEGF for 2 hrs. Following incubation with the respective growth factor, the cells were washed and lysis buffer added for RNA preparation.

Each of the libraries is composed of a collection of cDNA clones that in turn are representative of the mRNAs expressed in the indicated mRNA source. In order to facilitate the analysis of the millions of sequences in each library, the sequences were assigned to clusters. The concept of "cluster of clones" is derived from a sorting/grouping of cDNA clones based on their hybridization pattern to a panel of roughly 300 7bp oligonucleotide probes (see Drmanac *et al.*, *Genomics* (1996) *37*(1):29). Random cDNA clones from a tissue library are hybridized at moderate stringency to 300 7bp oligonucleotides. Each oligonucleotide has some measure of specific hybridization to that specific clone. The combination of 300 of these measures of hybridization for 300 probes equals the "hybridization signature" for a specific clone. Clones with similar sequence will have similar hybridization signatures. By developing a sorting/grouping algorithm to analyze these signatures, groups of clones in a library can be identified and brought together computationally. These groups of clones are termed "clusters". Depending on the stringency of the selection in the algorithm (similar to the stringency of hybridization in a

classic library cDNA screening protocol), the "purity" of each cluster can be controlled. For example, artifacts of clustering may occur in computational clustering just as artifacts can occur in "wet-lab" screening of a cDNA library with 400 bp cDNA fragments, at even the highest stringency. The stringency used in the implementation of cluster herein provides groups of clones that are in general from the same cDNA or closely related cDNAs. Closely related clones can be a result of different length clones of the same cDNA, closely related clones from highly related gene families, or splice variants of the same cDNA.

Differential expression for a selected cluster was assessed by first determining the number of cDNA clones corresponding to the selected cluster in the first library (Clones in 1st), and the determining the number of cDNA clones corresponding to the selected cluster in the second library (Clones in 2nd). Differential expression of the selected cluster in the first library relative to the second library is expressed as a "ratio" of percent expression between the two libraries. In general, the "ratio" is calculated by: 1) calculating the percent expression of the selected cluster in the first library by dividing the number of clones corresponding to a selected cluster in the first library by the total number of clones analyzed from the first library; 2) calculating the percent expression of the selected cluster in the second library by dividing the number of clones corresponding to a selected cluster in a second library by the total number of clones analyzed from the second library; 3) dividing the calculated percent expression from the first library by the calculated percent expression from the second library. If the "number of clones" corresponding to a selected cluster in a library is zero, the value is set at 1 to aid in calculation. The formula used in calculating the ratio takes into account the "depth" of each of the libraries being compared, *i.e.*, the total number of clones analyzed in each library.

In general, a polynucleotide is said to be significantly differentially expressed between two samples when the ratio value is greater than at least about 2, preferably greater than at least about 3, more preferably greater than at least about 5 , where the ratio value is calculated using the method described above. The significance of differential expression is determined using a z score test (Zar, Biostatistical Analysis, Prentice Hall, Inc., USA, "Differences between Proportions," pp 296-298 (1974).

Example 5: Polynucleotides Differentially Expressed in High Metastatic Potential Breast Cancer Cells Versus Low Metastatic Breast Cancer Cells

A number of polynucleotide sequences have been identified that are differentially expressed between cells derived from high metastatic potential breast cancer tissue and low metastatic breast cancer cells. Expression of these sequences in breast cancer can be valuable in determining diagnostic, prognostic and/or treatment information. For example, sequences that are highly expressed in the high metastatic potential cells can be indicative of increased expression of genes or regulatory sequences involved in the metastatic process. A patient sample displaying an increased level of one or more of these polynucleotides may thus warrant more aggressive treatment. In another example, sequences that display higher expression in the low metastatic potential cells can be associated with genes or regulatory sequences that inhibit metastasis, and thus the expression of these polynucleotides in a sample may warrant a more positive prognosis than the gross pathology would suggest.

The differential expression of these polynucleotides can be used as a diagnostic marker, a prognostic marker, for risk assessment, patient treatment and the like. These polynucleotide sequences can also be used in combination with other known molecular and/or biochemical markers.

The following tables summarize polynucleotides that are differentially expressed between high metastatic potential breast cancer cells and low metastatic potential breast cancer cells.

Table 5. Differentially expressed polynucleotides: Higher expression in high metastatic potential breast cancer (lib3) relative to low metastatic breast cancer cells (lib4)

SEQ ID NOS:	Sequence Name	Cluster ID	Lib3 clones	Lib4 clones	lib3/lib4	Zscore
45	RTA00000197AR.f.12.1	3513	17	5	3.317240	2.287632
146	RTA00000185AF.a.19.2	5749	9	0	8.780930	2.629923
154	RTA00000196F.e.7.1	1039	10	2	4.878294	1.978215
159	RTA00000182AF.l.12.1	1027	41	17	2.353059	2.926571
165	RTA00000192AF.g.23.1	6455	6	0	5.853953	2.011224
174	RTA00000181AF.e.22.3	3442	17	4	4.146550	2.562391
183	RTA00000198AF.c.17.1	6923	6	0	5.853953	2.011224
364	RTA00000187AF.g.13.1	2991	10	1	9.756589	2.371428
366	RTA00000192AF.o.19.1	3549	10	1	9.756589	2.371428
387	RTA00000191AF.j.14.1	1002	42	20	2.048883	2.570309
496	RTA00000190AF.p.3.1	2378	34	0	33.17240	5.588184
510	RTA00000178AF.n.23.1	3298	12	1	11.70790	2.729313
512	RTA00000191AF.c.3.1	3549	10	1	9.756589	2.371428
529	RTA00000178AF.b.13.1	3114	9	1	8.780930	2.174815
560	RTA00000184AF.i.23.3	1577	25	3	8.130490	3.903813
606	RTA00000179AR.e.01.4	2493	33	9	3.577416	3.469507

SEQ ID NOS:	Sequence Name	Cluster ID	Lib3 clones	Lib4 clones	lib3/lib4	Zscore
644	RTA00000197F.i.12.1	3605	14	1	13.65922	3.050936
646	RTA00000186AF.d.24.1	3114	9	1	8.780930	2.174815
754	RTA00000187AF.l.11.1	4482	14	3	4.553074	2.374769
875	RTA00000401F.m.02.1	1573	34	7	4.738914	3.982056
902	RTA00000422F.c.02.1	2902	18	5	3.512372	2.443314
921	RTA00000418F.m.19.1	8890	6	0	5.853953	2.011224
942	RTA00000351R.g.11.1	3077	17	4	4.146550	2.562391
1095	RTA00000408F.l.13.1	4423	12	1	11.70790	2.729313
1104	RTA00000404F.m.10.2	779	60	22	2.660887	3.974953
1131	RTA00000400F.k.22.1	2512	7	0	6.829612	2.235371
1170	RTA00000340R.f.05.1	3202	18	3	5.853953	2.998867
1184	RTA00000422F.c.17.1	1360	26	11	2.306102	2.226876
1205	RTA00000118A.a.23.1	3500	12	3	3.902635	2.018050
1354	RTA00000401F.k.14.1	211	121	43	2.745458	5.856098
2124	RTA00000191AF.j.14.1	1002	42	20	2.048883	2.570309
1535	RTA00000405F.l.11.1	2055	29	8	3.536763	3.213373
1751	RTA00000423F.j.03.1	5391	6	0	5.853953	2.011224
1764	RTA00000399F.o.24.1	2272	17	1	16.58620	3.483575
1777	RTA00000401F.j.15.1	3061	14	0	13.65922	3.428594
1795	RTA00000348R.o.12.1	2263	6	0	5.853953	2.011224
1869	RTA00000340F.f.22.1	1720	57	8	6.951569	5.855075
1882	RTA00000401F.g.22.1	1147	28	12	2.276537	2.294031
1890	RTA00000346F.o.16.1	176	170	44	3.769591	8.366611
1915	RTA00000400F.g.02.1	1508	21	5	4.097767	2.879196
2040	RTA00000527F.j.02.2	4896	11	0	10.73224	2.974502
2059	RTA00000528F.i.22.1	2478	17	5	3.317240	2.287632
2223	RTA00000528F.j.11.1	1070	26	6	4.227855	3.289393
2245	RTA00000527F.k.09.1	213	17	4	4.146550	2.562391
2300	RTA00000528F.b.03.1	2078	11	2	5.366124	2.174565
2325	RTA00000525F.d.13.1	349	77	1	75.12573	8.384408
2462	RTA00000528F.g.22.2	920	76	32	2.317189	4.010278
2488	RTA00000528F.h.02.2	1701	18	4	4.390465	2.714073
2492	RTA00000528F.c.11.1	1701	18	4	4.390465	2.714073

Table 6. Differentially expressed polynucleotides: Higher expression in low metastatic breast cancer cells (lib4) relative to high metastatic potential breast cancer (lib3)

SEQ ID NOS:	Sequence Name	Cluster ID	Lib4 Clones	Lib 3 Clones	lib4/lib3	Zscore
15	RTA00000177AR.n.8.1	4188	4	13	3.33108	1.99126
36	RTA00000181AF.p.4.3	40392	1	8	8.19958	2.03713
44	RTA00000199F.f.08.2	12445	0	11	11.2744	3.05623
89	RTA00000177AF.n.8.3	4188	4	13	3.33108	1.99126
172	RTA00000186AF.p.09.2	6879	3	43	14.6909	5.83444
203	RTA00000201F.d.09.1	1827	37	157	4.34910	8.71727
261	RTA00000192AF.a.24.1	13183	0	7	7.17463	2.30057
419	RTA00000182AF.j.20.1	4769	2	20	10.2494	3.68254
420	RTA00000181AF.c.11.1	4769	2	20	10.2494	3.68254
503	RTA00000197AF.k.9.1	3138	1	10	10.2494	2.45316
552	RTA00000193AF.b.24.1	35	386	1967	5.22298	33.2328
564	RTA00000200AF.g.18.1	1600	0	23	23.5738	4.64683

SEQ ID NOS:	Sequence Name	Cluster ID	Lib4 Clones	Lib 3 Clones	lib4/lib3	Zscore
570	RTA00000183AF.a.19.2	3788	0	6	6.14969	2.07158
590	RTA00000190AF.d.2.1	2444	26	55	2.16815	3.22244
693	RTA00000198F.m.12.1	4	987	2807	2.91492	30.3819
707	RTA00000179AF.p.15.1	5622	2	13	6.66216	2.62993
711	RTA00000198F.i.2.1	8076	0	9	9.22453	2.70385
726	RTA00000200R.f.10.1	4	987	2807	2.91492	30.3819
746	RTA00000178AF.i.01.2	4	987	2807	2.91492	30.3819
756	RTA00000404F.a.02.1	9738	1	13	13.3243	2.98623
990	RTA00000126A.o.23.1	6268	3	18	6.14969	3.11179
1122	RTA00000401F.o.06.1	2679	4	23	5.89345	3.52846
1142	RTA00000411F.a.15.1	73812	0	12	12.2993	3.21838
1286	RTA00000345F.n.12.1	7337	3	16	5.46639	2.80694
1289	RTA00000126A.g.7.1	1902	13	48	3.78442	4.45002
1435	RTA00000345F.e.11.1	4392	1	8	8.19958	2.03713
1860	RTA00000340F.p.18.1	287	6	173	29.5526	12.5749
1933	RTA00000400F.f.11.1	4088	0	82	84.0457	9.05778
1934	RTA00000341F.o.12.1	2883	9	21	2.39154	2.07600
1979	RTA00000122A.h.24.1	48	412	1020	2.53749	16.5262
1980	RTA00000346F.j.13.1	5337	5	17	3.48482	2.40321
2007	RTA00000400F.g.08.1	1275	15	32	2.18655	2.41857
2023	RTA00000523F.d.19.1	26489	1	8	8.19958	2.03713
2409	RTA00000526F.d.17.1	2757	4	16	4.09979	2.51500
1220	RTA00000528F.d.04.1	2395	12	37	3.16025	3.51521

Example 6: Polynucleotides Differentially Expressed in High Metastatic Potential Lung Cancer Cells Versus Low Metastatic Lung Cancer Cells

A number of polynucleotide sequences have been identified that are differentially expressed between cells derived from high metastatic potential lung cancer tissue and low metastatic lung cancer cells. Expression of these sequences in lung cancer tissue can be valuable in determining diagnostic, prognostic and/or treatment information. For example, sequences that are highly expressed in the high metastatic potential cells are associated can be indicative of increased expression of genes or regulatory sequences involved in the metastatic process. A patient sample displaying an increased level of one or more of these polynucleotides may thus warrant more aggressive treatment. In another example, sequences that display higher expression in the low metastatic potential cells can be associated with genes or regulatory sequences that inhibit metastasis, and thus the expression of these polynucleotides in a sample may warrant a more positive prognosis than the gross pathology would suggest.

The differential expression of these polynucleotides can be used as a diagnostic marker, a prognostic marker, for risk assessment, patient treatment and the like. These

polynucleotide sequences can also be used in combination with other known molecular and/or biochemical markers.

The following tables summarize polynucleotides that are differentially expressed between high metastatic potential lung cancer cells and low metastatic potential lung cancer cells:

Table 7 Differentially expressed polynucleotides: Higher expression in high metastatic potential lung cancer cells (lib8) relative to low metastatic lung cancer cells (lib9)

SEQ ID NO:	Sequence Name	Cluster ID	Lib8 clones	Lib9 clones	lib8/lib9	Zscore
10	RTA00000198AF.n.16.1	3721	9	0	12.5772	3.20845
54	RTA00000200F.o.22.1	983	8	1	11.1797	2.53243
65	RTA00000198AF.m.16.1	51	348	66	7.36849	17.4315
171	RTA00000198R.c.07.1	19181	6	0	8.38484	2.48169
203	RTA00000201F.d.09.1	1827	45	15	4.19242	5.09891
252	RTA00000181AF.e.18.3	8	1355	122	15.5211	39.0214
253	RTA00000181AF.e.17.3	8	1355	122	15.5211	39.0214
285	RTA00000181AR.j.14.3	5399	12	0	16.7696	3.80239
419	RTA00000182AF.j.20.1	4769	10	3	4.65824	2.29362
420	RTA00000181AF.c.11.1	4769	10	3	4.65824	2.29362
491	RTA00000196F.k.11.1	3	986	392	3.51507	22.4683
525	RTA00000198AF.c.7.1	19181	6	0	8.38484	2.48169
526	RTA00000185AF.e.20.1	5865	12	0	16.7696	3.80239
552	RTA00000193AF.b.24.1	35	868	11	110.273	34.2897
693	RTA00000198F.m.12.1	4	506	209	3.38335	15.7309
700	RTA00000183AF.i.18.2	40129	7	0	9.78231	2.74441
726	RTA00000200R.f.10.1	4	506	209	3.38335	15.7309
742	RTA00000177AF.m.1.1	14929	23	16	2.00886	2.02420
746	RTA00000178AF.i.01.2	4	506	209	3.38335	15.7309
861	RTA00000339F.f.11.1	5832	5	0	6.98736	2.18988
990	RTA00000126A.o.23.1	6268	5	0	6.98736	2.18988
1088	RTA00000399F.f.11.1	40167	8	0	11.1797	2.98512
1288	RTA00000423F.e.11.1	2566	11	2	7.68610	2.85611
1417	RTA00000339F.o.07.1	2566	11	2	7.68610	2.85611
1444	RTA00000419F.p.03.1	1937	10	3	4.65824	2.29362
1454	RTA00000340F.l.05.1	38935	7	0	9.78231	2.74441
1570	RTA00000403F.a.17.1	13686	8	0	11.1797	2.98512
1597	RTA00000401F.n.23.1	1552	8	1	11.1797	2.53243
1979	RTA00000122A.h.24.1	48	342	155	3.08345	12.2138
2024	RTA00000528F.b.23.1	1605	22	4	7.68610	4.23808
2034	RTA00000528F.m.16.1	4468	6	1	8.38484	1.97787
2126	RTA00000526F.d.01.1	4468	6	1	8.38484	1.97787

Table 8 Differentially expressed polynucleotides: Higher expression in low metastatic lung cancer cells (lib9) relative to high metastatic potntial lung cancer cells

SEQ ID NO:	Sequence Name	Cluster ID	Lib8 clones	Lib9 clones	lib9/lib8	Zscore
174	RTA00000181AF.e.22.3	3442	5	23	3.291654	2.368262
254	RTA00000178AF.n.2.1	17083	0	8	5.724617	2.034117
466	RTA00000177AF.p.20.1	4141	4	27	4.830145	3.070829
571	RTA00000198AF.b.14.1	801	16	46	2.057284	2.411087
574	RTA00000192AF.f.3.1	5257	5	25	3.577885	2.596857
590	RTA00000190AF.d.2.1	2444	12	37	2.206362	2.299984
922	RTA00000399F.l.14.1	3354	5	20	2.862308	1.998763
1355	RTA00000406F.m.04.1	14959	11	41	2.667151	2.865855
1422	RTA00000405F.h.07.2	4984	3	16	3.816411	2.058861
2007	RTA00000400F.g.08.1	1275	10	42	3.005423	3.147111
2038	RTA00000527F.p.06.1	1292	8	33	2.951755	2.724411
2245	RTA00000527F.k.09.1	213	137	403	2.104945	7.661033

Example 7: Polynucleotides Differentially Expressed in High Metastatic Potential Colon Cancer Cells Versus Low Metastatic Colon Cancer Cells

A number of polynucleotide sequences have been identified that are differentially expressed between cells derived from high metastatic potential colon cancer tissue and low metastatic colon cancer cells. Expression of these sequences in colon cancer tissue can be valuable in determining diagnostic, prognostic and/or treatment information. For example, sequences that are highly expressed in the high metastatic potential cells can be indicative of increased expression of genes or regulatory sequences involved in the metastatic process. A patient sample displaying an increased level of one or more of these polynucleotides may thus warrant more aggressive treatment. In another example, sequences that display higher expression in the low metastatic potential cells can be associated with genes or regulatory sequences that inhibit metastasis, and thus the expression of these polynucleotides in a sample may warrant a more positive prognosis than the gross pathology would suggest.

The differential expression of these polynucleotides can be used as a diagnostic marker, a prognostic marker, for risk assessment, patient treatment and the like. These polynucleotide sequences can also be used in combination with other known molecular and/or biochemical markers.

The following table summarizes identified polynucleotides with differential expression between high metastatic potential colon cancer cells and low metastatic potential colon cancer cells:

Table 9 Differentially expressed polynucleotides: Higher expression in high metastatic potential colon cancer (lib1) relative to low metastatic colon cancer cells (lib2)

SEQ ID NO:	Sequence Name	Cluster ID	Lib1 clones	Lib2 clones	lib1/lib2	Zscore
228	RTA00000187AR.h.15.2	6660	7	0	6.489973399	2.169320547
280	RTA00000193AF.b.18.1	7542	8	0	7.417112456	2.36964728
355	RTA00000184AR.b.24.1	5777	9	1	8.344251513	2.09555146
491	RTA00000196F.k.11.1	3	5268	2164	2.257009497	32.96556438
603	RTA00000183AR.d.11.3	6420	8	0	7.417112456	2.36964728
680	RTA00000177AF.f.10.1	6420	8	0	7.417112456	2.36964728
752	RTA00000192AF.o.7.1	5275	11	2	5.099264814	2.083995588
753	RTA00000192AF.o.17.1	5275	11	2	5.099264814	2.083995588
1241	RTA00000346F.l.13.1	7542	8	0	7.417112456	2.36964728
1264	RTA00000349R.g.10.1	5777	9	1	8.344251513	2.09555146
1401	RTA00000421F.m.14.1	3524	21	6	3.2449867	2.499690198
1442	RTA00000350R.g.10.1	9026	7	0	6.489973399	2.169320547
1514	RTA00000399F.o.06.1	13574	7	0	6.489973399	2.169320547
1851	RTA00000421F.a.06.1	2385	27	4	6.258188635	3.743586088
1915	RTA00000400F.g.02.1	1508	46	17	2.508729213	3.230059264
2024	RTA00000528F.b.23.1	1605	36	11	3.034273278	3.244010467
2066	RTA00000528F.m.12.1	5768	12	0		3.046665462

Table 10 Differentially expressed polynucleotides: Higher expression in low metastatic colon cancer cells (lib2)relative to high metastatic potential colon cancer (lib1)

SEQ ID NOS:	Sequence Name	Cluster ID	Lib1 clones	Lib2 clones	lib2/lib1	Zscore
33	RTA00000178AR.a.20.1	945	9	21	2.51670	2.21703
250	RTA00000192AF.j.21.1	2289	3	23	8.26916	3.92187
282	RTA00000193AF.c.15.1	3726	3	14	5.03340	2.58312
370	RTA00000179AF.c.15.3	2995	4	13	3.50540	2.09770
387	RTA00000191AF.j.14.1	1002	12	65	5.84234	6.26259
443	RTA00000197AR.i.17.1	3516	5	17	3.66719	2.52439
460	RTA00000179AF.c.15.1	2995	4	13	3.50540	2.09770
545	RTA00000196F.a.2.1	3575	5	14	3.02004	2.00158
560	RTA00000184AF.i.23.3	1577	12	40	3.59528	4.01991
703	RTA00000198F.l.09.1	3611	2	13	7.01081	2.73040
704	RTA00000190AF.o.12.1	3438	5	14	3.02004	2.00158
1095	RTA00000408F.l.13.1	4423	1	8	8.62869	2.11495
1104	RTA00000404F.m.10.2	779	27	54	2.15717	3.23169
1205	RTA00000118A.a.23.1	3500	3	13	4.67387	2.40298
1354	RTA00000401F.k.14.1	211	109	206	2.03843	6.08597
1387	RTA00000191AF.j.14.1	1002	12	65	5.84234	6.26259
1734	RTA00000345F.b.17.1	945	9	21	2.51670	2.21703
1742	RTA00000422F.b.22.1	2368	14	34	2.61942	3.00662
1954	RTA00000401F.j.23.1	570	59	148	2.70560	6.66631
2262	RTA00000527F.o.12.1	688	29	60	2.23155	3.53946
2325	RTA00000525F.d.13.1	349	69	138	2.15717	5.27497

Example 8: Polynucleotides Differentially Expressed in High Metastatic Potential Colon Cancer Patient Tissue Versus Normal Patient Tissue

A number of polynucleotide sequences have been identified that are differentially expressed between cells derived from high metastatic potential colon cancer tissue and normal tissue. Expression of these sequences in colon cancer tissue can be valuable in determining diagnostic, prognostic and/or treatment information. For example, sequences that are highly expressed in the high metastatic potential cells are associated can be indicative of increased expression of genes or regulatory sequences involved in the advanced disease state which involves processes such as angiogenesis, dedifferentiation, cell replication, and metastasis. A patient sample displaying an increased level of one or more of these polynucleotides may thus warrant more aggressive treatment.

The differential expression of these polynucleotides can be used as a diagnostic marker, a prognostic marker, for risk assessment, patient treatment and the like. These polynucleotide sequences can also be used in combination with other known molecular and/or biochemical markers.

The following tables summarize polynucleotides that are differentially expressed between high metastatic potential colon cancer cells and normal colon cells:

Table 11 Differentially expressed polynucleotides isolated from samples from two patients (UC#2 and UC#3) : Higher expression in high metastatic potential colon tissue (UC#2:lib17; UC#3:lib20) vs. normal colon tissue (UC#2:lib15; UC#3:lib18)

SEQ ID NO:	Sequence Name	Cluster ID	lib15 clones	lib17 clones	lib17/lib15	Zscore
65	RTA00000198AF.m.16.1	51	1	10	9.27022	2.28830
1780	RTA00000118A.j.24.1	18	4	23	5.33037	3.27028
1899	RTA00000345F.j.09.1	13	14	80	5.29727	6.34580
SEQ ID NO:	Sequence Name	Cluster ID	lib18 clones	lib20 clones	lib20/lib18	Zscore
1899	RTA00000345F.j.09.1	13	12	23	2.24234	2.16077

Table 12 Differentially expressed polynucleotides isolated from samples from two patients (UC#2 and UC#3) : Higher expression in normal colon tissue (UC#2:lib15; UC#3:lib18)vs. high metastatic potential colon tissue (UC#2:lib17; UC#3:lib20).

SEQ ID NO:	Sequence Name	Cluster ID	Lib5 Clones	L1ib7 Clones	lib15/lib17	Z Score: >2.5899%; >1.96
491	RTA00000196F.k.11.1	3	242	26	10.04	13.78900072
SEQ ID	Sequence Name	Cluster	Lib18	Lib20	lib18/lib20	Zscore

NO:		ID	clones	clones		
491	RTA00000196F.k.11.1	3	409	46	7.59993	15.3998

Example 9: Polynucleotides Differentially Expressed in High Colon Tumor Potential Patient Tissue Versus Metastasized Colon Cancer Patient Tissue

A number of polynucleotide sequences have been identified that are differentially expressed between cells derived from high tumor potential colon cancer tissue and cells derived from high metastatic potential colon cancer cells. Expression of these sequences in colon cancer tissue can be valuable in determining diagnostic, prognostic and/or treatment information associated with the transformation of precancerous tissue to malignant tissue. This information can be useful in the prevention of achieving the advanced malignant state in these tissues, and can be important in risk assessment for a patient.

The following table summarizes identified polynucleotides with differential expression between high tumor potential colon cancer tissue and cells derived from high metastatic potential colon cancer cells:

Table 13 Differentially expressed polynucleotides: High tumor potential colon tissue vs. metastatic colon tissue

SEQ ID NO:	Sequence Name	Cluster ID	L19 clones	L20 clones	lib19/lib20	Zscore
252	RTA00000181AF.e.18.3	8	14	1	10.4712	2.56699
253	RTA00000181AF.e.17.3	8	14	1	10.4712	2.56699
491	RTA00000196F.k.11.1	3	328	46	5.33318	11.8962
581	RTA00000191AF.p.3.2	17	24	2	8.97535	3.41950
693	RTA00000198F.m.12.1	4	26	8	2.43082	2.09705
726	RTA00000200R.f.10.1	4	26	8	2.43082	2.09705
746	RTA00000178AF.i.01.2	4	26	8	2.43082	2.09705
1780	RTA00000118A.j.24.1	18	80	13	4.60274	5.51440
1899	RTA00000345F.j.09.1	13	148	23	4.81287	7.68618

Example 10: Polynucleotides Differentially Expressed in High Tumor Potential Colon Cancer Patient Tissue Versus Normal Patient Tissue

A number of polynucleotide sequences have been identified that are differentially expressed between cells derived from high tumor potential colon cancer tissue and normal tissue. Expression of these sequences in colon cancer tissue can be valuable in determining diagnostic, prognostic and/or treatment information associated with the prevention of achieving the malignant state in these tissues, and can be important in risk assessment for a

patient. For example, sequences that are highly expressed in the potential colon cancer cells are associated with or can be indicative of increased expression of genes or regulatory sequences involved in early tumor progression. A patient sample displaying an increased level of one or more of these polynucleotides may thus warrant closer attention or more frequent screening procedures to catch the malignant state as early as possible.

The following tables summarize polynucleotides that are differentially expressed between high metastatic potential colon cancer cells and normal colon cells:

Table 14 Differentially expressed polynucleotides detected in samples from two patients (UC#2 and UC#3): Higher expression in tumor potential colon tissue (UC#2:lib16; UC#3:lib19)vs. normal colon tissue (UC#2:lib15; UC#3:lib18)

SEQ ID NO:	Sequence Name	Cluster ID	Lib15 clones	Lib16 clones	lib16/lib15	Zscore
1899	RTA00000345F.j.09.1	13	14	50	3.43709	4.22436
SEQ ID NO:	Sequence Name	Cluster ID	Lib18 clones	Lib19 clones	lib19/lib18	Zscore
65	RTA00000198AF.m.16.1	51	0	14	12.2505	3.23250
252	RTA00000181AF.e.18.3	8	1	14	12.2505	2.84687
253	RTA00000181AF.e.17.3	8	1	14	12.2505	2.84687
581	RTA00000191AF.p.3.2	17	4	24	5.25021	3.24580
693	RTA00000198F.m.12.1	4	6	26	3.79182	2.98901
716	RTA00000200F.p.05.1	3984	0	7	6.12525	2.09621
726	RTA00000200R.f.10.1	4	6	26	3.79182	2.98901
746	RTA00000178AF.i.01.2	4	6	26	3.79182	2.98901
1780	RTA00000118A.j.24.1	18	10	80	7.00028	6.65963
1899	RTA00000345F.j.09.1	13	12	148	10.7921	9.86174

Table 15 Differentially expressed polynucleotides: Higher expression in normal colon tissue (UC#2:lib15) vs. tumor potential colon tissue (UC#2:lib16)

SEQ ID NO:	Sequence Name	Cluster ID	Lib15 clones	Lib16 clones	lib15/lib16	Zscore
491	RTA00000196F.k.11.1	3	242	39	6.44765	12.3988

Example 11: Polynucleotides Differentially Expressed in Growth Factor-Stimulated Human Microvascular Endothelial Cells (HMEC) Relative to Untreated HMEC

A number of polynucleotide sequences have been identified that are differentially expressed between human microvascular endothelial cells (HMEC) that have been treated with growth factors relative to untreated HMEC.

Sequences that are differentially expressed between growth factor-treated HMEC and untreated HMEC can represent sequences encoding gene products involved in angiogenesis, metastasis (cell migration), and other development and oncogenic processes. For example, sequences that are more highly expressed in HMEC treated with growth factors (such as bFGF or VEGF) relative to untreated HMEC can serve as markers of

cancer cells of higher metastatic potential. Detection of expression of these sequences in colon cancer tissue can be valuable in determining diagnostic, prognostic and/or treatment information associated with the prevention of achieving the malignant state in these tissues, and can be important in risk assessment for a patient. A patient sample displaying an increased level of one or more of these polynucleotides may thus warrant closer attention or more frequent screening procedures to catch the malignant state as early as possible.

The following table summarizes identified polynucleotides with differential expression between growth factor-treated and untreated HMEC.

Table 16 Differentially expressed polynucleotides: Higher expression in bFGF treated HMEC (lib13) vs. untreated HMEC (lib12)

SEQ ID NO:	Sequence Name	Cluster ID	Lib12 clones	Lib13 clones	lib13/lib12	Zscore
648	RTA00000199F.i.9.1	7	25	52	2.07199	2.94741

Table 17 Differentially expressed polynucleotides: Higher expression in VEGF treated HMEC (lib14) vs. untreated HMEC (lib12)

SEQ ID NO:	Sequence Name	Cluster ID	Lib12 clones	Lib14 clones	lib14/lib12	Zscore
648	RTA00000199F.i.9.1	7	25	67	2.62449	4.17666
1899	RTA00000345F.j.09.1	13	22	49	2.18114	2.99887

Example 12: Polynucleotides Differentially Expressed Across Multiple Libraries

A number of polynucleotide sequences have been identified that are differentially expressed between cancerous cells and normal cells across all three tissue types tested (*i.e.*, breast, colon, and lung). Expression of these sequences in a tissue or any origin can be valuable in determining diagnostic, prognostic and/or treatment information associated with the prevention of achieving the malignant state in these tissues, and can be important in risk assessment for a patient. These polynucleotides can also serve as non-tissue specific markers of, for example, risk of metastasis of a tumor. The following table summarizes identified polynucleotides that were differentially expressed but without tissue type-specificity in the breast, colon, and lung libraries tested.

Table 18 Polynucleotides Differentially Expressed Across Multiple Library Comparisons

SEQ ID NO.	Cluster	Clones in 1st Lib	Clones in 2nd Lib	Ratio	Cell or Tissue Sample and Cancer State Compared (Z Score)

SEQ ID NO.	Cluster	Clones in 1st Lib	Clones in 2nd Lib	Ratio	Cell or Tissue Sample and Cancer State Compared (Z Score)
2024	1605	lib1	lib2	lib1/lib2	colon: high met > low met
		36	11	3.0342732	(3.2440104)
		lib8	lib9	lib8/lib9	lung: high met > low met
		22	4	7.6861036	(4.2380835)
65	51	lib8	lib9	lib8/lib9	lung: high met > low met
		348	66	7.3684960	(17.431560)
		lib18	lib19	lib19/lib18	pt #3 colon: tumor > normal
		0	14	12.250507	(3.2325073)
		lib15	lib17	lib17/lib15	pt #2 colon: met > normal
		1	10	9.2702249	(2.2883061)
174	3442	lib8	lib9	lib9/lib8	lung: low met > high met
		5	23	3.2916548	(2.3682625)
		lib3	lib4	lib3/lib4	breast: high met > low met
		17	4	4.1465504	(2.5623912)
203	1827	lib8	lib9	lib8/lib9	lung: high met > low met
		45	15	4.1924201	(5.0989192)
		lib3	lib4	lib4/lib3	breast: low met > high met
		37	157	4.3491051	(8.7172773)
2245	213	lib8	lib9	lib9/lib8	lung: low met > high met
		137	403	2.1049458	(7.6610331)
		lib3	lib4	lib3/lib4	breast: high met > low met
		17	4	4.1465504	(2.5623912)
990	6268	lib8	lib9	lib8/lib9	lung: high met > low met
		5	0	6.9873669	(2.1898837)
		lib3	lib4	lib4/lib3	breast: low met > high met
		3	18	6.1496901	(3.1117967)
252	8	lib8	lib9	lib8/lib9	lung: high met > low met
		1355	122	15.521118	(39.021411)
		lib19	lib20	lib19/lib20	pt. #3 colon: tumor > met
		14	1	10.471247	(2.5669948)
		lib18	lib19	lib19/lib18	pt #3 colon: tumor > normal
		1	14	12.250507	(2.8468716)
253	8	lib8	lib9	lib8/lib9	lung: high met > low met
		1355	122	15.521118	(39.021411)
		lib19	lib20	lib19/lib20	pt. #3 colon: tumor > met
		14	1	10.471247	(2.5669948)
		lib18	lib19	lib19/lib18	pt #3 colon: tumor > normal
		1	14	12.250507	(2.8468716)
2325	349	lib3	lib4	lib3/lib4	breast: high met > low met
		77	1	75.125736	(8.3844087)
		lib1	lib2	lib2/lib1	colon: low met > high met
		69	138	2.1571737	(5.2749799)

SEQ ID NO.	Cluster	Clones in 1st Lib	Clones in 2nd Lib	Ratio	Cell or Tissue Sample and Cancer State Compared (Z Score)
1095	4423	lib3	lib4	lib3/lib4	breast: high met > low met
		12	1	11.707907	(2.7293134)
		lib1	lib2	lib2/lib1	colon: low met > high met
		1	8	8.6286948	(2.1149516)
1124	779	lib3	lib4	lib3/lib4	breast: high met > low met
		60	22	2.6608879	(3.9749537)
		lib1	lib2	lib2/lib1	colon: low met > high met
		27	54	2.1571737	(3.2316908)
387	1002	lib3	lib4	lib3/lib4	breast: high met > low met
		42	20	2.0488837	(2.5703094)
		lib1	lib2	lib2/lib1	colon: low met > high met
		12	65	5.8423454	(6.2625969)
419	4769	lib8	lib9	lib8/lib9	lung: high met > low met
		10	3	4.6582446	(2.2936274)
		lib3	lib4	lib4/lib3	breast: low met > high met
		2	20	10.249483	(3.6825426)
420	4769	lib8	lib9	lib8/lib9	lung: high met > low met
		10	3	4.6582446	(2.2936274)
		lib3	lib4	lib4/lib3	breast: low met > high met
		2	20	10.249483	(3.6825426)
1205	3500	lib3	lib4	lib3/lib4	breast: high met > low met
		12	3	3.9026356	(2.0180506)
		lib1	lib2	lib2/lib1	colon: low met > high met
		3	13	4.6738763	(2.4029818)
491	3	lib1	lib2	lib1/lib2	colon: high met > low met
		5268	2164	2.2570094	(32.965564)
		lib8	lib9	lib8/lib9	lung: high met > low met
		986	392	3.5150733	(22.468331)
		lib19	lib20	lib19/lib20	pt #3 colon: tumor > met
		328	46	5.3331820	(11.896271)
		lib18	lib20	lib18/lib20	pt #3 colon: normal > met
		409	46	7.5999342	(15.399861)
		lib15	lib17	lib15/lib17	pt#2 colon: normal > met
		242	26	10.04	(13.789000)
		lib15	lib16	lib15/lib16	pt#2 colon: normal > tumor
		242	39	6.44765	12.39883
552	35	lib8	lib9	lib8/lib9	lung: high met > low met
		868	11	110.27335	(34.289704)
		lib3	lib4	lib4/lib3	breast: low met > high met
		386	1967	5.2229880	(33.232871)
560	1577	lib3	lib4	lib3/lib4	breast: high met > low met
		25	3	8.1304909	(3.9038139)

SEQ ID NO.	Cluster	Clones in 1st Lib	Clones in 2nd Lib	Ratio	Cell or Tissue Sample and Cancer State Compared (Z Score)
		lib1	lib2	lib2/lib1	colon: low met > high met
		12	40	3.5952895	(4.0199130)
581	17	lib19	lib20	lib19/lib20	pt #3 colon: tumor > met
		24	2	8.9753551	(3.4195074)
		lib18	lib19	lib19/lib18	pt #3 colon: tumor > normal
		4	24	5.2502174	(3.2458055)
590	2444	lib3	lib4	lib4/lib3	breast: low met > high met
		26	55	2.1681599	(3.2224421)
		lib8	lib9	lib9/lib8	lung: low met > high met
		12	37	2.2063628	(2.2999846)
1354	211	lib3	lib4	lib3/lib4	breast: high met > low met
		121	43	2.7454588	(5.8560985)
		lib1	lib2	lib2/lib1	colon: low met > high met
		109	206	2.0384302	(6.0859794)
1387	1002	lib3	lib4	lib3/lib4	breast: high met > low met
		42	20	2.0488837	(2.5703094)
		lib1	lib2	lib2/lib1	colon: low met > high met
		12	65	5.8423454	(6.2625969)
648	7	lib12	lib14	lib14/lib12	HMEC: VEGF > untreated
		25	67	2.6244913	(4.1766696)
		lib12	lib13	lib13/lib12	HMEC: bFGF > untreated
		25	52	2.0719962	(2.9474155)
693	4	lib8	lib9	lib8/lib9	lung: high met > low met
		506	209	3.3833566	(15.730912)
		lib3	lib4	lib4/lib3	breast: low met > high met
		987	2807	2.9149240	(30.381945)
		lib19	lib20	lib19/lib20	pt#3 colon: tumor > met
		26	8	2.4308253	(2.0970580)
		lib18	lib19	lib19/lib18	pt#3 colon: tumor > normal
		6	26	3.7918237	(2.9890107)
726	4	lib8	lib9	lib8/lib9	lung: high met > low met
		506	209	3.3833566	(15.730912)
		lib3	lib4	lib4/lib3	breast: low met > high met
		987	2807	2.9149240	(30.381945)
		lib19	lib20	lib19/lib20	pt#3 colon: tumor > met
		26	8	2.4308253	(2.0970580)
		lib18	lib19	lib19/lib18	pt#3 colon: tumor > normal
		6	26	3.7918237	(2.9890107)
746	4	lib8	lib9	lib8/lib9	lung: high met > low met
		506	209	3.3833566	(15.730912)
		lib3	lib4	lib4/lib3	breast: low met > high met
		987	2807	2.9149240	(30.381945)

SEQ ID NO.	Cluster	Clones in 1st Lib	Clones in 2nd Lib	Ratio	Cell or Tissue Sample and Cancer State Compared (Z Score)
		lib19	lib20	lib19/lib20	pt#3 colon: tumor > met
		26	8	2.4308253	(2.0970580)
		lib18	lib19	lib19/lib18	pt#3 colon: tumor > normal
		6	26	3.7918237	(2.9890107)
1780	18	lib19	lib20	lib19/lib20	pt#3 colon: tumor > met
		80	13	4.6027462	(5.5144093)
		lib18	lib19	lib19/lib18	pt#3 colon: tumor > normal
		10	80	7.0002899	(6.6596394)
		lib15	lib17	lib17/lib15	pt#3 colon: met > normal
		4	23	5.3303793	(3.2702852)
1899	13	lib19	lib20	lib19/lib20	pt#3 colon: tumor > met
		148	23	4.8128716	(7.6861840)
		lib18	lib20	lib20/lib18	pt#3 colon: met > normal
		12	23	2.2423439	(2.1607719)
		lib18	lib19	lib19/lib18	pt#3 colon: tumor > normal
		12	148	10.792113	(9.8617485)
		lib15	lib17	lib17/lib15	pt#2 colon: met > normal
		14	80	5.2972714	(6.3458044)
		lib15	lib16	lib16/lib15	pt#2 colon: tumor > normal
		14	50	3.4370927	(4.2243697)
		lib12	lib14	lib14/lib12	HMEC: VEGF > untreated
		22	49	2.1811410	(2.9988774)
1915	1508	lib1	lib2	lib1/lib2	colon: high met > low met
		46	17	2.5087292	(3.2300592)
		lib3	lib4	lib3/lib4	breast: high met > low met
		21	5	4.0977674	(2.8791960)
1979	48	lib8	lib9	lib8/lib9	lung: high met > low met
		342	155	3.0834574	(12.213852)
		lib3	lib4	lib4/lib3	breast: low met > high met
		412	1020	2.5374934	(16.526285)
2007	1275	lib3	lib4	lib4/lib3	breast: low met > high met
		15	32	2.1865564	(2.4185764)
		lib8	lib9	lib9/lib8	lung: low met > high met
		10	42	3.0054239	3.1471113

high met = high metastatic potential; low met = low metastatic potential;
met = metastasized; tumor = non-metastasized tumor;
pt = patient; #2 = UC#2; #3 = UC#3;
HMEC = human microvascular endothelial cell;
bFGF = bFGF treated; VEGF = VEGF treated

Example 12: Polynucleotides Exhibiting Colon-Specific Expression

The cDNA libraries described herein were also analyzed to identify those polynucleotides that were specifically expressed in colon cells or tissue, *i.e.*, the polynucleotides were identified in libraries prepared from colon cell lines or tissue, but not in libraries of breast or lung origin. The polynucleotides that were expressed in a colon cell line and/or in colon tissue, but were present in the breast or lung cDNA libraries described herein, are shown in Table 19 (inserted before claims).

No clones corresponding to the colon-specific polynucleotides in the table above were present in any of Libraries 3, 4, 8, 9, 12, 13, 14, or 15. The polynucleotide provided above can be used as markers of cells of colon origin, and find particular use in reference arrays, as described above.

Example 13: Identification of Contiguous Sequences Having a Polynucleotide of the Invention

The novel polynucleotides were used to screen publicly available and proprietary databases to determine if any of the polynucleotides of SEQ ID NOS:1-2502 would facilitate identification of a contiguous sequence, *e.g.*, the polynucleotides would provide sequence that would result in 5' extension of another DNA sequence, resulting in production of a longer contiguous sequence composed of the provided polynucleotide and the other DNA sequence(s). Contiging was performed using the Gelmerge application (default settings) of GCG from the Univ. of Wisconsin.

Using these parameters, 146 contiged sequences were generated. These contiged sequences are provided as SEQ ID NOS:5107-5252 (see Table 1). The contiged sequences can be correlated with the sequences of SEQ ID NOS:1-2502 upon which the contiged sequences are based by, for example, identifying those sequences of SEQ ID NOS:1-2502 and the contiged sequences of SEQ ID NOS:5107-5252 that share the same clone name in Table 1.

The contiged sequences (SEQ ID NO:5107-5252) thus represent longer sequences that encompass a polynucleotide sequence of the invention. The contiged sequences were then translated in all three reading frames to determine the best alignment with individual sequences using the BLAST programs as described above for SEQ ID NOS:1-2502 and the validation sequences "SEQ ID NOS:2503-5106." Again the sequences were masked using the XBLAST program for masking low complexity as described above in Example 1

(Table 2). Several of the contiged sequences were found to encode polypeptides having characteristics of a polypeptide belonging to a known protein families (and thus represent new members of these protein families) and/or comprising a known functional domain (Table 20). Thus the invention encompasses fragments, fusions, and variants of such polynucleotides that retain biological activity associated with the protein family and/or functional domain identified herein.

Table 20 Profile hits using contiged sequences

SEQ ID NO	Biological Activity (Profile)	Start	Stop	Score	Direction	Sequence Name
5111	7tm_2	71	915	8090	for	RTA00000399F.o.01.1
5120	7tm_2	101	919	8475	rev	RTA00000341F.m.21.1
5174	7tm_2	3	963	9431	for	RTA00000192AF.h.19.1
5197	7tm_2	214	1073	8528	rev	RTA00000192AF.f.3.1
5208	ANK	546	629	4920	for	RTA00000190AF.f.5.1
5120	asp	126	1067	6620	rev	RTA00000341F.m.21.1.
5241	asp	112	1094	6553	for	RTA00000418F.i.06.1
5243	asp	347	1028	5981	for	RTA00000339F.b.02.1
5197	ATPases	113	781	5690	for	RTA00000192AF.f.3.1
5239	ATPases	1	348	15955	for	RTA00000401F.m.07.1
5241	ATPases	110	823	6782	for	RTA00000418F.i.06.1
5243	ATPases	338	874	5832	for	RTA00000339F.b.02.1
5125	protkinase	59	685	5791	for	RTA00000182AF.c.5.1
5217	protkinase	75	1035	5405	for	RTA00000181AF.p.12.3
5237	protkinase	25	546	5107	rev	RTA00000118A.n.5.1
5248	protkinase	14	422	5103	rev	RTA00000419F.k.05.1
5252	protkinase	89	755	5499	for	RTA00000404F.m.17.2
5120	Wnt_dev_sign	3	948	11036	for	RTA00000341F.m.21.1

All stop/start sequences are provided in the forward direction.

Descriptions of the profiles for the indicated protein families and functional domains are provided in Example 3 above.

Those skilled in the art will recognize, or be able to ascertain, using not more than routine experimentation, many equivalents to the specific embodiments of the invention described herein. Such specific embodiments and equivalents are intended to be encompassed by the following claims.

All publications and patent applications cited in this specification are herein incorporated by reference as if each individual publication or patent application were specifically and individually indicated to be incorporated by reference. The citation of any publication is for its disclosure prior to the filing date and should not be construed as an admission that the present invention is not entitled to antedate such publication by virtue of prior invention.

Although the foregoing invention has been described in some detail by way of illustration and example for purposes of clarity of understanding, it is readily apparent to those of ordinary skill in the art in light of the teachings of this invention that certain changes and modifications may be made thereto without departing from the spirit or scope of the appended claims.

Deposit Information:

The following materials were deposited with the American Type Culture Collection: CMCC = (Chiron Master Culture Collection)

Cell Lines Deposited with ATCC

Cell Line	Deposit Date	ATCC Accession No.	CMCC Accession No.
KM12L4-A	March 19, 1998	CRL-12496	11606
Km12C	May 15, 1998	CRL-12533	11611
MDA-MB-231	May 15, 1998	CRL-12532	10583
MCF-7	October 9, 1998	CRL-12584	10377

cDNA Libraries Deposited with ATCC

cDNA Library No. Deposit Date ATCC Accession No.	cDNA Library ES21 January 22, 1999 ATCC No.	cDNA Library ES22 January 22, 1999 ATCC No.	cDNA Library ES23 January 22, 1999 ATCC No.
Clone Names	M00001575D:G05 M00001460A:A03 M00001655C:E04 M00001676C:C11 M00001679D:D05 M00001546B:C05 M00001453B:E10	M00001364A:E11 M00001694C:H10 M00003841D:E03 M00004176D:B12 M00001387B:E02 M00004282B:A04 M00001376B:F03 M00001445D:A06 M00001399C:H12 M00004208D:H08	M00001489B:A06 M00001585A:D06 M00001637B:E07 M00001529D:H02 M00001500C:C08 M00001483B:D03 M00001623C:H07 M00003975B:F03

cDNA Library No.	cDNA Library ES24	cDNA Library ES25	cDNA Library ES26
Deposit Date	January 22, 1999	January 22, 1999	January 22, 1999
ATCC Accession No.	ATCC No.	ATCC No.	ATCC No.
Clone Names	M00003987D:D06	M00001675D:B08	M00001479C:F10
	M00004073A:H12	M00001589B:E12	M00003842D:F08
	M00004104B:F11	M00001607D:A11	M00003901A:C09
	M00004237D:D08	M00001636A:E07	M00003982A:B06
	M00004111D:B07	M00001530A:B12	M00003824A:A06
	M00004138B:B11	M00001495B:B08	M00003845D:C03
	M00001391C:C04	M00001487C:F01	M00003856A:B07
	M00001448D:E12	M00001644B:D06	M00004104B:A02
	M00001450A:B03	M00003751C:A04	M00004110C:E03
	M00001451B:F01		

In addition, libraries of selected clones were deposited. The details of these deposits are provided in Tables 21-24.

This deposit is provided merely as convenience to those of skill in the art, and is not an admission that a deposit is required under 35 U.S.C. §112. The sequence of the polynucleotides contained within the deposited material, as well as the amino acid sequence of the polypeptides encoded thereby, are incorporated herein by reference and are controlling in the event of any conflict with the written description of sequences herein. A license may be required to make, use, or sell the deposited material, and no such license is granted hereby.

Retrieval of Individual Clones from Deposit of Pooled Clones

Where the ATCC deposit is composed of a pool of cDNA clones, the deposit was prepared by first transfecting each of the clones into separate bacterial cells. The clones were then deposited as a pool of equal mixtures in the composite deposit. Particular clones can be obtained from the composite deposit using methods well known in the art. For example, a bacterial cell containing a particular clone can be identified by isolating single colonies, and identifying colonies containing the specific clone through standard colony hybridization techniques, using an oligonucleotide probe or probes designed to specifically hybridize to a sequence of the clone insert (*e.g.*, a probe based upon unmasked sequence of the encoded polynucleotide having the indicated SEQ ID NO). The probe should be designed to have a T_m of approximately 80°C (assuming 2°C for each A or T and 4°C for each G or C). Positive colonies can then be picked, grown in culture, and the recombinant clone isolated. Alternatively, probes designed in this manner can be used to PCR to isolate a nucleic acid molecule from the pooled clones according to methods well known in the art,

e.g., by purifying the cDNA from the deposited culture pool, and using the probes in PCR reactions to produce an amplified product having the corresponding desired polynucleotide sequence.

Table 1.

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
1	1/28/98	1	RTA00000197AF.i.16.1	M00001490A:D11	16402
2	1/28/98	2	RTA00000188AF.n.15.1	M00003804A:H04	0
3	1/28/98	3	RTA00000197AF.e.24.1	M00001456B:F10	39250
4	1/28/98	4	RTA00000198R.f.04.1	M00001607D:F07	5023
5	1/28/98	5	RTA00000195R.c.11.1	M00003811A:E03	66087
6	1/28/98	6	RTA00000195AF.c.16.1	M00003829C:A11	23508
7	1/28/98	7	RTA00000197AR.e.12.1	M00001454B:G07	22095
8	1/28/98	8	RTA00000200AF.h.11.2	M00004146A:C08	8399
9	1/28/98	9	RTA00000177AF.g.22.1	M00001347C:G08	7031
10	1/28/98	10	RTA00000198AF.n.16.1	M00001694C:H10	3721
11	1/28/98	11	RTA00000199AF.i.17.1	M00003880C:F10	9615
12	1/28/98	12	RTA00000183AF.i.15.2	M00001529B:C04	2642
13	1/28/98	13	RTA00000190AF.i.5.1	M00003919A:A10	0
14	1/28/98	14	RTA00000196R.c.11.2	M00001352A:E12	13658
15	1/28/98	15	RTA00000177AR.n.8.1	M00001356D:F06	4188
16	1/28/98	16	RTA00000196AF.e.16.1	M00001363C:H02	39252
17	1/28/98	17	RTA00000183AR.e.14.2	M00001506B:D09	17437
18	1/28/98	18	RTA00000196AF.c.17.1	M00001352C:F06	39602
19	1/28/98	19	RTA00000185AF.a.8.1	M00001570D:A03	4868
20	1/28/98	20	RTA00000181AF.l.14.2	M00001454D:D06	2364
21	1/28/98	21	RTA00000131A.g.19.2	M00001449A:G10	36535
22	1/28/98	22	RTA00000187AR.o.10.2	M00001718D:F07	8984
23	1/28/98	23	RTA00000198R.b.08.1	M00001567C:H12	22636
24	1/28/98	24	RTA00000200AF.f.11.1	M00004111D:D11	0
25	1/28/98	25	RTA00000196AF.c.1.1	M00001349C:C05	8171
26	1/28/98	26	RTA00000200R.g.09.1	M00004131B:H09	22785
27	1/28/98	27	RTA00000192AF.i.12.1	M00004169C:C12	5319
28	1/28/98	28	RTA00000178AR.o.01.5	M00001387B:H07	0
29	1/28/98	29	RTA00000200AF.b.19.1	M00004042D:H02	22847
30	1/28/98	30	RTA00000184AR.n.07.2	M00001561C:F06	0
31	1/28/98	31	RTA00000200F.m.15.1	M00004236C:D10	22601
32	1/28/98	32	RTA00000198R.m.19.1	M00001680D:D02	40041
33	1/28/98	33	RTA00000178AR.a.20.1	M00001362C:H11	945
34	1/28/98	34	RTA00000197AF.n.8.1	M00001536D:A12	4101
35	1/28/98	35	RTA00000191AF.n.17.1	M00004091B:D11	7848
36	1/28/98	36	RTA00000181AF.p.4.3	M00001460A:A03	40392
37	1/28/98	37	RTA00000181AF.n.15.2	M00001457A:B07	86128
38	1/28/98	38	RTA00000196R.k.07.1	M00001399C:D09	22443
39	1/28/98	39	RTA00000189AR.b.19.1	M00003832B:E01	5294
40	1/28/98	40	RTA00000200AR.e.02.1	M00004090A:F09	36059
41	1/28/98	41	RTA00000184F.k.12.1	M00001557D:D09	8761
42	1/28/98	42	RTA00000184F.j.21.1	M00001557A:D02	7065
43	1/28/98	43	RTA00000179AF.c.14.3	M00001392D:H04	0
44	1/28/98	44	RTA00000199F.f.08.2	M00003841D:E03	12445
45	1/28/98	45	RTA00000197AR.f.12.1	M00001458C:E01	3513
46	1/28/98	46	RTA00000182AF.f.13.1	M00001470C:B10	8010
47	1/28/98	47	RTA00000192AF.m.12.1	M00004191D:B11	0
48	1/28/98	48	RTA00000177AR.a.23.5	M00001339D:G02	6995
49	1/28/98	49	RTA00000198R.o.05.1	M00003750A:D01	26702

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
50	1/28/98	50	RTA00000201R.a.02.1	M00004295B:D02	35362
51	1/28/98	51	RTA00000199R.k.07.1	M00003901C:A03	12973
52	1/28/98	52	RTA00000201R.b.02.1	M00004319D:G09	22660
53	1/28/98	53	RTA00000199AF.p.9.1	M00003988A:E10	10430
54	1/28/98	54	RTA00000200F.o.22.1	M00004282B:A04	983
55	1/28/98	55	RTA00000186AF.i.21.1	M00001636C:H09	6033
56	1/28/98	56	RTA00000177AF.e.9.1	M00001343D:C04	37442
57	1/28/98	57	RTA00000198AF.k.20.1	M00001660C:B12	22553
58	1/28/98	58	RTA00000199F.b.01.2	M00003778A:D08	19118
59	1/28/98	59	RTA00000195AF.b.13.1	M00001560D:A03	12605
59	2/24/98	78	RTA00000195AF.b.13.1	M00001560D:A03	12605
60	1/28/98	60	RTA00000196AR.i.12.3	M00001389D:G11	38800
61	1/28/98	61	RTA00000197AF.h.11.1	M00001476D:G03	22264
62	1/28/98	62	RTA00000190AF.a.18.2	M00003900D:B10	0
63	1/28/98	63	RTA00000184AF.k.19.1	M00001558B:D08	8022
64	1/28/98	64	RTA00000198AF.p.12.1	M00003763D:E10	8878
65	1/28/98	65	RTA00000198AF.m.16.1	M00001679D:D05	51
66	1/28/98	66	RTA00000199F.c.09.2	M00003800A:C09	16824
67	1/28/98	67	RTA00000200AF.g.07.1	M00004128B:G01	0
68	1/28/98	68	RTA00000184F.k.19.1	M00001558B:D08	8022
69	1/28/98	69	RTA00000186AF.h.8.1	M00001632C:C09	35547
70	1/28/98	70	RTA00000192AF.e.3.1	M00004138B:H02	13272
71	1/28/98	71	RTA00000193AR.o.16.3	M00004409B:A11	52972
72	1/28/98	72	RTA00000200F.a.6.1	M00004029B:F11	36952
73	1/28/98	73	RTA00000177AF.e.21.3	M00001344A:H07	4306
74	1/28/98	74	RTA00000196AF.h.20.1	M00001385B:F10	0
75	1/28/98	75	RTA00000180AR.h.19.2	M00001428A:H10	84182
76	1/28/98	76	RTA00000200AF.h.05.2	M00004142D:E10	10950
77	1/28/98	77	RTA00000197AF.n.2.1	M00001535A:D02	6229
78	1/28/98	78	RTA00000199R.f.09.1	M00003842B:D09	22907
79	1/28/98	79	RTA00000199AF.p.4.1	M00003985C:F01	10282
80	1/28/98	80	RTA00000196AF.p.13.2	M00001432A:E06	6125
81	1/28/98	81	RTA00000196AF.b.15.1	M00001347B:E01	5102
82	1/28/98	82	RTA00000183AF.l.18.1	M00001535D:C01	3484
83	1/28/98	83	RTA00000186AF.f.24.2	M00001629B:E06	0
84	1/28/98	84	RTA00000191AF.h.14.1	M00004056B:D09	13553
85	1/28/98	85	RTA00000200R.o.03.1	M00004257C:H06	22807
86	1/28/98	86	RTA00000189AF.l.22.1	M00003879C:G10	33333
87	2/24/98	245	RTA00000195AF.d.20.1	M00004117A:D11	37574
87	1/28/98	87	RTA00000195AF.d.20.1	M00004117A:D11	37574
88	1/28/98	88	RTA00000197AF.e.23.1	M00001456B:C09	37157
89	1/28/98	89	RTA00000177AF.n.8.3	M00001356D:F06	4188
90	1/28/98	90	RTA00000199F.f.15.2	M00003845A:H12	8772
91	1/28/98	91	RTA00000198AF.j.19.1	M00001653C:F12	38914
92	1/28/98	92	RTA00000198AF.j.18.1	M00001653B:G07	22759
93	1/28/98	93	RTA00000200F.o.11.1	M00004270A:F11	0
94	1/28/98	94	RTA00000195AF.b.4.1	M00001490C:D07	0
95	1/28/98	95	RTA00000180AF.g.3.1	M00001425A:C11	9024
96	1/28/98	96	RTA00000197AF.j.20.1	M00001496C:C11	4915
97	1/28/98	97	RTA00000197AF.o.2.1	M00001541C:B07	5739

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
98	1/28/98	98	RTA00000200AF.f.14.1	M00004115D:C08	22051
99	1/28/98	99	RTA00000184AF.d.8.1	M00001548A:A08	4393
100	1/28/98	100	RTA00000200R.f.14.1	M00004115D:C08	22051
101	1/28/98	101	RTA00000191AF.d.08.2	M00003997B:G07	970
102	1/28/98	102	RTA00000199R.j.08.1	M00003884D:G07	37844
103	1/28/98	103	RTA00000199F.e.10.1	M00003822A:F02	22906
104	1/28/98	104	RTA00000196R.h.03.1	M00001381A:D02	6636
105	1/28/98	105	RTA00000179AF.g.12.3	M00001398A:G03	36390
106	1/28/98	106	RTA00000197AF.n.21.1	M00001540B:C09	0
107	1/28/98	107	RTA00000196R.i.13.1	M00001390A:A09	9857
108	1/28/98	108	RTA00000183AR.h.23.2	M00001528A:F09	18957
109	1/28/98	109	RTA00000197AF.d.12.1	M00001451D:C10	39546
110	1/28/98	110	RTA00000197R.h.01.1	M00001470A:H01	13075
111	1/28/98	111	RTA00000198AF.o.12.1	M00003751D:B02	22038
112	1/28/98	112	RTA00000177AF.m.8.1	M00001354C:C10	8010
113	1/28/98	113	RTA00000196AF.d.09.1	M00001354B:B10	16934
114	1/28/98	114	RTA00000200R.f.02.1	M00004108A:A09	7138
115	1/28/98	115	RTA00000179AR.o.20.3	M00001409D:F11	2409
116	1/28/98	116	RTA00000181AR.k.24.3	M00001454B:C12	7005
117	1/28/98	117	RTA00000199AF.j.18.1	M00003889D:B09	5140
118	1/28/98	118	RTA00000199F.b.24.2	M00003794A:B03	0
119	1/28/98	119	RTA00000181AR.k.24.2	M00001454B:C12	7005
120	1/28/98	120	RTA00000178AR.m.19.5	M00001384D:H07	0
121	1/28/98	121	RTA00000199AF.o.16.1	M00003979A:F03	16721
122	1/28/98	122	RTA00000197AF.l.15.1	M00001517B:G08	4947
123	1/28/98	123	RTA00000191AF.k.6.1	M00004078B:A11	5451
124	1/28/98	124	RTA00000199AR.m.06.1	M00003933C:D06	19122
125	1/28/98	125	RTA00000197AF.k.15.1	M00001504D:D11	22750
126	1/28/98	126	RTA00000201F.d.16.1	M00004388B:A08	0
127	1/28/98	127	RTA00000178AF.k.18.1	M00001382A:F04	9755
128	1/28/98	128	RTA00000196F.i.12.1	M00001389D:G11	38800
129	1/28/98	129	RTA00000134A.d.10.1	M00001528A:F09	18957
130	1/28/98	130	RTA00000196AF.h.23.1	M00001386A:C02	13357
131	1/28/98	131	RTA00000185AF.d.11.2	M00001579D:C03	6539
132	1/28/98	132	RTA00000178AF.f.20.3	M00001372C:F07	39881
133	1/28/98	133	RTA00000181AR.n.20.3	M00001457B:E03	0
134	1/28/98	134	RTA00000197F.e.11.1	M00001454B:G03	2306
135	1/28/98	135	RTA00000196AF.c.22.1	M00001352D:C05	22548
136	1/28/98	136	RTA00000197AF.c.10.1	M00001448B:F06	10400
137	1/28/98	137	RTA00000181AF.m.4.3	M00001455A:E09	13238
138	1/28/98	138	RTA00000182AF.a.3.3	M00001462B:A10	0
139	1/28/98	139	RTA00000191AF.d.01.2	M00003996A:A06	7031
140	1/28/98	140	RTA00000199F.a.2.1	M00003772A:D07	12674
141	1/28/98	141	RTA00000196AF.c.6.1	M00001350A:D06	23148
142	1/28/98	142	RTA00000198AF.k.19.1	M00001660B:C04	75879
143	1/28/98	143	RTA00000199R.h.09.1	M00003867C:H09	76020
144	1/28/98	144	RTA00000198AF.o.18.1	M00003755A:A09	13018
145	1/28/98	145	RTA00000178AF.h.24.1	M00001376B:C06	6745
146	1/28/98	146	RTA00000185AF.a.19.2	M00001571C:H06	5749
147	1/28/98	147	RTA00000185AF.c.24.2	M00001578B:E04	23001

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
148	1/28/98	148	RTA00000199F.h.17.2	M00003871A:A05	36254
149	1/28/98	149	RTA00000181AR.h.06.3	M00001450D:D04	87226
150	1/28/98	150	RTA00000184F.k.09.1	M00001557C:H07	7065
151	1/28/98	151	RTA00000200R.l.17.1	M00004217C:D03	12771
152	1/28/98	152	RTA00000196AF.c.20.1	M00001352C:H02	8934
153	1/28/98	153	RTA00000200F.n.17.2	M00004252C:E03	19064
154	1/28/98	154	RTA00000196F.e.7.1	M00001360D:E11	1039
155	1/28/98	155	RTA00000197F.e.8.1	M00001454A:C11	3135
156	1/28/98	156	RTA00000199R.o.12.1	M00003977A:E04	16128
157	1/28/98	157	RTA00000188AF.n.01.1	M00003801A:B10	36412
158	1/28/98	158	RTA00000198AF.k.03.1	M00001655A:F06	22765
159	1/28/98	159	RTA00000182AF.l.12.1	M00001487A:A05	1027
160	1/28/98	160	RTA00000192AF.b.20.1	M00004118D:E08	0
161	1/28/98	161	RTA00000183AF.e.23.2	M00001506D:A09	0
162	1/28/98	162	RTA00000201F.e.15.1	M00004444B:D11	9960
163	1/28/98	163	RTA00000192AR.e.13.3	M00004142A:B12	9457
164	1/28/98	164	RTA00000193AR.i.14.4	M00004307C:A06	9457
165	1/28/98	165	RTA00000192AF.g.23.1	M00004157C:A09	6455
166	1/28/98	166	RTA00000198AF.f.21.1	M00001614D:D09	22676
167	1/28/98	167	RTA00000179AF.d.22.3	M00001394C:C11	7955
168	1/28/98	168	RTA00000177AR.k.23.1	M00001352D:D02	35550
169	1/28/98	169	RTA00000196AF.g.24.1	M00001380C:F02	8685
170	1/28/98	170	RTA00000197AF.d.23.1	M00001453A:E11	16130
171	1/28/98	171	RTA00000198R.c.07.1	M00001575D:G05	19181
172	1/28/98	172	RTA00000186AF.p.09.2	M00001655C:E04	6879
173	1/28/98	173	RTA00000200AR.b.07.1	M00004039C:C01	17125
174	1/28/98	174	RTA00000181AF.e.22.3	M00001448D:F09	3442
175	1/28/98	175	RTA00000200F.i.5.1	M00004156B:A12	22892
176	1/28/98	176	RTA00000183AF.h.19.1	M00001528A:A01	5175
177	1/28/98	177	RTA00000197AF.c.3.1	M00001447C:C01	3145
178	1/28/98	178	RTA00000200F.o.03.1	M00004257C:H06	22807
179	1/28/98	179	RTA00000179AF.f.20.3	M00001397B:B09	16154
180	1/28/98	180	RTA00000199AF.j.12.1	M00003887A:A06	22461
181	1/28/98	181	RTA00000198AF.d.2.1	M00001585A:F07	0
182	1/28/98	182	RTA00000196AF.h.16.1	M00001384C:E03	39895
183	1/28/98	183	RTA00000198AF.c.17.1	M00001579C:E08	6923
184	1/28/98	184	RTA00000197AF.f.7.1	M00001457C:C11	19261
185	2/24/98	234	RTA00000195AF.d.4.1	M00003881D:D06	22766
185	1/28/98	185	RTA00000195AF.d.4.1	M00003881D:D06	22766
186	1/28/98	186	RTA00000198R.p.09.1	M00003761D:E02	10473
187	1/28/98	187	RTA00000180AR.j.04.4	M00001429C:G12	22300
188	1/28/98	188	RTA00000188AF.o.05.1	M00003806D:G05	4668
189	1/28/98	189	RTA00000197AF.h.10.1	M00001476B:F10	15554
190	1/28/98	190	RTA00000134A.c.7.1	M00001528A:A01	5175
191	1/28/98	191	RTA00000187AF.p.23.1	M00003748B:F02	39804
192	1/28/98	192	RTA00000185AF.m.7.1	M00001605C:D12	39804
193	1/28/98	193	RTA00000199AF.n.3.1	M00003946D:C11	0
194	1/28/98	194	RTA00000200R.k.01.1	M00004188C:A09	40049
195	1/28/98	195	RTA00000198AF.c.10.1	M00001577B:H02	77149
196	1/28/98	196	RTA00000198F.e.10.1	M00001599B:E09	9727

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
197	1/28/98	197	RTA00000198F.l.12.1	M00001669C:B01	8592
198	1/28/98	198	RTA00000197AR.e.07.1	M00001453D:G12	86969
199	1/28/98	199	RTA00000199R.c.09.1	M00003800A:C09	16824
200	1/28/98	200	RTA00000182AF.f.2.1	M00001469D:D02	4794
201	1/28/98	201	RTA00000198AF.p.18.1	M00003769B:D03	23081
202	1/28/98	202	RTA00000200R.l.17.2	M00004217C:D03	12771
203	1/28/98	203	RTA00000201F.d.09.1	M00004380B:A05	1827
204	1/28/98	204	RTA00000180AR.o.5.2	M00001437D:C04	7848
205	1/28/98	205	RTA00000189AF.g.11.1	M00003858D:F12	0
206	1/28/98	206	RTA00000181AF.o.04.2	M00001457C:C12	22205
207	1/28/98	207	RTA00000199AF.l.19.1	M00003924B:D04	22460
208	1/28/98	208	RTA00000198AF.h.22.1	M00001635C:A03	22366
209	1/28/98	209	RTA00000182AF.c.5.1	M00001464D:F06	6397
210	1/28/98	210	RTA00000189AR.b.12.1	M00003829B:G03	17233
211	1/28/98	211	RTA00000199AF.m.15.1	M00003939A:A02	10101
212	1/28/98	212	RTA00000197AF.j.9.1	M00001494B:C01	13236
213	1/28/98	213	RTA00000200F.o.04.1	M00004260D:C12	12514
214	1/28/98	214	RTA00000200AF.f.22.1	M00004121C:F06	16521
215	1/28/98	215	RTA00000192AR.e.14.3	M00004142A:D08	3300
216	1/28/98	216	RTA00000188AF.g.9.1	M00003774B:B08	4959
217	1/28/98	217	RTA00000198AF.h.3.1	M00001625D:C07	22562
218	1/28/98	218	RTA00000188AF.o.18.1	M00003811D:A12	13678
219	1/28/98	219	RTA00000198AF.m.19.1	M00001680D:D02	40041
220	1/28/98	220	RTA00000200AF.h.01.2	M00004141D:A09	0
221	1/28/98	221	RTA00000189AF.i.17.1	M00003868C:H10	16814
222	1/28/98	222	RTA00000185AF.i.4.1	M00001594A:B12	13942
223	1/28/98	223	RTA00000197F.i.9.1	M00001488D:C10	0
224	1/28/98	224	RTA00000188AF.m.11.1	M00003799A:D09	0
225	1/28/98	225	RTA00000189AF.b.5.1	M00003828A:E04	3784
226	1/28/98	226	RTA00000191AR.o.09.4	M00004096A:G02	0
227	1/28/98	227	RTA00000201R.d.02.2	M00004375A:H01	2599
228	1/28/98	228	RTA00000187AR.h.15.2	M00001679A:A06	6660
229	1/28/98	229	RTA00000198AF.g.3.1	M00001615C:F03	0
230	1/28/98	230	RTA00000185AR.b.18.1	M00001575B:C09	12171
231	1/28/98	231	RTA00000192AF.l.13.2	M00004185C:C03	11443
232	1/28/98	232	RTA00000186AF.j.03.2	M00001638A:E07	0
233	1/28/98	233	RTA00000197AF.l.8.1	M00001511B:C06	39954
234	1/28/98	234	RTA00000191AF.f.8.1	M00004035A:A04	6541
235	1/28/98	235	RTA00000201AF.a.02.1	M00004295B:D02	35362
236	1/28/98	236	RTA00000183AR.h.23.1	M00001528A:F09	18957
237	1/28/98	237	RTA00000197AF.k.10.1	M00001500D:B11	0
238	1/28/98	238	RTA00000187AR.k.12.1	M00001679D:F02	78415
239	1/28/98	239	RTA00000201R.d.02.1	M00004375A:H01	2599
240	1/28/98	240	RTA00000178AF.e.1.1	M00001369A:H12	2664
241	1/28/98	241	RTA00000200AF.l.17.1	M00004217C:D03	12771
242	1/28/98	242	RTA00000198AF.m.17.1	M00001679D:F06	77992
243	1/28/98	243	RTA00000181AF.m.15.3	M00001455D:A11	12081
244	1/28/98	244	RTA00000199F.f.12.2	M00003844C:A08	8131
245	1/28/98	245	RTA00000200AF.k.7.1	M00004193C:G11	0
246	1/28/98	246	RTA00000199AF.l.4.1	M00003911D:B04	4410

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
247	1/28/98	247	RTA00000198AF.k.08.1	M00001656C:G08	17436
248	1/28/98	248	RTA00000198R.c.14.1	M00001578D:C04	39814
249	1/28/98	249	RTA00000200R.o.03.2	M00004257C:H06	22807
250	1/28/98	250	RTA00000192AF.j.21.1	M00004176D:B12	2289
251	1/28/98	251	RTA00000192AF.n.13.1	M00004197D:H01	8210
252	1/28/98	252	RTA00000181AF.e.18.3	M00001448D:C09	8
253	1/28/98	253	RTA00000181AF.e.17.3	M00001448D:C09	8
254	1/28/98	254	RTA00000178AF.n.2.1	M00001385C:H11	17083
255	1/28/98	255	RTA00000199AF.j.17.1	M00003889A:D10	5121
256	1/28/98	256	RTA00000184AR.e.15.1	M00001549C:E06	16347
257	1/28/98	257	RTA00000198AF.e.20.1	M00001604C:E09	9810
258	1/28/98	258	RTA00000199F.h.12.2	M00003868B:D12	16621
259	1/28/98	259	RTA00000197AF.j.4.1	M00001492D:A11	17209
260	1/28/98	260	RTA00000198R.m.17.1	M00001679D:F06	77992
261	1/28/98	261	RTA00000192AF.a.24.1	M00004114C:F11	13183
262	1/28/98	262	RTA00000186AF.c.17.1	M00001619D:G05	8551
263	1/28/98	263	RTA00000190AF.n.6.1	M00003965A:B11	0
264	1/28/98	264	RTA00000179AF.k.3.3	M00001401A:H07	0
265	1/28/98	265	RTA00000177AF.e.14.1	M00001343D:H07	23255
266	1/28/98	266	RTA00000199F.f.21.2	M00003847C:E09	13344
267	1/28/98	267	RTA00000186AF.g.11.2	M00001630B:H09	5214
268	1/28/98	268	RTA00000186AF.h.01.2	M00001632A:F12	0
269	1/28/98	269	RTA00000183AF.k.13.1	M00001534B:C12	0
270	1/28/98	270	RTA00000178R.l.08.1	M00001383A:C03	39648
271	1/28/98	271	RTA00000201F.d.02.1	M00004375A:H01	2599
272	1/28/98	272	RTA00000199F.g.08.2	M00003853D:G08	0
273	1/28/98	273	RTA00000201F.c.08.1	M00004353C:H07	0
274	1/28/98	274	RTA00000191AF.o.17.1	M00004102A:H02	5957
275	1/28/98	275	RTA00000191AF.o.17.2	M00004102A:H02	5957
276	1/28/98	276	RTA00000198AF.j.15.1	M00001653B:E09	4369
277	1/28/98	277	RTA00000198AR.i.08.1	M00001639A:F10	9807
278	1/28/98	278	RTA00000198AF.p.16.1	M00003768A:E02	71877
279	1/28/98	279	RTA00000196AF.h.24.1	M00001386A:D11	7308
280	1/28/98	280	RTA00000193AF.b.18.1	M00004233C:H09	7542
281	1/28/98	281	RTA00000188AF.n.10.1	M00003802D:B11	10283
282	1/28/98	282	RTA00000193AF.c.15.1	M00004248B:E08	3726
283	1/28/98	283	RTA00000177AF.i.8.4	M00001350A:H01	7187
284	1/28/98	284	RTA00000199F.d.10.2	M00003808C:B05	22049
285	1/28/98	285	RTA00000181AR.j.14.3	M00001453B:E10	5399
286	1/28/98	286	RTA00000181AR.k.2.3	M00001453C:A11	0
287	1/28/98	287	RTA00000200AF.b.07.1	M00004039C:C01	17125
288	1/28/98	288	RTA00000181AR.i.06.3	M00001452A:C07	19119
289	1/28/98	289	RTA00000196F.k.07.1	M00001399C:D09	22443
290	1/28/98	290	RTA00000201F.f.10.1	M00004498D:D05	5231
291	1/28/98	291	RTA00000200AF.e.16.1	M00004101C:G08	12068
292	1/28/98	292	RTA00000199AF.m.18.1	M00003939C:F04	0
293	1/28/98	293	RTA00000197AF.e.13.1	M00001454C:F02	662
294	1/28/98	294	RTA00000198AF.k.23.1	M00001661B:C08	8995
295	1/28/98	295	RTA00000181AR.i.19.2	M00001452C:B06	16970
296	1/28/98	296	RTA00000196AF.f.20.1	M00001371D:G01	22774

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
297	1/28/98	297	RTA00000178AF.f.9.3	M00001371C:E09	7172
298	1/28/98	298	RTA00000197AR.e.11.1	M00001454B:G03	2306
299	1/28/98	299	RTA00000196AF.f.5.1	M00001366D:G02	11937
300	2/24/98	464	RTA00000195AF.c.12.1	M00003818B:G12	37582
300	1/28/98	300	RTA00000195AF.c.12.1	M00003818B:G12	37582
301	1/28/98	301	RTA00000181AR.i.19.3	M00001452C:B06	16970
302	1/28/98	302	RTA00000186AF.d.1.2	M00001621C:C08	40044
303	1/28/98	303	RTA00000186AR.e.03.3	M00001623D:C10	22110
304	1/28/98	304	RTA00000182AR.c.5.1	M00001464D:F06	6397
305	1/28/98	305	RTA00000200AF.b.15.1	M00004040D:F01	10627
306	1/28/98	306	RTA00000199AF.p.12.1	M00003989A:H11	12578
307	1/28/98	307	RTA00000200F.n.05.2	M00004246C:A09	18989
308	1/28/98	308	RTA00000178AF.j.20.1	M00001380C:E05	15066
309	1/28/98	309	RTA00000198AF.h.12.1	M00001632C:A02	9503
310	1/28/98	310	RTA00000188AF.m.08.1	M00003798D:H08	22155
311	1/28/98	311	RTA00000191AR.j.4.2	M00004071D:A10	5198
312	1/28/98	312	RTA00000193AF.h.2.1	M00004290A:B03	3273
313	1/28/98	313	RTA00000183AF.o.11.1	M00001540D:D02	0
314	1/28/98	314	RTA00000182AF.o.5.1	M00001493B:D09	5007
315	1/28/98	315	RTA00000199R.d.23.1	M00003815D:H09	37477
316	1/28/98	316	RTA00000198AF.h.24.1	M00001636C:C01	8390
317	1/28/98	317	RTA00000198AF.p.09.1	M00003761D:E02	10473
318	1/28/98	318	RTA00000200AF.g.17.1	M00004138A:H09	0
319	1/28/98	319	RTA00000200F.n.05.1	M00004246C:A09	18989
320	1/28/98	320	RTA00000196AF.m.13.1	M00001415B:E09	16290
321	1/28/98	321	RTA00000181AR.b.21.1	M00001444C:D05	3266
322	1/28/98	322	RTA00000184AR.b.21.1	M00001546B:B02	39788
323	1/28/98	323	RTA00000182AF.m.21.1	M00001490C:C12	18699
324	1/28/98	324	RTA00000184F.j.06.1	M00001556B:G02	11294
325	1/28/98	325	RTA00000182AF.d.18.4	M00001467D:H05	37435
326	1/28/98	326	RTA00000197AR.e.19.1	M00001455D:A09	8047
327	1/28/98	327	RTA00000182AF.i.1.3	M00001479B:A01	7033
328	1/28/98	328	RTA00000200AF.g.09.1	M00004131B:H09	22785
329	1/28/98	329	RTA00000186AF.b.9.1	M00001616C:F07	0
330	1/28/98	330	RTA00000177AR.m.17.4	M00001355B:G10	14391
331	1/28/98	331	RTA00000197AR.c.20.1	M00001449D:A06	16282
332	1/28/98	332	RTA00000193AR.n.04.3	M00004375C:D01	9850
333	1/28/98	333	RTA00000196F.k.15.1	M00001400A:F06	8320
334	1/28/98	334	RTA00000181AR.b.21.3	M00001444C:D05	3266
335	1/28/98	335	RTA00000182AF.e.3.2	M00001468B:H06	0
336	1/28/98	336	RTA00000186AF.f.24.1	M00001629B:E06	0
337	1/28/98	337	RTA00000177AR.m.17.3	M00001355B:G10	14391
338	1/28/98	338	RTA00000184AF.i.1.1	M00001554B:C07	0
339	1/28/98	339	RTA00000193AF.d.1.1	M00004250D:D10	0
340	1/28/98	340	RTA00000185AF.n.8.1	M00001608B:A03	0
341	1/28/98	341	RTA00000181AF.l.06.2	M00001454C:C08	0
342	1/28/98	342	RTA00000196AF.d.10.1	M00001354C:B06	22256
343	1/28/98	343	RTA00000201F.a.18.1	M00004314B:G07	16837
344	1/28/98	344	RTA00000198AF.o.02.1	M00003748A:B07	68756
345	1/28/98	345	RTA00000187AF.h.21.1	M00001679A:F01	39171

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
346	1/28/98	346	RTA00000197AR.k.22.1	M00001505C:H01	11394
347	1/28/98	347	RTA00000199F.b.03.2	M00003779B:E12	38340
348	1/28/98	348	RTA00000200F.n.07.2	M00004247C:C12	8663
349	1/28/98	349	RTA00000191AF.j.15.1	M00004073B:B01	6308
350	1/28/98	350	RTA00000193AR.c.7.2	M00004241D:F11	9850
351	1/28/98	351	RTA00000179AF.c.22.1	M00001393B:B09	22515
352	1/28/98	352	RTA00000197AF.p.3.1	M00001550A:A03	7239
353	1/28/98	353	RTA00000198F.a.9.1	M00001557D:C08	0
354	1/28/98	354	RTA00000198R.k.03.1	M00001655A:F06	22765
355	1/28/98	355	RTA00000184AR.b.24.1	M00001546B:C05	5777
356	1/28/98	356	RTA00000180AF.l.12.2	M00001433B:H11	0
357	1/28/98	357	RTA00000184AF.o.15.1	M00001564D:C09	0
358	1/28/98	358	RTA00000198AF.g.7.1	M00001616C:C09	13386
359	1/28/98	359	RTA00000196AF.b.17.1	M00001348A:D04	12193
360	1/28/98	360	RTA00000198F.i.5.1	M00001638A:D10	39989
361	1/28/98	361	RTA00000177AR.g.16.4	M00001347A:B10	13576
362	1/28/98	362	RTA00000197AR.c.24.1	M00001450A:B12	82498
363	1/28/98	363	RTA00000196AF.e.14.1	M00001362C:A10	12850
364	1/28/98	364	RTA00000187AF.g.13.1	M00001676C:C11	2991
365	1/28/98	365	RTA00000196F.l.20.2	M00001410B:G05	22678
366	1/28/98	366	RTA00000192AF.o.19.1	M00004208D:H08	3549
367	1/28/98	367	RTA00000196F.i.24.1	M00001392C:D10	4233
368	1/28/98	368	RTA00000198AF.k.18.1	M00001660A:C12	17432
369	1/28/98	369	RTA00000196F.m.3.1	M00001413A:F02	10453
370	1/28/98	370	RTA00000179AF.c.15.3	M00001392D:H06	2995
371	1/28/98	371	RTA00000197F.e.7.1	M00001453D:G12	86969
372	1/28/98	372	RTA00000186AF.d.23.1	M00001623B:G07	22187
373	1/28/98	373	RTA00000196F.e.12.1	M00001361C:H11	10147
374	1/28/98	374	RTA00000178AF.l.11.1	M00001383A:G04	23286
375	1/28/98	375	RTA00000177AF.m.18.1	M00001355B:G11	0
376	1/28/98	376	RTA00000177AF.m.18.3	M00001355B:G11	0
377	1/28/98	377	RTA00000178AF.m.19.1	M00001384D:H07	0
378	1/28/98	378	RTA00000181AF.k.24.3	M00001454B:C12	7005
379	1/28/98	379	RTA00000180AF.l.06.2	M00001433A:G07	5625
380	1/28/98	380	RTA00000182AF.k.24.1	M00001485D:B10	5625
381	1/28/98	381	RTA00000199AF.m.14.1	M00003938A:B04	10580
382	1/28/98	382	RTA00000200AF.j.6.1	M00004176B:E08	22902
383	1/28/98	383	RTA00000199F.f.20.2	M00003847B:G03	0
384	1/28/98	384	RTA00000196AF.h.17.1	M00001384C:F12	39215
385	1/28/98	385	RTA00000201F.c.24.1	M00004374D:E10	35731
386	1/28/98	386	RTA00000197AR.j.04.1	M00001492D:A11	17209
387	2/24/98	632	RTA00000191AF.j.14.1	M00004073A:H12	1002
387	1/28/98	387	RTA00000191AF.j.14.1	M00004073A:H12	1002
388	1/28/98	388	RTA00000185AF.n.17.1	M00001609B:A11	5336
389	1/28/98	389	RTA00000181AR.k.2.2	M00001453C:A11	0
390	1/28/98	390	RTA00000197AR.f.07.1	M00001457C:C11	19261
391	1/28/98	391	RTA00000179AF.e.20.3	M00001396A:C03	4009
392	1/28/98	392	RTA00000185AF.b.11.2	M00001573C:D03	9024
393	1/28/98	393	RTA00000188AF.b.14.1	M00003754D:D02	0
394	1/28/98	394	RTA00000198AF.p.22.1	M00003771A:G10	0

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
395	1/28/98	395	RTA00000196R.c.21.2	M00001352C:H10	0
396	1/28/98	396	RTA00000179AR.b.02.3	M00001391B:G12	0
397	1/28/98	397	RTA00000198AF.b.22.1	M00001571B:E03	38956
398	1/28/98	398	RTA00000177AR.l.13.3	M00001353A:G12	8078
399	1/28/98	399	RTA00000186AF.m.15.2	M00001649C:B10	40122
400	1/28/98	400	RTA00000186AR.e.07.3	M00001623D:G03	4175
401	1/28/98	401	RTA00000195F.e.04.1	M00004465B:D04	6731
402	1/28/98	402	RTA00000177AF.b.21.4	M00001341A:F12	4443
403	1/28/98	403	RTA00000184AF.f.13.1	M00001550D:H02	3784
404	1/28/98	404	RTA00000195AF.b.6.1	M00001496C:G10	39490
405	1/28/98	405	RTA00000197AF.b.24.1	M00001446C:D09	23171
406	1/28/98	406	RTA00000199F.f.09.2	M00003842B:D09	22907
407	1/28/98	407	RTA00000178AF.e.20.1	M00001370D:E12	3135
408	1/28/98	408	RTA00000183AR.l.15.1	M00001535C:E01	39383
409	1/28/98	409	RTA00000180AF.d.1.3	M00001418D:B06	8526
410	1/28/98	410	RTA00000201F.a.20.1	M00004316A:G09	22639
411	1/28/98	411	RTA00000179AF.j.13.3	M00001400B:H06	0
412	2/24/98	678	RTA00000195AF.c.24.1	M00003860D:H07	0
412	1/28/98	412	RTA00000195AF.c.24.1	M00003860D:H07	0
413	1/28/98	413	RTA00000200F.a.12.1	M00004031D:B05	16751
414	1/28/98	414	RTA00000185AR.b.15.1	M00001573D:F04	39813
415	1/28/98	415	RTA00000200AF.f.09.1	M00004111C:E11	12863
416	1/28/98	416	RTA00000199F.a.5.1	M00003773B:G01	22134
417	1/28/98	417	RTA00000200R.d.16.1	M00004085A:B02	39875
418	1/28/98	418	RTA00000187AR.k.01.1	M00001679D:B05	78356
419	1/28/98	419	RTA00000182AF.j.20.1	M00001483B:D03	4769
420	1/28/98	420	RTA00000181AF.c.11.1	M00001445D:A06	4769
421	1/28/98	421	RTA00000200AF.i.21.1	M00004167D:A07	5316
422	1/28/98	422	RTA00000189AF.b.12.1	M00003829B:G03	17233
423	1/28/98	423	RTA00000188AR.b.17.1	M00003755A:B03	10662
424	1/28/98	424	RTA00000187AR.j.24.1	M00001679D:B05	78356
425	1/28/98	425	RTA00000200AF.c.16.1	M00004064D:A11	23433
426	1/28/98	426	RTA00000199AF.o.19.1	M00003980D:E09	36927
427	1/28/98	427	RTA00000187AR.d.9.2	M00001664D:G07	5483
428	1/28/98	428	RTA00000185AF.b.15.2	M00001573D:F04	39813
429	1/28/98	429	RTA00000196F.i.19.1	M00001390C:C11	39498
430	1/28/98	430	RTA00000198R.k.23.1	M00001661B:C08	8995
431	1/28/98	431	RTA00000199AF.k.15.1	M00003905C:G10	8275
432	1/28/98	432	RTA00000198AF.o.05.1	M00003750A:D01	26702
433	1/28/98	433	RTA00000198R.j.18.1	M00001653B:G07	22759
434	1/28/98	434	RTA00000187AR.d.2.2	M00001664C:H10	4892
435	1/28/98	435	RTA00000182AR.c.22.1	M00001467A:D08	16283
436	1/28/98	436	RTA00000200AF.k.11.1	M00004197C:F03	9796
437	1/28/98	437	RTA00000198R.a.23.1	M00001563B:D11	10700
438	1/28/98	438	RTA00000180AR.g.03.4	M00001425A:C11	9024
439	1/28/98	439	RTA00000185AF.d.14.2	M00001579D:G07	8071
440	1/28/98	440	RTA00000177AR.f.13.4	M00001345A:G11	10480
441	1/28/98	441	RTA00000185AF.e.6.1	M00001583B:E10	0
442	1/28/98	442	RTA00000191AF.l.9.1	M00004081C:H06	0
443	1/28/98	443	RTA00000197AR.i.17.1	M00001490A:E11	3516

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
444	1/28/98	444	RTA00000189AF.l.16.1	M00003879A:G05	0
445	1/28/98	445	RTA00000196AF.n.13.1	M00001422C:F12	8396
446	1/28/98	446	RTA00000182AF.a.23.3	M00001463A:F06	9755
447	1/28/98	447	RTA00000198AF.d.8.1	M00001587A:H03	0
448	1/28/98	448	RTA00000200AF.j.9.1	M00004177C:A01	8608
449	1/28/98	449	RTA00000181AF.m.22.3	M00001455D:F09	9283
450	1/28/98	450	RTA00000181AF.m.21.3	M00001455D:F09	9283
451	1/28/98	451	RTA00000200AF.b.20.1	M00004043A:D02	40403
452	1/28/98	452	RTA00000199F.d.19.2	M00003813D:H12	6707
453	1/28/98	453	RTA00000199AF.i.20.1	M00003881A:D09	9544
454	1/28/98	454	RTA00000200R.d.04.1	M00004078A:A06	5506
455	1/28/98	455	RTA00000198AF.d.12.1	M00001589A:C01	21142
456	1/28/98	456	RTA00000200AF.b.12.1	M00004040B:F10	22053
457	1/28/98	457	RTA00000191AR.l.7.2	M00004081C:D12	14391
458	1/28/98	458	RTA00000199R.d.16.1	M00003812C:A05	24191
459	1/28/98	459	RTA00000179AF.c.22.3	M00001393B:B09	22515
460	1/28/98	460	RTA00000179AF.c.15.1	M00001392D:H06	2995
461	1/28/98	461	RTA00000190AF.e.13.1	M00003908A:H09	38961
462	1/28/98	462	RTA00000196AF.n.17.1	M00001423D:A09	12477
463	1/28/98	463	RTA00000177AR.k.23.4	M00001352D:D02	35550
464	1/28/98	464	RTA00000199AF.l.14.1	M00003917A:D02	22865
465	1/28/98	465	RTA00000187AF.k.20.1	M00001680B:C01	3648
466	1/28/98	466	RTA00000177AF.p.20.1	M00001361A:A05	4141
467	1/28/98	467	RTA00000195AF.b.19.1	M00001589A:D12	77678
468	1/28/98	468	RTA00000198AF.a.18.1	M00001561C:E11	0
469	1/28/98	469	RTA00000190AF.n.2.1	M00003963A:E03	5650
470	1/28/98	470	RTA00000198AF.f.16.1	M00001614A:E06	0
471	1/28/98	471	RTA00000188AF.e.2.1	M00003763B:H01	0
472	1/28/98	472	RTA00000192AF.p.17.1	M00004214C:H05	11451
473	1/28/98	473	RTA00000196F.i.3.1	M00001387A:E10	0
474	1/28/98	474	RTA00000192AR.d.1.3	M00004130D:H01	14507
475	1/28/98	475	RTA00000187AR.m.3.3	M00001682C:B12	17055
476	1/28/98	476	RTA00000200R.g.15.1	M00004135B:G01	22898
477	1/28/98	477	RTA00000180AR.e.22.2	M00001423A:G05	7714
478	1/28/98	478	RTA00000192AR.o.24.2	M00004210B:B05	7191
479	1/28/98	479	RTA00000197R.l.22.1	M00001528A:C11	6962
480	1/28/98	480	RTA00000181AF.o.08.2	M00001457C:H12	849
481	1/28/98	481	RTA00000179AR.l.22.2	M00001405B:E09	4314
482	1/28/98	482	RTA00000187AF.j.7.1	M00001679C:F01	78091
483	1/28/98	483	RTA00000192AF.h.19.1	M00004162C:A07	4642
484	1/28/98	484	RTA00000199F.g.20.2	M00003860D:A01	15767
485	1/28/98	485	RTA00000196AF.c.14.1	M00001352B:F04	23105
486	1/28/98	486	RTA00000190AR.p.22.2	M00003979A:E11	16368
487	1/28/98	487	RTA00000198F.i.8.1	M00001639A:F10	9807
488	1/28/98	488	RTA00000179AR.l.22.4	M00001405B:E09	4314
489	1/28/98	489	RTA00000186AF.h.22.1	M00001634B:C10	16485
490	1/28/98	490	RTA00000198AF.n.05.1	M00001687A:G01	24157
491	1/28/98	491	RTA00000196F.k.11.1	M00001399C:H12	3
492	1/28/98	492	RTA00000198AF.b.8.1	M00001567C:H12	22636
493	1/28/98	493	RTA00000177AF.m.17.1	M00001355B:G10	14391

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
494	1/28/98	494	RTA00000200AF.k.1.1	M00004188C:A09	40049
495	1/28/98	495	RTA00000185AF.j.21.1	M00001597A:E12	0
496	1/28/98	496	RTA00000190AF.p.3.1	M00003975B:F03	2378
497	1/28/98	497	RTA00000198AF.o.09.1	M00003751B:A05	4310
498	1/28/98	498	RTA00000190AF.h.12.1	M00003917C:D03	12977
499	1/28/98	499	RTA00000199F.b.22.2	M00003791C:E09	17018
500	1/28/98	500	RTA00000179AR.m.07.5	M00001405D:D11	0
501	1/28/98	501	RTA00000200R.k.11.1	M00004197C:F03	9796
502	1/28/98	502	RTA00000197AF.o.23.1	M00001549A:A09	12682
503	1/28/98	503	RTA00000197AF.k.9.1	M00001500C:C08	3138
504	1/28/98	504	RTA00000198AF.g.2.1	M00001615C:D02	16640
505	1/28/98	505	RTA00000188AF.n.03.1	M00003801B:B10	9443
506	1/28/98	506	RTA00000198R.o.09.1	M00003751B:A05	4310
507	1/28/98	507	RTA00000198AF.c.5.1	M00001573D:F10	53802
508	1/28/98	508	RTA00000187AF.i.14.2	M00001679B:H07	19406
509	1/28/98	509	RTA00000183AF.p.17.1	M00001543A:H12	5158
510	1/28/98	510	RTA00000178AF.n.23.1	M00001387B:E02	3298
511	1/28/98	511	RTA00000196AF.g.10.1	M00001376B:A02	12498
512	1/28/98	512	RTA00000191AF.c.3.1	M00003987D:D06	3549
513	1/28/98	513	RTA00000197AF.h.14.1	M00001477B:F04	7045
514	1/28/98	514	RTA00000196AF.n.02.1	M00001417D:A04	39260
515	1/28/98	515	RTA00000196AF.f.18.1	M00001370D:A12	14506
516	1/28/98	516	RTA00000200AF.e.23.1	M00004107B:A06	14686
517	1/28/98	517	RTA00000184AF.e.14.1	M00001549C:D02	16347
518	1/28/98	518	RTA00000199AF.n.22.1	M00003971A:A06	23064
519	1/28/98	519	RTA00000183AF.a.24.2	M00001499B:A11	10539
520	1/28/98	520	RTA00000195AF.c.8.1	M00001678B:H01	0
520	2/24/98	958	RTA00000195AF.c.8.1	M00001678B:H01	0
521	1/28/98	521	RTA00000197AF.p.12.1	M00001552B:G05	0
522	1/28/98	522	RTA00000178AR.h.17.2	M00001376A:C05	23824
523	1/28/98	523	RTA00000198AF.d.4.1	M00001586D:E02	22435
524	1/28/98	524	RTA00000191AF.j.24.1	M00004076B:G03	0
525	1/28/98	525	RTA00000198AF.c.7.1	M00001575D:G05	19181
526	1/28/98	526	RTA00000185AF.e.20.1	M00001585A:D06	5865
527	1/28/98	527	RTA00000198R.m.23.1	M00001684B:G03	38469
528	1/28/98	528	RTA00000200F.n.09.2	M00004249D:B08	12391
529	1/28/98	529	RTA00000178AF.b.13.1	M00001364A:E11	3114
530	1/28/98	530	RTA00000185AF.d.24.2	M00001582D:F05	0
531	1/28/98	531	RTA00000195F.a.3.1	M00001368A:A03	27179
532	1/28/98	532	RTA00000177AF.o.4.1	M00001358C:C06	0
533	1/28/98	533	RTA00000177AR.m.13.4	M00001355A:C12	4175
534	1/28/98	534	RTA00000201AF.e.01.1	M00004405D:C04	11397
535	1/28/98	535	RTA00000196AF.n.19.1	M00001423D:D12	6881
536	1/28/98	536	RTA00000193AR.a.2.3	M00004216D:D03	0
537	1/28/98	537	RTA00000188AF.g.14.1	M00003774C:D02	0
538	1/28/98	538	RTA00000177AR.m.13.3	M00001355A:C12	4175
539	1/28/98	539	RTA00000197AR.b.13.1	M00001445B:E04	9560
540	1/28/98	540	RTA00000179AF.b.10.3	M00001391D:D10	0
541	1/28/98	541	RTA00000197AR.b.16.1	M00001445C:A08	0
542	1/28/98	542	RTA00000198R.p.12.1	M00003763D:E10	8878

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
543	1/28/98	543	RTA00000200AF.i.19.1	M00004167A:H03	14722
544	1/28/98	544	RTA00000196F.j.13.1	M00001396D:B03	23170
545	1/28/98	545	RTA00000196F.a.2.1	M00001338B:E02	3575
546	1/28/98	546	RTA00000197F.i.6.1	M00001487C:D06	12149
547	1/28/98	547	RTA00000196AF.g.8.1	M00001375B:G12	39665
548	1/28/98	548	RTA00000179AF.f.23.3	M00001397B:G03	35258
549	1/28/98	549	RTA00000198AF.c.16.1	M00001579C:B11	26801
550	1/28/98	550	RTA00000183AF.g.14.1	M00001513D:A03	0
551	1/28/98	551	RTA00000200AR.c.24.1	M00004076D:D04	15972
552	1/28/98	552	RTA00000193AF.b.24.1	M00004237D:D08	35
553	1/28/98	553	RTA00000201F.b.22.1	M00004344B:H04	35728
554	1/28/98	554	RTA00000186AR.e.07.4	M00001623D:G03	4175
555	1/28/98	555	RTA00000198AF.j.08.1	M00001651B:A11	10983
556	1/28/98	556	RTA00000199F.f.17.2	M00003845D:B04	22905
557	1/28/98	557	RTA00000198AF.d.9.1	M00001587D:A10	8841
558	1/28/98	558	RTA00000186AR.h.14.1	M00001632D:H07	0
559	1/28/98	559	RTA00000197AF.p.20.1	M00001554B:B07	22795
560	1/28/98	560	RTA00000184AF.i.23.3	M00001556A:F11	1577
561	1/28/98	561	RTA00000185AR.d.10.1	M00001579C:H10	0
562	1/28/98	562	RTA00000196F.j.12.1	M00001396A:H03	19294
563	1/28/98	563	RTA00000192AR.o.16.2	M00004208B:F05	9061
564	1/28/98	564	RTA00000200AF.g.18.1	M00004138B:B11	1600
565	1/28/98	565	RTA00000191AF.c.10.1	M00003989B:F11	40422
566	1/28/98	566	RTA00000195F.a.4.1	M00001372C:G12	20470
567	1/28/98	567	RTA00000177AR.m.13.1	M00001355A:C12	4175
568	1/28/98	568	RTA00000196AF.p.01.2	M00001430A:A02	87143
569	1/28/98	569	RTA00000196AF.l.23.1	M00001412A:E04	12052
570	1/28/98	570	RTA00000183AF.a.19.2	M00001499A:A05	3788
571	1/28/98	571	RTA00000198AF.b.14.1	M00001569C:B06	801
572	1/28/98	572	RTA00000181AF.l.16.2	M00001454D:E05	13532
573	1/28/98	573	RTA00000196AF.b.7.1	M00001344A:G07	7774
574	1/28/98	574	RTA00000192AF.f.3.1	M00004146C:C11	5257
575	1/28/98	575	RTA00000186AF.l.12.2	M00001645A:C12	19267
576	1/28/98	576	RTA00000196AF.c.7.1	M00001350B:G11	0
577	1/28/98	577	RTA00000190AF.a.24.2	M00003901B:A05	0
578	1/28/98	578	RTA00000180AF.g.17.1	M00001426A:A09	16653
579	1/28/98	579	RTA00000200F.i.7.1	M00004157D:B03	22322
580	1/28/98	580	RTA00000197F.a.12.1	M00001438B:B09	7895
581	1/28/98	581	RTA00000191AF.p.3.2	M00004104B:F11	17
582	1/28/98	582	RTA00000178AR.d.12.4	M00001368A:D07	2476
583	1/28/98	583	RTA00000190AR.h.12.2	M00003917C:D03	12977
584	1/28/98	584	RTA00000190AR.c.03.1	M00003904C:A08	0
585	1/28/98	585	RTA00000198AF.n.18.1	M00001771A:A07	16715
586	1/28/98	586	RTA00000199R.o.11.1	M00003976C:A10	23172
587	1/28/98	587	RTA00000199F.a.3.1	M00003772D:E10	16617
588	1/28/98	588	RTA00000191AF.b.4.1	M00003983C:F03	14936
589	1/28/98	589	RTA00000192AF.l.1.1	M00004183C:D07	16392
590	1/28/98	590	RTA00000190AF.d.2.1	M00003906B:F12	2444
591	1/28/98	591	RTA00000197AF.h.1.1	M00001470A:H01	13075
592	1/28/98	592	RTA00000186AF.e.18.1	M00001624C:A06	0

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
593	1/28/98	593	RTA00000196R.c.14.2	M00001352B:F04	23105
594	1/28/98	594	RTA00000181AR.e.04.3	M00001448A:G09	11825
595	1/28/98	595	RTA00000195R.a.06.1	M00001394A:E04	35265
595	2/24/98	1065	RTA00000195R.a.06.1	M00001394A:E04	35265
596	1/28/98	596	RTA00000184AF.d.9.1	M00001548A:B11	6515
597	1/28/98	597	RTA00000198F.a.4.1	M00001557A:F01	9635
598	1/28/98	598	RTA00000197F.e.10.1	M00001454B:D08	13154
599	1/28/98	599	RTA00000179AF.o.5.1	M00001408D:D04	6172
600	1/28/98	600	RTA00000177AF.g.4.1	M00001346B:B07	4119
601	1/28/98	601	RTA00000184AF.i.10.2	M00001555A:B01	3744
602	1/28/98	602	RTA00000195AF.b.21.1	M00001595B:A09	39055
602	2/24/98	317	RTA00000195AF.b.21.1	M00001595B:A09	39055
603	1/28/98	603	RTA00000183AR.d.11.3	M00001504D:G06	6420
604	1/28/98	604	RTA00000200AF.j.15.1	M00004185D:E04	5849
605	1/28/98	605	RTA00000196F.e.9.1	M00001361A:H07	23300
606	1/28/98	606	RTA00000179AR.e.01.4	M00001395A:C09	2493
607	1/28/98	607	RTA00000200AF.k.12.1	M00004198B:D02	7359
608	1/28/98	608	RTA00000192AF.p.8.1	M00004212B:C07	2379
609	1/28/98	609	RTA00000196AF.n.05.1	M00001418B:F07	12531
610	1/28/98	610	RTA00000200AF.k.2.1	M00004188D:G08	35924
611	1/28/98	611	RTA00000196F.l.13.2	M00001408A:H04	0
612	1/28/98	612	RTA00000197AR.e.22.1	M00001456A:H02	78758
613	1/28/98	613	RTA00000177AF.k.18.4	M00001352C:A05	53729
614	1/28/98	614	RTA00000201F.f.03.1	M00004493B:D09	22633
615	1/28/98	615	RTA00000197R.p.20.1	M00001554B:B07	22795
616	1/28/98	616	RTA00000188AF.m.07.1	M00003798D:E03	23183
617	1/28/98	617	RTA00000179AF.d.13.3	M00001394A:F01	6583
618	1/28/98	618	RTA00000192AF.a.14.1	M00004111D:A08	6874
619	1/28/98	619	RTA00000201F.g.08.1	M00004692A:E07	0
620	1/28/98	620	RTA00000201R.g.08.1	M00004692A:E07	0
621	1/28/98	621	RTA00000201R.g.08.2	M00004692A:E07	0
622	1/28/98	622	RTA00000186AR.m.14.2	M00001649B:G12	9800
623	1/28/98	623	RTA00000198R.b.24.1	M00001571D:B11	19047
624	1/28/98	624	RTA00000200F.o.15.1	M00004275A:B03	7866
625	1/28/98	625	RTA00000196AF.c.19.1	M00001352C:G09	5935
626	1/28/98	626	RTA00000185AR.d.11.1	M00001579D:C03	6539
627	1/28/98	627	RTA00000199F.h.15.2	M00003870A:C05	22269
628	1/28/98	628	RTA00000198AF.g.16.1	M00001621D:D03	6602
629	1/28/98	629	RTA00000199R.m.23.1	M00003945A:E09	40166
630	1/28/98	630	RTA00000183AR.g.03.2	M00001512D:G09	3956
631	1/28/98	631	RTA00000200AF.h.19.2	M00004151D:E03	0
632	1/28/98	632	RTA00000183AR.g.03.1	M00001512D:G09	3956
633	1/28/98	633	RTA00000197F.i.8.1	M00001488A:E01	6292
634	1/28/98	634	RTA00000192AF.j.6.1	M00004172C:D08	11494
635	1/28/98	635	RTA00000181AF.p.7.3	M00001460A:E01	38773
636	1/28/98	636	RTA00000196F.k.20.1	M00001402B:F12	6324
637	1/28/98	637	RTA00000200AF.g.15.1	M00004135B:G01	22898
638	1/28/98	638	RTA00000193AF.l.05.2	M00004348A:A02	2815
639	1/28/98	639	RTA00000199AF.j.1.1	M00003881C:G09	6006
640	1/28/98	640	RTA00000190AF.f.5.1	M00003909A:H04	5015

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
641	1/28/98	641	RTA00000198F.a.10.1	M00001558A:E11	6695
642	1/28/98	642	RTA00000189AF.i.14.1	M00003868B:G11	0
643	1/28/98	643	RTA00000184AF.c.9.1	M00001546C:G10	16245
644	1/28/98	644	RTA00000197F.i.12.1	M00001489B:A06	3605
645	1/28/98	645	RTA00000177AF.k.9.1	M00001352A:E02	16245
646	1/28/98	646	RTA00000186AF.d.24.1	M00001623C:H07	3114
647	1/28/98	647	RTA00000197F.m.11.1	M00001530B:D10	16488
648	1/28/98	648	RTA00000199F.i.9.1	M00003878C:E04	7
649	1/28/98	649	RTA00000190AR.l.19.2	M00003946A:H10	88204
650	1/28/98	650	RTA00000183AR.n.17.1	M00001539B:H06	9800
651	1/28/98	651	RTA00000189AR.d.22.2	M00003844C:B11	6539
652	1/28/98	652	RTA00000178AR.m.21.4	M00001385A:F12	7861
653	1/28/98	653	RTA00000178AR.m.21.5	M00001385A:F12	7861
654	1/28/98	654	RTA00000186AF.j.21.2	M00001639D:B07	22506
655	1/28/98	655	RTA00000186AF.g.8.2	M00001630B:A11	8065
656	1/28/98	656	RTA00000178AR.h.22.3	M00001376B:A08	19230
657	1/28/98	657	RTA00000178AR.h.22.2	M00001376B:A08	19230
658	1/28/98	658	RTA00000193AF.a.1.1	M00004216D:C03	16501
659	1/28/98	659	RTA00000185AR.k.23.2	M00001601A:E09	0
660	1/28/98	660	RTA00000197AF.p.16.1	M00001552D:G08	6013
661	1/28/98	661	RTA00000198R.b.04.1	M00001565A:H09	0
662	1/28/98	662	RTA00000201R.a.15.1	M00004312B:H07	57347
663	1/28/98	663	RTA00000199F.g.21.2	M00003861C:H02	34826
664	1/28/98	664	RTA00000195R.a.23.1	M00001449C:H12	86432
665	1/28/98	665	RTA00000197AF.l.22.1	M00001528A:C11	6962
666	1/28/98	666	RTA00000198F.i.10.1	M00001640B:F03	12792
667	1/28/98	667	RTA00000197AF.d.16.1	M00001452A:E07	23505
668	1/28/98	668	RTA00000178AF.i.17.1	M00001377C:E12	0
669	1/28/98	669	RTA00000192AF.c.2.1	M00004121B:G01	0
670	1/28/98	670	RTA00000186AF.p.17.3	M00001656B:A07	38383
671	1/28/98	671	RTA00000185AR.d.08.1	M00001579C:E09	6562
672	1/28/98	672	RTA00000196AF.h.09.1	M00001382B:F12	8015
673	1/28/98	673	RTA00000199F.m.3.1	M00003931B:A11	0
674	1/28/98	674	RTA00000197AR.e.24.1	M00001456B:F10	39250
675	1/28/98	675	RTA00000179AR.b.21.3	M00001392C:D05	4366
676	1/28/98	676	RTA00000197AR.m.14.1	M00001531B:E09	14879
677	1/28/98	677	RTA00000197AF.i.19.1	M00001490B:H11	39554
678	1/28/98	678	RTA00000190AF.j.3.1	M00003922A:D02	2705
679	1/28/98	679	RTA00000197AF.d.11.1	M00001451C:E01	27260
680	1/28/98	680	RTA00000177AF.f.10.1	M00001345A:E01	6420
681	1/28/98	681	RTA00000180AF.l.04.2	M00001432D:F05	11159
682	1/28/98	682	RTA00000125A.j.16.1	M00001544A:E06	0
683	1/28/98	683	RTA00000187AR.j.01.1	M00001679C:D01	79028
684	1/28/98	684	RTA00000200AR.b.11.1	M00004040A:G12	12043
685	1/28/98	685	RTA00000200F.i.9.1	M00004159C:F09	36756
686	1/28/98	686	RTA00000201F.f.07.1	M00004497A:H03	51116
687	1/28/98	687	RTA00000197AF.g.4.1	M00001464B:B03	8821
688	1/28/98	688	RTA00000193AF.g.3.1	M00004050D:A06	5567
689	1/28/98	689	RTA00000197AF.o.4.1	M00001542B:C06	4121
690	1/28/98	690	RTA00000198R.l.21.1	M00001673A:A04	19194

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
691	1/28/98	691	RTA00000195F.a.10.1	M00001401C:H03	6803
692	1/28/98	692	RTA00000199F.e.4.1	M00003820B:C05	0
693	1/28/98	693	RTA00000198F.m.12.1	M00001679C:D05	4
694	1/28/98	694	RTA00000201R.c.19.1	M00004370A:G05	22357
695	1/28/98	695	RTA00000197F.m.5.1	M00001528C:H04	10872
696	1/28/98	696	RTA00000180AR.d.16.3	M00001419D:C10	11393
697	1/28/98	697	RTA00000193AF.e.21.1	M00004271B:B06	0
698	1/28/98	698	RTA00000179AF.g.1.3	M00001397C:A10	7588
699	1/28/98	699	RTA00000178AF.a.12.1	M00001362B:H06	0
700	1/28/98	700	RTA00000183AF.i.18.2	M00001529D:H02	40129
701	1/28/98	701	RTA00000199AF.o.10.1	M00003974C:E04	0
702	1/28/98	702	RTA00000177AR.b.8.5	M00001340B:A06	17062
703	1/28/98	703	RTA00000198F.l.09.1	M00001664B:D06	3611
704	1/28/98	704	RTA00000190AF.o.12.1	M00003972D:C09	3438
705	1/28/98	705	RTA00000196F.i.5.1	M00001387B:A06	0
706	1/28/98	706	RTA00000177AF.i.6.4	M00001350A:B08	0
707	1/28/98	707	RTA00000179AF.p.15.1	M00001411D:F05	5622
708	1/28/98	708	RTA00000201F.f.06.1	M00004496C:H03	23771
709	1/28/98	709	RTA00000192AF.d.18.1	M00004135D:G02	0
710	1/28/98	710	RTA00000196AF.l.3.1	M00001405B:D07	20864
711	1/28/98	711	RTA00000198F.i.2.1	M00001637B:E07	8076
712	1/28/98	712	RTA00000201F.b.21.1	M00004341B:G03	9071
713	1/28/98	713	RTA00000198AF.g.21.1	M00001624A:F09	6273
714	1/28/98	714	RTA00000199R.g.07.1	M00003853D:D03	0
715	1/28/98	715	RTA00000197AR.k.11.1	M00001500D:E10	53758
716	1/28/98	716	RTA00000200F.p.05.1	M00004285C:A08	3984
717	1/28/98	717	RTA00000200F.o.10.2	M00004269B:C08	36432
718	1/28/98	718	RTA00000196F.l.14.2	M00001408B:G06	23144
719	1/28/98	719	RTA00000183AF.b.12.1	M00001500A:B02	0
720	1/28/98	720	RTA00000197AF.f.14.1	M00001459B:C09	3732
721	1/28/98	721	RTA00000180AF.c.4.1	M00001417B:C04	5415
722	1/28/98	722	RTA00000199R.j.24.1	M00003895C:A10	0
723	1/28/98	723	RTA00000183AF.p.24.1	M00001543C:F01	3116
724	1/28/98	724	RTA00000177AR.f.15.4	M00001345B:E10	9062
725	1/28/98	725	RTA00000197AF.b.1.1	M00001441D:E04	12134
726	1/28/98	726	RTA00000200R.f.10.1	M00004111D:B07	4
727	1/28/98	727	RTA00000184AF.n.12.2	M00001561D:C11	3727
728	1/28/98	728	RTA00000177AR.f.17.4	M00001345C:B01	8594
729	1/28/98	729	RTA00000184AF.a.19.1	M00001544C:C06	2628
730	1/28/98	730	RTA00000192AF.o.11.1	M00004205D:F06	0
731	1/28/98	731	RTA00000184F.k.02.1	M00001557B:H10	5192
732	1/28/98	732	RTA00000186AF.p.01.2	M00001654D:G11	40440
733	1/28/98	733	RTA00000200AF.d.20.1	M00004087A:G08	26600
734	1/28/98	734	RTA00000200AF.d.21.1	M00004087C:D03	0
735	1/28/98	735	RTA00000192AF.b.11.1	M00004117A:G01	40014
736	1/28/98	736	RTA00000196AF.o.13.1	M00001428B:A09	0
737	1/28/98	737	RTA00000189AR.m.9.1	M00003880B:C08	2917
738	1/28/98	738	RTA00000183AF.o.8.1	M00001540C:B10	8927
739	1/28/98	739	RTA00000181AF.p.12.3	M00001460C:H02	22204
740	1/28/98	740	RTA00000198AF.d.15.1	M00001590C:H08	5997

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
741	1/28/98	741	RTA00000196AF.n.22.1	M00001424B:H04	9572
742	1/28/98	742	RTA00000177AF.m.1.1	M00001353D:D10	14929
743	1/28/98	743	RTA00000178AF.k.9.1	M00001381B:F06	16342
744	1/28/98	744	RTA00000196F.m.4.1	M00001413A:F03	7958
745	1/28/98	745	RTA00000183AF.m.11.1	M00001536D:G02	8927
746	1/28/98	746	RTA00000178AF.i.01.2	M00001376B:F03	4
747	1/28/98	747	RTA00000190AF.c.6.1	M00003904D:D10	4780
748	1/28/98	748	RTA00000198AF.b.24.1	M00001571D:B11	19047
749	1/28/98	749	RTA00000178AR.i.13.4	M00001377B:H01	0
750	1/28/98	750	RTA00000198AF.a.19.1	M00001561D:C05	0
751	1/28/98	751	RTA00000179AF.c.4.3	M00001392D:B11	0
752	1/28/98	752	RTA00000192AF.o.7.1	M00004204D:C03	5275
753	1/28/98	753	RTA00000192AF.o.17.1	M00004208D:B10	5275
754	1/28/98	754	RTA00000187AF.l.11.1	M00001681A:F03	4482
755	1/28/98	755	RTA00000199F.c.21.2	M00003803C:D09	5070
756	2/24/98	1	RTA00000404F.a.02.1	M00001589B:E12	9738
757	2/24/98	2	RTA00000406F.d.16.1	M00003875C:G02	15040
758	2/24/98	3	RTA00000420F.d.18.1	M00004105C:B05	63074
759	2/24/98	4	RTA00000339F.i.20.1	M00001438D:C06	4356
760	2/24/98	5	RTA00000408F.o.12.2	M00001572A:A10	78578
761	2/24/98	6	RTA00000119A.j.15.1	M00001460A:E11	79623
762	2/24/98	7	RTA00000413F.d.12.1	M00004088C:A12	66467
763	2/24/98	8	RTA00000423F.i.12.1	M00003914D:E03	9118
764	2/24/98	9	RTA00000406F.n.02.1	M00003918C:H10	15051
765	2/24/98	10	RTA00000350R.c.12.1	M00001550D:A04	9728
766	2/24/98	11	RTA00000411F.k.05.1	M00003850D:B05	64777
767	2/24/98	12	RTA00000339F.b.17.1	M00001366D:E12	10020
768	2/24/98	13	RTA00000406F.f.18.1	M00003879B:G02	38587
769	2/24/98	14	RTA00000419F.b.09.1	M00001694C:F12	78128
770	2/24/98	15	RTA00000419F.c.19.1	M00003820A:A08	64346
771	2/24/98	16	RTA00000399F.a.02.1	M00001366D:C12	0
772	2/24/98	17	RTA00000411F.m.15.1	M00003868D:B09	78014
773	2/24/98	18	RTA00000420F.g.12.1	M00004895B:G04	0
774	2/24/98	19	RTA00000123A.k.23.1	M00001533A:G05	80313
775	2/24/98	20	RTA00000404F.m.04.2	M00001641A:A11	22720
776	2/24/98	21	RTA00000411F.g.08.1	M00003822D:D04	45815
777	2/24/98	22	RTA00000130A.m.15.1	M00001622A:H12	81630
778	2/24/98	23	RTA00000411F.k.20.1	M00003854B:A07	64973
779	2/24/98	24	RTA00000423F.l.09.1	M00004118A:H08	9752
780	2/24/98	25	RTA00000418F.k.05.1	M00001637A:A06	73021
781	2/24/98	26	RTA00000423F.h.18.1	M00003876C:D02	37972
782	2/24/98	27	RTA00000420F.n.19.2	M00005259B:C01	0
783	2/24/98	28	RTA00000422F.p.06.2	M00001661A:B11	39282
784	2/24/98	29	RTA00000404F.n.16.2	M00001649C:D05	39095
785	2/24/98	30	RTA00000411F.m.24.1	M00003870B:B08	77568
786	2/24/98	31	RTA00000134A.j.10.1	M00001534A:G06	81383
787	2/24/98	32	RTA00000409F.j.02.1	M00001611B:E06	76417
788	2/24/98	33	RTA00000403F.j.15.1	M00001539B:G07	23840
789	2/24/98	34	RTA00000411F.n.11.1	M00003875A:B01	77276
790	2/24/98	35	RTA00000339F.i.13.1	M00001434A:B10	5970

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
791	2/24/98	36	RTA00000414F.e.22.1	M00005257D:A06	0
792	2/24/98	37	RTA00000406F.o.15.1	M00003988D:A08	37482
793	2/24/98	38	RTA00000412F.g.04.2	M00003971B:B07	64457
794	2/24/98	39	RTA00000187AF.l.7.1	M00001680D:F08	10539
795	2/24/98	40	RTA00000352R.l.06.1	M00004187D:H06	40343
796	2/24/98	41	RTA00000419F.b.12.1	M00003806B:C09	63148
797	2/24/98	42	RTA00000423F.k.17.2	M00004038A:F02	37512
798	2/24/98	43	RTA00000420F.g.04.1	M00004891B:B12	0
799	2/24/98	44	RTA00000418F.k.14.1	M00001639A:H06	76133
800	2/24/98	45	RTA00000409F.l.12.1	M00001615A:D06	26755
801	2/24/98	46	RTA00000404F.c.20.1	M00001594A:D08	39088
802	2/24/98	47	RTA00000423F.g.09.1	M00003904C:B06	38958
803	2/24/98	48	RTA00000411F.b.24.1	M00001677B:A12	30041
804	2/24/98	49	RTA00000406F.d.12.1	M00003875C:A01	38575
805	2/24/98	50	RTA00000411F.f.02.1	M00003813A:D08	63386
806	2/24/98	51	RTA00000129A.n.21.1	M00001604A:C11	79381
807	2/24/98	52	RTA00000409F.m.12.1	M00001618B:D09	73490
808	2/24/98	53	RTA00000410F.c.04.1	M00001633D:G09	74099
809	2/24/98	54	RTA00000399F.o.01.1	M00001595C:E01	3055
810	2/24/98	55	RTA00000406F.m.09.1	M00003914C:H05	26891
811	2/24/98	56	RTA00000411F.b.06.1	M00001676C:A04	77884
812	2/24/98	57	RTA00000409F.l.21.1	M00001615B:G07	73143
813	2/24/98	58	RTA00000420F.m.18.1	M00005254D:A10	0
814	2/24/98	59	RTA00000346F.j.08.1	M00003879B:A06	39951
815	2/24/98	60	RTA00000413F.p.17.2	M00005136D:G06	0
816	2/24/98	61	RTA00000410F.n.07.1	M00001662A:G01	78823
817	2/24/98	62	RTA00000339F.n.10.1	M00001453B:F08	13719
818	2/24/98	63	RTA00000404F.l.20.2	M00001639B:H05	38638
819	2/24/98	64	RTA00000413F.d.18.1	M00004090B:B04	65305
820	2/24/98	65	RTA00000404F.p.04.2	M00001652D:E05	39069
821	2/24/98	66	RTA00000405F.g.19.2	M00001673A:G08	37150
822	2/24/98	67	RTA00000409F.a.22.1	M00001583B:F02	75200
823	2/24/98	68	RTA00000339F.n.03.1	M00001449B:B03	0
824	2/24/98	69	RTA00000405F.o.18.1	M00003839A:D07	11016
825	2/24/98	70	RTA00000409F.m.13.1	M00001618B:E05	0
826	2/24/98	71	RTA00000120A.d.24.1	M00001464A:E10	5085
827	2/24/98	72	RTA00000347F.a.08.1	M00001592C:G04	3135
828	2/24/98	73	RTA00000413F.p.15.2	M00005136D:D06	0
829	2/24/98	74	RTA00000408F.e.22.2	M00001476B:F08	26930
830	2/24/98	75	RTA00000350R.i.22.1	M00001608B:A03	0
831	2/24/98	76	RTA00000413F.d.16.1	M00004088C:F01	63331
832	2/24/98	77	RTA00000420F.j.22.1	M00005173B:F01	0
833	1/28/98	59	RTA00000195AF.b.13.1	M00001560D:A03	12605
833	2/24/98	78	RTA00000195AF.b.13.1	M00001560D:A03	12605
834	2/24/98	79	RTA00000419F.g.08.1	M00003842C:D11	66700
835	2/24/98	80	RTA00000122A.g.16.1	M00001514A:B04	81366
836	2/24/98	81	RTA00000419F.c.16.1	M00003819D:B01	65254
837	2/24/98	82	RTA00000411F.b.03.1	M00001676B:E01	23634
838	2/24/98	83	RTA00000405F.e.11.2	M00001663D:C06	9331
839	2/24/98	84	RTA00000352R.i.15.1	M00004153B:B03	4363

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
840	2/24/98	85	RTA00000339F.k.22.1	M00001427C:D01	5556
841	2/24/98	86	RTA00000346F.g.22.1	M00003794D:G03	6371
842	2/24/98	87	RTA00000403F.l.20.1	M00001573A:A06	18267
843	2/24/98	88	RTA00000420F.i.24.1	M00005134B:E08	0
844	2/24/98	89	RTA00000406F.c.08.1	M00003870C:A10	22387
845	2/24/98	90	RTA00000411F.a.02.1	M00001675B:E02	78537
846	2/24/98	91	RTA00000355R.e.15.1	M00004316A:G09	22639
847	2/24/98	92	RTA00000412F.l.04.1	M00003989D:F12	66372
848	2/24/98	93	RTA00000413F.p.24.1	M00005139A:H03	0
849	2/24/98	94	RTA00000406F.a.23.1	M00003867B:D10	38712
850	2/24/98	95	RTA00000423F.h.05.1	M00003906A:F04	14837
851	2/24/98	96	RTA00000120A.n.19.3	M00001467A:H07	80004
852	2/24/98	97	RTA00000403F.e.01.1	M00001473A:C11	38965
853	2/24/98	98	RTA00000411F.l.03.1	M00003854D:A12	62702
854	2/24/98	99	RTA00000420F.m.19.1	M00005254D:B08	0
855	2/24/98	100	RTA00000339F.o.23.1	M00001473C:D09	7801
856	2/24/98	101	RTA00000121A.m.2.1	M00001507A:A11	81064
857	2/24/98	102	RTA00000420F.g.06.1	M00004891C:D04	0
858	2/24/98	103	RTA00000418F.j.12.1	M00001626C:G08	73316
859	2/24/98	104	RTA00000421F.n.03.1	M00001675C:A04	1638
860	2/24/98	105	RTA00000346F.d.08.1	M00001671A:A10	39955
861	2/24/98	106	RTA00000339F.f.11.1	M00001391C:H02	5832
862	2/24/98	107	RTA00000125A.g.16.1	M00001544A:C09	21497
863	2/24/98	108	RTA00000418F.o.18.1	M00001661B:F06	78676
864	2/24/98	109	RTA00000422F.p.24.2	M00001658A:G09	5823
865	2/24/98	110	RTA00000408F.k.14.1	M00001486B:E12	73856
866	2/24/98	111	RTA00000128A.i.20.1	M00001560A:F03	9900
867	2/24/98	112	RTA00000422F.c.11.1	M00003841D:A04	2643
868	2/24/98	113	RTA00000401F.e.02.1	M00003805B:C04	0
869	2/24/98	114	RTA00000341F.m.21.1	M00004051D:E01	0
870	2/24/98	115	RTA00000418F.h.19.1	M00001590B:C05	0
871	2/24/98	116	RTA00000403F.o.15.1	M00001582B:E12	39140
872	2/24/98	117	RTA00000341F.m.13.1	M00003987B:E12	26502
873	2/24/98	118	RTA00000408F.h.03.1	M00001479D:H03	78382
874	2/24/98	119	RTA00000423F.k.05.1	M00004036D:F02	37472
875	2/24/98	120	RTA00000401F.m.02.1	M00003907A:F01	1573
876	2/24/98	121	RTA00000418F.p.19.1	M00001677D:B01	78544
877	2/24/98	122	RTA00000420F.f.06.1	M00004115D:D08	64812
878	2/24/98	123	RTA00000122A.j.18.1	M00001516A:D05	81317
879	2/24/98	124	RTA00000420F.d.05.1	M00004092B:E05	64432
880	2/24/98	125	RTA00000403F.m.18.1	M00001576A:B09	39185
881	2/24/98	126	RTA00000422F.j.20.1	M00001653A:G07	22388
882	2/24/98	127	RTA00000411F.j.05.1	M00003841C:F06	40709
883	2/24/98	128	RTA00000403F.a.04.1	M00001448A:B12	23529
884	2/24/98	129	RTA00000118A.d.24.1	M00001416A:H02	81488
885	2/24/98	130	RTA00000406F.f.12.1	M00003879A:C11	21895
886	2/24/98	131	RTA00000418F.g.22.1	M00001585B:F01	74837
887	2/24/98	132	RTA00000418F.m.05.1	M00001650B:C10	73600
888	2/24/98	133	RTA00000404F.l.20.1	M00001639B:H05	38638
889	2/24/98	134	RTA00000408F.i.08.2	M00001482A:H05	75811

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
890	2/24/98	135	RTA00000122A.d.5.1	M00001513A:F05	81155
891	2/24/98	136	RTA00000419F.l.12.1	M00003901C:B01	75710
892	2/24/98	137	RTA00000339R.a.06.1	M00001346A:E04	58694
893	2/24/98	138	RTA00000406F.f.03.1	M00003878C:D08	38687
894	2/24/98	139	RTA00000419F.b.19.1	M00003809A:C01	65534
895	2/24/98	140	RTA00000128A.j.6.2	M00001560A:H10	5316
896	2/24/98	141	RTA00000418F.k.19.1	M00001639C:C02	74932
897	2/24/98	142	RTA00000420F.j.19.1	M00005140C:B10	0
898	2/24/98	143	RTA00000420F.h.13.1	M00004899D:G06	0
899	2/24/98	144	RTA00000349R.f.15.1	M00001472A:D08	75097
900	2/24/98	145	RTA00000419F.g.12.1	M00003842C:G03	66171
901	2/24/98	146	RTA00000404F.n.11.2	M00001649A:E11	38001
902	2/24/98	147	RTA00000422F.c.02.1	M00004118B:A03	2902
903	2/24/98	148	RTA00000419F.n.04.1	M00003975C:F07	13102
904	2/24/98	149	RTA00000419F.o.24.1	M00004031A:F07	65092
905	2/24/98	150	RTA00000419F.k.19.1	M00003877C:G12	75447
906	2/24/98	151	RTA00000341F.c.21.1	M00003789C:F06	7899
907	2/24/98	152	RTA00000127A.i.20.1	M00001555A:B12	81418
908	2/24/98	153	RTA00000422F.g.22.1	M00001585B:A06	22561
909	2/24/98	154	RTA00000340F.b.21.1	M00001533D:A08	8001
910	2/24/98	155	RTA00000413F.h.13.1	M00004107A:D01	65190
911	2/24/98	156	RTA00000125A.k.1.1	M00001545A:B12	0
912	2/24/98	157	RTA00000339F.a.23.1	M00001361B:C07	4022
913	2/24/98	158	RTA00000348R.j.16.1	M00001410A:D07	7005
914	2/24/98	159	RTA00000348R.j.17.1	M00001391D:C06	2641
915	2/24/98	160	RTA00000414F.f.19.1	M00005260B:E11	0
916	2/24/98	161	RTA00000418F.n.22.1	M00001659D:B05	79062
917	2/24/98	162	RTA00000406F.l.08.1	M00003908D:D12	39016
918	2/24/98	163	RTA00000422F.l.23.1	M00001616D:C11	4240
919	2/24/98	164	RTA00000345F.k.06.1	M00001475A:A12	0
920	2/24/98	165	RTA00000409F.j.07.1	M00001611C:H11	75190
921	2/24/98	166	RTA00000418F.m.19.1	M00001654D:A03	8890
922	2/24/98	167	RTA00000399F.l.14.1	M00001590B:G08	3354
923	2/24/98	168	RTA00000411F.e.22.1	M00003812B:D07	63638
924	2/24/98	169	RTA00000347F.a.17.1	M00001366D:C06	16723
925	2/24/98	170	RTA00000422F.n.08.1	M00001632B:E05	38655
926	2/24/98	171	RTA00000404F.n.20.1	M00001650A:C11	26865
927	2/24/98	172	RTA00000420F.i.17.1	M00005101C:B09	0
928	2/24/98	173	RTA00000418F.d.13.1	M00001570A:H01	74309
929	2/24/98	174	RTA00000404F.b.02.1	M00001591B:B12	38984
930	2/24/98	175	RTA00000410F.d.09.1	M00001635B:H01	76964
931	2/24/98	176	RTA00000403F.b.10.1	M00001455C:G07	73268
932	2/24/98	177	RTA00000406F.i.12.1	M00003903D:H11	39080
933	2/24/98	178	RTA00000406F.h.08.1	M00003901C:A08	16228
934	2/24/98	179	RTA00000418F.i.19.1	M00001596D:E03	79180
935	2/24/98	180	RTA00000400F.j.19.1	M00001653C:D10	4086
936	2/24/98	181	RTA00000412F.h.21.1	M00003974D:F02	64348
937	2/24/98	182	RTA00000404F.g.14.1	M00001614D:B08	8858
938	2/24/98	183	RTA00000120A.g.18.1	M00001465A:C12	81255
939	2/24/98	184	RTA00000133A.j.13.1	M00001507A:B02	16846

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
940	2/24/98	185	RTA00000423F.j.05.1	M00003903C:C05	37958
941	2/24/98	186	RTA00000132A.k.6.1	M00001464A:E07	81284
942	2/24/98	187	RTA00000351R.g.11.1	M00003779D:E08	3077
943	2/24/98	188	RTA00000406F.p.04.1	M00004030D:F11	37458
944	2/24/98	189	RTA00000347F.a.13.1	M00001402D:F02	22446
945	2/24/98	190	RTA00000419F.p.23.1	M00004039B:A05	64748
946	2/24/98	191	RTA00000419F.d.17.1	M00003828B:F09	64353
947	2/24/98	192	RTA00000421F.k.15.1	M00001613D:B03	2222
948	2/24/98	193	RTA00000347F.b.10.1	M00001546C:C07	8044
949	2/24/98	194	RTA00000124A.k.5.1	M00001538A:F12	80252
950	2/24/98	195	RTA00000404F.h.22.1	M00001619C:C07	18735
951	2/24/98	196	RTA00000418F.k.10.1	M00001639A:G07	74454
952	2/24/98	197	RTA00000410F.o.05.1	M00001669A:B02	75262
953	2/24/98	198	RTA00000339R.l.14.1	M00001452A:C07	19119
954	2/24/98	199	RTA00000403F.m.13.2	M00001575D:A10	39077
955	2/24/98	200	RTA00000339F.c.02.1	M00001381C:B08	12975
956	2/24/98	201	RTA00000404F.l.09.1	M00001638B:E12	39176
957	2/24/98	202	RTA00000419F.g.22.1	M00003845D:A09	64515
958	2/24/98	203	RTA00000404F.g.21.1	M00001615C:A11	37947
959	2/24/98	204	RTA00000351R.k.19.1	M00003841B:E03	936
960	2/24/98	205	RTA00000138A.n.4.1	M00001624A:G11	21920
961	2/24/98	206	RTA00000410F.b.15.1	M00001633C:F09	77100
962	2/24/98	207	RTA00000414F.b.08.1	M00005212C:H02	0
963	2/24/98	208	RTA00000419F.j.23.1	M00003871A:C11	74470
964	2/24/98	209	RTA00000411F.j.02.1	M00003841C:D07	65310
965	2/24/98	210	RTA00000419F.p.24.1	M00004039B:E12	63477
966	2/24/98	211	RTA00000404F.a.19.1	M00001590B:C07	38624
967	2/24/98	212	RTA00000408F.k.06.1	M00001485C:H10	78393
968	2/24/98	213	RTA00000123A.f.3.1	M00001531A:H07	44017
969	2/24/98	214	RTA00000404F.h.19.1	M00001619A:E05	8096
970	2/24/98	215	RTA00000403F.j.18.1	M00001539D:E10	5790
971	2/24/98	216	RTA00000420F.i.18.1	M00005101C:E09	0
972	2/24/98	217	RTA00000399F.o.17.1	M00001599D:A09	1106
973	2/24/98	218	RTA00000346F.e.13.1	M00001660B:D03	74653
974	2/24/98	219	RTA00000419F.c.18.1	M00003819D:B11	41394
975	2/24/98	220	RTA00000413F.k.02.1	M00004690A:G08	0
976	2/24/98	221	RTA00000414F.f.13.1	M00005259D:H08	0
977	2/24/98	222	RTA00000405F.e.09.1	M00001663C:F12	38978
978	2/24/98	223	RTA00000404F.e.22.1	M00001610A:H05	11344
979	2/24/98	224	RTA00000341F.g.21.1	M00003914C:F09	8823
980	2/24/98	225	RTA00000414F.d.07.1	M00005229D:H09	0
981	2/24/98	226	RTA00000125A.k.10.1	M00001545A:F02	81644
982	2/24/98	227	RTA00000347F.c.06.1	M00001444D:C01	18846
983	2/24/98	228	RTA00000411F.k.19.1	M00003852D:E08	64200
984	2/24/98	229	RTA00000345F.i.09.1	M00001450A:D08	27250
985	2/24/98	230	RTA00000423F.k.01.1	M00004034D:E09	40426
986	2/24/98	231	RTA00000408F.d.06.1	M00001458D:C11	78997
987	2/24/98	232	RTA00000128A.b.20.1	M00001558A:G09	79761
988	2/24/98	233	RTA00000403F.i.08.1	M00001485C:B10	6176
989	2/24/98	234	RTA00000195AF.d.4.1	M00003881D:D06	22766

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
989	1/28/98	185	RTA00000195AF.d.4.1	M00003881D:D06	22766
990	2/24/98	235	RTA00000126A.o.23.1	M00001551A:B10	6268
991	2/24/98	236	RTA00000403F.h.12.1	M00001483C:G09	15205
992	2/24/98	237	RTA00000119A.j.22.1	M00001460A:F07	80336
993	2/24/98	238	RTA00000340F.j.12.1	M00001624A:B06	3277
994	2/24/98	239	RTA00000346F.j.02.1	M00003832B:E01	5294
995	2/24/98	240	RTA00000126A.n.7.2	M00001551A:D06	79557
996	2/24/98	241	RTA00000339F.d.13.1	M00001395C:F11	0
997	2/24/98	242	RTA00000404F.j.08.1	M00001629B:B08	39066
998	2/24/98	243	RTA00000410F.c.14.1	M00001634A:H05	77809
999	2/24/98	244	RTA00000120A.g.23.1	M00001465A:E10	81189
1000	2/24/98	245	RTA00000195AF.d.20.1	M00004117A:D11	37574
1000	1/28/98	87	RTA00000195AF.d.20.1	M00004117A:D11	37574
1001	2/24/98	246	RTA00000414F.c.14.1	M00005218A:G05	0
1002	2/24/98	247	RTA00000412F.j.17.1	M00003982C:G04	64071
1003	2/24/98	248	RTA00000404F.k.24.1	M00001636A:C03	15256
1004	2/24/98	249	RTA00000119A.j.10.1	M00001460A:C10	79646
1005	2/24/98	250	RTA00000410F.o.12.1	M00001669A:G12	77376
1006	2/24/98	251	RTA00000119A.i.9.1	M00001457A:G03	0
1007	2/24/98	252	RTA00000412F.g.24.1	M00003973C:C03	28741
1008	2/24/98	253	RTA00000400F.f.18.1	M00001637A:E10	3764
1009	2/24/98	254	RTA00000341F.l.15.1	M00003986B:A08	5294
1010	2/24/98	255	RTA00000419F.o.16.1	M00003989C:G05	62867
1011	2/24/98	256	RTA00000404F.m.03.2	M00001640A:H02	11799
1012	2/24/98	257	RTA00000411F.c.17.1	M00001678D:G03	77664
1013	2/24/98	258	RTA00000406F.k.15.1	M00003907C:C04	38549
1014	2/24/98	259	RTA00000406F.a.02.1	M00003855C:F10	37744
1015	2/24/98	260	RTA00000414F.e.08.1	M00005236A:E04	0
1016	2/24/98	261	RTA00000341F.b.06.1	M00003794A:E12	17008
1017	2/24/98	262	RTA00000409F.n.14.1	M00001621B:G05	78190
1018	2/24/98	263	RTA00000410F.p.17.1	M00001674D:C10	47425
1019	2/24/98	264	RTA00000345F.j.08.1	M00001451B:A04	16731
1020	2/24/98	265	RTA00000340F.k.16.1	M00001647B:C09	13157
1021	2/24/98	266	RTA00000419F.g.15.1	M00003844D:A07	32519
1022	2/24/98	267	RTA00000423F.a.19.1	M00001676D:A02	21396
1023	2/24/98	268	RTA00000403F.e.23.1	M00001476A:D11	9626
1024	2/24/98	269	RTA00000422F.e.08.1	M00001573A:E01	39020
1025	2/24/98	270	RTA00000411F.d.15.1	M00001692A:B06	74890
1026	2/24/98	271	RTA00000414F.e.16.1	M00005236B:H10	0
1027	2/24/98	272	RTA00000411F.l.15.1	M00003857C:F11	66704
1028	2/24/98	273	RTA00000400F.a.11.1	M00001612B:D11	0
1029	2/24/98	274	RTA00000405F.e.08.1	M00001663C:F10	37916
1030	2/24/98	275	RTA00000353R.j.24.1	M00001428B:D01	23089
1031	2/24/98	276	RTA00000423F.a.18.1	M00001675A:G10	26761
1032	2/24/98	277	RTA00000418F.o.06.1	M00001660C:D11	75930
1033	2/24/98	278	RTA00000404F.c.10.1	M00001593B:E11	23534
1034	2/24/98	279	RTA00000418F.i.21.1	M00001596D:E10	78728
1035	2/24/98	280	RTA00000418F.p.15.1	M00001671C:C11	31066
1036	2/24/98	281	RTA00000411F.l.13.1	M00003857C:C09	43114
1037	2/24/98	282	RTA00000407F.a.24.1	M00004083A:E08	37560

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
1038	2/24/98	283	RTA00000346F.n.06.1	M00004139C:A12	12439
1039	2/24/98	284	RTA00000412F.l.21.1	M00004029C:G10	65183
1040	2/24/98	285	RTA00000413F.i.02.1	M00004110D:A10	65857
1041	2/24/98	286	RTA00000404F.i.19.1	M00001625B:C10	38698
1042	2/24/98	287	RTA00000410F.n.09.1	M00001662C:A04	11736
1043	2/24/98	288	RTA00000403F.a.11.1	M00001448C:F10	73109
1044	2/24/98	289	RTA00000420F.n.08.1	M00005257A:H11	0
1045	2/24/98	290	RTA00000411F.k.16.1	M00003852C:B06	64759
1046	2/24/98	291	RTA00000405F.c.01.1	M00001657D:A04	19236
1047	2/24/98	292	RTA00000423F.i.18.1	M00003918A:D08	14996
1048	2/24/98	293	RTA00000403F.l.04.1	M00001571C:A04	39278
1049	2/24/98	294	RTA00000405F.l.17.1	M00003805A:F02	17225
1050	2/24/98	295	RTA00000406F.a.07.1	M00003856C:H09	26607
1051	2/24/98	296	RTA00000347F.d.06.1	M00001457C:F02	39122
1052	2/24/98	297	RTA00000419F.b.18.1	M00003808D:D08	67034
1053	2/24/98	298	RTA00000406F.h.07.1	M00003901B:H04	38003
1054	2/24/98	299	RTA00000405F.l.15.1	M00001694A:E03	19575
1055	2/24/98	300	RTA00000406F.g.17.1	M00003881B:F10	37979
1056	2/24/98	301	RTA00000401F.m.23.1	M00003914C:C02	2801
1057	2/24/98	302	RTA00000356R.f.18.1	M00004692A:H10	0
1058	2/24/98	303	RTA00000130A.h.22.1	M00001617A:D06	80933
1059	2/24/98	304	RTA00000403F.n.18.2	M00001577D:H06	8811
1060	2/24/98	305	RTA00000418F.p.06.1	M00001664A:F08	32628
1061	2/24/98	306	RTA00000404F.d.13.1	M00001595D:A04	39036
1062	2/24/98	307	RTA00000420F.l.12.2	M00005230B:H09	0
1063	2/24/98	308	RTA00000353R.d.11.1	M00004692A:H08	0
1064	2/24/98	309	RTA00000340F.n.01.1	M00001679A:G06	39081
1065	2/24/98	310	RTA00000419F.d.06.1	M00003820B:D07	65496
1066	2/24/98	311	RTA00000419F.n.09.1	M00003977C:A06	66070
1067	2/24/98	312	RTA00000399F.i.08.1	M00001575D:B10	38927
1068	2/24/98	313	RTA00000406F.g.07.1	M00003880C:E11	37925
1069	2/24/98	314	RTA00000423F.g.13.1	M00003905A:E07	38028
1070	2/24/98	315	RTA00000419F.p.12.1	M00004037A:E04	13767
1071	2/24/98	316	RTA00000414F.a.02.1	M00005178D:H04	0
1072	2/24/98	317	RTA00000195AF.b.21.1	M00001595B:A09	39055
1072	1/28/98	602	RTA00000195AF.b.21.1	M00001595B:A09	39055
1073	2/24/98	318	RTA00000403F.h.05.1	M00001482D:A04	39096
1074	2/24/98	319	RTA00000420F.b.21.1	M00004088D:B10	65057
1075	2/24/98	320	RTA00000422F.p.07.2	M00001661A:E06	39024
1076	2/24/98	321	RTA00000339F.c.21.1	M00001389C:A08	5325
1077	2/24/98	322	RTA00000339F.c.24.1	M00001364B:B06	5516
1078	2/24/98	323	RTA00000421F.n.19.1	M00001679A:D10	16409
1079	2/24/98	324	RTA00000340F.p.17.1	M00003750C:H05	0
1080	2/24/98	325	RTA00000345F.k.21.1	M00001464B:C11	40204
1081	2/24/98	326	RTA00000419F.b.15.1	M00003806D:D11	43969
1082	2/24/98	327	RTA00000405F.a.11.1	M00001655A:B11	39124
1083	2/24/98	328	RTA00000423F.k.19.2	M00003985D:E10	17615
1084	2/24/98	329	RTA00000413F.e.16.1	M00004093C:C02	63836
1085	2/24/98	330	RTA00000403F.i.04.1	M00001485B:D09	8930
1086	2/24/98	331	RTA00000404F.o.18.2	M00001651C:C05	39110

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
1087	2/24/98	332	RTA00000409F.i.24.1	M00001611B:A09	76967
1088	2/24/98	333	RTA00000399F.f.11.1	M00001487C:F01	40167
1089	2/24/98	334	RTA00000408F.p.05.1	M00001575B:B02	9649
1090	2/24/98	335	RTA00000413F.d.02.1	M00004087B:A12	66172
1091	2/24/98	336	RTA00000340F.n.13.1	M00001688D:B10	17055
1092	2/24/98	337	RTA00000340F.p.04.1	M00001679D:B02	78533
1093	2/24/98	338	RTA00000411F.c.05.1	M00001677B:H06	73368
1094	2/24/98	339	RTA00000403F.g.10.1	M00001481A:G06	20211
1095	2/24/98	340	RTA00000408F.l.13.1	M00001530A:B12	4423
1096	2/24/98	341	RTA00000412F.g.20.2	M00003972C:F08	25018
1097	2/24/98	342	RTA00000404F.i.02.1	M00001619D:D10	39015
1098	2/24/98	343	RTA00000422F.g.21.1	M00001583A:F07	17232
1099	2/24/98	344	RTA00000403F.m.15.2	M00001575D:D12	26901
1100	2/24/98	345	RTA00000412F.h.23.2	M00003974D:H04	65118
1101	2/24/98	346	RTA00000418F.j.08.1	M00001626C:C11	73382
1102	2/24/98	347	RTA00000125A.n.4.1	M00001546A:D08	81984
1103	2/24/98	348	RTA00000412F.l.19.1	M00004029C:C05	65825
1104	2/24/98	349	RTA00000404F.m.10.2	M00001641D:E02	779
1105	2/24/98	350	RTA00000129A.p.3.1	M00001604A:B08	32644
1106	2/24/98	351	RTA00000340F.p.20.1	M00003752B:C02	17008
1107	2/24/98	352	RTA00000411F.a.10.1	M00001675C:G01	73073
1108	2/24/98	353	RTA00000409F.n.17.1	M00001621C:C10	76725
1109	2/24/98	354	RTA00000404F.c.03.2	M00001592C:F11	39198
1110	2/24/98	355	RTA00000420F.a.19.1	M00004076A:D12	34192
1111	2/24/98	356	RTA00000409F.m.24.1	M00001620D:H02	3942
1112	2/24/98	357	RTA00000406F.n.16.1	M00003972A:G09	5660
1113	2/24/98	358	RTA00000414F.e.06.1	M00005235A:A03	0
1114	2/24/98	359	RTA00000420F.d.12.1	M00004096D:H03	64095
1115	2/24/98	360	RTA00000409F.j.19.1	M00001613A:F03	73792
1116	2/24/98	361	RTA00000422F.d.16.1	M00001570C:G03	39133
1117	2/24/98	362	RTA00000418F.m.16.1	M00001653B:E06	74986
1118	2/24/98	363	RTA00000405F.c.11.1	M00001659A:D12	39068
1119	2/24/98	364	RTA00000404F.k.22.1	M00001635D:C12	39084
1120	2/24/98	365	RTA00000418F.k.07.1	M00001637A:F10	75067
1121	2/24/98	366	RTA00000403F.c.10.1	M00001456D:F05	75261
1122	2/24/98	367	RTA00000401F.o.06.1	M00004029C:C12	2679
1123	2/24/98	368	RTA00000346F.o.08.1	M00004149C:B02	0
1124	2/24/98	369	RTA00000410F.m.05.1	M00001657B:B04	74964
1125	2/24/98	370	RTA00000405F.i.20.1	M00001677A:G11	38532
1126	2/24/98	371	RTA00000403F.j.17.1	M00001539D:B10	38563
1127	2/24/98	372	RTA00000408F.p.24.1	M00001579A:E03	74286
1128	2/24/98	373	RTA00000418F.k.18.1	M00001639C:A10	75385
1129	2/24/98	374	RTA00000422F.m.04.1	M00001615B:A09	38702
1130	2/24/98	375	RTA00000405F.g.16.2	M00001672D:D04	9021
1131	2/24/98	376	RTA00000400F.k.22.1	M00001656A:B07	2512
1132	2/24/98	377	RTA00000346F.i.01.1	M00003797A:D06	22260
1133	2/24/98	378	RTA00000403F.a.07.1	M00001448B:F09	73559
1134	2/24/98	379	RTA00000349R.j.07.1	M00001529B:C04	2642
1135	2/24/98	380	RTA00000403F.b.19.1	M00001456B:A06	22327
1136	2/24/98	381	RTA00000418F.m.23.1	M00001654D:F11	77195

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
1137	2/24/98	382	RTA00000341F.h.10.1	M00003901B:G11	0
1138	2/24/98	383	RTA00000404F.i.18.1	M00001621C:H12	21912
1139	2/24/98	384	RTA00000422F.i.14.1	M00001487A:F10	39300
1140	2/24/98	385	RTA00000418F.m.14.1	M00001651B:E06	75711
1141	2/24/98	386	RTA00000406F.o.12.1	M00003986D:D02	37459
1142	2/24/98	387	RTA00000411F.a.15.1	M00001675D:B08	73812
1143	2/24/98	388	RTA00000411F.a.07.1	M00001675C:C03	74547
1144	2/24/98	389	RTA00000411F.c.02.1	M00001677B:B04	72852
1145	2/24/98	390	RTA00000355R.a.14.1	M00004187D:G09	10207
1146	2/24/98	391	RTA00000130A.h.16.1	M00001617A:A08	80761
1147	2/24/98	392	RTA00000410F.p.23.1	M00001675B:C01	73948
1148	2/24/98	393	RTA00000418F.m.24.1	M00001654D:F12	77114
1149	2/24/98	394	RTA00000420F.m.02.1	M00005233A:G08	0
1150	2/24/98	395	RTA00000408F.j.19.2	M00001485C:C08	73752
1151	2/24/98	396	RTA00000406F.e.21.1	M00003877D:G05	9090
1152	2/24/98	397	RTA00000118A.d.17.1	M00001416A:D09	81921
1153	2/24/98	398	RTA00000407F.b.04.1	M00004086D:B09	63221
1154	2/24/98	399	RTA00000411F.e.07.1	M00003810C:A03	65008
1155	2/24/98	400	RTA00000403F.f.08.1	M00001477A:G07	19107
1156	2/24/98	401	RTA00000132A.c.11.1	M00001454A:G03	87278
1157	2/24/98	402	RTA00000420F.e.16.1	M00004110A:E04	63639
1158	2/24/98	403	RTA00000403F.d.22.1	M00001473A:A07	10692
1159	2/24/98	404	RTA00000404F.b.11.1	M00001591D:F06	39079
1160	2/24/98	405	RTA00000418F.k.17.1	M00001639C:A09	75390
1161	2/24/98	406	RTA00000129A.k.12.1	M00001601A:A06	79322
1162	2/24/98	407	RTA00000340R.m.07.1	M00001679D:F02	78415
1163	2/24/98	408	RTA00000405F.d.14.1	M00001662A:C12	35209
1164	2/24/98	409	RTA00000406F.f.11.1	M00003879A:B08	38601
1165	2/24/98	410	RTA00000120A.h.5.1	M00001465A:G06	80344
1166	2/24/98	411	RTA00000420F.m.12.1	M00005234D:B04	0
1167	2/24/98	412	RTA00000411F.g.06.1	M00003822D:C06	66065
1168	2/24/98	413	RTA00000408F.d.16.1	M00001459B:D03	76318
1169	2/24/98	414	RTA00000120A.p.18.1	M00001468A:C05	6478
1170	2/24/98	415	RTA00000340R.f.05.1	M00001569B:G11	3202
1171	2/24/98	416	RTA00000404F.c.19.1	M00001594A:D06	39026
1172	2/24/98	417	RTA00000423F.l.02.1	M00003978C:A03	5639
1173	2/24/98	418	RTA00000410F.a.01.1	M00001631D:B10	73354
1174	2/24/98	419	RTA00000408F.h.08.1	M00001480A:D03	74575
1175	2/24/98	420	RTA00000422F.b.16.1	M00003813B:A11	17045
1176	2/24/98	421	RTA00000419F.f.10.1	M00003835D:G06	66193
1177	2/24/98	422	RTA00000418F.l.04.1	M00001641C:D02	74140
1178	2/24/98	423	RTA00000410F.a.16.1	M00001633A:E06	73548
1179	2/24/98	424	RTA00000138A.e.13.1	M00001605A:E06	79608
1180	2/24/98	425	RTA00000130A.b.5.1	M00001605A:E09	79579
1181	2/24/98	426	RTA00000408F.j.15.2	M00001485B:F05	74759
1182	2/24/98	427	RTA00000410F.m.20.1	M00001660B:E03	74285
1183	2/24/98	428	RTA00000422F.f.14.1	M00001478B:D07	2036
1184	2/24/98	429	RTA00000422F.c.17.1	M00004099D:F01	1360
1185	2/24/98	430	RTA00000419F.e.04.1	M00003831C:G05	62963
1186	2/24/98	431	RTA00000399F.j.15.1	M00001578C:G06	1261

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
1187	2/24/98	432	RTA00000418F.g.05.1	M00001579C:H06	73075
1188	2/24/98	433	RTA00000419F.n.02.1	M00003958B:H08	65963
1189	2/24/98	434	RTA00000348R.b.16.1	M00001347B:H04	6510
1190	2/24/98	435	RTA00000340F.b.02.1	M00001503C:G05	10185
1191	2/24/98	436	RTA00000119A.m.15.1	M00001461A:E05	80989
1192	2/24/98	437	RTA00000403F.m.20.2	M00001576A:F11	707
1193	2/24/98	438	RTA00000195R.d.09.1	M00003981C:B04	8537
1194	2/24/98	439	RTA00000413F.g.23.1	M00004103B:E09	40700
1195	2/24/98	440	RTA00000403F.a.18.1	M00001448D:F12	75726
1196	2/24/98	441	RTA00000404F.m.20.2	M00001647A:H08	39144
1197	2/24/98	442	RTA00000347F.b.02.1	M00001450A:A02	39304
1198	2/24/98	443	RTA00000414F.f.15.1	M00005260A:A12	0
1199	2/24/98	444	RTA00000419F.h.04.1	M00003846A:D03	65034
1200	2/24/98	445	RTA00000408F.d.12.1	M00001459B:A12	75782
1201	2/24/98	446	RTA00000133A.m.19.2	M00001512A:G05	80167
1202	2/24/98	447	RTA00000423F.b.04.3	M00001675D:E10	6311
1203	2/24/98	448	RTA00000127A.a.3.1	M00001552A:H10	13232
1204	2/24/98	449	RTA00000411F.j.16.1	M00003843A:E08	17237
1205	2/24/98	450	RTA00000118A.a.23.1	M00001395A:H02	3500
1206	2/24/98	451	RTA00000126A.o.22.1	M00001551A:A11	81752
1207	2/24/98	452	RTA00000419F.n.13.1	M00003977D:A06	66026
1208	2/24/98	453	RTA00000130A.h.13.1	M00001617A:A01	80790
1209	2/24/98	454	RTA00000418F.n.19.1	M00001659C:F02	28761
1210	2/24/98	455	RTA00000399F.d.23.1	M00001481B:A07	3310
1211	2/24/98	456	RTA00000413F.o.06.1	M00005100A:B02	0
1212	2/24/98	457	RTA00000411F.m.19.1	M00003868D:D11	74924
1213	2/24/98	458	RTA00000130A.a.19.1	M00001605A:A06	0
1214	2/24/98	459	RTA00000419F.k.06.1	M00003871D:A10	78493
1215	2/24/98	460	RTA00000341F.j.12.1	M00003987C:G03	12195
1216	2/24/98	461	RTA00000412F.d.16.1	M00003906B:H06	26829
1217	2/24/98	462	RTA00000119A.j.23.1	M00001460A:G07	79835
1218	2/24/98	463	RTA00000403F.o.22.1	M00001583A:D01	25076
1219	2/24/98	464	RTA00000195AF.c.12.1	M00003818B:G12	37582
1219	1/28/98	300	RTA00000195AF.c.12.1	M00003818B:G12	37582
1220	2/24/98	465	RTA00000350R.p.18.1	M00001676B:F05	11460
1221	2/24/98	466	RTA00000406F.i.24.1	M00003904D:B12	12767
1222	2/24/98	467	RTA00000123A.n.13.2	M00001534A:D03	39167
1223	2/24/98	468	RTA00000423F.c.19.1	M00001680B:E10	40472
1224	2/24/98	469	RTA00000405F.g.24.1	M00001673D:D06	39076
1225	2/24/98	470	RTA00000411F.j.06.1	M00003841C:H08	63545
1226	2/24/98	471	RTA00000419F.c.11.1	M00003817B:C04	65504
1227	2/24/98	472	RTA00000135A.f.14.2	M00001542A:G12	79969
1228	2/24/98	473	RTA00000403F.a.05.1	M00001448A:E11	18808
1229	2/24/98	474	RTA00000405F.e.17.1	M00001669A:C10	38662
1230	2/24/98	475	RTA00000411F.d.05.1	M00001681C:A08	75812
1231	2/24/98	476	RTA00000345F.h.01.1	M00001441B:D11	10834
1232	2/24/98	477	RTA00000418F.d.03.1	M00001567B:G11	76824
1233	2/24/98	478	RTA00000418F.h.08.1	M00001589B:E07	76401
1234	2/24/98	479	RTA00000418F.m.10.1	M00001651A:H11	79110
1235	2/24/98	480	RTA00000411F.i.15.1	M00003837C:G08	31612

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
1236	2/24/98	481	RTA00000413F.i.23.1	M00004118B:F01	63073
1237	2/24/98	482	RTA00000411F.e.24.1	M00003813A:B02	64781
1238	2/24/98	483	RTA00000406F.g.22.1	M00003881D:C12	38590
1239	2/24/98	484	RTA00000126A.n.13.2	M00001551A:H06	79735
1240	2/24/98	485	RTA00000419F.a.02.1	M00001678A:F05	77993
1241	2/24/98	486	RTA00000346F.l.13.1	M00003980B:C11	7542
1242	2/24/98	487	RTA00000420F.g.05.1	M00004891B:D01	0
1243	2/24/98	488	RTA00000339F.k.23.1	M00001429D:H12	0
1244	2/24/98	489	RTA00000406F.j.19.1	M00003906A:F12	1685
1245	2/24/98	490	RTA00000120A.d.15.1	M00001464A:B02	80533
1246	2/24/98	491	RTA00000418F.f.21.1	M00001579B:F04	75157
1247	2/24/98	492	RTA00000340F.o.18.1	M00001669D:C03	4261
1248	2/24/98	493	RTA00000129A.d.1.2	M00001587A:F05	80058
1249	2/24/98	494	RTA00000419F.k.12.1	M00003876C:F02	0
1250	2/24/98	495	RTA00000400F.o.21.1	M00001669C:C08	16259
1251	2/24/98	496	RTA00000419F.m.20.1	M00003914A:B07	76720
1252	2/24/98	497	RTA00000350R.f.21.1	M00001610C:E07	22110
1253	2/24/98	498	RTA00000406F.e.15.1	M00003877C:A11	39074
1254	2/24/98	499	RTA00000126A.p.18.2	M00001552A:E10	80881
1255	2/24/98	500	RTA00000411F.c.10.1	M00001678D:B11	73117
1256	2/24/98	501	RTA00000414F.f.05.1	M00005257D:H11	0
1257	2/24/98	502	RTA00000341F.d.08.1	M00003824C:D07	0
1258	2/24/98	503	RTA00000420F.m.08.1	M00005233B:D04	0
1259	2/24/98	504	RTA00000413F.d.05.1	M00004087C:A01	64788
1260	2/24/98	505	RTA00000121A.o.3.1	M00001511A:A02	81437
1261	2/24/98	506	RTA00000403F.f.09.1	M00001477B:C02	0
1262	2/24/98	507	RTA00000420F.e.02.1	M00004107B:D07	40259
1263	2/24/98	508	RTA00000420F.i.20.1	M00005101C:E12	0
1264	2/24/98	509	RTA00000349R.g.10.1	M00001495B:B08	5777
1265	2/24/98	510	RTA00000131A.g.16.2	M00001449A:F01	0
1266	2/24/98	511	RTA00000341F.b.13.1	M00003762B:H09	0
1267	2/24/98	512	RTA00000414F.c.16.1	M00005228A:B03	0
1268	2/24/98	513	RTA00000126A.k.7.2	M00001550A:E07	79866
1269	2/24/98	514	RTA00000404F.e.13.1	M00001608D:E09	12046
1270	2/24/98	515	RTA00000419F.l.03.1	M00003879A:D02	79060
1271	2/24/98	516	RTA00000339F.f.20.1	M00001399A:C03	6494
1272	2/24/98	517	RTA00000118A.a.2.1	M00001395A:A12	38067
1273	2/24/98	518	RTA00000410F.m.18.1	M00001660B:A09	76365
1274	2/24/98	519	RTA00000404F.l.10.1	M00001638B:F10	23136
1275	2/24/98	520	RTA00000406F.c.20.1	M00003871D:G06	38578
1276	2/24/98	521	RTA00000413F.b.14.1	M00004078A:C11	66591
1277	2/24/98	522	RTA00000406F.c.18.1	M00003871C:F12	14368
1278	2/24/98	523	RTA00000418F.j.09.1	M00001626C:D12	76352
1279	2/24/98	524	RTA00000419F.f.23.1	M00003840D:H10	65002
1280	2/24/98	525	RTA00000348R.d.24.1	M00001349B:G05	5774
1281	2/24/98	526	RTA00000411F.a.05.1	M00001675B:H03	76699
1282	2/24/98	527	RTA00000419F.m.21.1	M00003914A:E04	77947
1283	2/24/98	528	RTA00000405F.n.16.1	M00003825B:B10	21503
1284	2/24/98	529	RTA00000422F.o.19.2	M00001655C:E01	13084
1285	2/24/98	530	RTA00000408F.n.02.2	M00001539A:E01	76993

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
1286	2/24/98	531	RTA00000345F.n.12.1	M00001528A:C04	7337
1287	2/24/98	532	RTA00000403F.a.24.1	M00001455B:A09	24128
1288	2/24/98	533	RTA00000423F.e.11.1	M00003809B:E10	2566
1289	2/24/98	534	RTA00000126A.g.7.1	M00001548A:H04	1902
1290	2/24/98	535	RTA00000119A.g.7.1	M00001454A:F11	83580
1291	2/24/98	536	RTA00000411F.i.02.1	M00003835B:H11	66975
1292	2/24/98	537	RTA00000408F.l.09.1	M00001530A:A09	75487
1293	2/24/98	538	RTA00000423F.g.04.1	M00003903D:C12	23012
1294	2/24/98	539	RTA00000346F.m.15.1	M00004037B:C04	13553
1295	2/24/98	540	RTA00000418F.i.18.1	M00001595C:B05	78024
1296	2/24/98	541	RTA00000411F.h.15.1	M00003832A:A09	65160
1297	2/24/98	542	RTA00000410F.i.19.1	M00001641B:C10	78988
1298	2/24/98	543	RTA00000419F.k.24.1	M00003878C:G08	75596
1299	2/24/98	544	RTA00000420F.l.21.2	M00005232A:H12	0
1300	2/24/98	545	RTA00000420F.e.15.1	M00004110A:A10	20190
1301	2/24/98	546	RTA00000409F.i.09.1	M00001610B:C07	75279
1302	2/24/98	547	RTA00000419F.h.02.1	M00003845D:G08	63985
1303	2/24/98	548	RTA00000413F.b.12.1	M00004077B:H11	64932
1304	2/24/98	549	RTA00000121A.h.18.1	M00001471A:B04	16376
1305	2/24/98	550	RTA00000411F.n.20.1	M00003875C:A09	75816
1306	2/24/98	551	RTA00000340F.b.05.1	M00001513A:G07	0
1307	2/24/98	552	RTA00000411F.n.12.1	M00003875A:C04	73308
1308	2/24/98	553	RTA00000408F.j.12.2	M00001485B:C03	18226
1309	2/24/98	554	RTA00000409F.i.03.1	M00001610A:E09	75968
1310	2/24/98	555	RTA00000133A.d.22.1	M00001469A:G11	11797
1311	2/24/98	556	RTA00000400F.i.11.1	M00001649C:H10	2587
1312	2/24/98	557	RTA00000409F.j.05.1	M00001611C:C12	74128
1313	2/24/98	558	RTA00000419F.m.04.1	M00003906C:C05	74367
1314	2/24/98	559	RTA00000418F.k.03.1	M00001634D:G11	78901
1315	2/24/98	560	RTA00000419F.d.16.1	M00003828B:E07	64357
1316	2/24/98	561	RTA00000420F.e.10.1	M00004108D:G04	65899
1317	2/24/98	562	RTA00000401F.j.17.1	M00003901B:C05	5483
1318	2/24/98	563	RTA00000406F.b.08.1	M00003867D:A06	18258
1319	2/24/98	564	RTA00000418F.k.08.1	M00001639A:C03	18259
1320	2/24/98	565	RTA00000420F.k.17.2	M00005217B:A06	0
1321	2/24/98	566	RTA00000414F.d.05.1	M00005229D:H03	0
1322	2/24/98	567	RTA00000410F.c.02.1	M00001633D:D12	75055
1323	2/24/98	568	RTA00000403F.m.03.1	M00001573D:D10	39179
1324	2/24/98	569	RTA00000403F.h.18.1	M00001484C:A04	39241
1325	2/24/98	570	RTA00000405F.n.13.1	M00003824A:G10	23810
1326	2/24/98	571	RTA00000355R.e.14.1	M00004314B:G07	16837
1327	2/24/98	572	RTA00000422F.l.03.1	M00001610D:D05	39147
1328	2/24/98	573	RTA00000414F.c.23.1	M00005229B:G12	0
1329	2/24/98	574	RTA00000403F.o.14.1	M00001579D:H09	38971
1330	2/24/98	575	RTA00000345F.a.18.1	M00001351C:B06	5517
1331	2/24/98	576	RTA00000401F.d.15.2	M00001693C:C12	5297
1332	2/24/98	577	RTA00000419F.e.11.1	M00003833B:C12	36780
1333	2/24/98	578	RTA00000127A.f.11.1	M00001554A:A08	81463
1334	2/24/98	579	RTA00000413F.m.16.1	M00004898C:F03	0
1335	2/24/98	580	RTA00000403F.o.07.1	M00001579C:A01	39037

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
1336	2/24/98	581	RTA00000403F.d.19.1	M00001472C:A01	39243
1337	2/24/98	582	RTA00000414F.e.14.1	M00005236B:F10	0
1338	2/24/98	583	RTA00000406F.i.17.1	M00003904B:C03	37902
1339	2/24/98	584	RTA00000418F.d.22.1	M00001573B:C06	75324
1340	2/24/98	585	RTA00000340R.o.12.1	M00003746C:E02	53732
1341	2/24/98	586	RTA00000125A.g.24.1	M00001544A:F05	80397
1342	2/24/98	587	RTA00000130A.o.21.1	M00001623A:F04	80218
1343	2/24/98	588	RTA00000420F.a.23.1	M00004078B:F12	42158
1344	2/24/98	589	RTA00000411F.m.18.1	M00003868D:D09	75629
1345	2/24/98	590	RTA00000407F.b.22.1	M00004108B:B02	37487
1346	2/24/98	591	RTA00000409F.a.16.1	M00001583A:A05	73990
1347	2/24/98	592	RTA00000421F.p.18.1	M00003877B:H10	750
1348	2/24/98	593	RTA00000341F.k.12.1	M00004103C:D04	62985
1349	2/24/98	594	RTA00000129A.c.18.2	M00001587A:B10	37216
1350	2/24/98	595	RTA00000410F.d.10.1	M00001635B:H02	77561
1351	2/24/98	596	RTA00000351R.i.03.1	M00003846B:D06	6874
1352	2/24/98	597	RTA00000135A.l.1.2	M00001545A:B10	39426
1353	2/24/98	598	RTA00000420F.b.18.1	M00004086D:G08	66136
1354	2/24/98	599	RTA00000401F.k.14.1	M00003903A:H09	211
1355	2/24/98	600	RTA00000406F.m.04.1	M00003914B:A11	14959
1356	2/24/98	601	RTA00000403F.o.13.1	M00001579D:F04	39049
1357	2/24/98	602	RTA00000411F.f.06.1	M00003813B:E09	64186
1358	2/24/98	603	RTA00000399F.o.19.1	M00001607A:F11	2594
1359	2/24/98	604	RTA00000351R.c.13.1	M00003747D:C05	11476
1360	2/24/98	605	RTA00000403F.c.14.1	M00001457D:A07	0
1361	2/24/98	606	RTA00000420F.l.20.2	M00005232A:C10	0
1362	2/24/98	607	RTA00000420F.d.16.1	M00004103D:F10	64485
1363	2/24/98	608	RTA00000404F.i.12.1	M00001620D:G11	39001
1364	2/24/98	609	RTA00000404F.o.10.2	M00001651B:B12	16785
1365	2/24/98	610	RTA00000419F.d.07.1	M00003820B:D10	21421
1366	2/24/98	611	RTA00000404F.p.02.2	M00001652D:A06	39097
1367	2/24/98	612	RTA00000125A.k.14.1	M00001545A:G05	79457
1368	2/24/98	613	RTA00000122A.j.22.1	M00001516A:F06	81151
1369	2/24/98	614	RTA00000406F.i.13.1	M00003904A:C04	37904
1370	2/24/98	615	RTA00000135A.b.23.1	M00001538A:D12	35241
1371	2/24/98	616	RTA00000423F.c.11.1	M00001677D:B02	0
1372	2/24/98	617	RTA00000423F.f.23.1	M00003816C:E09	15390
1373	2/24/98	618	RTA00000423F.l.04.1	M00004039B:G08	14320
1374	2/24/98	619	RTA00000420F.b.04.1	M00004081A:E02	63820
1375	2/24/98	620	RTA00000420F.a.07.1	M00004072C:F08	63405
1376	2/24/98	621	RTA00000408F.i.18.2	M00001482C:D02	74410
1377	2/24/98	622	RTA00000404F.l.07.1	M00001637C:C06	10798
1378	2/24/98	623	RTA00000341F.j.05.1	M00003963D:B05	36177
1379	2/24/98	624	RTA00000420F.a.16.1	M00004075D:C10	63345
1380	2/24/98	625	RTA00000126A.h.22.2	M00001549A:F01	0
1381	2/24/98	626	RTA00000410F.j.01.1	M00001641B:F12	73399
1382	2/24/98	627	RTA00000408F.p.21.1	M00001579A:C03	77930
1383	2/24/98	628	RTA00000412F.d.19.1	M00003907B:C03	75743
1384	2/24/98	629	RTA00000352R.c.04.1	M00003924A:D08	71976
1385	2/24/98	630	RTA00000413F.f.19.1	M00004100B:C07	65189

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
1386	2/24/98	631	RTA00000411F.e.03.1	M00001694D:C12	73648
1387	2/24/98	632	RTA00000191AF.j.14.1	M00004073A:H12	1002
1387	1/28/98	387	RTA00000191AF.j.14.1	M00004073A:H12	1002
1388	2/24/98	633	RTA00000341F.d.02.1	M00003797A:G03	4706
1389	2/24/98	634	RTA00000418F.c.04.1	M00001487B:A11	41587
1390	2/24/98	635	RTA00000418F.o.17.1	M00001661B:F03	79069
1391	2/24/98	636	RTA00000418F.e.21.1	M00001577B:A03	74773
1392	2/24/98	637	RTA00000419F.d.14.1	M00003828A:D05	64945
1393	2/24/98	638	RTA00000418F.b.09.1	M00001478B:H08	19700
1394	2/24/98	639	RTA00000414F.d.09.1	M00005231C:B01	0
1395	2/24/98	640	RTA00000405F.f.02.1	M00001669B:G02	38665
1396	2/24/98	641	RTA00000410F.j.20.1	M00001642D:G10	73601
1397	2/24/98	642	RTA00000341F.h.19.1	M00003916C:C05	0
1398	2/24/98	643	RTA00000420F.l.14.2	M00005230D:F06	0
1399	2/24/98	644	RTA00000119A.j.9.1	M00001460A:B12	82060
1400	2/24/98	645	RTA00000422F.p.12.2	M00001661C:F10	9840
1401	2/24/98	646	RTA00000421F.m.14.1	M00001642A:F03	3524
1402	2/24/98	647	RTA00000418F.b.23.1	M00001485A:C05	28767
1403	2/24/98	648	RTA00000340F.i.13.1	M00001624B:B10	79299
1404	2/24/98	649	RTA00000412F.g.03.1	M00003971B:A10	64740
1405	2/24/98	650	RTA00000122A.g.17.1	M00001514A:B08	32655
1406	2/24/98	651	RTA00000403F.g.11.1	M00001481A:H08	24238
1407	2/24/98	652	RTA00000419F.n.12.1	M00003977D:A03	66086
1408	2/24/98	653	RTA00000352R.m.12.1	M00004212B:C07	2379
1409	2/24/98	654	RTA00000421F.a.05.1	M00001570C:G06	5278
1410	2/24/98	655	RTA00000351R.p.14.1	M00003915C:H04	13166
1411	2/24/98	656	RTA00000403F.e.08.1	M00001473D:B11	19126
1412	2/24/98	657	RTA00000124A.k.20.1	M00001538A:C08	80913
1413	2/24/98	658	RTA00000121A.n.2.1	M00001511A:A05	33585
1414	2/24/98	659	RTA00000422F.m.24.1	M00001641D:C04	39159
1415	2/24/98	660	RTA00000408F.e.24.2	M00001476C:C11	75002
1416	2/24/98	661	RTA00000341F.l.16.1	M00003986D:C08	8479
1417	2/24/98	662	RTA00000339F.o.07.1	M00001473D:G01	2566
1418	2/24/98	663	RTA00000403F.b.12.1	M00001455D:A06	78775
1419	2/24/98	664	RTA00000404F.a.09.1	M00001589C:E06	38985
1420	2/24/98	665	RTA00000419F.p.20.1	M00004039A:C03	9458
1421	2/24/98	666	RTA00000403F.o.19.1	M00001582D:F02	78615
1422	2/24/98	667	RTA00000405F.h.07.2	M00001674A:G11	4984
1423	2/24/98	668	RTA00000408F.m.05.2	M00001530C:G10	23384
1424	2/24/98	669	RTA00000410F.b.10.1	M00001633C:B09	74504
1425	2/24/98	670	RTA00000131A.i.6.1	M00001450A:B08	0
1426	2/24/98	671	RTA00000413F.h.12.1	M00004107A:A12	66929
1427	2/24/98	672	RTA00000406F.k.14.1	M00003907C:C02	38651
1428	2/24/98	673	RTA00000406F.d.09.1	M00003875B:F12	38591
1429	2/24/98	674	RTA00000411F.f.17.1	M00003814B:F12	65661
1430	2/24/98	675	RTA00000411F.k.10.1	M00003850D:H11	64506
1431	2/24/98	676	RTA00000411F.g.21.1	M00003823D:G05	64500
1432	2/24/98	677	RTA00000119A.h.24.1	M00001457A:C05	82266
1433	1/28/98	412	RTA00000195AF.c.24.1	M00003860D:H07	0
1433	2/24/98	678	RTA00000195AF.c.24.1	M00003860D:H07	0

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
1434	2/24/98	679	RTA00000408F.m.22.2	M00001539A:C12	72949
1435	2/24/98	680	RTA00000345F.e.11.1	M00001391C:C04	4392
1436	2/24/98	681	RTA00000120A.c.24.1	M00001464A:D03	34278
1437	2/24/98	682	RTA00000410F.i.17.1	M00001641B:B01	78147
1438	2/24/98	683	RTA00000403F.j.21.1	M00001540D:E02	24723
1439	2/24/98	684	RTA00000339F.k.20.1	M00001426D:D12	6662
1440	2/24/98	685	RTA00000129A.a.13.2	M00001582A:A03	79780
1441	2/24/98	686	RTA00000129A.k.21.1	M00001601A:E12	82067
1442	2/24/98	687	RTA00000350R.g.10.1	M00001587C:C10	9026
1443	2/24/98	688	RTA00000413F.d.23.1	M00004090B:H06	66030
1444	2/24/98	689	RTA00000419F.p.03.1	M00004035A:G10	1937
1445	2/24/98	690	RTA00000341F.b.05.1	M00003793D:A11	0
1446	2/24/98	691	RTA00000354R.n.08.1	M00003835A:A09	8802
1447	2/24/98	692	RTA00000411F.d.10.1	M00001681D:C12	76445
1448	2/24/98	693	RTA00000404F.b.19.1	M00001592B:A04	39281
1449	2/24/98	694	RTA00000418F.c.07.1	M00001529D:C05	73245
1450	2/24/98	695	RTA00000418F.j.15.1	M00001632C:H07	74855
1451	2/24/98	696	RTA00000404F.p.12.2	M00001653B:C06	0
1452	2/24/98	697	RTA00000412F.d.14.1	M00003905D:C08	76757
1453	2/24/98	698	RTA00000413F.b.16.1	M00004078A:E05	65126
1454	2/24/98	699	RTA00000340F.l.05.1	M00001644B:D06	38935
1455	2/24/98	700	RTA00000350R.m.14.1	M00001644C:B07	39171
1456	2/24/98	701	RTA00000418F.l.11.1	M00001641C:H07	77158
1457	2/24/98	702	RTA00000130A.d.5.1	M00001605A:H03	82051
1458	2/24/98	703	RTA00000339F.n.05.1	M00001449D:B01	39648
1459	2/24/98	704	RTA00000355R.a.12.1	M00004159C:F09	36756
1460	2/24/98	705	RTA00000407F.a.23.1	M00004081C:A10	23489
1461	2/24/98	706	RTA00000403F.a.09.1	M00001448B:H05	77820
1462	2/24/98	707	RTA00000403F.h.11.1	M00001483B:D04	39219
1463	2/24/98	708	RTA00000406F.j.13.1	M00003905D:B08	38688
1464	2/24/98	709	RTA00000352R.p.09.1	M00004228C:H03	16915
1465	2/24/98	710	RTA00000413F.g.24.1	M00004104D:A04	65481
1466	2/24/98	711	RTA00000404F.l.03.2	M00001636B:G11	40272
1467	2/24/98	712	RTA00000407F.b.18.1	M00004102C:D09	37569
1468	2/24/98	713	RTA00000414F.b.10.1	M00005212D:D09	0
1469	2/24/98	714	RTA00000420F.a.08.1	M00004073A:D10	19473
1470	2/24/98	715	RTA00000418F.b.01.1	M00001475C:G11	76040
1471	2/24/98	716	RTA00000420F.l.03.2	M00005217D:F12	0
1472	2/24/98	717	RTA00000404F.i.22.1	M00001625C:G05	39082
1473	2/24/98	718	RTA00000124A.k.23.1	M00001538A:D03	81350
1474	2/24/98	719	RTA00000404F.e.11.1	M00001608C:E11	38991
1475	2/24/98	720	RTA00000129A.d.2.4	M00001587A:G06	80119
1476	2/24/98	721	RTA00000422F.k.14.1	M00001649D:A08	0
1477	2/24/98	722	RTA00000411F.l.22.1	M00003858B:G05	64439
1478	2/24/98	723	RTA00000419F.o.15.1	M00003989C:D03	32487
1479	2/24/98	724	RTA00000119A.m.17.1	M00001461A:F05	79536
1480	2/24/98	725	RTA00000410F.b.07.1	M00001633C:A05	78916
1481	2/24/98	726	RTA00000420F.b.19.1	M00004088D:A11	36873
1482	2/24/98	727	RTA00000414F.d.02.1	M00005229B:H06	0
1483	2/24/98	728	RTA00000411F.b.21.1	M00001677B:A02	10051

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
1484	2/24/98	729	RTA00000403F.m.20.1	M00001576A:F11	707
1485	2/24/98	730	RTA00000356R.c.16.1	M00004294C:C08	16915
1486	2/24/98	731	RTA00000119A.d.17.1	M00001453A:B01	0
1487	2/24/98	732	RTA00000412F.h.11.1	M00003974B:B11	63175
1488	2/24/98	733	RTA00000405F.d.18.1	M00001662C:B02	10494
1489	2/24/98	734	RTA00000414F.e.09.1	M00005236A:G10	0
1490	2/24/98	735	RTA00000420F.a.11.1	M00004073C:D04	66460
1491	2/24/98	736	RTA00000120A.c.7.1	M00001462A:D03	80985
1492	2/24/98	737	RTA00000404F.e.15.1	M00001609B:C09	39101
1493	2/24/98	738	RTA00000422F.n.20.1	M00001669B:B12	38676
1494	2/24/98	739	RTA00000423F.h.20.1	M00003914A:G06	38639
1495	2/24/98	740	RTA00000399F.l.19.1	M00001590D:G07	40145
1496	2/24/98	741	RTA00000414F.b.12.1	M00005212D:H01	0
1497	2/24/98	742	RTA00000410F.b.18.1	M00001633C:H11	76701
1498	2/24/98	743	RTA00000345F.i.08.1	M00001449D:G10	0
1499	2/24/98	744	RTA00000423F.g.15.1	M00003905A:F09	35173
1500	2/24/98	745	RTA00000413F.b.04.1	M00004076D:H07	66427
1501	2/24/98	746	RTA00000345F.e.02.1	M00001395A:E03	0
1502	2/24/98	747	RTA00000413F.n.24.1	M00004960C:E10	0
1503	2/24/98	748	RTA00000346F.f.11.1	M00003793C:D09	38528
1504	2/24/98	749	RTA00000351R.i.13.1	M00003858D:F12	0
1505	2/24/98	750	RTA00000403F.c.05.1	M00001456C:C11	74935
1506	2/24/98	751	RTA00000422F.i.02.1	M00001456C:B12	76436
1507	2/24/98	752	RTA00000410F.a.08.1	M00001632A:B10	73324
1508	2/24/98	753	RTA00000345F.o.13.1	M00001546B:F12	11500
1509	2/24/98	754	RTA00000419F.e.02.1	M00003830C:A03	65010
1510	2/24/98	755	RTA00000423F.d.17.1	M00001663A:C11	20630
1511	2/24/98	756	RTA00000403F.g.13.1	M00001481B:D09	38718
1512	2/24/98	757	RTA00000423F.h.13.1	M00003871A:B09	14398
1513	2/24/98	758	RTA00000407F.a.01.1	M00004039A:H11	12501
1514	2/24/98	759	RTA00000399F.o.06.1	M00001595D:G03	13574
1515	2/24/98	760	RTA00000423F.d.04.1	M00001694A:B12	11307
1516	2/24/98	761	RTA00000411F.f.14.1	M00003814B:C12	62984
1517	2/24/98	762	RTA00000411F.c.04.1	M00001677B:E06	76858
1518	2/24/98	763	RTA00000135A.m.18.1	M00001545A:C03	19255
1519	2/24/98	764	RTA00000413F.c.17.1	M00004085B:B05	36831
1520	2/24/98	765	RTA00000137A.j.15.4	M00001559A:C08	4213
1521	2/24/98	766	RTA00000404F.j.01.1	M00001625D:G10	26859
1522	2/24/98	767	RTA00000138A.p.10.1	M00001644A:H01	81625
1523	2/24/98	768	RTA00000121A.k.5.1	M00001507A:E04	17530
1524	2/24/98	769	RTA00000340F.i.10.1	M00001618A:F10	38561
1525	2/24/98	770	RTA00000421F.f.05.1	M00001477B:E02	5266
1526	2/24/98	771	RTA00000423F.h.07.1	M00003911B:F08	37933
1527	2/24/98	772	RTA00000413F.e.04.1	M00004090C:C07	64176
1528	2/24/98	773	RTA00000406F.h.03.1	M00003901B:A09	38585
1529	2/24/98	774	RTA00000403F.e.24.1	M00001476B:D10	16432
1530	2/24/98	775	RTA00000405F.c.22.1	M00001660C:B06	39053
1531	2/24/98	776	RTA00000403F.i.11.1	M00001485D:E05	23535
1532	2/24/98	777	RTA00000419F.g.02.1	M00003842A:A03	62839
1533	2/24/98	778	RTA00000347F.e.05.1	M00001578D:C04	39814

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
1534	2/24/98	779	RTA00000408F.l.16.1	M00001530A:F12	73468
1535	2/24/98	780	RTA00000405F.l.11.1	M00001693D:E08	2055
1536	2/24/98	781	RTA00000423F.f.09.1	M00003808C:A05	64823
1537	2/24/98	782	RTA00000419F.k.03.1	M00003871C:B05	40822
1538	2/24/98	783	RTA00000406F.b.02.1	M00003867B:G08	38744
1539	2/24/98	784	RTA00000418F.o.14.1	M00001661B:B05	33524
1540	2/24/98	785	RTA00000404F.l.03.1	M00001636B:G11	40272
1541	2/24/98	786	RTA00000404F.b.09.1	M00001591D:C07	39166
1542	2/24/98	787	RTA00000345F.i.24.1	M00001449C:C05	0
1543	2/24/98	788	RTA00000419F.i.04.1	M00003860B:F11	65791
1544	2/24/98	789	RTA00000423F.b.13.1	M00001676C:E07	20619
1545	2/24/98	790	RTA00000345F.n.08.1	M00001517A:B11	0
1546	2/24/98	791	RTA00000399F.n.15.1	M00001594D:C03	3213
1547	2/24/98	792	RTA00000406F.k.11.1	M00003907B:D05	38715
1548	2/24/98	793	RTA00000414F.e.21.1	M00005257C:G01	0
1549	2/24/98	794	RTA00000406F.c.06.1	M00003870C:A01	37924
1550	2/24/98	795	RTA00000418F.n.07.1	M00001658B:A07	76316
1551	2/24/98	796	RTA00000419F.n.15.1	M00003977D:D04	63484
1552	2/24/98	797	RTA00000408F.n.06.2	M00001539A:H12	76642
1553	2/24/98	798	RTA00000420F.c.04.1	M00004089A:B08	65007
1554	2/24/98	799	RTA00000411F.j.15.1	M00003843A:E04	66871
1555	2/24/98	800	RTA00000403F.m.12.1	M00001575D:A02	16933
1556	2/24/98	801	RTA00000128A.m.23.1	M00001561A:D01	81441
1557	2/24/98	802	RTA00000406F.g.03.1	M00003880B:D11	38690
1558	2/24/98	803	RTA00000405F.h.05.2	M00001674A:G07	75706
1559	2/24/98	804	RTA00000129A.n.24.1	M00001604A:C07	81409
1560	2/24/98	805	RTA00000406F.j.08.1	M00003905B:C06	6688
1561	2/24/98	806	RTA00000345F.f.08.1	M00001413B:H09	0
1562	2/24/98	807	RTA00000418F.n.11.1	M00001658D:G12	78977
1563	2/24/98	808	RTA00000418F.p.08.1	M00001669D:D06	73983
1564	2/24/98	809	RTA00000420F.i.23.1	M00005134A:D11	0
1565	2/24/98	810	RTA00000120A.h.9.1	M00001465A:B12	80736
1566	2/24/98	811	RTA00000413F.a.12.1	M00004072D:F09	63403
1567	2/24/98	812	RTA00000412F.o.05.1	M00004034A:A01	63575
1568	2/24/98	813	RTA00000346F.o.06.1	M00004136D:B02	4937
1569	2/24/98	814	RTA00000408F.l.24.1	M00001530B:G09	34263
1570	2/24/98	815	RTA00000403F.a.17.1	M00001448D:E12	13686
1571	2/24/98	816	RTA00000354R.n.04.1	M00003808C:B05	22049
1572	2/24/98	817	RTA00000420F.l.08.2	M00005228C:C05	0
1573	2/24/98	818	RTA00000406F.h.05.1	M00003901B:C03	38542
1574	2/24/98	819	RTA00000410F.b.24.1	M00001633D:D09	75104
1575	2/24/98	820	RTA00000423F.d.11.1	M00001678C:C06	38950
1576	2/24/98	821	RTA00000420F.h.16.1	M00004927A:E06	0
1577	2/24/98	822	RTA00000419F.o.21.1	M00004031A:E01	10336
1578	2/24/98	823	RTA00000119A.k.1.1	M00001460A:H11	81282
1579	2/24/98	824	RTA00000420F.f.07.1	M00004119A:C09	66312
1580	2/24/98	825	RTA00000404F.k.22.2	M00001635D:C12	39084
1581	2/24/98	826	RTA00000422F.e.07.1	M00001579C:G05	38964
1582	2/24/98	827	RTA00000410F.f.12.1	M00001637C:E03	73883
1583	2/24/98	828	RTA00000419F.n.05.1	M00003976C:D06	63713

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
1584	2/24/98	829	RTA00000411F.m.11.1	M00003867A:D12	73196
1585	2/24/98	830	RTA00000347F.b.08.1	M00001541B:E05	17591
1586	2/24/98	831	RTA00000420F.d.21.1	M00004107B:B04	65313
1587	2/24/98	832	RTA00000403F.o.10.2	M00001579C:G05	38964
1588	2/24/98	833	RTA00000420F.j.20.1	M00005140D:C06	0
1589	2/24/98	834	RTA00000407F.b.11.1	M00004090C:C10	0
1590	2/24/98	835	RTA00000413F.c.10.1	M00004083B:C01	65600
1591	2/24/98	836	RTA00000411F.b.17.1	M00001676D:B02	72893
1592	2/24/98	837	RTA00000420F.h.01.1	M00004897C:D06	0
1593	2/24/98	838	RTA00000408F.k.19.1	M00001487C:G03	77593
1594	2/24/98	839	RTA00000414F.b.01.1	M00005212B:A02	0
1595	2/24/98	840	RTA00000420F.b.20.1	M00004088D:B05	0
1596	2/24/98	841	RTA00000119A.i.8.1	M00001457A:G12	82593
1597	2/24/98	842	RTA00000401F.n.23.1	M00003982A:B06	1552
1598	2/24/98	843	RTA00000418F.g.03.1	M00001579C:E06	78737
1599	2/24/98	844	RTA00000411F.a.09.1	M00001675C:F01	78629
1600	2/24/98	845	RTA00000348R.b.04.1	M00001342B:E01	1890
1601	2/24/98	846	RTA00000419F.j.11.1	M00003868C:C07	73183
1602	2/24/98	847	RTA00000403F.i.11.1	M00001571D:F05	25073
1603	2/24/98	848	RTA00000404F.n.18.2	M00001649C:E11	37169
1604	2/24/98	849	RTA00000122A.n.16.1	M00001517A:G08	80553
1605	2/24/98	850	RTA00000420F.c.07.1	M00004089A:E02	65555
1606	2/24/98	851	RTA00000423F.d.07.1	M00001678B:B12	0
1607	2/24/98	852	RTA00000414F.f.03.1	M00005257D:G07	0
1608	2/24/98	853	RTA00000408F.j.13.2	M00001485B:D10	42275
1609	2/24/98	854	RTA00000345F.a.07.1	M00001338C:E10	0
1610	2/24/98	855	RTA00000423F.a.01.1	M00001659C:F10	39103
1611	2/24/98	856	RTA00000408F.d.02.1	M00001458D:A01	79169
1612	2/24/98	857	RTA00000404F.e.09.1	M00001608B:A09	39121
1613	2/24/98	858	RTA00000341F.e.20.1	M00003891D:B10	67422
1614	2/24/98	859	RTA00000419F.m.22.1	M00003914A:G09	75600
1615	2/24/98	860	RTA00000419F.m.23.1	M00003958B:E11	64263
1616	2/24/98	861	RTA00000419F.b.06.1	M00001694B:B08	76728
1617	2/24/98	862	RTA00000414F.c.07.1	M00005216A:H01	0
1618	2/24/98	863	RTA00000406F.p.08.1	M00004032C:B02	37573
1619	2/24/98	864	RTA00000129A.n.17.1	M00001604A:A09	79811
1620	2/24/98	865	RTA00000414F.c.03.1	M00005216A:D09	0
1621	2/24/98	866	RTA00000407F.b.08.1	M00004088D:B03	37513
1622	2/24/98	867	RTA00000339F.l.21.1	M00001455D:D11	9781
1623	2/24/98	868	RTA00000406F.i.08.1	M00003903C:E12	37946
1624	2/24/98	869	RTA00000403F.h.07.1	M00001482D:H11	26856
1625	2/24/98	870	RTA00000418F.n.24.1	M00001659D:C09	73153
1626	2/24/98	871	RTA00000403F.f.23.1	M00001479C:E01	39223
1627	2/24/98	872	RTA00000409F.l.20.1	M00001615B:G01	74394
1628	2/24/98	873	RTA00000418F.l.06.1	M00001641C:F01	73317
1629	2/24/98	874	RTA00000346F.o.22.1	M00004300C:H09	7381
1630	2/24/98	875	RTA00000129A.k.22.1	M00001601A:E02	79639
1631	2/24/98	876	RTA00000423F.d.16.1	M00001678D:C11	39173
1632	2/24/98	877	RTA00000418F.m.22.1	M00001654D:E12	74567
1633	2/24/98	878	RTA00000413F.c.12.1	M00004083B:G03	65334

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
1634	2/24/98	879	RTA00000409F.b.19.1	M00001584D:H02	14479
1635	2/24/98	880	RTA00000418F.g.20.1	M00001585B:C03	74626
1636	2/24/98	881	RTA00000413F.d.15.1	M00004088C:E04	64943
1637	2/24/98	882	RTA00000355R.c.03.1	M00004244C:G07	3986
1638	2/24/98	883	RTA00000406F.c.09.1	M00003870C:E10	5671
1639	2/24/98	884	RTA00000412F.c.10.1	M00003903C:C04	76372
1640	2/24/98	885	RTA00000122A.j.17.1	M00001516A:D02	62736
1641	2/24/98	886	RTA00000420F.m.15.1	M00005235B:F10	0
1642	2/24/98	887	RTA00000339F.p.06.1	M00001484A:A10	4880
1643	2/24/98	888	RTA00000339R.c.04.1	M00001362D:H01	1805
1644	2/24/98	889	RTA00000346F.b.16.1	M00001615C:G05	16485
1645	2/24/98	890	RTA00000418F.j.19.1	M00001634D:D02	78399
1646	2/24/98	891	RTA00000137A.p.12.1	M00001587A:B01	80614
1647	2/24/98	892	RTA00000339F.m.17.1	M00001453B:H12	20854
1648	2/24/98	893	RTA00000418F.p.10.1	M00001669D:F05	75323
1649	2/24/98	894	RTA00000408F.k.12.1	M00001486B:D07	77246
1650	2/24/98	895	RTA00000137A.j.11.4	M00001559A:A11	79752
1651	2/24/98	896	RTA00000423F.l.20.1	M00004105C:E09	12580
1652	2/24/98	897	RTA00000419F.n.24.1	M00003980A:F04	65995
1653	2/24/98	898	RTA00000418F.l.03.1	M00001641C:C06	79058
1654	2/24/98	899	RTA00000406F.h.10.1	M00003901C:F09	22732
1655	2/24/98	900	RTA00000419F.m.13.1	M00003908A:F12	79052
1656	2/24/98	901	RTA00000418F.j.14.1	M00001632C:B10	32623
1657	2/24/98	902	RTA00000403F.a.10.1	M00001448C:E11	73952
1658	2/24/98	903	RTA00000420F.a.21.1	M00004078B:C11	66241
1659	2/24/98	904	RTA00000127A.e.6.1	M00001553A:E07	5885
1660	2/24/98	905	RTA00000405F.g.21.2	M00001673B:F07	38966
1661	2/24/98	906	RTA00000405F.g.21.1	M00001673B:F07	38966
1662	2/24/98	907	RTA00000419F.m.06.1	M00003906C:D06	75749
1663	2/24/98	908	RTA00000423F.g.03.1	M00003905C:G11	38007
1664	2/24/98	909	RTA00000420F.i.04.1	M00004959D:H12	0
1665	2/24/98	910	RTA00000418F.f.03.1	M00001577B:F10	78911
1666	2/24/98	911	RTA00000406F.p.13.1	M00004034C:G02	8584
1667	2/24/98	912	RTA00000404F.g.13.1	M00001614C:E06	9436
1668	2/24/98	913	RTA00000120A.c.20.1	M00001464A:B07	43235
1669	2/24/98	914	RTA00000138A.m.15.1	M00001624A:A03	41603
1670	2/24/98	915	RTA00000408F.f.14.2	M00001476D:F03	73024
1671	2/24/98	916	RTA00000418F.p.20.1	M00001677D:B07	78023
1672	2/24/98	917	RTA00000423F.e.21.1	M00003806B:G05	66961
1673	2/24/98	918	RTA00000419F.j.22.1	M00003871A:A02	73525
1674	2/24/98	919	RTA00000410F.d.18.1	M00001635D:D05	75458
1675	2/24/98	920	RTA00000403F.b.24.1	M00001456B:G01	78838
1676	2/24/98	921	RTA00000422F.j.02.1	M00001594D:B08	10368
1677	2/24/98	922	RTA00000410F.e.09.1	M00001636A:F08	76093
1678	2/24/98	923	RTA00000126A.d.19.1	M00001548A:G01	79474
1679	2/24/98	924	RTA00000354R.m.02.1	M00003890B:C08	12766
1680	2/24/98	925	RTA00000353R.h.10.1	M00001390C:C11	39498
1681	2/24/98	926	RTA00000399F.k.20.1	M00001585C:D10	3003
1682	2/24/98	927	RTA00000411F.d.21.1	M00001692B:E01	74794
1683	2/24/98	928	RTA00000340F.m.04.1	M00001679B:H07	19406

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
1684	2/24/98	929	RTA00000411F.n.09.1	M00003875A:A07	78962
1685	2/24/98	930	RTA00000127A.h.22.2	M00001554A:E04	13155
1686	2/24/98	931	RTA00000420F.e.09.1	M00004108D:E07	66325
1687	2/24/98	932	RTA00000405F.p.03.1	M00003844A:A11	11346
1688	2/24/98	933	RTA00000419F.a.18.1	M00001680A:B02	78484
1689	2/24/98	934	RTA00000414F.e.01.1	M00005233D:H07	0
1690	2/24/98	935	RTA00000420F.i.07.1	M00004960A:B08	0
1691	2/24/98	936	RTA00000121A.n.23.1	M00001511A:G01	26981
1692	2/24/98	937	RTA00000121A.n.15.1	M00001511A:G08	40849
1693	2/24/98	938	RTA00000403F.i.23.1	M00001487B:E10	11364
1694	2/24/98	939	RTA00000405F.a.03.1	M00001654C:E04	39065
1695	2/24/98	940	RTA00000414F.f.17.1	M00005260A:F04	0
1696	2/24/98	941	RTA00000419F.p.08.1	M00004036D:B04	65560
1697	2/24/98	942	RTA00000126A.n.6.2	M00001551A:D04	79917
1698	2/24/98	943	RTA00000413F.c.03.1	M00004081D:H09	64527
1699	2/24/98	944	RTA00000422F.k.24.1	M00001610C:E06	39118
1700	2/24/98	945	RTA00000412F.c.17.1	M00003905A:A06	75620
1701	2/24/98	946	RTA00000414F.b.07.1	M00005212C:D02	0
1702	2/24/98	947	RTA00000347F.g.08.1	M00004096B:F05	23121
1703	2/24/98	948	RTA00000419F.o.06.1	M00003986C:D09	64643
1704	2/24/98	949	RTA00000340R.j.07.1	M00001654C:D05	38954
1705	2/24/98	950	RTA00000423F.j.02.1	M00003903B:C02	38617
1706	2/24/98	951	RTA00000419F.c.04.1	M00003815C:D12	63749
1707	2/24/98	952	RTA00000411F.a.01.1	M00001675B:D02	74524
1708	2/24/98	953	RTA00000406F.f.05.1	M00003878C:F06	22961
1709	2/24/98	954	RTA00000410F.n.05.1	M00001662A:C07	77830
1710	2/24/98	955	RTA00000404F.e.06.1	M00001607D:F06	39315
1711	2/24/98	956	RTA00000423F.l.06.1	M00004062A:H06	38136
1712	2/24/98	957	RTA00000411F.c.03.1	M00001677B:B06	79280
1713	2/24/98	958	RTA00000195AF.c.8.1	M00001678B:H01	0
1713	1/28/98	520	RTA00000195AF.c.8.1	M00001678B:H01	0
1714	2/24/98	959	RTA00000340F.g.20.1	M00001609D:G10	4089
1715	2/24/98	960	RTA00000404F.l.19.2	M00001639B:H01	16196
1716	2/24/98	961	RTA00000420F.n.21.2	M00005259B:D12	0
1717	2/24/98	962	RTA00000404F.p.05.2	M00001652D:E09	1896
1718	2/24/98	963	RTA00000405F.l.07.1	M00001693C:E09	38636
1719	2/24/98	964	RTA00000423F.l.15.1	M00004075B:G09	11219
1720	2/24/98	965	RTA00000411F.n.06.1	M00003871D:E11	73886
1721	2/24/98	966	RTA00000422F.k.15.1	M00001594A:G09	19253
1722	2/24/98	967	RTA00000406F.h.16.1	M00003902B:D06	38618
1723	2/24/98	968	RTA00000419F.f.24.1	M00003841B:E06	18717
1724	2/24/98	969	RTA00000411F.d.18.1	M00001692A:G06	76063
1725	2/24/98	970	RTA00000414F.e.15.1	M00005236B:G03	0
1726	2/24/98	971	RTA00000411F.i.11.1	M00003837C:E05	66849
1727	2/24/98	972	RTA00000408F.d.15.1	M00001459B:C11	78467
1728	2/24/98	973	RTA00000339F.b.22.1	M00001373D:B03	6867
1729	2/24/98	974	RTA00000340F.h.07.1	M00001608D:D11	19254
1730	2/24/98	975	RTA00000411F.n.02.1	M00003870B:F04	78049
1731	2/24/98	976	RTA00000419F.b.17.1	M00003808D:D04	63261
1732	2/24/98	977	RTA00000350R.p.12.1	M00001657C:C07	0

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
1733	2/24/98	978	RTA00000130A.e.20.1	M00001606A:H09	79502
1734	2/24/98	979	RTA00000345F.b.17.1	M00001362C:H11	945
1735	2/24/98	980	RTA00000411F.i.13.1	M00003837C:F10	66138
1736	2/24/98	981	RTA00000420F.e.20.1	M00004110B:A07	64762
1737	2/24/98	982	RTA00000126A.p.23.2	M00001552A:F06	80915
1738	2/24/98	983	RTA00000423F.f.11.1	M00003809A:H04	0
1739	2/24/98	984	RTA00000406F.g.08.1	M00003880C:H03	37963
1740	2/24/98	985	RTA00000409F.a.08.1	M00001582D:B01	74978
1741	2/24/98	986	RTA00000406F.d.24.1	M00003876B:C05	37997
1742	2/24/98	987	RTA00000422F.b.22.1	M00004117B:A12	2368
1743	2/24/98	988	RTA00000407F.a.22.1	M00004081A:G01	15570
1744	2/24/98	989	RTA00000418F.i.12.1	M00001592A:E02	78971
1745	2/24/98	990	RTA00000121A.h.19.1	M00001471A:D04	80334
1746	2/24/98	991	RTA00000419F.b.10.1	M00001694C:G04	78566
1747	2/24/98	992	RTA00000406F.m.10.1	M00003914D:B02	38004
1748	2/24/98	993	RTA00000406F.o.05.1	M00003985B:G04	37894
1749	2/24/98	994	RTA00000408F.b.04.2	M00001455A:F04	39933
1750	2/24/98	995	RTA00000411F.k.04.1	M00003850D:A05	65407
1751	2/24/98	996	RTA00000423F.j.03.1	M00003903B:D03	5391
1752	2/24/98	997	RTA00000134A.l.9.1	M00001535A:D10	81814
1753	2/24/98	998	RTA00000341F.g.22.1	M00003914D:D10	0
1754	2/24/98	999	RTA00000418F.k.04.1	M00001637A:A03	75864
1755	2/24/98	1000	RTA00000351R.j.21.1	M00003859D:C05	31604
1756	2/24/98	1001	RTA00000413F.p.07.2	M00005102C:D03	0
1757	2/24/98	1002	RTA00000419F.p.18.1	M00004038D:G06	63002
1758	2/24/98	1003	RTA00000420F.k.08.2	M00005176C:C09	0
1759	2/24/98	1004	RTA00000419F.a.24.1	M00001680B:D02	79290
1760	2/24/98	1005	RTA00000339F.e.17.1	M00001397D:G08	7568
1761	2/24/98	1006	RTA00000129A.e.14.1	M00001587A:F08	80053
1762	2/24/98	1007	RTA00000404F.a.01.1	M00001589B:B08	19251
1763	2/24/98	1008	RTA00000414F.f.07.1	M00005259C:B05	0
1764	2/24/98	1009	RTA00000399F.o.24.1	M00001607D:A11	2272
1765	2/24/98	1010	RTA00000408F.n.16.2	M00001540C:B03	73720
1766	2/24/98	1011	RTA00000400F.c.04.1	M00001618A:F08	6445
1767	2/24/98	1012	RTA00000403F.g.06.1	M00001480C:A05	10505
1768	2/24/98	1013	RTA00000404F.b.18.1	M00001592A:H05	13669
1769	2/24/98	1014	RTA00000412F.l.14.1	M00004029B:F01	62792
1770	2/24/98	1015	RTA00000129A.b.6.2	M00001582A:H01	39111
1771	2/24/98	1016	RTA00000406F.n.12.1	M00003960A:G07	37517
1772	2/24/98	1017	RTA00000418F.e.03.1	M00001573B:G08	73442
1773	2/24/98	1018	RTA00000413F.j.21.1	M00004688A:A02	0
1774	2/24/98	1019	RTA00000403F.g.03.1	M00001479D:G06	23537
1775	2/24/98	1020	RTA00000412F.p.06.1	M00004038B:H10	65485
1776	2/24/98	1021	RTA00000419F.b.21.1	M00003809A:F01	65366
1777	2/24/98	1022	RTA00000401F.j.15.1	M00003901A:C09	3061
1778	2/24/98	1023	RTA00000404F.f.12.1	M00001611B:A05	39209
1779	2/24/98	1024	RTA00000351R.j.16.1	M00003857B:F07	64773
1780	2/24/98	1025	RTA00000118A.j.24.1	M00001450A:B03	18
1781	2/24/98	1026	RTA00000419F.f.18.1	M00003839D:E11	64047
1782	2/24/98	1027	RTA00000423F.i.16.1	M00003907D:A12	38604

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
1783	2/24/98	1028	RTA00000346F.d.12.1	M00001676B:B09	11777
1784	2/24/98	1029	RTA00000411F.f.04.1	M00003813A:G04	64526
1785	2/24/98	1030	RTA00000125A.c.17.1	M00001542A:E04	80619
1786	2/24/98	1031	RTA00000404F.g.08.1	M00001613D:H10	38980
1787	2/24/98	1032	RTA00000423F.c.13.1	M00001678A:A11	39059
1788	2/24/98	1033	RTA00000414F.e.19.1	M00005257C:E05	0
1789	2/24/98	1034	RTA00000124A.f.16.3	M00001536A:F11	47430
1790	2/24/98	1035	RTA00000404F.k.15.1	M00001634A:B04	18225
1791	2/24/98	1036	RTA00000339F.k.08.1	M00001439B:A10	8133
1792	2/24/98	1037	RTA00000339F.l.12.1	M00001450A:G11	7711
1793	2/24/98	1038	RTA00000406F.b.01.1	M00003867B:G07	39006
1794	2/24/98	1039	RTA00000407F.c.08.1	M00004118D:B05	37549
1795	2/24/98	1040	RTA00000348R.o.12.1	M00001433C:F10	2263
1796	2/24/98	1041	RTA00000403F.b.05.1	M00001455B:E07	74300
1797	2/24/98	1042	RTA00000339F.g.10.1	M00001400C:D02	6327
1798	2/24/98	1043	RTA00000423F.b.17.1	M00001662B:F06	8200
1799	2/24/98	1044	RTA00000419F.n.11.1	M00003977C:B03	66477
1800	2/24/98	1045	RTA00000408F.j.05.2	M00001483C:G06	73878
1801	2/24/98	1046	RTA00000346F.j.06.1	M00003879A:A02	5767
1802	2/24/98	1047	RTA00000419F.c.14.1	M00003819B:G01	65727
1803	2/24/98	1048	RTA00000413F.o.07.2	M00005100A:C01	0
1804	2/24/98	1049	RTA00000405F.f.05.1	M00001669C:D09	14359
1805	2/24/98	1050	RTA00000405F.f.05.2	M00001669C:D09	14359
1806	2/24/98	1051	RTA00000346F.h.24.1	M00003797A:C11	4379
1807	2/24/98	1052	RTA00000420F.b.02.1	M00004081A:A08	64013
1808	2/24/98	1053	RTA00000413F.b.24.1	M00004080A:F01	65117
1809	2/24/98	1054	RTA00000412F.d.08.1	M00003905C:B02	75328
1810	2/24/98	1055	RTA00000346F.a.04.1	M00001607B:C05	5382
1811	2/24/98	1056	RTA00000419F.m.18.1	M00003908C:G09	76014
1812	2/24/98	1057	RTA00000419F.l.24.1	M00003904D:B10	74628
1813	2/24/98	1058	RTA00000408F.c.06.1	M00001456D:E08	78619
1814	2/24/98	1059	RTA00000405F.h.21.2	M00001675C:D12	39072
1815	2/24/98	1060	RTA00000346F.g.02.1	M00003792A:B10	6901
1816	2/24/98	1061	RTA00000405F.g.05.2	M00001671D:E10	38987
1817	2/24/98	1062	RTA00000411F.f.20.1	M00003816C:C01	63501
1818	2/24/98	1063	RTA00000132A.n.7.1	M00001466A:F08	0
1819	2/24/98	1064	RTA00000420F.d.19.1	M00004105C:C08	43146
1820	1/28/98	595	RTA00000195R.a.06.1	M00001394A:E04	35265
1820	2/24/98	1065	RTA00000195R.a.06.1	M00001394A:E04	35265
1821	2/24/98	1066	RTA00000123A.f.2.1	M00001531A:H03	80379
1822	2/24/98	1067	RTA00000411F.j.11.1	M00003841D:F06	66154
1823	2/24/98	1068	RTA00000341F.f.03.1	M00003850A:F06	0
1824	2/24/98	1069	RTA00000346F.k.05.1	M00003904C:A08	0
1825	2/24/98	1070	RTA00000346F.n.22.1	M00004137A:D06	0
1826	2/24/98	1071	RTA00000404F.k.18.2	M00001635A:C06	5475
1827	2/24/98	1072	RTA00000419F.j.03.1	M00003868B:G06	77578
1828	2/24/98	1073	RTA00000418F.a.10.1	M00001475B:C04	15245
1829	2/24/98	1074	RTA00000423F.h.11.1	M00003867C:E11	38977
1830	2/24/98	1075	RTA00000413F.b.17.1	M00004078A:F07	21704
1831	2/24/98	1076	RTA00000423F.k.09.1	M00004035B:H09	26630

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
1832	2/24/98	1077	RTA00000414F.e.11.1	M00005236B:A12	0
1833	2/24/98	1078	RTA00000423F.f.03.1	M00003829C:D10	63852
1834	2/24/98	1079	RTA00000419F.e.10.1	M00003833B:B03	63225
1835	2/24/98	1080	RTA00000351R.g.06.1	M00003771D:G05	0
1836	2/24/98	1081	RTA00000403F.d.02.1	M00001458D:D01	39224
1837	2/24/98	1082	RTA00000137A.o.22.1	M00001587A:D01	0
1838	2/24/98	1083	RTA00000418F.j.20.1	M00001634D:D04	77101
1839	2/24/98	1084	RTA00000403F.o.22.2	M00001583A:D01	25076
1840	2/24/98	1085	RTA00000403F.n.22.1	M00001578B:B05	26775
1841	2/24/98	1086	RTA00000403F.n.22.2	M00001578B:B05	26775
1842	2/24/98	1087	RTA00000401F.o.13.1	M00004040C:A01	3220
1843	2/24/98	1088	RTA00000339R.b.02.1	M00001344B:F12	0
1844	2/24/98	1089	RTA00000406F.j.21.1	M00003906A:H07	17822
1845	2/24/98	1090	RTA00000405F.g.22.1	M00001673C:A02	527
1846	2/24/98	1091	RTA00000356R.h.05.1	M00004107C:C02	35052
1847	2/24/98	1092	RTA00000125A.c.2.1	M00001542A:F06	40148
1848	2/24/98	1093	RTA00000340F.i.15.1	M00001629C:E07	26815
1849	2/24/98	1094	RTA00000405F.h.03.2	M00001673D:F10	20633
1850	2/24/98	1095	RTA00000345F.c.12.1	M00001376A:C05	23824
1851	2/24/98	1096	RTA00000421F.a.06.1	M00001589C:A11	2385
1852	2/24/98	1097	RTA00000412F.o.03.1	M00004033D:D07	65039
1853	2/24/98	1098	RTA00000409F.d.16.1	M00001590C:F10	76090
1854	2/24/98	1099	RTA00000400F.m.16.1	M00001660B:E04	3307
1855	2/24/98	1100	RTA00000414F.a.12.1	M00005210A:E06	0
1856	2/24/98	1101	RTA00000408F.j.17.2	M00001485B:H03	78935
1857	2/24/98	1102	RTA00000126A.j.15.2	M00001549A:H11	40425
1858	2/24/98	1103	RTA00000346F.a.16.1	M00001593A:B07	12082
1859	2/24/98	1104	RTA00000126A.b.10.1	M00001547A:F06	0
1860	2/24/98	1105	RTA00000340F.p.18.1	M00003751C:A04	287
1861	2/24/98	1106	RTA00000410F.b.17.1	M00001633C:H05	77458
1862	2/24/98	1107	RTA00000419F.l.22.1	M00003903D:C06	78444
1863	2/24/98	1108	RTA00000346F.c.16.1	M00001652B:G10	9579
1864	2/24/98	1109	RTA00000422F.f.22.1	M00001584A:G03	38703
1865	2/24/98	1110	RTA00000404F.j.24.1	M00001631D:G05	39067
1866	2/24/98	1111	RTA00000406F.m.20.1	M00003918C:C12	38038
1867	2/24/98	1112	RTA00000418F.c.05.1	M00001487B:F02	76475
1868	2/24/98	1113	RTA00000418F.p.21.1	M00001677D:F03	78068
1869	2/24/98	1114	RTA00000340F.f.22.1	M00001594B:F12	1720
1870	2/24/98	1115	RTA00000340F.i.08.1	M00001615B:F07	12005
1871	2/24/98	1116	RTA00000410F.o.04.1	M00001664D:F04	79018
1872	2/24/98	1117	RTA00000411F.l.16.1	M00003857C:G01	16122
1873	2/24/98	1118	RTA00000411F.j.03.1	M00003841C:F01	66263
1874	2/24/98	1119	RTA00000126A.k.24.1	M00001550A:F07	39428
1875	2/24/98	1120	RTA00000353R.l.23.1	M00001418B:F07	12531
1876	2/24/98	1121	RTA00000120A.m.10.3	M00001467A:B03	81376
1877	2/24/98	1122	RTA00000419F.f.16.1	M00003839D:E02	64679
1878	2/24/98	1123	RTA00000408F.c.23.1	M00001458C:D10	42261
1879	2/24/98	1124	RTA00000123A.h.22.1	M00001532A:C01	17124
1880	2/24/98	1125	RTA00000118A.n.5.1	M00001451A:C10	0
1881	2/24/98	1126	RTA00000136A.h.6.1	M00001550A:D09	81620

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
1882	2/24/98	1127	RTA00000401F.g.22.1	M00003871A:G09	1147
1883	2/24/98	1128	RTA00000423F.a.02.3	M00001656B:A08	39210
1884	2/24/98	1129	RTA00000401F.m.07.1	M00003907D:F11	2893
1885	2/24/98	1130	RTA00000354R.p.01.1	M00004104C:H12	0
1886	2/24/98	1131	RTA00000418F.e.20.1	M00001576C:G05	73741
1887	2/24/98	1132	RTA00000119A.c.12.1	M00001453A:D08	4882
1888	2/24/98	1133	RTA00000405F.l.03.1	M00001692D:B01	38580
1889	2/24/98	1134	RTA00000418F.m.02.1	M00001650A:A12	74550
1890	2/24/98	1135	RTA00000346F.o.16.1	M00004358D:C02	176
1891	2/24/98	1136	RTA00000406F.c.05.1	M00003870A:H01	22077
1892	2/24/98	1137	RTA00000345F.d.03.1	M00001376B:A08	19230
1893	2/24/98	1138	RTA00000411F.k.21.1	M00003854B:D04	65349
1894	2/24/98	1139	RTA00000404F.h.20.1	M00001619B:A09	15564
1895	2/24/98	1140	RTA00000339F.c.05.1	M00001365A:H10	3908
1896	2/24/98	1141	RTA00000347F.f.08.1	M00003972D:H02	5948
1897	2/24/98	1142	RTA00000418F.i.06.1	M00001591B:B06	75151
1898	2/24/98	1143	RTA00000423F.a.03.1	M00001656B:D05	26796
1899	2/24/98	1144	RTA00000345F.j.09.1	M00001451B:F01	13
1900	2/24/98	1145	RTA00000423F.k.21.2	M00003984D:B08	37499
1901	2/24/98	1146	RTA00000347F.h.02.1	M00004072D:H12	562
1902	2/24/98	1147	RTA00000404F.c.18.1	M00001594A:C01	38982
1903	2/24/98	1148	RTA00000345F.d.23.1	M00001390D:E03	5862
1904	2/24/98	1149	RTA00000339F.b.02.1	M00001344B:F12	0
1905	2/24/98	1150	RTA00000411F.g.24.1	M00003825B:B11	65233
1906	2/24/98	1151	RTA00000405F.g.18.2	M00001672D:E08	5255
1907	2/24/98	1152	RTA00000405F.m.07.1	M00003809B:B02	37733
1908	2/24/98	1153	RTA00000411F.j.07.1	M00003841C:H11	66963
1909	2/24/98	1154	RTA00000403F.m.09.2	M00001575B:G01	26814
1910	2/24/98	1155	RTA00000353R.h.04.1	M00001375B:C06	17123
1911	2/24/98	1156	RTA00000408F.f.10.2	M00001476D:C05	75309
1912	2/24/98	1157	RTA00000422F.m.18.1	M00001647B:E04	23829
1913	2/24/98	1158	RTA00000405F.o.03.1	M00003829C:H05	37575
1914	2/24/98	1159	RTA00000413F.b.18.1	M00004078C:F04	39873
1915	2/24/98	1160	RTA00000400F.g.02.1	M00001638B:E03	1508
1916	2/24/98	1161	RTA00000346F.m.05.1	M00003983B:C08	5644
1917	2/24/98	1162	RTA00000408F.c.10.1	M00001458A:A11	18247
1918	2/24/98	1163	RTA00000341F.b.14.1	M00003763A:C01	5992
1919	2/24/98	1164	RTA00000405F.m.21.1	M00003815C:C06	24218
1920	2/24/98	1165	RTA00000408F.c.08.1	M00001456D:G11	73473
1921	2/24/98	1166	RTA00000347F.h.01.1	M00004040A:G12	12043
1922	2/24/98	1167	RTA00000410F.c.06.1	M00001633D:H06	77784
1923	2/24/98	1168	RTA00000421F.b.06.1	M00001567A:B09	2113
1924	2/24/98	1169	RTA00000405F.b.08.1	M00001656B:E01	39182
1925	2/24/98	1170	RTA00000409F.l.24.1	M00001616C:A02	73174
1926	2/24/98	1171	RTA00000406F.j.06.1	M00003905A:F10	38952
1927	2/24/98	1172	RTA00000423F.h.03.1	M00003875D:D09	37903
1928	2/24/98	1173	RTA00000339R.b.07.1	M00001360A:G10	6826
1929	2/24/98	1174	RTA00000121A.k.22.1	M00001507A:C05	79523
1930	2/24/98	1175	RTA00000414F.b.04.1	M00005212B:E01	0
1931	2/24/98	1176	RTA00000411F.m.06.1	M00003858D:G06	24195

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
1932	2/24/98	1177	RTA00000126A.b.9.1	M00001547A:F11	81279
1933	2/24/98	1178	RTA00000400F.f.11.1	M00001636A:E07	4088
1934	2/24/98	1179	RTA00000341F.o.12.1	M00004144A:F04	2883
1935	2/24/98	1180	RTA00000404F.l.05.1	M00001636D:F09	38671
1936	2/24/98	1181	RTA00000346F.f.14.1	M00003800B:F03	16998
1937	2/24/98	1182	RTA00000346F.d.21.1	M00001670B:G12	6641
1938	2/24/98	1183	RTA00000346F.j.21.1	M00003879D:A08	3095
1939	2/24/98	1184	RTA00000345F.h.08.1	M00001419D:C10	11393
1940	2/24/98	1185	RTA00000413F.b.20.1	M00004079D:G08	66063
1941	2/24/98	1186	RTA00000419F.p.10.1	M00004036D:B09	41448
1942	2/24/98	1187	RTA00000120A.c.19.1	M00001464A:B03	81016
1943	2/24/98	1188	RTA00000341F.o.18.1	M00004169D:B11	37189
1944	2/24/98	1189	RTA00000339F.o.18.1	M00001469B:B01	6641
1945	2/24/98	1190	RTA00000405F.g.02.2	M00001671B:G05	10567
1946	2/24/98	1191	RTA00000340F.i.05.1	M00001614B:E08	0
1947	2/24/98	1192	RTA00000406F.m.17.1	M00003918A:F09	0
1948	2/24/98	1193	RTA00000411F.k.14.1	M00003851A:C10	63987
1949	2/24/98	1194	RTA00000420F.e.05.1	M00004107D:E12	63908
1950	2/24/98	1195	RTA00000422F.e.23.1	M00001567D:B03	19246
1951	2/24/98	1196	RTA00000413F.l.18.1	M00004895D:G07	0
1952	2/24/98	1197	RTA00000128A.j.10.1	M00001560A:H06	80085
1953	2/24/98	1198	RTA00000412F.f.10.2	M00003959A:A03	65405
1954	2/24/98	1199	RTA00000401F.j.23.1	M00003901C:D03	570
1955	2/24/98	1200	RTA00000422F.k.17.1	M00001652A:A01	38955
1956	2/24/98	1201	RTA00000409F.m.02.1	M00001616C:A11	9157
1957	2/24/98	1202	RTA00000347F.h.10.1	M00004206A:E02	22779
1958	2/24/98	1203	RTA00000413F.e.10.1	M00004092C:B03	31033
1959	2/24/98	1204	RTA00000419F.l.02.1	M00003879A:C01	75736
1960	2/24/98	1205	RTA00000419F.k.05.1	M00003871C:E04	11757
1961	2/24/98	1206	RTA00000418F.b.20.1	M00001484D:G05	73560
1962	2/24/98	1207	RTA00000401F.j.21.1	M00003901B:F10	0
1963	2/24/98	1208	RTA00000347F.e.24.1	M00003823B:F07	8188
1964	2/24/98	1209	RTA00000408F.n.05.2	M00001539A:H02	77883
1965	2/24/98	1210	RTA00000419F.o.09.1	M00003987B:F08	66396
1966	2/24/98	1211	RTA00000399F.f.14.1	M00001487D:C11	11483
1967	2/24/98	1212	RTA00000349R.o.03.1	M00001551D:H07	23006
1968	2/24/98	1213	RTA00000135A.a.23.1	M00001537A:H05	27054
1969	2/24/98	1214	RTA00000339F.j.07.1	M00001428D:B10	5673
1970	2/24/98	1215	RTA00000422F.o.08.2	M00001659D:D03	26832
1971	2/24/98	1216	RTA00000404F.e.07.1	M00001608A:D03	9034
1972	2/24/98	1217	RTA00000410F.j.17.1	M00001642D:F02	72912
1973	2/24/98	1218	RTA00000418F.m.18.1	M00001653B:G10	76479
1974	2/24/98	1219	RTA00000347F.e.20.1	M00003771B:E05	39911
1975	2/24/98	1220	RTA00000419F.e.23.1	M00003834B:G04	65772
1976	2/24/98	1221	RTA00000403F.o.17.1	M00001582D:A02	23085
1977	2/24/98	1222	RTA00000423F.e.13.1	M00003848A:C09	10998
1978	2/24/98	1223	RTA00000347F.a.14.1	M00001429D:F11	7421
1979	2/24/98	1224	RTA00000122A.h.24.1	M00001514A:A12	48
1980	2/24/98	1225	RTA00000346F.j.13.1	M00003841C:E04	5337
1981	2/24/98	1226	RTA00000414F.c.12.1	M00005218A:F09	0

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
1982	2/24/98	1227	RTA00000411F.g.05.1	M00003822D:B10	64664
1983	2/24/98	1228	RTA00000404F.h.10.1	M00001618A:A03	37148
1984	2/24/98	1229	RTA00000422F.n.14.1	M00001642C:G02	26787
1985	2/24/98	1230	RTA00000399F.j.14.1	M00001578C:F05	16942
1986	2/24/98	1231	RTA00000120A.m.13.3	M00001467A:C10	80608
1987	2/24/98	1232	RTA00000412F.i.03.1	M00003975D:C06	65617
1988	2/24/98	1233	RTA00000418F.l.02.1	M00001641C:C05	39316
1989	2/24/98	1234	RTA00000352R.c.20.1	M00003982A:B12	7339
1990	2/24/98	1235	RTA00000411F.j.04.1	M00003841C:F03	66219
1991	2/24/98	1236	RTA00000414F.b.06.1	M00005212C:C03	0
1992	2/24/98	1237	RTA00000414F.c.24.1	M00005229B:H04	0
1993	2/24/98	1238	RTA00000420F.g.09.1	M00004895B:E12	0
1994	2/24/98	1239	RTA00000340F.o.22.1	M00001673B:B07	7356
1995	2/24/98	1240	RTA00000404F.a.18.1	M00001590B:B02	36267
1996	2/24/98	1241	RTA00000408F.l.14.1	M00001530A:E10	12001
1997	2/24/98	1242	RTA00000405F.d.10.1	M00001661C:F11	39000
1998	2/24/98	1243	RTA00000404F.j.19.1	M00001630D:H10	0
1999	2/24/98	1244	RTA00000418F.h.23.1	M00001591A:B08	75153
2000	2/24/98	1245	RTA00000422F.k.22.1	M00001592C:E05	4098
2001	2/24/98	1246	RTA00000418F.j.11.1	M00001626C:E04	73853
2002	2/24/98	1247	RTA00000408F.o.13.1	M00001572A:B05	74895
2003	2/24/98	1248	RTA00000419F.o.07.1	M00003986C:E09	14059
2004	2/24/98	1249	RTA00000419F.n.17.1	M00003978D:G04	63186
2005	2/24/98	1250	RTA00000403F.f.15.1	M00001477D:F10	22768
2006	2/24/98	1251	RTA00000408F.d.03.1	M00001458D:A02	22768
2007	2/24/98	1252	RTA00000400F.g.08.1	M00001639A:C11	1275
2008	2/24/98	1253	RTA00000346F.f.02.1	M00003772C:B12	62757
2009	2/24/98	1254	RTA00000341F.p.11.1	M00004159C:G12	0
2010	2/24/98	1255	RTA00000413F.i.21.1	M00004118B:B04	64066
2011	2/24/98	1256	RTA00000401F.k.19.1	M00003903D:D10	799
2012	2/24/98	1257	RTA00000419F.h.21.1	M00003856C:B08	64828
2013	2/24/98	1258	RTA00000403F.p.05.2	M00001583D:B08	24528
2014	2/24/98	1259	RTA00000420F.l.19.2	M00005231A:H04	0
2015	2/24/98	1260	RTA00000422F.f.18.1	M00001583D:B08	24528
2016	2/24/98	1261	RTA00000404F.m.17.2	M00001643B:E05	0
2017	2/24/98	1262	RTA00000122A.h.4.1	M00001514A:G03	33576
2018	2/24/98	1263	RTA00000341F.i.22.1	M00003911A:F10	7825
2019	2/24/98	1264	RTA00000345F.e.13.1	M00001392C:D05	4366
2020	2/24/98	1265	RTA00000340F.d.07.1	M00001532D:A06	0
2021	2/24/98	1266	RTA00000121A.a.2.1	M00001468A:H10	81843
2022	3/24/98	1	RTA00000527F.g.13.1	M00003845D:A04	36035
2023	3/24/98	2	RTA00000523F.d.19.1	M00003824A:A06	26489
2024	3/24/98	3	RTA00000528F.b.23.1	M00001479C:F10	1605
2025	3/24/98	4	RTA00000426F.h.11.1	M00003905B:H05	75479
2026	3/24/98	5	RTA00000426F.p.04.1	M00004029B:H08	34149
2027	3/24/98	6	RTA00000523F.l.10.1	M00005134B:E01	0
2028	3/24/98	7	RTA00000523F.o.20.1	M00005177B:H02	0
2029	3/24/98	8	RTA00000428F.b.06.1	M00005228A:A09	0
2030	3/24/98	9	RTA00000522F.b.22.1	M00001573B:H12	75181
2031	3/24/98	10	RTA00000527F.f.12.1	M00003829D:D12	5945

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
2032	3/24/98	11	RTA00000427F.l.11.1	M00005139A:F01	0
2033	3/24/98	12	RTA00000522F.a.23.1	M00001570C:A05	38613
2034	3/24/98	13	RTA00000528F.m.16.1	M00003845D:C03	4468
2035	3/24/98	14	RTA00000523F.b.02.1	M00003806C:A06	65163
2036	3/24/98	15	RTA00000425F.j.14.1	M00001639D:C12	73397
2037	3/24/98	16	RTA00000426F.m.22.1	M00003983A:G02	30002
2038	3/24/98	17	RTA00000527F.p.06.1	M00004029B:G10	1292
2039	3/24/98	18	RTA00000522F.e.16.1	M00001590A:C08	75283
2040	3/24/98	19	RTA00000527F.j.02.2	M00003856A:B07	4896
2041	3/24/98	20	RTA00000522F.o.06.1	M00001659D:A09	26860
2042	3/24/98	21	RTA00000523F.h.17.1	M00003852A:B03	65586
2043	3/24/98	22	RTA00000527F.k.15.1	M00003982A:G03	22688
2044	3/24/98	23	RTA00000522F.p.07.1	M00001670A:C11	76888
2045	3/24/98	24	RTA00000522F.n.08.1	M00001656A:D10	76343
2046	3/24/98	25	RTA00000425F.c.06.1	M00001585D:D11	78041
2047	3/24/98	26	RTA00000427F.b.23.1	M00003973D:F08	64297
2048	3/24/98	27	RTA00000527F.p.02.1	M00004029B:A01	36844
2049	3/24/98	28	RTA00000427F.d.08.1	M00003980C:E12	63967
2050	3/24/98	29	RTA00000524F.b.03.1	M00005212A:D10	0
2051	3/24/98	30	RTA00000426F.m.07.1	M00004028A:G03	63504
2052	3/24/98	31	RTA00000427F.c.10.1	M00003976B:E06	65478
2053	3/24/98	32	RTA00000424F.n.14.1	M00001584D:C11	73008
2054	3/24/98	33	RTA00000524F.b.21.1	M00005216C:B09	0
2055	3/24/98	34	RTA00000424F.m.15.1	M00001612D:F06	73759
2056	3/24/98	35	RTA00000426F.f.11.1	M00003823C:B01	63102
2057	3/24/98	36	RTA00000428F.a.16.1	M00005212D:F08	0
2058	3/24/98	37	RTA00000426F.f.20.1	M00003854C:F01	65134
2059	3/24/98	38	RTA00000528F.i.22.1	M00001661D:D05	2478
2060	3/24/98	39	RTA00000527F.c.23.1	M00003822C:A07	37742
2061	3/24/98	40	RTA00000426F.h.23.1	M00003911A:D12	75964
2062	3/24/98	41	RTA00000525F.b.17.1	M00004037B:A04	24715
2063	3/24/98	42	RTA00000527F.i.19.2	M00003853C:C06	38089
2064	3/24/98	43	RTA00000527F.p.07.1	M00004029C:B03	23343
2065	3/24/98	44	RTA00000527F.p.17.1	M00004030C:D12	17223
2066	3/24/98	45	RTA00000528F.m.12.1	M00003842D:F08	5768
2067	3/24/98	46	RTA00000523F.c.09.1	M00003813C:D08	47389
2068	3/24/98	47	RTA00000523F.e.18.1	M00003829D:A11	62898
2069	3/24/98	48	RTA00000527F.k.21.1	M00003982B:H10	36051
2070	3/24/98	49	RTA00000527F.n.22.1	M00004027A:A08	24175
2071	3/24/98	50	RTA00000522F.k.15.1	M00001652D:G06	76866
2072	3/24/98	51	RTA00000522F.n.02.1	M00001655D:E08	74959
2073	3/24/98	52	RTA00000523F.l.07.1	M00004927C:H11	0
2074	3/24/98	53	RTA00000525F.c.17.1	M00004040A:C08	38160
2075	3/24/98	54	RTA00000425F.f.19.1	M00001653D:G07	32635
2076	3/24/98	55	RTA00000528F.e.23.1	M00001593B:D10	19242
2077	3/24/98	56	RTA00000522F.n.16.1	M00001657D:A10	26769
2078	3/24/98	57	RTA00000427F.c.20.1	M00003978A:E01	26527
2079	3/24/98	58	RTA00000527F.k.06.1	M00003981B:B12	12469
2080	3/24/98	59	RTA00000427F.n.14.1	M00004960B:D12	0
2081	3/24/98	60	RTA00000523F.i.06.1	M00003855A:A01	66341

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
2082	3/24/98	61	RTA00000427F.f.21.1	M00004118B:C11	36853
2083	3/24/98	62	RTA00000427F.j.19.1	M00004077A:G12	41395
2084	3/24/98	63	RTA00000522F.b.01.1	M00001570C:B02	75691
2085	3/24/98	64	RTA00000424F.i.24.1	M00001596A:G06	79101
2086	3/24/98	65	RTA00000523F.c.01.1	M00003810A:A02	65710
2087	3/24/98	66	RTA00000427F.b.15.1	M00003971C:F09	66891
2088	3/24/98	67	RTA00000527F.e.03.1	M00003825D:F01	25560
2089	3/24/98	68	RTA00000523F.n.04.1	M00005138B:D12	0
2090	3/24/98	69	RTA00000522F.j.15.2	M00001651C:G12	76535
2091	3/24/98	70	RTA00000525F.e.07.1	M00004115C:G03	38147
2092	3/24/98	71	RTA00000527F.j.20.2	M00003860D:E06	37603
2093	3/24/98	72	RTA00000426F.f.19.1	M00003854C:C09	66701
2094	3/24/98	73	RTA00000524F.b.12.1	M00005213C:G01	0
2095	3/24/98	74	RTA00000527F.d.19.1	M00003825B:F10	486
2096	3/24/98	75	RTA00000523F.i.22.1	M00003857A:E12	64688
2097	3/24/98	76	RTA00000523F.l.18.1	M00005134D:A06	0
2098	3/24/98	77	RTA00000425F.i.17.1	M00001633A:F11	43213
2099	3/24/98	78	RTA00000427F.o.05.1	M00004958B:D01	0
2100	3/24/98	79	RTA00000523F.l.15.1	M00005134C:E11	0
2101	3/24/98	80	RTA00000425F.p.12.1	M00001638C:G01	73219
2102	3/24/98	81	RTA00000427F.j.07.1	M00004105A:B10	64819
2103	3/24/98	82	RTA00000523F.h.15.1	M00003851C:F09	65137
2104	3/24/98	83	RTA00000527F.i.05.2	M00003851C:B06	37481
2105	3/24/98	84	RTA00000527F.k.18.1	M00003982B:C10	11332
2106	3/24/98	85	RTA00000427F.m.21.1	M00004900C:E11	0
2107	3/24/98	86	RTA00000523F.k.01.1	M00003966C:F03	41437
2108	3/24/98	87	RTA00000425F.j.11.1	M00001637C:H12	76667
2109	3/24/98	88	RTA00000424F.b.22.4	M00001530A:F11	72971
2110	3/24/98	89	RTA00000527F.n.02.1	M00003986C:G11	24190
2111	3/24/98	90	RTA00000525F.a.03.1	M00004031D:F05	36786
2112	3/24/98	91	RTA00000527F.i.21.2	M00003855A:F01	37490
2113	3/24/98	92	RTA00000424F.a.24.4	M00001448D:E11	73951
2114	3/24/98	93	RTA00000522F.k.14.1	M00001652D:G02	74280
2115	3/24/98	94	RTA00000522F.n.05.1	M00001655D:H11	73260
2116	3/24/98	95	RTA00000523F.c.18.1	M00003817C:A10	66179
2117	3/24/98	96	RTA00000523F.b.13.1	M00003809B:A03	66330
2118	3/24/98	97	RTA00000522F.j.14.2	M00001651C:D11	73123
2119	3/24/98	98	RTA00000527F.p.16.1	M00004030C:C02	23798
2120	3/24/98	99	RTA00000425F.c.20.1	M00001626D:A02	73581
2121	3/24/98	100	RTA00000424F.i.21.1	M00001596A:E07	73482
2122	3/24/98	101	RTA00000523F.j.19.1	M00003966B:D02	65910
2123	3/24/98	102	RTA00000522F.g.19.1	M00001595C:A01	78119
2124	3/24/98	103	RTA00000424F.b.22.1	M00001530A:F11	72971
2125	3/24/98	104	RTA00000527F.b.18.1	M00003810D:H09	37469
2126	3/24/98	105	RTA00000526F.d.01.1	M00004104B:A02	4468
2127	3/24/98	106	RTA00000424F.j.14.1	M00001592B:B02	74311
2128	3/24/98	107	RTA00000523F.n.20.1	M00005174D:H02	0
2129	3/24/98	108	RTA00000525F.e.16.1	M00004117B:G01	36837
2130	3/24/98	109	RTA00000424F.a.01.4	M00001575A:D05	43214
2131	3/24/98	110	RTA00000522F.d.08.1	M00001578B:A06	74284

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
2132	3/24/98	111	RTA00000425F.d.08.1	M00001631A:F06	74350
2133	3/24/98	112	RTA00000523F.n.12.1	M00005173C:A02	0
2134	3/24/98	113	RTA00000527F.g.07.1	M00003840C:C02	37488
2135	3/24/98	114	RTA00000524F.a.23.1	M00005211C:E09	0
2136	3/24/98	115	RTA00000525F.b.05.1	M00004034C:F05	21116
2137	3/24/98	116	RTA00000425F.n.05.1	M00001647D:G07	73965
2138	3/24/98	117	RTA00000523F.d.18.1	M00003822B:G01	64072
2139	3/24/98	118	RTA00000525F.a.02.1	M00004031C:H10	37454
2140	3/24/98	119	RTA00000523F.p.06.1	M00005177D:F09	0
2141	3/24/98	120	RTA00000426F.h.09.1	M00003905B:G03	78797
2142	3/24/98	121	RTA00000427F.n.02.1	M00004900D:B10	0
2143	3/24/98	122	RTA00000523F.o.12.1	M00005177A:B06	0
2144	3/24/98	123	RTA00000427F.g.05.1	M00004069C:C08	63138
2145	3/24/98	124	RTA00000424F.m.12.1	M00001586C:H07	77675
2146	3/24/98	125	RTA00000424F.a.01.1	M00001575A:D05	43214
2147	3/24/98	126	RTA00000527F.m.05.1	M00003985A:C01	17240
2148	3/24/98	127	RTA00000523F.n.10.1	M00005140D:G09	0
2149	3/24/98	128	RTA00000428F.c.02.1	M00005229D:H07	0
2150	3/24/98	129	RTA00000527F.p.18.1	M00004030D:B06	31635
2151	3/24/98	130	RTA00000427F.h.12.1	M00004092C:D08	36894
2152	3/24/98	131	RTA00000523F.c.15.1	M00003813D:G06	36935
2153	3/24/98	132	RTA00000427F.k.17.1	M00004101A:F07	64965
2154	3/24/98	133	RTA00000425F.f.04.1	M00001607A:B06	24633
2155	3/24/98	134	RTA00000424F.c.14.3	M00001476D:A09	76614
2156	3/24/98	135	RTA00000522F.k.10.2	M00001652D:B09	77619
2157	3/24/98	136	RTA00000424F.m.22.1	M00001614C:E11	72943
2158	3/24/98	137	RTA00000527F.h.17.1	M00003848D:G02	37799
2159	3/24/98	138	RTA00000527F.c.22.1	M00003822B:G12	37496
2160	3/24/98	139	RTA00000425F.k.22.1	M00001633C:E12	78123
2161	3/24/98	140	RTA00000424F.m.14.1	M00001612D:D12	77491
2162	3/24/98	141	RTA00000522F.k.19.1	M00001653A:A05	32625
2163	3/24/98	142	RTA00000523F.i.18.1	M00003856B:C04	64463
2164	3/24/98	143	RTA00000425F.j.22.1	M00001633B:E03	73882
2165	3/24/98	144	RTA00000527F.g.23.1	M00003846C:F08	37538
2166	3/24/98	145	RTA00000426F.m.24.1	M00003981A:A07	63943
2167	3/24/98	146	RTA00000527F.i.17.2	M00003853B:C08	37539
2168	3/24/98	147	RTA00000425F.d.21.1	M00001631B:H04	78920
2169	3/24/98	148	RTA00000427F.n.18.1	M00004891D:C11	0
2170	3/24/98	149	RTA00000424F.d.04.3	M00001478A:F12	76505
2171	3/24/98	150	RTA00000424F.d.04.1	M00001478A:F12	76505
2172	3/24/98	151	RTA00000427F.c.12.1	M00003976B:H07	66995
2173	3/24/98	152	RTA00000425F.d.07.1	M00001631A:F12	43197
2174	3/24/98	153	RTA00000527F.l.13.1	M00003983C:F10	36904
2175	3/24/98	154	RTA00000522F.h.13.1	M00001596C:F09	40823
2176	3/24/98	155	RTA00000424F.l.19.1	M00001609C:A12	75454
2177	3/24/98	156	RTA00000525F.b.22.1	M00004037C:D07	16679
2178	3/24/98	157	RTA00000523F.g.10.1	M00003848B:E07	40694
2179	3/24/98	158	RTA00000427F.a.06.1	M00004036A:A11	66550
2180	3/24/98	159	RTA00000525F.c.19.1	M00004040B:F07	38159
2181	3/24/98	160	RTA00000523F.f.06.1	M00003833D:H08	62871

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
2182	3/24/98	161	RTA00000424F.h.10.1	M00001485C:G06	72925
2183	3/24/98	162	RTA00000522F.a.12.1	M00001567A:H05	33515
2184	3/24/98	163	RTA00000522F.h.01.1	M00001595C:E05	75010
2185	3/24/98	164	RTA00000523F.n.17.1	M00005174D:B02	0
2186	3/24/98	165	RTA00000425F.e.21.1	M00001629D:D10	77203
2187	3/24/98	166	RTA00000523F.f.07.1	M00003833D:H10	62799
2188	3/24/98	167	RTA00000424F.i.20.1	M00001596A:D01	44010
2189	3/24/98	168	RTA00000424F.j.12.1	M00001594C:E05	73827
2190	3/24/98	169	RTA00000425F.f.05.1	M00001607A:D10	24090
2191	3/24/98	170	RTA00000523F.d.12.1	M00003822B:D08	64888
2192	3/24/98	171	RTA00000523F.e.10.1	M00003829A:F03	62878
2193	3/24/98	172	RTA00000425F.f.11.1	M00001656C:C04	79275
2194	3/24/98	173	RTA00000426F.m.18.1	M00003986D:G07	62974
2195	3/24/98	174	RTA00000424F.b.21.4	M00001530A:B02	24686
2196	3/24/98	175	RTA00000528F.d.18.1	M00001582C:E01	2684
2197	3/24/98	176	RTA00000522F.g.15.1	M00001595B:G07	76536
2198	3/24/98	177	RTA00000522F.n.12.1	M00001656A:H12	74117
2199	3/24/98	178	RTA00000428F.a.12.1	M00005179B:H02	0
2200	3/24/98	179	RTA00000424F.d.10.3	M00001530D:A11	73110
2201	3/24/98	180	RTA00000523F.k.02.1	M00004687A:C03	0
2202	3/24/98	181	RTA00000523F.b.06.1	M00003808A:F09	28736
2203	3/24/98	182	RTA00000524F.b.17.1	M00005214B:A06	0
2204	3/24/98	183	RTA00000527F.c.04.1	M00003813C:H08	23090
2205	3/24/98	184	RTA00000524F.b.18.1	M00005214B:D11	0
2206	3/24/98	185	RTA00000527F.h.21.1	M00003850C:G09	37630
2207	3/24/98	186	RTA00000425F.c.07.1	M00001585D:F03	76042
2208	3/24/98	187	RTA00000428F.b.23.1	M00005231D:H10	0
2209	3/24/98	188	RTA00000525F.c.15.1	M00004040A:A07	7692
2210	3/24/98	189	RTA00000424F.d.22.3	M00001448B:G07	76189
2211	3/24/98	190	RTA00000523F.h.12.1	M00003851C:D07	65745
2212	3/24/98	191	RTA00000522F.g.22.1	M00001595C:B12	77504
2213	3/24/98	192	RTA00000523F.m.02.1	M00005134D:H03	0
2214	3/24/98	193	RTA00000428F.b.12.1	M00005231C:B07	0
2215	3/24/98	194	RTA00000522F.j.12.2	M00001651C:A04	74341
2216	3/24/98	195	RTA00000523F.i.08.1	M00003855A:C12	65099
2217	3/24/98	196	RTA00000523F.f.12.1	M00003840A:C10	63751
2218	3/24/98	197	RTA00000425F.j.20.1	M00001633B:A12	26760
2219	3/24/98	198	RTA00000523F.o.05.1	M00005175B:H04	0
2220	3/24/98	199	RTA00000427F.f.24.1	M00004076D:B09	64572
2221	3/24/98	200	RTA00000527F.a.13.1	M00003805D:E06	37740
2222	3/24/98	201	RTA00000427F.n.17.1	M00004891D:A07	0
2223	3/24/98	202	RTA00000528F.j.11.1	M00001669B:C12	1070
2224	3/24/98	203	RTA00000427F.p.10.2	M00005102C:F09	0
2225	3/24/98	204	RTA00000424F.a.09.4	M00001575C:C11	77833
2226	3/24/98	205	RTA00000426F.h.12.1	M00003905C:F12	78093
2227	3/24/98	206	RTA00000525F.f.07.1	M00004119A:A06	37500
2228	3/24/98	207	RTA00000424F.j.07.1	M00001596B:C11	79211
2229	3/24/98	208	RTA00000424F.m.10.1	M00001586C:E06	34251
2230	3/24/98	209	RTA00000427F.g.16.1	M00004069A:E12	63011
2231	3/24/98	210	RTA00000522F.g.06.1	M00001594D:G11	78221

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
2232	3/24/98	211	RTA00000424F.h.03.1	M00001487C:G09	74447
2233	3/24/98	212	RTA00000424F.n.06.1	M00001613A:D02	74737
2234	3/24/98	213	RTA00000427F.c.22.1	M00003978A:E09	63990
2235	3/24/98	214	RTA00000424F.k.12.1	M00001610C:B07	77666
2236	3/24/98	215	RTA00000425F.f.02.1	M00001607A:A01	76982
2237	3/24/98	216	RTA00000427F.h.11.1	M00004092C:B12	26494
2238	3/24/98	217	RTA00000425F.j.16.1	M00001639D:F02	75631
2239	3/24/98	218	RTA00000427F.i.19.1	M00004102C:D01	64206
2240	3/24/98	219	RTA00000427F.f.17.1	M00004115A:B12	63803
2241	3/24/98	220	RTA00000522F.o.18.1	M00001669B:H06	76366
2242	3/24/98	221	RTA00000427F.j.22.1	M00004097D:B05	66367
2243	3/24/98	222	RTA00000426F.p.10.1	M00004033D:C05	65845
2244	3/24/98	223	RTA00000522F.m.02.1	M00001654C:G07	76834
2245	3/24/98	224	RTA00000527F.k.09.1	M00003981C:F05	213
2246	3/24/98	225	RTA00000527F.d.09.1	M00003824A:G11	10848
2247	3/24/98	226	RTA00000425F.e.15.1	M00001608D:F11	75921
2248	3/24/98	227	RTA00000427F.i.11.1	M00004097C:H08	26635
2249	3/24/98	228	RTA00000523F.o.14.1	M00005177A:H09	0
2250	3/24/98	229	RTA00000424F.n.13.1	M00001584D:B06	74942
2251	3/24/98	230	RTA00000424F.g.14.1	M00001572A:B06	74879
2252	3/24/98	231	RTA00000426F.e.17.1	M00003810C:B06	64089
2253	3/24/98	232	RTA00000527F.i.13.2	M00003852B:G04	2924
2254	3/24/98	233	RTA00000426F.f.13.1	M00003851A:A06	65384
2255	3/24/98	234	RTA00000524F.c.16.1	M00005218D:G10	0
2256	3/24/98	235	RTA00000427F.g.19.1	M00004087A:B05	64611
2257	3/24/98	236	RTA00000527F.o.01.1	M00004027A:D06	19088
2258	3/24/98	237	RTA00000522F.c.01.1	M00001576A:C11	74938
2259	3/24/98	238	RTA00000522F.g.17.1	M00001595B:G10	76486
2260	3/24/98	239	RTA00000523F.j.17.1	M00003966B:A04	63610
2261	3/24/98	240	RTA00000522F.n.14.1	M00001657C:C11	73410
2262	3/24/98	241	RTA00000527F.o.12.1	M00004028B:G08	688
2263	3/24/98	242	RTA00000523F.e.20.1	M00003829D:F03	65164
2264	3/24/98	243	RTA00000424F.c.15.3	M00001476D:F12	73533
2265	3/24/98	244	RTA00000426F.p.09.1	M00004033D:B07	66665
2266	3/24/98	245	RTA00000522F.p.09.1	M00001670A:F09	75204
2267	3/24/98	246	RTA00000426F.m.21.1	M00003983A:F06	64915
2268	3/24/98	247	RTA00000425F.j.21.1	M00001633B:B11	77373
2269	3/24/98	248	RTA00000527F.i.14.1	M00003983D:A09	14935
2270	3/24/98	249	RTA00000523F.h.21.1	M00003853B:C10	41440
2271	3/24/98	250	RTA00000427F.h.24.1	M00004091B:H09	65193
2272	3/24/98	251	RTA00000425F.f.24.1	M00001656D:C04	40841
2273	3/24/98	252	RTA00000425F.m.03.1	M00001642D:G08	76045
2274	3/24/98	253	RTA00000426F.m.08.1	M00004030B:A12	63781
2275	3/24/98	254	RTA00000523F.d.24.1	M00003824D:D08	64799
2276	3/24/98	255	RTA00000523F.c.14.1	M00003813D:C02	66015
2277	3/24/98	256	RTA00000523F.b.20.1	M00003809C:H07	66492
2278	3/24/98	257	RTA00000522F.h.07.1	M00001595D:C11	75149
2279	3/24/98	258	RTA00000527F.g.10.1	M00003845A:E12	37820
2280	3/24/98	259	RTA00000528F.m.04.1	M00003830D:H11	10815
2281	3/24/98	260	RTA00000524F.b.02.1	M00005212A:A02	0

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
2282	3/24/98	261	RTA00000427F.i.22.1	M00004104D:B05	63199
2283	3/24/98	262	RTA00000424F.k.03.1	M00001590D:B04	21289
2284	3/24/98	263	RTA00000527F.n.07.1	M00003986D:H12	15939
2285	3/24/98	264	RTA00000425F.e.09.1	M00001608C:G04	75550
2286	3/24/98	265	RTA00000427F.h.02.1	M00004085B:G01	63652
2287	3/24/98	266	RTA00000426F.f.16.1	M00003813B:F02	65613
2288	3/24/98	267	RTA00000425F.i.21.1	M00001635B:B02	75305
2289	3/24/98	268	RTA00000427F.k.19.1	M00004103B:B07	62851
2290	3/24/98	269	RTA00000427F.p.02.2	M00005100B:D02	0
2291	3/24/98	270	RTA00000426F.g.16.1	M00003814B:C01	41446
2292	3/24/98	271	RTA00000527F.l.05.1	M00003983A:D02	13016
2293	3/24/98	272	RTA00000426F.m.02.1	M00004034C:C06	66237
2294	3/24/98	273	RTA00000424F.a.02.4	M00001575A:D06	78806
2295	3/24/98	274	RTA00000523F.h.06.1	M00003851B:D03	28745
2296	3/24/98	275	RTA00000522F.l.22.1	M00001654C:D10	75801
2297	3/24/98	276	RTA00000427F.h.19.1	M00004092D:B11	63047
2298	3/24/98	277	RTA00000427F.e.08.1	M00003974D:E01	47387
2299	3/24/98	278	RTA00000522F.g.21.1	M00001595C:A09	77310
2300	3/24/98	279	RTA00000528F.b.03.1	M00001455A:D10	2078
2301	3/24/98	280	RTA00000522F.g.20.1	M00001595C:A05	77688
2302	3/24/98	281	RTA00000527F.k.20.1	M00003982B:H07	17148
2303	3/24/98	282	RTA00000427F.h.22.1	M00004108C:E01	64547
2304	3/24/98	283	RTA00000425F.k.20.1	M00001633C:A08	74048
2305	3/24/98	284	RTA00000524F.b.19.1	M00005216B:D02	0
2306	3/24/98	285	RTA00000522F.b.07.1	M00001570D:E05	78634
2307	3/24/98	286	RTA00000426F.g.19.1	M00003858B:G02	63672
2308	3/24/98	287	RTA00000525F.d.19.1	M00004114B:D09	36860
2309	3/24/98	288	RTA00000427F.l.04.1	M00005136D:C01	0
2310	3/24/98	289	RTA00000427F.d.10.1	M00003978C:A12	40685
2311	3/24/98	290	RTA00000427F.l.03.1	M00005136D:B07	0
2312	3/24/98	291	RTA00000523F.o.23.1	M00005177C:G04	0
2313	3/24/98	292	RTA00000424F.a.05.4	M00001575B:C01	77976
2314	3/24/98	293	RTA00000525F.c.02.1	M00004038A:E05	14618
2315	3/24/98	294	RTA00000424F.a.05.1	M00001575B:C01	77976
2316	3/24/98	295	RTA00000522F.l.15.1	M00001654B:A01	74691
2317	3/24/98	296	RTA00000425F.e.02.1	M00001625C:F10	76143
2318	3/24/98	297	RTA00000525F.c.11.1	M00004039C:E02	37895
2319	3/24/98	298	RTA00000527F.e.08.1	M00003826B:B04	19015
2320	3/24/98	299	RTA00000522F.c.14.1	M00001577A:A03	75449
2321	3/24/98	300	RTA00000424F.m.08.1	M00001584A:A07	19402
2322	3/24/98	301	RTA00000527F.f.18.1	M00003830D:B11	37577
2323	3/24/98	302	RTA00000427F.p.04.2	M00005100B:H07	0
2324	3/24/98	303	RTA00000522F.a.06.1	M00001567A:C11	73662
2325	3/24/98	304	RTA00000525F.d.13.1	M00004110C:E03	349
2326	3/24/98	305	RTA00000523F.n.16.1	M00005173D:H02	0
2327	3/24/98	306	RTA00000522F.d.23.1	M00001579D:F02	73868
2328	3/24/98	307	RTA00000427F.p.03.2	M00005100B:G11	0
2329	3/24/98	308	RTA00000424F.k.23.1	M00001614A:B10	31061
2330	3/24/98	309	RTA00000523F.j.10.1	M00003860B:G09	63384
2331	3/24/98	310	RTA00000527F.p.08.1	M00004029C:F02	36013

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
2332	3/24/98	311	RTA00000428F.b.02.1	M00005214D:D10	0
2333	3/24/98	312	RTA00000426F.f.17.1	M00003811C:C02	66334
2334	3/24/98	313	RTA00000523F.j.21.1	M00003966C:A12	36925
2335	3/24/98	314	RTA00000522F.e.09.1	M00001589D:A01	32599
2336	3/24/98	315	RTA00000427F.n.19.1	M00004891D:E07	0
2337	3/24/98	316	RTA00000523F.h.16.1	M00003851D:H11	66031
2338	3/24/98	317	RTA00000428F.a.01.1	M00004897D:G05	0
2339	3/24/98	318	RTA00000523F.a.01.1	M00001671C:F11	74923
2340	3/24/98	319	RTA00000523F.p.15.1	M00005178B:H01	0
2341	3/24/98	320	RTA00000427F.j.06.1	M00004102D:B05	63676
2342	3/24/98	321	RTA00000424F.m.04.1	M00001609C:G05	79017
2343	3/24/98	322	RTA00000523F.i.17.1	M00003856B:A12	65779
2344	3/24/98	323	RTA00000524F.c.12.1	M00005218B:D09	0
2345	3/24/98	324	RTA00000523F.o.09.1	M00005176A:C12	0
2346	3/24/98	325	RTA00000525F.c.18.1	M00004040B:C05	24208
2347	3/24/98	326	RTA00000527F.e.09.1	M00003826B:E11	37521
2348	3/24/98	327	RTA00000424F.j.08.1	M00001596B:D09	73972
2349	3/24/98	328	RTA00000523F.n.01.1	M00005137A:E01	0
2350	3/24/98	329	RTA00000527F.c.09.1	M00003817C:G06	64859
2351	3/24/98	330	RTA00000523F.d.23.1	M00003824C:A10	63633
2352	3/24/98	331	RTA00000528F.k.10.1	M00001678C:F09	1981
2353	3/24/98	332	RTA00000523F.c.03.1	M00003810B:B11	36913
2354	3/24/98	333	RTA00000427F.k.21.1	M00004090D:F12	62880
2355	3/24/98	334	RTA00000427F.n.11.1	M00004960B:A09	0
2356	3/24/98	335	RTA00000427F.d.09.1	M00003980C:F12	66486
2357	3/24/98	336	RTA00000426F.n.17.1	M00004039D:B10	66572
2358	3/24/98	337	RTA00000525F.e.08.1	M00004115C:H04	24193
2359	3/24/98	338	RTA00000523F.e.15.1	M00003829C:E08	7919
2360	3/24/98	339	RTA00000426F.m.03.1	M00004034C:E08	66480
2361	3/24/98	340	RTA00000424F.h.06.1	M00001485C:D07	77552
2362	3/24/98	341	RTA00000425F.d.06.1	M00001631A:D03	77660
2363	3/24/98	342	RTA00000427F.e.12.1	M00003959C:G06	62813
2364	3/24/98	343	RTA00000527F.c.11.1	M00003817D:D12	37484
2365	3/24/98	344	RTA00000425F.p.15.1	M00001638C:H07	31680
2366	3/24/98	345	RTA00000426F.n.23.1	M00004030C:A08	18176
2367	3/24/98	346	RTA00000522F.m.19.1	M00001655C:C07	41544
2368	3/24/98	347	RTA00000522F.a.05.1	M00001567A:C04	32611
2369	3/24/98	348	RTA00000427F.i.09.1	M00004097C:E03	65916
2370	3/24/98	349	RTA00000424F.j.09.1	M00001596B:H05	74387
2371	3/24/98	350	RTA00000424F.n.11.1	M00001582C:C04	73874
2372	3/24/98	351	RTA00000523F.l.03.1	M00004927A:A02	0
2373	3/24/98	352	RTA00000527F.e.13.1	M00003826C:F05	37588
2374	3/24/98	353	RTA00000428F.a.18.1	M00005214C:A09	0
2375	3/24/98	354	RTA00000425F.j.19.1	M00001639D:G06	77925
2376	3/24/98	355	RTA00000522F.g.12.1	M00001595A:E07	78783
2377	3/24/98	356	RTA00000523F.a.07.1	M00001693A:H06	75804
2378	3/24/98	357	RTA00000425F.e.19.1	M00001629D:B10	73409
2379	3/24/98	358	RTA00000425F.n.19.1	M00001638B:C08	78324
2380	3/24/98	359	RTA00000523F.d.21.1	M00003824B:C09	33424
2381	3/24/98	360	RTA00000523F.j.03.1	M00003860A:A08	64535

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
2382	3/24/98	361	RTA00000523F.p.08.1	M00005178A:A07	0
2383	3/24/98	362	RTA00000523F.p.09.1	M00005178A:A08	0
2384	3/24/98	363	RTA00000427F.k.07.1	M00004099A:F11	63742
2385	3/24/98	364	RTA00000523F.m.07.1	M00005136A:D10	0
2386	3/24/98	365	RTA00000527F.k.16.1	M00003982B:B06	1015
2387	3/24/98	366	RTA00000522F.a.17.1	M00001567C:B08	79032
2388	3/24/98	367	RTA00000527F.l.19.1	M00003983D:E08	36856
2389	3/24/98	368	RTA00000424F.i.11.1	M00001485D:A05	41569
2390	3/24/98	369	RTA00000524F.c.08.1	M00005217C:C01	0
2391	3/24/98	370	RTA00000424F.d.19.3	M00001448B:A07	73180
2392	3/24/98	371	RTA00000522F.j.09.2	M00001650D:F11	78522
2393	3/24/98	372	RTA00000424F.m.24.1	M00001614C:G07	77045
2394	3/24/98	373	RTA00000522F.j.19.2	M00001652B:D06	76224
2395	3/24/98	374	RTA00000528F.f.10.1	M00001596C:G05	3600
2396	3/24/98	375	RTA00000427F.p.19.2	M00004895C:G05	0
2397	3/24/98	376	RTA00000525F.b.21.1	M00004037C:D04	9486
2398	3/24/98	377	RTA00000527F.j.12.2	M00003857C:E05	37503
2399	3/24/98	378	RTA00000522F.g.11.1	M00001595A:D12	75432
2400	3/24/98	379	RTA00000522F.k.02.2	M00001652C:B09	77622
2401	3/24/98	380	RTA00000427F.e.13.1	M00003959D:A04	66080
2402	3/24/98	381	RTA00000426F.f.18.1	M00003854C:C02	63271
2403	3/24/98	382	RTA00000427F.a.12.1	M00003982C:H10	63377
2404	3/24/98	383	RTA00000424F.b.23.4	M00001530A:H05	77322
2405	3/24/98	384	RTA00000527F.p.03.1	M00004029B:A06	5940
2406	3/24/98	385	RTA00000426F.f.12.1	M00003823C:C04	19096
2407	3/24/98	386	RTA00000523F.l.16.1	M00005134C:G04	0
2408	3/24/98	387	RTA00000427F.f.02.1	M00004118D:A11	36822
2409	3/24/98	388	RTA00000526F.d.17.1	M00004235A:A12	2757
2410	3/24/98	389	RTA00000424F.i.15.1	M00001596A:A02	78043
2411	3/24/98	390	RTA00000524F.a.11.1	M00005210D:C09	0
2412	3/24/98	391	RTA00000522F.m.03.1	M00001654C:G09	79194
2413	3/24/98	392	RTA00000522F.a.20.1	M00001567C:E07	74070
2414	3/24/98	393	RTA00000424F.b.15.4	M00001539B:B10	74958
2415	3/24/98	394	RTA00000527F.g.14.1	M00003845D:B02	37532
2416	3/24/98	395	RTA00000522F.d.06.1	M00001578B:A02	74809
2417	3/24/98	396	RTA00000528F.g.05.2	M00001615C:E07	3770
2418	3/24/98	397	RTA00000427F.e.10.1	M00003974D:H07	64599
2419	3/24/98	398	RTA00000527F.c.16.1	M00003821A:H09	22908
2420	3/24/98	399	RTA00000524F.c.07.1	M00005217A:G10	0
2421	3/24/98	400	RTA00000523F.f.17.1	M00003840B:E08	63984
2422	3/24/98	401	RTA00000525F.c.16.1	M00004040A:B04	38209
2423	3/24/98	402	RTA00000527F.p.24.1	M00004031B:A06	36832
2424	3/24/98	403	RTA00000425F.n.17.1	M00001636A:H12	78304
2425	3/24/98	404	RTA00000522F.b.18.1	M00001573B:A06	3460
2426	3/24/98	405	RTA00000425F.e.07.1	M00001608C:D02	75992
2427	3/24/98	406	RTA00000523F.o.07.1	M00005176A:A05	0
2428	3/24/98	407	RTA00000523F.h.08.1	M00003851B:E01	62893
2429	3/24/98	408	RTA00000522F.o.10.1	M00001660D:E05	78798
2430	3/24/98	409	RTA00000425F.l.10.1	M00001638A:C08	26893
2431	3/24/98	410	RTA00000427F.f.16.1	M00004119D:H06	64122

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
2432	3/24/98	411	RTA00000424F.n.12.1	M00001582C:G02	41589
2433	3/24/98	412	RTA00000425F.i.11.1	M00001664B:F06	21716
2434	3/24/98	413	RTA00000425F.i.10.1	M00001664B:E08	78736
2435	3/24/98	414	RTA00000426F.m.12.1	M00004030B:D08	63740
2436	3/24/98	415	RTA00000527F.g.12.1	M00003845C:D04	37746
2437	3/24/98	416	RTA00000527F.i.12.2	M00003852B:D11	0
2438	3/24/98	417	RTA00000524F.b.10.1	M00005213C:A01	0
2439	3/24/98	418	RTA00000425F.i.18.1	M00001633A:G10	42255
2440	3/24/98	419	RTA00000428F.b.22.1	M00005231D:B09	0
2441	3/24/98	420	RTA00000424F.j.13.1	M00001594C:H03	74485
2442	3/24/98	421	RTA00000523F.i.10.1	M00003855B:B09	64876
2443	3/24/98	422	RTA00000527F.f.03.1	M00003829A:B08	17788
2444	3/24/98	423	RTA00000427F.p.06.2	M00005102C:C01	0
2445	3/24/98	424	RTA00000424F.k.10.1	M00001592D:H02	73232
2446	3/24/98	425	RTA00000522F.i.07.2	M00001649A:E10	78377
2447	3/24/98	426	RTA00000424F.k.21.1	M00001614A:A04	73197
2448	3/24/98	427	RTA00000522F.b.08.1	M00001570D:E06	26915
2449	3/24/98	428	RTA00000522F.l.08.1	M00001654A:E08	78781
2450	3/24/98	429	RTA00000525F.a.14.1	M00004033B:C02	37566
2451	3/24/98	430	RTA00000424F.g.08.1	M00001482C:F09	74928
2452	3/24/98	431	RTA00000425F.l.09.1	M00001638A:B04	75251
2453	3/24/98	432	RTA00000522F.o.20.1	M00001669C:B09	74853
2454	3/24/98	433	RTA00000527F.j.04.2	M00003856A:G04	11809
2455	3/24/98	434	RTA00000522F.c.11.1	M00001576C:H02	31064
2456	3/24/98	435	RTA00000523F.c.13.1	M00003813D:B12	40668
2457	3/24/98	436	RTA00000427F.i.21.1	M00004102C:F03	65540
2458	3/24/98	437	RTA00000427F.n.10.1	M00004960B:A08	0
2459	3/24/98	438	RTA00000522F.h.02.1	M00001595C:E09	74947
2460	3/24/98	439	RTA00000522F.g.10.1	M00001595A:C07	74294
2461	3/24/98	440	RTA00000523F.o.22.1	M00005177C:B04	0
2462	3/24/98	441	RTA00000528F.g.22.2	M00001630C:F09	920
2463	3/24/98	442	RTA00000425F.d.14.1	M00001629A:H09	13417
2464	3/24/98	443	RTA00000425F.k.16.1	M00001640A:F05	75282
2465	3/24/98	444	RTA00000525F.b.09.1	M00004035B:F05	23472
2466	3/24/98	445	RTA00000522F.j.08.2	M00001650D:D10	76613
2467	3/24/98	446	RTA00000425F.f.20.1	M00001653D:H07	74071
2468	3/24/98	447	RTA00000523F.f.19.1	M00003840B:F05	34169
2469	3/24/98	448	RTA00000425F.j.18.1	M00001639D:G12	75561
2470	3/24/98	449	RTA00000426F.m.04.1	M00004028A:B10	36865
2471	3/24/98	450	RTA00000527F.g.21.1	M00003846B:C05	36028
2472	3/24/98	451	RTA00000527F.i.15.2	M00003852C:F07	14235
2473	3/24/98	452	RTA00000525F.a.22.1	M00004033D:G06	36848
2474	3/24/98	453	RTA00000522F.p.22.1	M00001671B:F02	73322
2475	3/24/98	454	RTA00000424F.d.12.2	M00001530D:E06	74342
2476	3/24/98	455	RTA00000424F.g.24.1	M00001487C:A11	79156
2477	3/24/98	456	RTA00000427F.a.10.1	M00004038B:D01	65370
2478	3/24/98	457	RTA00000426F.h.20.1	M00003905A:H11	23187
2479	3/24/98	458	RTA00000424F.d.12.3	M00001530D:E06	74342
2480	3/24/98	459	RTA00000425F.c.03.1	M00001585D:B12	74643
2481	3/24/98	460	RTA00000523F.f.16.1	M00003840B:E07	26522

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
2482	3/24/98	461	RTA00000427F.f.15.1	M00004119D:A07	66734
2483	3/24/98	462	RTA00000427F.p.13.2	M00004695B:E04	0
2484	3/24/98	463	RTA00000523F.p.16.1	M00005179D:B03	0
2485	3/24/98	464	RTA00000522F.p.18.1	M00001671A:H06	76376
2486	3/24/98	465	RTA00000528F.d.04.1	M00001570D:E07	2395
2487	3/24/98	466	RTA00000427F.d.06.1	M00003980B:C06	33446
2488	3/24/98	467	RTA00000528F.h.02.2	M00001632C:D08	1701
2489	3/24/98	468	RTA00000524F.a.18.1	M00005211A:E09	0
2490	3/24/98	469	RTA00000522F.e.20.1	M00001590B:H10	26770
2491	3/24/98	470	RTA00000427F.p.24.2	M00004897D:F03	0
2492	3/24/98	471	RTA00000528F.c.11.1	M00001486D:D12	1701
2493	3/24/98	472	RTA00000522F.g.18.1	M00001595B:H11	73226
2494	3/24/98	473	RTA00000523F.o.21.1	M00005177C:A01	0
2495	3/24/98	474	RTA00000522F.h.05.1	M00001595C:H11	73358
2496	3/24/98	475	RTA00000427F.i.06.1	M00004097B:D03	41450
2497	3/24/98	476	RTA00000425F.n.16.1	M00001636A:C02	18265
2498	3/24/98	477	RTA00000527F.l.21.1	M00003983D:H02	36439
2499	3/24/98	478	RTA00000527F.p.09.1	M00004029C:F05	7694
2500	3/24/98	479	RTA00000527F.l.23.1	M00003984A:B06	36018
2501	3/24/98	480	RTA00000424F.d.17.3	M00001455A:E11	73958
2502	3/24/98	481	RTA00000523F.j.02.1	M00003857A:H10	62853
2503	2/24/98	1132	RTA00000119A.c.12.1	M00001453A:D08	4882
2504	2/24/98	6	RTA00000119A.j.15.1	M00001460A:E11	79623
2505	2/24/98	1041	RTA00000403F.b.05.1	M00001455B:E07	74300
2506	2/24/98	994	RTA00000408F.b.04.2	M00001455A:F04	39933
2507	2/24/98	401	RTA00000132A.c.11.1	M00001454A:G03	87278
2508	2/24/98	535	RTA00000119A.g.7.1	M00001454A:F11	83580
2509	2/24/98	867	RTA00000339F.l.21.1	M00001455D:D11	9781
2510	2/24/98	62	RTA00000339F.n.10.1	M00001453B:F08	13719
2511	2/24/98	380	RTA00000403F.b.19.1	M00001456B:A06	22327
2512	1/28/98	288	RTA00000181AR.i.06.3	M00001452A:C07	19119
2512	2/24/98	198	RTA00000339R.l.14.1	M00001452A:C07	19119
2513	1/28/98	288	RTA00000181AR.i.06.3	M00001452A:C07	19119
2513	2/24/98	198	RTA00000339R.l.14.1	M00001452A:C07	19119
2514	2/24/98	264	RTA00000345F.j.08.1	M00001451B:A04	16731
2515	2/24/98	1125	RTA00000118A.n.5.1	M00001451A:C10	0
2516	2/24/98	229	RTA00000345F.i.09.1	M00001450A:D08	27250
2517	2/24/98	670	RTA00000131A.i.6.1	M00001450A:B08	0
2518	2/24/98	892	RTA00000339F.m.17.1	M00001453B:H12	20854
2519	2/24/98	1123	RTA00000408F.c.23.1	M00001458C:D10	42261
2520	2/24/98	680	RTA00000345F.e.11.1	M00001391C:C04	4392
2521	2/24/98	644	RTA00000119A.j.9.1	M00001460A:B12	82060
2522	2/24/98	972	RTA00000408F.d.15.1	M00001459B:C11	78467
2523	2/24/98	1081	RTA00000403F.d.02.1	M00001458D:D01	39224
2524	2/24/98	231	RTA00000408F.d.06.1	M00001458D:C11	78997
2525	2/24/98	663	RTA00000403F.b.12.1	M00001455D:A06	78775
2526	2/24/98	856	RTA00000408F.d.02.1	M00001458D:A01	79169
2527	2/24/98	743	RTA00000345F.i.08.1	M00001449D:G10	0
2528	2/24/98	1162	RTA00000408F.c.10.1	M00001458A:A11	18247
2529	2/24/98	841	RTA00000119A.i.8.1	M00001457A:G12	82593

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
2530	2/24/98	677	RTA00000119A.h.24.1	M00001457A:C05	82266
2531	2/24/98	750	RTA00000403F.c.05.1	M00001456C:C11	74935
2532	2/24/98	751	RTA00000422F.i.02.1	M00001456C:B12	76436
2533	2/24/98	920	RTA00000403F.b.24.1	M00001456B:G01	78838
2534	2/24/98	1251	RTA00000408F.d.03.1	M00001458D:A02	22768
2535	2/24/98	450	RTA00000118A.a.23.1	M00001395A:H02	3500
2536	2/24/98	85	RTA00000339F.k.22.1	M00001427C:D01	5556
2537	2/24/98	684	RTA00000339F.k.20.1	M00001426D:D12	6662
2538	2/24/98	129	RTA00000118A.d.24.1	M00001416A:H02	81488
2539	2/24/98	397	RTA00000118A.d.17.1	M00001416A:D09	81921
2540	2/24/98	158	RTA00000348R.j.16.1	M00001410A:D07	7005
2541	2/24/98	1025	RTA00000118A.j.24.1	M00001450A:B03	18
2542	2/24/98	1005	RTA00000339F.e.17.1	M00001397D:G08	7568
2543	2/24/98	1040	RTA00000348R.o.12.1	M00001433C:F10	2263
2544	2/24/98	746	RTA00000345F.e.02.1	M00001395A:E03	0
2545	2/24/98	517	RTA00000118A.a.2.1	M00001395A:A12	38067
2546	2/24/98	1065	RTA00000195R.a.06.1	M00001394A:E04	35265
2546	1/28/98	595	RTA00000195R.a.06.1	M00001394A:E04	35265
2547	1/28/98	595	RTA00000195R.a.06.1	M00001394A:E04	35265
2547	2/24/98	1065	RTA00000195R.a.06.1	M00001394A:E04	35265
2548	1/28/98	675	RTA00000179AR.b.21.3	M00001392C:D05	4366
2548	2/24/98	1264	RTA00000345F.e.13.1	M00001392C:D05	4366
2549	1/28/98	562	RTA00000196F.j.12.1	M00001396A:H03	19294
2550	2/24/98	1042	RTA00000339F.g.10.1	M00001400C:D02	6327
2551	2/24/98	706	RTA00000403F.a.09.1	M00001448B:H05	77820
2552	2/24/98	823	RTA00000119A.k.1.1	M00001460A:H11	81282
2553	2/24/98	703	RTA00000339F.n.05.1	M00001449D:B01	39648
2554	2/24/98	787	RTA00000345F.i.24.1	M00001449C:C05	0
2555	2/24/98	68	RTA00000339F.n.03.1	M00001449B:B03	0
2556	2/24/98	440	RTA00000403F.a.18.1	M00001448D:F12	75726
2557	2/24/98	815	RTA00000403F.a.17.1	M00001448D:E12	13686
2558	2/24/98	275	RTA00000353R.j.24.1	M00001428B:D01	23089
2559	2/24/98	902	RTA00000403F.a.10.1	M00001448C:E11	73952
2560	2/24/98	1214	RTA00000339F.j.07.1	M00001428D:B10	5673
2561	2/24/98	378	RTA00000403F.a.07.1	M00001448B:F09	73559
2562	2/24/98	473	RTA00000403F.a.05.1	M00001448A:E11	18808
2563	2/24/98	128	RTA00000403F.a.04.1	M00001448A:B12	23529
2564	2/24/98	227	RTA00000347F.c.06.1	M00001444D:C01	18846
2565	2/24/98	35	RTA00000339F.i.13.1	M00001434A:B10	5970
2566	2/24/98	442	RTA00000347F.b.02.1	M00001450A:A02	39304
2567	2/24/98	288	RTA00000403F.a.11.1	M00001448C:F10	73109
2568	2/24/98	853	RTA00000408F.j.13.2	M00001485B:D10	42275
2569	2/24/98	249	RTA00000119A.j.10.1	M00001460A:C10	79646
2570	2/24/98	634	RTA00000418F.c.04.1	M00001487B:A11	41587
2571	2/24/98	110	RTA00000408F.k.14.1	M00001486B:E12	73856
2572	2/24/98	894	RTA00000408F.k.12.1	M00001486B:D07	77246
2573	2/24/98	395	RTA00000408F.j.19.2	M00001485C:C08	73752
2574	2/24/98	509	RTA00000349R.g.10.1	M00001495B:B08	5777
2575	2/24/98	426	RTA00000408F.j.15.2	M00001485B:F05	74759
2576	2/24/98	101	RTA00000121A.m.2.1	M00001507A:A11	81064

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
2577	2/24/98	330	RTA00000403F.i.04.1	M00001485B:D09	8930
2578	2/24/98	647	RTA00000418F.b.23.1	M00001485A:C05	28767
2579	2/24/98	569	RTA00000403F.h.18.1	M00001484C:A04	39241
2580	2/24/98	236	RTA00000403F.h.12.1	M00001483C:G09	15205
2581	2/24/98	707	RTA00000403F.h.11.1	M00001483B:D04	39219
2582	2/24/98	869	RTA00000403F.h.07.1	M00001482D:H11	26856
2583	2/24/98	1101	RTA00000408F.j.17.2	M00001485B:H03	78935
2584	2/24/98	344	RTA00000403F.m.15.2	M00001575D:D12	26901
2585	2/24/98	768	RTA00000121A.k.5.1	M00001507A:E04	17530
2586	2/24/98	1174	RTA00000121A.k.22.1	M00001507A:C05	79523
2587	2/24/98	184	RTA00000133A.j.13.1	M00001507A:B02	16846
2588	2/24/98	1230	RTA00000399F.j.14.1	M00001578C:F05	16942
2589	2/24/98	304	RTA00000403F.n.18.2	M00001577D:H06	8811
2590	2/24/98	938	RTA00000403F.i.23.1	M00001487B:E10	11364
2591	2/24/98	1131	RTA00000418F.e.20.1	M00001576C:G05	73741
2592	2/24/98	651	RTA00000403F.g.11.1	M00001481A:H08	24238
2593	2/24/98	312	RTA00000399F.i.08.1	M00001575D:B10	38927
2594	2/24/98	800	RTA00000403F.m.12.1	M00001575D:A02	16933
2595	2/24/98	1017	RTA00000418F.e.03.1	M00001573B:G08	73442
2596	2/24/98	269	RTA00000422F.e.08.1	M00001573A:E01	39020
2597	2/24/98	1247	RTA00000408F.o.13.1	M00001572A:B05	74895
2598	2/24/98	847	RTA00000403F.l.11.1	M00001571D:F05	25073
2599	2/24/98	910	RTA00000418F.f.03.1	M00001577B:F10	78911
2600	2/24/98	244	RTA00000120A.g.23.1	M00001465A:E10	81189
2601	2/24/98	1189	RTA00000339F.o.18.1	M00001469B:B01	6641
2602	2/24/98	1266	RTA00000121A.a.2.1	M00001468A:H10	81843
2603	2/24/98	414	RTA00000120A.p.18.1	M00001468A:C05	6478
2604	2/24/98	96	RTA00000120A.n.19.3	M00001467A:H07	80004
2605	2/24/98	1231	RTA00000120A.m.13.3	M00001467A:C10	80608
2606	2/24/98	134	RTA00000408F.i.08.2	M00001482A:H05	75811
2607	2/24/98	410	RTA00000120A.h.5.1	M00001465A:G06	80344
2608	2/24/98	403	RTA00000403F.d.22.1	M00001473A:A07	10692
2609	2/24/98	183	RTA00000120A.g.18.1	M00001465A:C12	81255
2610	2/24/98	810	RTA00000120A.h.9.1	M00001465A:B12	80736
2611	2/24/98	71	RTA00000120A.d.24.1	M00001464A:E10	5085
2612	2/24/98	490	RTA00000120A.d.15.1	M00001464A:B02	80533
2613	2/24/98	736	RTA00000120A.c.7.1	M00001462A:D03	80985
2614	2/24/98	724	RTA00000119A.m.17.1	M00001461A:F05	79536
2615	2/24/98	1063	RTA00000132A.n.7.1	M00001466A:F08	0
2616	2/24/98	74	RTA00000408F.e.22.2	M00001476B:F08	26930
2617	1/28/98	656	RTA00000178AR.h.22.3	M00001376B:A08	19230
2617	1/28/98	657	RTA00000178AR.h.22.2	M00001376B:A08	19230
2617	2/24/98	1137	RTA00000345F.d.03.1	M00001376B:A08	19230
2618	2/24/98	1012	RTA00000403F.g.06.1	M00001480C:A05	10505
2619	2/24/98	419	RTA00000408F.h.08.1	M00001480A:D03	74575
2620	2/24/98	871	RTA00000403F.f.23.1	M00001479C:E01	39223
2621	2/24/98	638	RTA00000418F.b.09.1	M00001478B:H08	19700
2622	2/24/98	770	RTA00000421F.f.05.1	M00001477B:E02	5266
2623	2/24/98	549	RTA00000121A.h.18.1	M00001471A:B04	16376
2624	2/24/98	660	RTA00000408F.e.24.2	M00001476C:C11	75002

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
2625	2/24/98	144	RTA00000349R.f.15.1	M00001472A:D08	75097
2626	2/24/98	774	RTA00000403F.e.24.1	M00001476B:D10	16432
2627	2/24/98	268	RTA00000403F.e.23.1	M00001476A:D11	9626
2628	2/24/98	715	RTA00000418F.b.01.1	M00001475C:G11	76040
2629	2/24/98	1073	RTA00000418F.a.10.1	M00001475B:C04	15245
2630	2/24/98	100	RTA00000339F.o.23.1	M00001473C:D09	7801
2631	2/24/98	756	RTA00000403F.g.13.1	M00001481B:D09	38718
2632	2/24/98	915	RTA00000408F.f.14.2	M00001476D:F03	73024
2633	1/28/98	389	RTA00000181AR.k.2.2	M00001453C:A11	0
2633	1/28/98	286	RTA00000181AR.k.2.3	M00001453C:A11	0
2634	1/28/98	565	RTA00000191AF.c.10.1	M00003989B:F11	40422
2635	1/28/98	449	RTA00000181AF.m.22.3	M00001455D:F09	9283
2635	1/28/98	450	RTA00000181AF.m.21.3	M00001455D:F09	9283
2636	1/28/98	449	RTA00000181AF.m.22.3	M00001455D:F09	9283
2636	1/28/98	450	RTA00000181AF.m.21.3	M00001455D:F09	9283
2637	1/28/98	449	RTA00000181AF.m.22.3	M00001455D:F09	9283
2637	1/28/98	450	RTA00000181AF.m.21.3	M00001455D:F09	9283
2638	1/28/98	449	RTA00000181AF.m.22.3	M00001455D:F09	9283
2638	1/28/98	450	RTA00000181AF.m.21.3	M00001455D:F09	9283
2639	1/28/98	390	RTA00000197AR.f.07.1	M00001457C:C11	19261
2639	1/28/98	184	RTA00000197AF.f.7.1	M00001457C:C11	19261
2640	1/28/98	598	RTA00000197F.e.10.1	M00001454B:D08	13154
2641	1/28/98	184	RTA00000197AF.f.7.1	M00001457C:C11	19261
2641	1/28/98	390	RTA00000197AR.f.07.1	M00001457C:C11	19261
2642	1/28/98	286	RTA00000181AR.k.2.3	M00001453C:A11	0
2642	1/28/98	389	RTA00000181AR.k.2.2	M00001453C:A11	0
2643	1/28/98	667	RTA00000197AF.d.16.1	M00001452A:E07	23505
2644	1/28/98	679	RTA00000197AF.d.11.1	M00001451C:E01	27260
2645	1/28/98	664	RTA00000195R.a.23.1	M00001449C:H12	86432
2646	1/28/98	594	RTA00000181AR.e.04.3	M00001448A:G09	11825
2647	1/28/98	405	RTA00000197AF.b.24.1	M00001446C:D09	23171
2648	1/28/98	572	RTA00000181AF.l.16.2	M00001454D:E05	13532
2649	1/28/98	590	RTA00000190AF.d.2.1	M00003906B:F12	2444
2650	1/28/98	675	RTA00000179AR.b.21.3	M00001392C:D05	4366
2650	2/24/98	1264	RTA00000345F.e.13.1	M00001392C:D05	4366
2651	1/28/98	486	RTA00000190AR.p.22.2	M00003979A:E11	16368
2652	1/28/98	701	RTA00000199AF.o.10.1	M00003974C:E04	0
2653	1/28/98	704	RTA00000190AF.o.12.1	M00003972D:C09	3438
2654	1/28/98	469	RTA00000190AF.n.2.1	M00003963A:E03	5650
2655	1/28/98	612	RTA00000197AR.e.22.1	M00001456A:H02	78758
2656	1/28/98	640	RTA00000190AF.f.5.1	M00003909A:H04	5015
2657	1/28/98	539	RTA00000197AR.b.13.1	M00001445B:E04	9560
2658	1/28/98	431	RTA00000199AF.k.15.1	M00003905C:G10	8275
2659	1/28/98	747	RTA00000190AF.c.6.1	M00003904D:D10	4780
2660	1/28/98	584	RTA00000190AR.c.03.1	M00003904C:A08	0
2660	2/24/98	1069	RTA00000346F.k.05.1	M00003904C:A08	0
2661	1/28/98	584	RTA00000190AR.c.03.1	M00003904C:A08	0
2661	2/24/98	1069	RTA00000346F.k.05.1	M00003904C:A08	0
2662	1/28/98	577	RTA00000190AF.a.24.2	M00003901B:A05	0
2663	1/28/98	639	RTA00000199AF.j.1.1	M00003881C:G09	6006

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
2664	1/28/98	649	RTA00000190AR.l.19.2	M00003946A:H10	88204
2665	1/28/98	488	RTA00000179AR.l.22.4	M00001405B:E09	4314
2665	1/28/98	481	RTA00000179AR.l.22.2	M00001405B:E09	4314
2666	1/28/98	721	RTA00000180AF.c.4.1	M00001417B:C04	5415
2667	1/28/98	744	RTA00000196F.m.4.1	M00001413A:F03	7958
2668	1/28/98	569	RTA00000196AF.l.23.1	M00001412A:E04	12052
2669	1/28/98	707	RTA00000179AF.p.15.1	M00001411D:F05	5622
2670	1/28/98	599	RTA00000179AF.o.5.1	M00001408D:D04	6172
2671	1/28/98	420	RTA00000181AF.c.11.1	M00001445D:A06	4769
2672	1/28/98	500	RTA00000179AR.m.07.5	M00001405D:D11	0
2673	1/28/98	609	RTA00000196AF.n.05.1	M00001418B:F07	12531
2673	2/24/98	1120	RTA00000353R.l.23.1	M00001418B:F07	12531
2674	1/28/98	481	RTA00000179AR.l.22.2	M00001405B:E09	4314
2674	1/28/98	488	RTA00000179AR.l.22.4	M00001405B:E09	4314
2675	1/28/98	481	RTA00000179AR.l.22.2	M00001405B:E09	4314
2675	1/28/98	488	RTA00000179AR.l.22.4	M00001405B:E09	4314
2676	1/28/98	481	RTA00000179AR.l.22.2	M00001405B:E09	4314
2676	1/28/98	488	RTA00000179AR.l.22.4	M00001405B:E09	4314
2677	1/28/98	636	RTA00000196F.k.20.1	M00001402B:F12	6324
2678	1/28/98	691	RTA00000195F.a.10.1	M00001401C:H03	6803
2679	2/24/98	161	RTA00000418F.n.22.1	M00001659D:B05	79062
2680	1/28/98	611	RTA00000196F.l.13.2	M00001408A:H04	0
2681	1/28/98	535	RTA00000196AF.n.19.1	M00001423D:D12	6881
2682	1/28/98	413	RTA00000200F.a.12.1	M00004031D:B05	16751
2683	1/28/98	580	RTA00000197F.a.12.1	M00001438B:B09	7895
2684	1/28/98	681	RTA00000180AF.l.04.2	M00001432D:F05	11159
2685	1/28/98	568	RTA00000196AF.p.01.2	M00001430A:A02	87143
2686	1/28/98	736	RTA00000196AF.o.13.1	M00001428B:A09	0
2687	1/28/98	438	RTA00000180AR.g.03.4	M00001425A:C11	9024
2687	1/28/98	95	RTA00000180AF.g.3.1	M00001425A:C11	9024
2688	1/28/98	514	RTA00000196AF.n.02.1	M00001417D:A04	39260
2689	1/28/98	741	RTA00000196AF.n.22.1	M00001424B:H04	9572
2690	1/28/98	609	RTA00000196AF.n.05.1	M00001418B:F07	12531
2690	2/24/98	1120	RTA00000353R.l.23.1	M00001418B:F07	12531
2691	1/28/98	462	RTA00000196AF.n.17.1	M00001423D:A09	12477
2692	1/28/98	477	RTA00000180AR.e.22.2	M00001423A:G05	7714
2693	1/28/98	445	RTA00000196AF.n.13.1	M00001422C:F12	8396
2694	1/28/98	696	RTA00000180AR.d.16.3	M00001419D:C10	11393
2694	2/24/98	1184	RTA00000345F.h.08.1	M00001419D:C10	11393
2695	1/28/98	696	RTA00000180AR.d.16.3	M00001419D:C10	11393
2695	2/24/98	1184	RTA00000345F.h.08.1	M00001419D:C10	11393
2696	1/28/98	541	RTA00000197AR.b.16.1	M00001445C:A08	0
2697	1/28/98	95	RTA00000180AF.g.3.1	M00001425A:C11	9024
2697	1/28/98	438	RTA00000180AR.g.03.4	M00001425A:C11	9024
2698	1/28/98	536	RTA00000193AR.a.2.3	M00004216D:D03	0
2699	1/28/98	588	RTA00000191AF.b.4.1	M00003983C:F03	14936
2700	1/28/98	401	RTA00000195F.e.04.1	M00004465B:D04	6731
2701	2/24/98	91	RTA00000355R.e.15.1	M00004316A:G09	22639
2701	1/28/98	410	RTA00000201F.a.20.1	M00004316A:G09	22639
2702	1/28/98	410	RTA00000201F.a.20.1	M00004316A:G09	22639

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
2702	2/24/98	91	RTA00000355R.e.15.1	M00004316A:G09	22639
2703	1/28/98	716	RTA00000200F.p.05.1	M00004285C:A08	3984
2704	2/24/98	434	RTA00000348R.b.16.1	M00001347B:H04	6510
2705	1/28/98	528	RTA00000200F.n.09.2	M00004249D:B08	12391
2706	2/24/98	575	RTA00000345F.a.18.1	M00001351C:B06	5517
2707	1/28/98	658	RTA00000193AF.a.1.1	M00004216D:C03	16501
2708	1/28/98	472	RTA00000192AF.p.17.1	M00004214C:H05	11451
2709	1/28/98	478	RTA00000192AR.o.24.2	M00004210B:B05	7191
2710	1/28/98	753	RTA00000192AF.o.17.1	M00004208D:B10	5275
2711	1/28/98	563	RTA00000192AR.o.16.2	M00004208B:F05	9061
2712	1/28/98	730	RTA00000192AF.o.11.1	M00004205D:F06	0
2713	1/28/98	624	RTA00000200F.o.15.1	M00004275A:B03	7866
2714	2/24/98	169	RTA00000347F.a.17.1	M00001366D:C06	16723
2715	1/28/98	656	RTA00000178AR.h.22.3	M00001376B:A08	19230
2715	1/28/98	657	RTA00000178AR.h.22.2	M00001376B:A08	19230
2715	2/24/98	1137	RTA00000345F.d.03.1	M00001376B:A08	19230
2716	1/28/98	657	RTA00000178AR.h.22.2	M00001376B:A08	19230
2716	1/28/98	656	RTA00000178AR.h.22.3	M00001376B:A08	19230
2716	2/24/98	1137	RTA00000345F.d.03.1	M00001376B:A08	19230
2717	1/28/98	522	RTA00000178AR.h.17.2	M00001376A:C05	23824
2717	2/24/98	1095	RTA00000345F.c.12.1	M00001376A:C05	23824
2718	1/28/98	522	RTA00000178AR.h.17.2	M00001376A:C05	23824
2718	2/24/98	1095	RTA00000345F.c.12.1	M00001376A:C05	23824
2719	2/24/98	1155	RTA00000353R.h.04.1	M00001375B:C06	17123
2720	1/28/98	614	RTA00000201F.f.03.1	M00004493B:D09	22633
2721	2/24/98	16	RTA00000399F.a.02.1	M00001366D:C12	0
2722	1/28/98	436	RTA00000200AF.k.11.1	M00004197C:F03	9796
2722	1/28/98	501	RTA00000200R.k.11.1	M00004197C:F03	9796
2723	2/24/98	1140	RTA00000339F.c.05.1	M00001365A:H10	3908
2724	2/24/98	322	RTA00000339F.c.24.1	M00001364B:B06	5516
2725	2/24/98	888	RTA00000339R.c.04.1	M00001362D:H01	1805
2726	1/28/98	33	RTA00000178AR.a.20.1	M00001362C:H11	945
2726	2/24/98	979	RTA00000345F.b.17.1	M00001362C:H11	945
2727	1/28/98	33	RTA00000178AR.a.20.1	M00001362C:H11	945
2727	2/24/98	979	RTA00000345F.b.17.1	M00001362C:H11	945
2728	2/24/98	1173	RTA00000339R.b.07.1	M00001360A:G10	6826
2729	2/24/98	973	RTA00000339F.b.22.1	M00001373D:B03	6867
2730	1/28/98	581	RTA00000191AF.p.3.2	M00004104B:F11	17
2731	1/28/98	637	RTA00000200AF.g.15.1	M00004135B:G01	22898
2731	1/28/98	476	RTA00000200R.g.15.1	M00004135B:G01	22898
2732	1/28/98	637	RTA00000200AF.g.15.1	M00004135B:G01	22898
2732	1/28/98	476	RTA00000200R.g.15.1	M00004135B:G01	22898
2733	1/28/98	474	RTA00000192AR.d.1.3	M00004130D:H01	14507
2734	1/28/98	735	RTA00000192AF.b.11.1	M00004117A:G01	40014
2735	1/28/98	726	RTA00000200R.f.10.1	M00004111D:B07	4
2736	1/28/98	752	RTA00000192AF.o.7.1	M00004204D:C03	5275
2737	1/28/98	516	RTA00000200AF.e.23.1	M00004107B:A06	14686
2738	1/28/98	685	RTA00000200F.i.9.1	M00004159C:F09	36756
2738	2/24/98	704	RTA00000355R.a.12.1	M00004159C:F09	36756
2739	1/28/98	417	RTA00000200R.d.16.1	M00004085A:B02	39875

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
2740	1/28/98	454	RTA00000200R.d.04.1	M00004078A:A06	5506
2741	1/28/98	551	RTA00000200AR.c.24.1	M00004076D:D04	15972
2742	1/28/98	524	RTA00000191AF.j.24.1	M00004076B:G03	0
2743	2/24/98	1166	RTA00000347F.h.01.1	M00004040A:G12	12043
2743	1/28/98	684	RTA00000200AR.b.11.1	M00004040A:G12	12043
2744	2/24/98	1166	RTA00000347F.h.01.1	M00004040A:G12	12043
2744	1/28/98	684	RTA00000200AR.b.11.1	M00004040A:G12	12043
2745	1/28/98	415	RTA00000200AF.f.09.1	M00004111C:E11	12863
2746	1/28/98	448	RTA00000200AF.j.9.1	M00004177C:A01	8608
2747	2/24/98	446	RTA00000133A.m.19.2	M00001512A:G05	80167
2748	1/28/98	436	RTA00000200AF.k.11.1	M00004197C:F03	9796
2748	1/28/98	501	RTA00000200R.k.11.1	M00004197C:F03	9796
2749	1/28/98	436	RTA00000200AF.k.11.1	M00004197C:F03	9796
2749	1/28/98	501	RTA00000200R.k.11.1	M00004197C:F03	9796
2750	1/28/98	436	RTA00000200AF.k.11.1	M00004197C:F03	9796
2750	1/28/98	501	RTA00000200R.k.11.1	M00004197C:F03	9796
2751	1/28/98	610	RTA00000200AF.k.2.1	M00004188D:G08	35924
2752	1/28/98	494	RTA00000200AF.k.1.1	M00004188C:A09	40049
2752	1/28/98	194	RTA00000200R.k.01.1	M00004188C:A09	40049
2753	1/28/98	574	RTA00000192AF.f.3.1	M00004146C:C11	5257
2754	1/28/98	604	RTA00000200AF.j.15.1	M00004185D:E04	5849
2755	1/28/98	579	RTA00000200F.i.7.1	M00004157D:B03	22322
2756	1/28/98	634	RTA00000192AF.j.6.1	M00004172C:D08	11494
2757	1/28/98	421	RTA00000200AF.i.21.1	M00004167D:A07	5316
2758	1/28/98	543	RTA00000200AF.i.19.1	M00004167A:H03	14722
2759	1/28/98	483	RTA00000192AF.h.19.1	M00004162C:A07	4642
2760	2/24/98	704	RTA00000355R.a.12.1	M00004159C:F09	36756
2760	1/28/98	685	RTA00000200F.i.9.1	M00004159C:F09	36756
2761	1/28/98	607	RTA00000200AF.k.12.1	M00004198B:D02	7359
2762	1/28/98	494	RTA00000200AF.k.1.1	M00004188C:A09	40049
2762	1/28/98	194	RTA00000200R.k.01.1	M00004188C:A09	40049
2763	2/24/98	554	RTA00000409F.i.03.1	M00001610A:E09	75968
2764	2/24/98	1228	RTA00000404F.h.10.1	M00001618A:A03	37148
2765	2/24/98	332	RTA00000409F.i.24.1	M00001611B:A09	76967
2766	2/24/98	1023	RTA00000404F.f.12.1	M00001611B:A05	39209
2767	2/24/98	572	RTA00000422F.l.03.1	M00001610D:D05	39147
2768	2/24/98	497	RTA00000350R.f.21.1	M00001610C:E07	22110
2769	2/24/98	557	RTA00000409F.j.05.1	M00001611C:C12	74128
2770	2/24/98	223	RTA00000404F.e.22.1	M00001610A:H05	11344
2771	2/24/98	165	RTA00000409F.j.07.1	M00001611C:H11	75190
2772	2/24/98	959	RTA00000340F.g.20.1	M00001609D:G10	4089
2773	2/24/98	737	RTA00000404F.e.15.1	M00001609B:C09	39101
2774	2/24/98	974	RTA00000340F.h.07.1	M00001608D:D11	19254
2775	2/24/98	857	RTA00000404F.e.09.1	M00001608B:A09	39121
2776	1/28/98	340	RTA00000185AF.n.8.1	M00001608B:A03	0
2776	2/24/98	75	RTA00000350R.i.22.1	M00001608B:A03	0
2777	1/28/98	340	RTA00000185AF.n.8.1	M00001608B:A03	0
2777	2/24/98	75	RTA00000350R.i.22.1	M00001608B:A03	0
2778	2/24/98	546	RTA00000409F.i.09.1	M00001610B:C07	75279
2779	2/24/98	374	RTA00000422F.m.04.1	M00001615B:A09	38702

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
2780	2/24/98	505	RTA00000121A.o.3.1	M00001511A:A02	81437
2781	2/24/98	453	RTA00000130A.h.13.1	M00001617A:A01	80790
2782	2/24/98	163	RTA00000422F.l.23.1	M00001616D:C11	4240
2783	2/24/98	889	RTA00000346F.b.16.1	M00001615C:G05	16485
2784	2/24/98	203	RTA00000404F.g.21.1	M00001615C:A11	37947
2785	2/24/98	32	RTA00000409F.j.02.1	M00001611B:E06	76417
2786	2/24/98	872	RTA00000409F.l.20.1	M00001615B:G01	74394
2787	2/24/98	978	RTA00000130A.e.20.1	M00001606A:H09	79502
2788	2/24/98	45	RTA00000409F.l.12.1	M00001615A:D06	26755
2789	2/24/98	182	RTA00000404F.g.14.1	M00001614D:B08	8858
2790	2/24/98	912	RTA00000404F.g.13.1	M00001614C:E06	9436
2791	2/24/98	1191	RTA00000340F.i.05.1	M00001614B:E08	0
2792	2/24/98	192	RTA00000421F.k.15.1	M00001613D:B03	2222
2793	2/24/98	360	RTA00000409F.j.19.1	M00001613A:F03	73792
2794	2/24/98	57	RTA00000409F.l.21.1	M00001615B:G07	73143
2795	2/24/98	354	RTA00000404F.c.03.2	M00001592C:F11	39198
2796	2/24/98	791	RTA00000399F.n.15.1	M00001594D:C03	3213
2797	2/24/98	921	RTA00000422F.j.02.1	M00001594D:B08	10368
2798	2/24/98	1114	RTA00000340F.f.22.1	M00001594B:F12	1720
2799	2/24/98	966	RTA00000422F.k.15.1	M00001594A:G09	19253
2800	2/24/98	46	RTA00000404F.c.20.1	M00001594A:D08	39088
2801	2/24/98	955	RTA00000404F.e.06.1	M00001607D:F06	39315
2802	2/24/98	1103	RTA00000346F.a.16.1	M00001593A:B07	12082
2803	2/24/98	540	RTA00000418F.i.18.1	M00001595C:B05	78024
2804	2/24/98	1245	RTA00000422F.k.22.1	M00001592C:E05	4098
2805	2/24/98	693	RTA00000404F.b.19.1	M00001592B:A04	39281
2806	2/24/98	1013	RTA00000404F.b.18.1	M00001592A:H05	13669
2807	2/24/98	989	RTA00000418F.i.12.1	M00001592A:E02	78971
2808	2/24/98	404	RTA00000404F.b.11.1	M00001591D:F06	39079
2809	2/24/98	786	RTA00000404F.b.09.1	M00001591D:C07	39166
2810	2/24/98	1147	RTA00000404F.c.18.1	M00001594A:C01	38982
2811	2/24/98	686	RTA00000129A.k.21.1	M00001601A:E12	82067
2812	2/24/98	1011	RTA00000400F.c.04.1	M00001618A:F08	6445
2813	2/24/98	702	RTA00000130A.d.5.1	M00001605A:H03	82051
2814	2/24/98	425	RTA00000130A.b.5.1	M00001605A:E09	79579
2815	2/24/98	458	RTA00000130A.a.19.1	M00001605A:A06	0
2816	2/24/98	51	RTA00000129A.n.21.1	M00001604A:C11	79381
2817	2/24/98	804	RTA00000129A.n.24.1	M00001604A:C07	81409
2818	2/24/98	317	RTA00000195AF.b.21.1	M00001595B:A09	39055
2818	1/28/98	602	RTA00000195AF.b.21.1	M00001595B:A09	39055
2819	2/24/98	864	RTA00000129A.n.17.1	M00001604A:A09	79811
2820	2/24/98	317	RTA00000195AF.b.21.1	M00001595B:A09	39055
2820	1/28/98	602	RTA00000195AF.b.21.1	M00001595B:A09	39055
2821	2/24/98	875	RTA00000129A.k.22.1	M00001601A:E02	79639
2822	2/24/98	406	RTA00000129A.k.12.1	M00001601A:A06	79322
2823	2/24/98	179	RTA00000418F.i.19.1	M00001596D:E03	79180
2824	2/24/98	759	RTA00000399F.o.06.1	M00001595D:G03	13574
2825	2/24/98	306	RTA00000404F.d.13.1	M00001595D:A04	39036
2826	2/24/98	1055	RTA00000346F.a.04.1	M00001607B:C05	5382
2827	2/24/98	350	RTA00000129A.p.3.1	M00001604A:B08	32644

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
2828	2/24/98	721	RTA00000422F.k.14.1	M00001649D:A08	0
2829	2/24/98	391	RTA00000130A.h.16.1	M00001617A:A08	80761
2830	2/24/98	962	RTA00000404F.p.05.2	M00001652D:E09	1896
2831	2/24/98	65	RTA00000404F.p.04.2	M00001652D:E05	39069
2832	2/24/98	1108	RTA00000346F.c.16.1	M00001652B:G10	9579
2833	2/24/98	1200	RTA00000422F.k.17.1	M00001652A:A01	38955
2834	2/24/98	1218	RTA00000418F.m.18.1	M00001653B:G10	76479
2835	2/24/98	171	RTA00000404F.n.20.1	M00001650A:C11	26865
2836	2/24/98	180	RTA00000400F.j.19.1	M00001653C:D10	4086
2837	2/24/98	556	RTA00000400F.i.11.1	M00001649C:H10	2587
2838	2/24/98	848	RTA00000404F.n.18.2	M00001649C:E11	37169
2839	2/24/98	29	RTA00000404F.n.16.2	M00001649C:D05	39095
2840	2/24/98	146	RTA00000404F.n.11.2	M00001649A:E11	38001
2841	2/24/98	700	RTA00000350R.m.14.1	M00001644C:B07	39171
2842	2/24/98	699	RTA00000340F.l.05.1	M00001644B:D06	38935
2843	2/24/98	479	RTA00000418F.m.10.1	M00001651A:H11	79110
2844	2/24/98	1169	RTA00000405F.b.08.1	M00001656B:E01	39182
2845	2/24/98	855	RTA00000423F.a.01.1	M00001659C:F10	39103
2846	2/24/98	363	RTA00000405F.c.11.1	M00001659A:D12	39068
2847	2/24/98	807	RTA00000418F.n.11.1	M00001658D:G12	78977
2848	2/24/98	795	RTA00000418F.n.07.1	M00001658B:A07	76316
2849	2/24/98	109	RTA00000422F.p.24.2	M00001658A:G09	5823
2850	2/24/98	696	RTA00000404F.p.12.2	M00001653B:C06	0
2851	2/24/98	369	RTA00000410F.m.05.1	M00001657B:B04	74964
2852	2/24/98	1229	RTA00000422F.n.14.1	M00001642C:G02	26787
2853	2/24/98	529	RTA00000422F.o.19.2	M00001655C:E01	13084
2854	2/24/98	327	RTA00000405F.a.11.1	M00001655A:B11	39124
2855	2/24/98	393	RTA00000418F.m.24.1	M00001654D:F12	77114
2856	2/24/98	381	RTA00000418F.m.23.1	M00001654D:F11	77195
2857	2/24/98	877	RTA00000418F.m.22.1	M00001654D:E12	74567
2858	2/24/98	166	RTA00000418F.m.19.1	M00001654D:A03	8890
2859	2/24/98	291	RTA00000405F.c.01.1	M00001657D:A04	19236
2860	2/24/98	356	RTA00000409F.m.24.1	M00001620D:H02	3942
2861	2/24/98	717	RTA00000404F.i.22.1	M00001625C:G05	39082
2862	2/24/98	648	RTA00000340F.i.13.1	M00001624B:B10	79299
2863	2/24/98	914	RTA00000138A.m.15.1	M00001624A:A03	41603
2864	2/24/98	587	RTA00000130A.o.21.1	M00001623A:F04	80218
2865	2/24/98	22	RTA00000130A.m.15.1	M00001622A:H12	81630
2866	2/24/98	767	RTA00000138A.p.10.1	M00001644A:H01	81625
2867	2/24/98	262	RTA00000409F.n.14.1	M00001621B:G05	78190
2868	2/24/98	960	RTA00000404F.l.19.2	M00001639B:H01	16196
2869	2/24/98	608	RTA00000404F.i.12.1	M00001620D:G11	39001
2870	2/24/98	342	RTA00000404F.i.02.1	M00001619D:D10	39015
2871	2/24/98	195	RTA00000404F.h.22.1	M00001619C:C07	18735
2872	2/24/98	214	RTA00000404F.h.19.1	M00001619A:E05	8096
2873	2/24/98	52	RTA00000409F.m.12.1	M00001618B:D09	73490
2874	2/24/98	769	RTA00000340F.i.10.1	M00001618A:F10	38561
2875	2/24/98	383	RTA00000404F.i.18.1	M00001621C:H12	21912
2876	2/24/98	256	RTA00000404F.m.03.2	M00001640A:H02	11799
2877	2/24/98	519	RTA00000404F.l.10.1	M00001638B:F10	23136

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
2878	2/24/98	646	RTA00000421F.m.14.1	M00001642A:F03	3524
2879	2/24/98	659	RTA00000422F.m.24.1	M00001641D:C04	39159
2880	2/24/98	701	RTA00000418F.l.11.1	M00001641C:H07	77158
2881	2/24/98	873	RTA00000418F.l.06.1	M00001641C:F01	73317
2882	2/24/98	422	RTA00000418F.l.04.1	M00001641C:D02	74140
2883	2/24/98	766	RTA00000404F.j.01.1	M00001625D:G10	26859
2884	2/24/98	20	RTA00000404F.m.04.2	M00001641A:A11	22720
2885	2/24/98	346	RTA00000418F.j.08.1	M00001626C:C11	73382
2886	2/24/98	141	RTA00000418F.k.19.1	M00001639C:C02	74932
2887	2/24/98	373	RTA00000418F.k.18.1	M00001639C:A10	75385
2888	2/24/98	405	RTA00000418F.k.17.1	M00001639C:A09	75390
2889	2/24/98	63	RTA00000404F.l.20.2	M00001639B:H05	38638
2889	2/24/98	133	RTA00000404F.l.20.1	M00001639B:H05	38638
2890	2/24/98	133	RTA00000404F.l.20.1	M00001639B:H05	38638
2890	2/24/98	63	RTA00000404F.l.20.2	M00001639B:H05	38638
2891	2/24/98	1261	RTA00000404F.m.17.2	M00001643B:E05	0
2892	2/24/98	626	RTA00000410F.j.01.1	M00001641B:F12	73399
2893	2/24/98	982	RTA00000126A.p.23.2	M00001552A:F06	80915
2894	2/24/98	196	RTA00000418F.k.10.1	M00001639A:G07	74454
2895	2/24/98	765	RTA00000137A.j.15.4	M00001559A:C08	4213
2896	2/24/98	895	RTA00000137A.j.11.4	M00001559A:A11	79752
2897	2/24/98	232	RTA00000128A.b.20.1	M00001558A:G09	79761
2898	2/24/98	152	RTA00000127A.i.20.1	M00001555A:B12	81418
2899	2/24/98	78	RTA00000195AF.b.13.1	M00001560D:A03	12605
2899	1/28/98	59	RTA00000195AF.b.13.1	M00001560D:A03	12605
2900	2/24/98	448	RTA00000127A.a.3.1	M00001552A:H10	13232
2901	2/24/98	801	RTA00000128A.m.23.1	M00001561A:D01	81441
2902	2/24/98	499	RTA00000126A.p.18.2	M00001552A:E10	80881
2903	2/24/98	1212	RTA00000349R.o.03.1	M00001551D:H07	23006
2904	2/24/98	484	RTA00000126A.n.13.2	M00001551A:H06	79735
2905	2/24/98	240	RTA00000126A.n.7.2	M00001551A:D06	79557
2906	2/24/98	451	RTA00000126A.o.22.1	M00001551A:A11	81752
2907	2/24/98	513	RTA00000126A.k.7.2	M00001550A:E07	79866
2908	2/24/98	578	RTA00000127A.f.11.1	M00001554A:A08	81463
2909	2/24/98	372	RTA00000408F.p.24.1	M00001579A:E03	74286
2910	2/24/98	985	RTA00000409F.a.08.1	M00001582D:B01	74978
2911	2/24/98	685	RTA00000129A.a.13.2	M00001582A:A03	79780
2912	2/24/98	574	RTA00000403F.o.14.1	M00001579D:H09	38971
2913	2/24/98	601	RTA00000403F.o.13.1	M00001579D:F04	39049
2914	2/24/98	432	RTA00000418F.g.05.1	M00001579C:H06	73075
2915	1/28/98	59	RTA00000195AF.b.13.1	M00001560D:A03	12605
2915	2/24/98	78	RTA00000195AF.b.13.1	M00001560D:A03	12605
2916	2/24/98	491	RTA00000418F.f.21.1	M00001579B:F04	75157
2917	2/24/98	612	RTA00000125A.k.14.1	M00001545A:G05	79457
2918	1/28/98	248	RTA00000198R.c.14.1	M00001578D:C04	39814
2918	2/24/98	778	RTA00000347F.e.05.1	M00001578D:C04	39814
2919	1/28/98	248	RTA00000198R.c.14.1	M00001578D:C04	39814
2919	2/24/98	778	RTA00000347F.e.05.1	M00001578D:C04	39814
2920	2/24/98	361	RTA00000422F.d.16.1	M00001570C:G03	39133
2921	2/24/98	173	RTA00000418F.d.13.1	M00001570A:H01	74309

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
2922	2/24/98	1195	RTA00000422F.e.23.1	M00001567D:B03	19246
2923	2/24/98	1168	RTA00000421F.b.06.1	M00001567A:B09	2113
2924	2/24/98	580	RTA00000403F.o.07.1	M00001579C:A01	39037
2925	2/24/98	531	RTA00000345F.n.12.1	M00001528A:C04	7337
2926	2/24/98	154	RTA00000340F.b.21.1	M00001533D:A08	8001
2927	2/24/98	19	RTA00000123A.k.23.1	M00001533A:G05	80313
2928	2/24/98	1265	RTA00000340F.d.07.1	M00001532D:A06	0
2929	2/24/98	1124	RTA00000123A.h.22.1	M00001532A:C01	17124
2930	2/24/98	1241	RTA00000408F.l.14.1	M00001530A:E10	12001
2931	2/24/98	534	RTA00000126A.g.7.1	M00001548A:H04	1902
2932	2/24/98	694	RTA00000418F.c.07.1	M00001529D:C05	73245
2933	2/24/98	1034	RTA00000124A.f.16.3	M00001536A:F11	47430
2934	2/24/98	790	RTA00000345F.n.08.1	M00001517A:B11	0
2935	2/24/98	613	RTA00000122A.j.22.1	M00001516A:F06	81151
2936	2/24/98	885	RTA00000122A.j.17.1	M00001516A:D02	62736
2937	2/24/98	1262	RTA00000122A.h.4.1	M00001514A:G03	33576
2938	2/24/98	135	RTA00000122A.d.5.1	M00001513A:F05	81155
2939	1/28/98	391	RTA00000179AF.e.20.3	M00001396A:C03	4009
2940	2/24/98	537	RTA00000408F.l.09.1	M00001530A:A09	75487
2941	2/24/98	683	RTA00000403F.j.21.1	M00001540D:E02	24723
2942	2/24/98	343	RTA00000422F.g.21.1	M00001583A:F07	17232
2943	2/24/98	226	RTA00000125A.k.10.1	M00001545A:F02	81644
2944	2/24/98	763	RTA00000135A.m.18.1	M00001545A:C03	19255
2945	2/24/98	156	RTA00000125A.k.1.1	M00001545A:B12	0
2946	2/24/98	597	RTA00000135A.l.1.2	M00001545A:B10	39426
2947	2/24/98	586	RTA00000125A.g.24.1	M00001544A:F05	80397
2948	2/24/98	467	RTA00000123A.n.13.2	M00001534A:D03	39167
2949	2/24/98	830	RTA00000347F.b.08.1	M00001541B:E05	17591
2950	2/24/98	997	RTA00000134A.l.9.1	M00001535A:D10	81814
2951	2/24/98	371	RTA00000403F.j.17.1	M00001539D:B10	38563
2952	2/24/98	33	RTA00000403F.j.15.1	M00001539B:G07	23840
2953	2/24/98	1209	RTA00000408F.n.05.2	M00001539A:H02	77883
2954	2/24/98	530	RTA00000408F.n.02.2	M00001539A:E01	76993
2955	2/24/98	1213	RTA00000135A.a.23.1	M00001537A:H05	27054
2956	2/24/98	347	RTA00000125A.n.4.1	M00001546A:D08	81984
2957	2/24/98	472	RTA00000135A.f.14.2	M00001542A:G12	79969
2958	2/24/98	243	RTA00000410F.c.14.1	M00001634A:H05	77809
2959	2/24/98	919	RTA00000410F.d.18.1	M00001635D:D05	75458
2960	2/24/98	825	RTA00000404F.k.22.2	M00001635D:C12	39084
2960	2/24/98	364	RTA00000404F.k.22.1	M00001635D:C12	39084
2961	2/24/98	825	RTA00000404F.k.22.2	M00001635D:C12	39084
2961	2/24/98	364	RTA00000404F.k.22.1	M00001635D:C12	39084
2962	2/24/98	595	RTA00000410F.d.10.1	M00001635B:H02	77561
2963	2/24/98	175	RTA00000410F.d.09.1	M00001635B:H01	76964
2964	2/24/98	206	RTA00000410F.b.15.1	M00001633C:F09	77100
2965	2/24/98	1083	RTA00000418F.j.20.1	M00001634D:D04	77101
2966	2/24/98	922	RTA00000410F.e.09.1	M00001636A:F08	76093
2967	2/24/98	1035	RTA00000404F.k.15.1	M00001634A:B04	18225
2968	2/24/98	1167	RTA00000410F.c.06.1	M00001633D:H06	77784
2969	2/24/98	53	RTA00000410F.c.04.1	M00001633D:G09	74099

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
2970	2/24/98	567	RTA00000410F.c.02.1	M00001633D:D12	75055
2971	2/24/98	819	RTA00000410F.b.24.1	M00001633D:D09	75104
2972	2/24/98	666	RTA00000403F.o.19.1	M00001582D:F02	78615
2973	2/24/98	559	RTA00000418F.k.03.1	M00001634D:G11	78901
2974	2/24/98	999	RTA00000418F.k.04.1	M00001637A:A03	75864
2975	2/24/98	936	RTA00000121A.n.23.1	M00001511A:G01	26981
2976	2/24/98	201	RTA00000404F.l.09.1	M00001638B:E12	39176
2977	2/24/98	1160	RTA00000400F.g.02.1	M00001638B:E03	1508
2978	2/24/98	827	RTA00000410F.f.12.1	M00001637C:E03	73883
2979	2/24/98	622	RTA00000404F.l.07.1	M00001637C:C06	10798
2980	2/24/98	365	RTA00000418F.k.07.1	M00001637A:F10	75067
2981	2/24/98	248	RTA00000404F.k.24.1	M00001636A:C03	15256
2982	2/24/98	25	RTA00000418F.k.05.1	M00001637A:A06	73021
2983	2/24/98	1178	RTA00000400F.f.11.1	M00001636A:E07	4088
2984	2/24/98	1180	RTA00000404F.l.05.1	M00001636D:F09	38671
2985	2/24/98	711	RTA00000404F.l.03.2	M00001636B:G11	40272
2985	2/24/98	785	RTA00000404F.l.03.1	M00001636B:G11	40272
2986	2/24/98	785	RTA00000404F.l.03.1	M00001636B:G11	40272
2986	2/24/98	711	RTA00000404F.l.03.2	M00001636B:G11	40272
2987	2/24/98	711	RTA00000404F.l.03.2	M00001636B:G11	40272
2987	2/24/98	785	RTA00000404F.l.03.1	M00001636B:G11	40272
2988	2/24/98	711	RTA00000404F.l.03.2	M00001636B:G11	40272
2988	2/24/98	785	RTA00000404F.l.03.1	M00001636B:G11	40272
2989	2/24/98	1106	RTA00000410F.b.17.1	M00001633C:H05	77458
2990	2/24/98	253	RTA00000400F.f.18.1	M00001637A:E10	3764
2991	2/24/98	562	RTA00000401F.j.17.1	M00003901B:C05	5483
2992	2/24/98	1082	RTA00000137A.o.22.1	M00001587A:D01	0
2993	2/24/98	594	RTA00000129A.c.18.2	M00001587A:B10	37216
2994	2/24/98	891	RTA00000137A.p.12.1	M00001587A:B01	80614
2995	2/24/98	131	RTA00000418F.g.22.1	M00001585B:F01	74837
2996	2/24/98	880	RTA00000418F.g.20.1	M00001585B:C03	74626
2997	2/24/98	742	RTA00000410F.b.18.1	M00001633C:H11	76701
2998	2/24/98	879	RTA00000409F.b.19.1	M00001584D:H02	14479
2999	2/24/98	167	RTA00000399F.l.14.1	M00001590B:G08	3354
3000	2/24/98	1260	RTA00000422F.f.18.1	M00001583D:B08	24528
3000	2/24/98	1258	RTA00000403F.p.05.2	M00001583D:B08	24528
3001	2/24/98	1260	RTA00000422F.f.18.1	M00001583D:B08	24528
3001	2/24/98	1258	RTA00000403F.p.05.2	M00001583D:B08	24528
3002	2/24/98	1260	RTA00000422F.f.18.1	M00001583D:B08	24528
3002	2/24/98	1258	RTA00000403F.p.05.2	M00001583D:B08	24528
3003	2/24/98	1260	RTA00000422F.f.18.1	M00001583D:B08	24528
3003	2/24/98	1258	RTA00000403F.p.05.2	M00001583D:B08	24528
3004	2/24/98	67	RTA00000409F.a.22.1	M00001583B:F02	75200
3005	2/24/98	564	RTA00000418F.k.08.1	M00001639A:C03	18259
3006	1/28/98	282	RTA00000193AF.c.15.1	M00004248B:E08	3726
3007	2/24/98	242	RTA00000404F.j.08.1	M00001629B:B08	39066
3008	2/24/98	669	RTA00000410F.b.10.1	M00001633C:B09	74504
3009	2/24/98	725	RTA00000410F.b.07.1	M00001633C:A05	78916
3010	2/24/98	423	RTA00000410F.a.16.1	M00001633A:E06	73548
3011	2/24/98	695	RTA00000418F.j.15.1	M00001632C:H07	74855

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
3012	2/24/98	901	RTA00000418F.j.14.1	M00001632C:B10	32623
3013	2/24/98	752	RTA00000410F.a.08.1	M00001632A:B10	73324
3014	2/24/98	1007	RTA00000404F.a.01.1	M00001589B:B08	19251
3015	2/24/98	1093	RTA00000340F.i.15.1	M00001629C:E07	26815
3016	2/24/98	664	RTA00000404F.a.09.1	M00001589C:E06	38985
3017	2/24/98	1246	RTA00000418F.j.11.1	M00001626C:E04	73853
3018	2/24/98	174	RTA00000404F.b.02.1	M00001591B:B12	38984
3019	2/24/98	1142	RTA00000418F.i.06.1	M00001591B:B06	75151
3020	2/24/98	740	RTA00000399F.l.19.1	M00001590D:G07	40145
3021	2/24/98	1098	RTA00000409F.d.16.1	M00001590C:F10	76090
3022	2/24/98	591	RTA00000409F.a.16.1	M00001583A:A05	73990
3023	2/24/98	1110	RTA00000404F.j.24.1	M00001631D:G05	39067
3024	1/28/98	108	RTA00000183AR.h.23.2	M00001528A:F09	18957
3024	1/28/98	236	RTA00000183AR.h.23.1	M00001528A:F09	18957
3024	1/28/98	129	RTA00000134A.d.10.1	M00001528A:F09	18957
3025	1/28/98	68	RTA00000184F.k.19.1	M00001558B:D08	8022
3025	1/28/98	63	RTA00000184AF.k.19.1	M00001558B:D08	8022
3026	1/28/98	269	RTA00000183AF.k.13.1	M00001534B:C12	0
3027	1/28/98	129	RTA00000134A.d.10.1	M00001528A:F09	18957
3027	1/28/98	108	RTA00000183AR.h.23.2	M00001528A:F09	18957
3027	1/28/98	236	RTA00000183AR.h.23.1	M00001528A:F09	18957
3028	1/28/98	129	RTA00000134A.d.10.1	M00001528A:F09	18957
3028	1/28/98	108	RTA00000183AR.h.23.2	M00001528A:F09	18957
3028	1/28/98	236	RTA00000183AR.h.23.1	M00001528A:F09	18957
3029	1/28/98	236	RTA00000183AR.h.23.1	M00001528A:F09	18957
3029	1/28/98	108	RTA00000183AR.h.23.2	M00001528A:F09	18957
3029	1/28/98	129	RTA00000134A.d.10.1	M00001528A:F09	18957
3030	1/28/98	34	RTA00000197AF.n.8.1	M00001536D:A12	4101
3031	1/28/98	108	RTA00000183AR.h.23.2	M00001528A:F09	18957
3031	1/28/98	129	RTA00000134A.d.10.1	M00001528A:F09	18957
3031	1/28/98	236	RTA00000183AR.h.23.1	M00001528A:F09	18957
3032	1/28/98	106	RTA00000197AF.n.21.1	M00001540B:C09	0
3033	1/28/98	236	RTA00000183AR.h.23.1	M00001528A:F09	18957
3033	1/28/98	129	RTA00000134A.d.10.1	M00001528A:F09	18957
3033	1/28/98	108	RTA00000183AR.h.23.2	M00001528A:F09	18957
3034	1/28/98	108	RTA00000183AR.h.23.2	M00001528A:F09	18957
3034	1/28/98	236	RTA00000183AR.h.23.1	M00001528A:F09	18957
3034	1/28/98	129	RTA00000134A.d.10.1	M00001528A:F09	18957
3035	1/28/98	129	RTA00000134A.d.10.1	M00001528A:F09	18957
3035	1/28/98	108	RTA00000183AR.h.23.2	M00001528A:F09	18957
3035	1/28/98	236	RTA00000183AR.h.23.1	M00001528A:F09	18957
3036	1/28/98	233	RTA00000197AF.l.8.1	M00001511B:C06	39954
3037	1/28/98	323	RTA00000182AF.m.21.1	M00001490C:C12	18699
3038	1/28/98	223	RTA00000197F.i.9.1	M00001488D:C10	0
3039	1/28/98	236	RTA00000183AR.h.23.1	M00001528A:F09	18957
3039	1/28/98	108	RTA00000183AR.h.23.2	M00001528A:F09	18957
3039	1/28/98	129	RTA00000134A.d.10.1	M00001528A:F09	18957
3040	1/28/98	352	RTA00000197AF.p.3.1	M00001550A:A03	7239
3041	1/28/98	301	RTA00000181AR.i.19.3	M00001452C:B06	16970
3041	1/28/98	295	RTA00000181AR.i.19.2	M00001452C:B06	16970

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
3042	1/28/98	68	RTA00000184F.k.19.1	M00001558B:D08	8022
3042	1/28/98	63	RTA00000184AF.k.19.1	M00001558B:D08	8022
3043	1/28/98	63	RTA00000184AF.k.19.1	M00001558B:D08	8022
3043	1/28/98	68	RTA00000184F.k.19.1	M00001558B:D08	8022
3044	1/28/98	41	RTA00000184F.k.12.1	M00001557D:D09	8761
3045	1/28/98	150	RTA00000184F.k.09.1	M00001557C:H07	7065
3046	1/28/98	82	RTA00000183AF.l.18.1	M00001535D:C01	3484
3047	1/28/98	338	RTA00000184AF.i.1.1	M00001554B:C07	0
3048	1/28/98	327	RTA00000182AF.i.1.3	M00001479B:A01	7033
3049	1/28/98	256	RTA00000184AR.e.15.1	M00001549C:E06	16347
3050	1/28/98	99	RTA00000184AF.d.8.1	M00001548A:A08	4393
3051	1/28/98	355	RTA00000184AR.b.24.1	M00001546B:C05	5777
3052	1/28/98	322	RTA00000184AR.b.21.1	M00001546B:B02	39788
3053	1/28/98	97	RTA00000197AF.o.2.1	M00001541C:B07	5739
3054	1/28/98	313	RTA00000183AF.o.11.1	M00001540D:D02	0
3055	1/28/98	42	RTA00000184F.j.21.1	M00001557A:D02	7065
3056	1/28/98	378	RTA00000181AF.k.24.3	M00001454B:C12	7005
3056	1/28/98	119	RTA00000181AR.k.24.2	M00001454B:C12	7005
3056	1/28/98	116	RTA00000181AR.k.24.3	M00001454B:C12	7005
3057	1/28/98	134	RTA00000197F.e.11.1	M00001454B:G03	2306
3057	1/28/98	298	RTA00000197AR.e.11.1	M00001454B:G03	2306
3058	1/28/98	134	RTA00000197F.e.11.1	M00001454B:G03	2306
3058	1/28/98	298	RTA00000197AR.e.11.1	M00001454B:G03	2306
3059	1/28/98	134	RTA00000197F.e.11.1	M00001454B:G03	2306
3059	1/28/98	298	RTA00000197AR.e.11.1	M00001454B:G03	2306
3060	1/28/98	116	RTA00000181AR.k.24.3	M00001454B:C12	7005
3060	1/28/98	378	RTA00000181AF.k.24.3	M00001454B:C12	7005
3060	1/28/98	119	RTA00000181AR.k.24.2	M00001454B:C12	7005
3061	1/28/98	116	RTA00000181AR.k.24.3	M00001454B:C12	7005
3061	1/28/98	378	RTA00000181AF.k.24.3	M00001454B:C12	7005
3061	1/28/98	119	RTA00000181AR.k.24.2	M00001454B:C12	7005
3062	1/28/98	159	RTA00000182AF.l.12.1	M00001487A:A05	1027
3063	1/28/98	119	RTA00000181AR.k.24.2	M00001454B:C12	7005
3063	1/28/98	116	RTA00000181AR.k.24.3	M00001454B:C12	7005
3063	1/28/98	378	RTA00000181AF.k.24.3	M00001454B:C12	7005
3064	1/28/98	341	RTA00000181AF.l.06.2	M00001454C:C08	0
3065	1/28/98	116	RTA00000181AR.k.24.3	M00001454B:C12	7005
3065	1/28/98	119	RTA00000181AR.k.24.2	M00001454B:C12	7005
3065	1/28/98	378	RTA00000181AF.k.24.3	M00001454B:C12	7005
3066	1/28/98	378	RTA00000181AF.k.24.3	M00001454B:C12	7005
3066	1/28/98	116	RTA00000181AR.k.24.3	M00001454B:C12	7005
3066	1/28/98	119	RTA00000181AR.k.24.2	M00001454B:C12	7005
3067	1/28/98	378	RTA00000181AF.k.24.3	M00001454B:C12	7005
3067	1/28/98	116	RTA00000181AR.k.24.3	M00001454B:C12	7005
3067	1/28/98	119	RTA00000181AR.k.24.2	M00001454B:C12	7005
3068	1/28/98	378	RTA00000181AF.k.24.3	M00001454B:C12	7005
3068	1/28/98	116	RTA00000181AR.k.24.3	M00001454B:C12	7005
3068	1/28/98	119	RTA00000181AR.k.24.2	M00001454B:C12	7005
3069	1/28/98	170	RTA00000197AF.d.23.1	M00001453A:E11	16130
3070	1/28/98	491	RTA00000196F.k.11.1	M00001399C:H12	3

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
3071	1/28/98	119	RTA00000181AR.k.24.2	M00001454B:C12	7005
3071	1/28/98	378	RTA00000181AF.k.24.3	M00001454B:C12	7005
3071	1/28/98	116	RTA00000181AR.k.24.3	M00001454B:C12	7005
3072	1/28/98	674	RTA00000197AR.e.24.1	M00001456B:F10	39250
3072	1/28/98	3	RTA00000197AF.e.24.1	M00001456B:F10	39250
3073	2/24/98	78	RTA00000195AF.b.13.1	M00001560D:A03	12605
3073	1/28/98	59	RTA00000195AF.b.13.1	M00001560D:A03	12605
3074	1/28/98	189	RTA00000197AF.h.10.1	M00001476B:F10	15554
3075	1/28/98	46	RTA00000182AF.f.13.1	M00001470C:B10	8010
3076	1/28/98	200	RTA00000182AF.f.2.1	M00001469D:D02	4794
3077	1/28/98	325	RTA00000182AF.d.18.4	M00001467D:H05	37435
3078	1/28/98	45	RTA00000197AR.f.12.1	M00001458C:E01	3513
3079	1/28/98	298	RTA00000197AR.e.11.1	M00001454B:G03	2306
3079	1/28/98	134	RTA00000197F.e.11.1	M00001454B:G03	2306
3080	1/28/98	37	RTA00000181AF.n.15.2	M00001457A:B07	86128
3081	1/28/98	7	RTA00000197AR.e.12.1	M00001454B:G07	22095
3082	1/28/98	674	RTA00000197AR.e.24.1	M00001456B:F10	39250
3082	1/28/98	3	RTA00000197AF.e.24.1	M00001456B:F10	39250
3083	1/28/98	88	RTA00000197AF.e.23.1	M00001456B:C09	37157
3084	1/28/98	243	RTA00000181AF.m.15.3	M00001455D:A11	12081
3085	1/28/98	326	RTA00000197AR.e.19.1	M00001455D:A09	8047
3086	1/28/98	293	RTA00000197AF.e.13.1	M00001454C:F02	662
3087	1/28/98	380	RTA00000182AF.k.24.1	M00001485D:B10	5625
3088	1/28/98	206	RTA00000181AF.o.04.2	M00001457C:C12	22205
3089	1/28/98	228	RTA00000187AR.h.15.2	M00001679A:A06	6660
3090	1/28/98	68	RTA00000184F.k.19.1	M00001558B:D08	8022
3090	1/28/98	63	RTA00000184AF.k.19.1	M00001558B:D08	8022
3091	1/28/98	191	RTA00000187AF.p.23.1	M00003748B:F02	39804
3092	1/28/98	10	RTA00000198AF.n.16.1	M00001694C:H10	3721
3093	1/28/98	219	RTA00000198AF.m.19.1	M00001680D:D02	40041
3093	1/28/98	32	RTA00000198R.m.19.1	M00001680D:D02	40041
3094	1/28/98	32	RTA00000198R.m.19.1	M00001680D:D02	40041
3094	1/28/98	219	RTA00000198AF.m.19.1	M00001680D:D02	40041
3095	1/28/98	317	RTA00000198AF.p.09.1	M00003761D:E02	10473
3095	1/28/98	186	RTA00000198R.p.09.1	M00003761D:E02	10473
3096	1/28/98	219	RTA00000198AF.m.19.1	M00001680D:D02	40041
3096	1/28/98	32	RTA00000198R.m.19.1	M00001680D:D02	40041
3097	1/28/98	64	RTA00000198AF.p.12.1	M00003763D:E10	8878
3097	1/28/98	542	RTA00000198R.p.12.1	M00003763D:E10	8878
3098	1/28/98	364	RTA00000187AF.g.13.1	M00001676C:C11	2991
3099	1/28/98	430	RTA00000198R.k.23.1	M00001661B:C08	8995
3099	1/28/98	294	RTA00000198AF.k.23.1	M00001661B:C08	8995
3100	1/28/98	430	RTA00000198R.k.23.1	M00001661B:C08	8995
3100	1/28/98	294	RTA00000198AF.k.23.1	M00001661B:C08	8995
3101	1/28/98	57	RTA00000198AF.k.20.1	M00001660C:B12	22553
3102	1/28/98	368	RTA00000198AF.k.18.1	M00001660A:C12	17432
3103	1/28/98	247	RTA00000198AF.k.08.1	M00001656C:G08	17436
3104	1/28/98	219	RTA00000198AF.m.19.1	M00001680D:D02	40041
3104	1/28/98	32	RTA00000198R.m.19.1	M00001680D:D02	40041
3105	1/28/98	199	RTA00000199R.c.09.1	M00003800A:C09	16824

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
3105	1/28/98	66	RTA00000199F.c.09.2	M00003800A:C09	16824
3106	1/28/98	225	RTA00000189AF.b.5.1	M00003828A:E04	3784
3107	1/28/98	5	RTA00000195R.c.11.1	M00003811A:E03	66087
3108	1/28/98	284	RTA00000199F.d.10.2	M00003808C:B05	22049
3108	2/24/98	816	RTA00000354R.n.04.1	M00003808C:B05	22049
3109	1/28/98	284	RTA00000199F.d.10.2	M00003808C:B05	22049
3109	2/24/98	816	RTA00000354R.n.04.1	M00003808C:B05	22049
3110	1/28/98	2	RTA00000188AF.n.15.1	M00003804A:H04	0
3111	1/28/98	317	RTA00000198AF.p.09.1	M00003761D:E02	10473
3111	1/28/98	186	RTA00000198R.p.09.1	M00003761D:E02	10473
3112	1/28/98	199	RTA00000199R.c.09.1	M00003800A:C09	16824
3112	1/28/98	66	RTA00000199F.c.09.2	M00003800A:C09	16824
3113	1/28/98	487	RTA00000198F.i.8.1	M00001639A:F10	9807
3113	1/28/98	277	RTA00000198AR.i.08.1	M00001639A:F10	9807
3114	1/28/98	66	RTA00000199F.c.09.2	M00003800A:C09	16824
3114	1/28/98	199	RTA00000199R.c.09.1	M00003800A:C09	16824
3115	1/28/98	224	RTA00000188AF.m.11.1	M00003799A:D09	0
3116	1/28/98	58	RTA00000199F.b.01.2	M00003778A:D08	19118
3117	1/28/98	216	RTA00000188AF.g.9.1	M00003774B:B08	4959
3118	1/28/98	201	RTA00000198AF.p.18.1	M00003769B:D03	23081
3119	1/28/98	542	RTA00000198R.p.12.1	M00003763D:E10	8878
3119	1/28/98	64	RTA00000198AF.p.12.1	M00003763D:E10	8878
3120	1/28/98	199	RTA00000199R.c.09.1	M00003800A:C09	16824
3120	1/28/98	66	RTA00000199F.c.09.2	M00003800A:C09	16824
3121	1/28/98	146	RTA00000185AF.a.19.2	M00001571C:H06	5749
3122	1/28/98	248	RTA00000198R.c.14.1	M00001578D:C04	39814
3122	2/24/98	778	RTA00000347F.e.05.1	M00001578D:C04	39814
3123	1/28/98	248	RTA00000198R.c.14.1	M00001578D:C04	39814
3123	2/24/98	778	RTA00000347F.e.05.1	M00001578D:C04	39814
3124	1/28/98	147	RTA00000185AF.c.24.2	M00001578B:E04	23001
3125	1/28/98	195	RTA00000198AF.c.10.1	M00001577B:H02	77149
3126	1/28/98	171	RTA00000198R.c.07.1	M00001575D:G05	19181
3126	1/28/98	525	RTA00000198AF.c.7.1	M00001575D:G05	19181
3127	1/28/98	172	RTA00000186AF.p.09.2	M00001655C:E04	6879
3128	1/28/98	230	RTA00000185AR.b.18.1	M00001575B:C09	12171
3129	1/28/98	192	RTA00000185AF.m.7.1	M00001605C:D12	39804
3130	1/28/98	19	RTA00000185AF.a.8.1	M00001570D:A03	4868
3131	1/28/98	492	RTA00000198AF.b.8.1	M00001567C:H12	22636
3131	1/28/98	23	RTA00000198R.b.08.1	M00001567C:H12	22636
3132	1/28/98	23	RTA00000198R.b.08.1	M00001567C:H12	22636
3132	1/28/98	492	RTA00000198AF.b.8.1	M00001567C:H12	22636
3133	1/28/98	357	RTA00000184AF.o.15.1	M00001564D:C09	0
3134	1/28/98	30	RTA00000184AR.n.07.2	M00001561C:F06	0
3135	1/28/98	59	RTA00000195AF.b.13.1	M00001560D:A03	12605
3135	2/24/98	78	RTA00000195AF.b.13.1	M00001560D:A03	12605
3136	1/28/98	525	RTA00000198AF.c.7.1	M00001575D:G05	19181
3136	1/28/98	171	RTA00000198R.c.07.1	M00001575D:G05	19181
3137	1/28/98	303	RTA00000186AR.e.03.3	M00001623D:C10	22110
3138	1/28/98	295	RTA00000181AR.i.19.2	M00001452C:B06	16970
3138	1/28/98	301	RTA00000181AR.i.19.3	M00001452C:B06	16970

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
3139	1/28/98	232	RTA00000186AF.j.03.2	M00001638A:E07	0
3140	1/28/98	309	RTA00000198AF.h.12.1	M00001632C:A02	9503
3141	1/28/98	268	RTA00000186AF.h.01.2	M00001632A:F12	0
3142	1/28/98	267	RTA00000186AF.g.11.2	M00001630B:H09	5214
3143	1/28/98	83	RTA00000186AF.f.24.2	M00001629B:E06	0
3143	1/28/98	336	RTA00000186AF.f.24.1	M00001629B:E06	0
3144	1/28/98	222	RTA00000185AF.i.4.1	M00001594A:B12	13942
3145	1/28/98	217	RTA00000198AF.h.3.1	M00001625D:C07	22562
3146	1/28/98	196	RTA00000198F.e.10.1	M00001599B:E09	9727
3147	1/28/98	372	RTA00000186AF.d.23.1	M00001623B:G07	22187
3148	1/28/98	302	RTA00000186AF.d.1.2	M00001621C:C08	40044
3149	1/28/98	262	RTA00000186AF.c.17.1	M00001619D:G05	8551
3150	1/28/98	358	RTA00000198AF.g.7.1	M00001616C:C09	13386
3151	1/28/98	166	RTA00000198AF.f.21.1	M00001614D:D09	22676
3152	1/28/98	277	RTA00000198AR.i.08.1	M00001639A:F10	9807
3152	1/28/98	487	RTA00000198F.i.8.1	M00001639A:F10	9807
3153	1/28/98	336	RTA00000186AF.f.24.1	M00001629B:E06	0
3153	1/28/98	83	RTA00000186AF.f.24.2	M00001629B:E06	0
3154	1/28/98	352	RTA00000197AF.p.3.1	M00001550A:A03	7239
3155	1/28/98	251	RTA00000192AF.n.13.1	M00004197D:H01	8210
3156	1/28/98	41	RTA00000184F.k.12.1	M00001557D:D09	8761
3157	1/28/98	731	RTA00000184F.k.02.1	M00001557B:H10	5192
3158	1/28/98	42	RTA00000184F.j.21.1	M00001557A:D02	7065
3159	1/28/98	42	RTA00000184F.j.21.1	M00001557A:D02	7065
3160	1/28/98	302	RTA00000186AF.d.1.2	M00001621C:C08	40044
3161	1/28/98	560	RTA00000184AF.i.23.3	M00001556A:F11	1577
3162	1/28/98	558	RTA00000186AR.h.14.1	M00001632D:H07	0
3163	1/28/98	256	RTA00000184AR.e.15.1	M00001549C:E06	16347
3164	1/28/98	682	RTA00000125A.j.16.1	M00001544A:E06	0
3165	1/28/98	129	RTA00000134A.d.10.1	M00001528A:F09	18957
3165	1/28/98	108	RTA00000183AR.h.23.2	M00001528A:F09	18957
3165	1/28/98	236	RTA00000183AR.h.23.1	M00001528A:F09	18957
3166	1/28/98	129	RTA00000134A.d.10.1	M00001528A:F09	18957
3166	1/28/98	108	RTA00000183AR.h.23.2	M00001528A:F09	18957
3166	1/28/98	236	RTA00000183AR.h.23.1	M00001528A:F09	18957
3167	1/28/98	108	RTA00000183AR.h.23.2	M00001528A:F09	18957
3167	1/28/98	236	RTA00000183AR.h.23.1	M00001528A:F09	18957
3167	1/28/98	129	RTA00000134A.d.10.1	M00001528A:F09	18957
3168	2/24/98	531	RTA00000345F.n.12.1	M00001528A:C04	7337
3169	1/28/98	324	RTA00000184F.j.06.1	M00001556B:G02	11294
3170	2/24/98	604	RTA00000351R.c.13.1	M00003747D:C05	11476
3171	1/28/98	301	RTA00000181AR.i.19.3	M00001452C:B06	16970
3171	1/28/98	295	RTA00000181AR.i.19.2	M00001452C:B06	16970
3172	1/28/98	231	RTA00000192AF.l.13.2	M00004185C:C03	11443
3173	1/28/98	634	RTA00000192AF.j.6.1	M00004172C:D08	11494
3174	1/28/98	165	RTA00000192AF.g.23.1	M00004157C:A09	6455
3175	1/28/98	574	RTA00000192AF.f.3.1	M00004146C:C11	5257
3176	1/28/98	146	RTA00000185AF.a.19.2	M00001571C:H06	5749
3177	1/28/98	651	RTA00000189AR.d.22.2	M00003844C:B11	6539
3178	1/28/98	161	RTA00000183AF.e.23.2	M00001506D:A09	0

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
3179	1/28/98	475	RTA00000187AR.m.3.3	M00001682C:B12	17055
3180	2/24/98	39	RTA00000187AF.l.7.1	M00001680D:F08	10539
3181	1/28/98	228	RTA00000187AR.h.15.2	M00001679A:A06	6660
3182	2/24/98	465	RTA00000350R.p.18.1	M00001676B:F05	11460
3183	1/28/98	575	RTA00000186AF.l.12.2	M00001645A:C12	19267
3184	2/24/98	700	RTA00000350R.m.14.1	M00001644C:B07	39171
3185	1/28/98	261	RTA00000192AF.a.24.1	M00004114C:F11	13183
3186	1/28/98	236	RTA00000183AR.h.23.1	M00001528A:F09	18957
3186	1/28/98	108	RTA00000183AR.h.23.2	M00001528A:F09	18957
3186	1/28/98	129	RTA00000134A.d.10.1	M00001528A:F09	18957
3187	1/28/98	398	RTA00000177AR.l.13.3	M00001353A:G12	8078
3188	1/28/98	645	RTA00000177AF.k.9.1	M00001352A:E02	16245
3189	1/28/98	283	RTA00000177AF.i.8.4	M00001350A:H01	7187
3190	1/28/98	361	RTA00000177AR.g.16.4	M00001347A:B10	13576
3191	1/28/98	680	RTA00000177AF.f.10.1	M00001345A:E01	6420
3192	1/28/98	632	RTA00000183AR.g.03.1	M00001512D:G09	3956
3192	1/28/98	630	RTA00000183AR.g.03.2	M00001512D:G09	3956
3193	1/28/98	702	RTA00000177AR.b.8.5	M00001340B:A06	17062
3194	1/28/98	330	RTA00000177AR.m.17.4	M00001355B:G10	14391
3194	1/28/98	493	RTA00000177AF.m.17.1	M00001355B:G10	14391
3194	1/28/98	337	RTA00000177AR.m.17.3	M00001355B:G10	14391
3195	1/28/98	236	RTA00000183AR.h.23.1	M00001528A:F09	18957
3195	1/28/98	129	RTA00000134A.d.10.1	M00001528A:F09	18957
3195	1/28/98	108	RTA00000183AR.h.23.2	M00001528A:F09	18957
3196	1/28/98	129	RTA00000134A.d.10.1	M00001528A:F09	18957
3196	1/28/98	236	RTA00000183AR.h.23.1	M00001528A:F09	18957
3196	1/28/98	108	RTA00000183AR.h.23.2	M00001528A:F09	18957
3197	1/28/98	435	RTA00000182AR.c.22.1	M00001467A:D08	16283
3198	1/28/98	635	RTA00000181AF.p.7.3	M00001460A:E01	38773
3199	1/28/98	362	RTA00000197AR.c.24.1	M00001450A:B12	82498
3200	2/24/98	442	RTA00000347F.b.02.1	M00001450A:A02	39304
3201	1/28/98	265	RTA00000177AF.e.14.1	M00001343D:H07	23255
3202	1/28/98	270	RTA00000178R.l.08.1	M00001383A:C03	39648
3203	1/28/98	472	RTA00000192AF.p.17.1	M00004214C:H05	11451
3204	1/28/98	603	RTA00000183AR.d.11.3	M00001504D:G06	6420
3205	1/28/98	519	RTA00000183AF.a.24.2	M00001499B:A11	10539
3206	1/28/98	435	RTA00000182AR.c.22.1	M00001467A:D08	16283
3207	2/24/98	158	RTA00000348R.j.16.1	M00001410A:D07	7005
3208	1/28/98	411	RTA00000179AF.j.13.3	M00001400B:H06	0
3209	1/28/98	742	RTA00000177AF.m.1.1	M00001353D:D10	14929
3210	1/28/98	270	RTA00000178R.l.08.1	M00001383A:C03	39648
3211	1/28/98	337	RTA00000177AR.m.17.3	M00001355B:G10	14391
3211	1/28/98	493	RTA00000177AF.m.17.1	M00001355B:G10	14391
3211	1/28/98	330	RTA00000177AR.m.17.4	M00001355B:G10	14391
3212	1/28/98	297	RTA00000178AF.f.9.3	M00001371C:E09	7172
3213	1/28/98	33	RTA00000178AR.a.20.1	M00001362C:H11	945
3213	2/24/98	979	RTA00000345F.b.17.1	M00001362C:H11	945
3214	1/28/98	33	RTA00000178AR.a.20.1	M00001362C:H11	945
3214	2/24/98	979	RTA00000345F.b.17.1	M00001362C:H11	945
3215	1/28/98	466	RTA00000177AF.p.20.1	M00001361A:A05	4141

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
3216	1/28/98	330	RTA00000177AR.m.17.4	M00001355B:G10	14391
3216	1/28/98	493	RTA00000177AF.m.17.1	M00001355B:G10	14391
3216	1/28/98	337	RTA00000177AR.m.17.3	M00001355B:G10	14391
3217	1/28/98	632	RTA00000183AR.g.03.1	M00001512D:G09	3956
3217	1/28/98	630	RTA00000183AR.g.03.2	M00001512D:G09	3956
3218	1/28/98	391	RTA00000179AF.e.20.3	M00001396A:C03	4009
3219	1/28/98	370	RTA00000179AF.c.15.3	M00001392D:H06	2995
3219	1/28/98	460	RTA00000179AF.c.15.1	M00001392D:H06	2995
3220	1/28/98	47	RTA00000192AF.m.12.1	M00004191D:B11	0
3221	1/28/98	438	RTA00000180AR.g.03.4	M00001425A:C11	9024
3221	1/28/98	95	RTA00000180AF.g.3.1	M00001425A:C11	9024
3222	1/28/98	438	RTA00000180AR.g.03.4	M00001425A:C11	9024
3222	1/28/98	95	RTA00000180AF.g.3.1	M00001425A:C11	9024
3223	1/28/98	320	RTA00000196AF.m.13.1	M00001415B:E09	16290
3224	1/28/98	365	RTA00000196F.l.20.2	M00001410B:G05	22678
3225	1/28/98	80	RTA00000196AF.p.13.2	M00001432A:E06	6125
3226	1/28/98	179	RTA00000179AF.f.20.3	M00001397B:B09	16154
3227	1/28/98	379	RTA00000180AF.l.06.2	M00001433A:G07	5625
3228	1/28/98	460	RTA00000179AF.c.15.1	M00001392D:H06	2995
3228	1/28/98	370	RTA00000179AF.c.15.3	M00001392D:H06	2995
3229	1/28/98	107	RTA00000196R.i.13.1	M00001390A:A09	9857
3230	1/28/98	120	RTA00000178AR.m.19.5	M00001384D:H07	0
3230	1/28/98	377	RTA00000178AF.m.19.1	M00001384D:H07	0
3231	1/28/98	120	RTA00000178AR.m.19.5	M00001384D:H07	0
3231	1/28/98	377	RTA00000178AF.m.19.1	M00001384D:H07	0
3232	1/28/98	384	RTA00000196AF.h.17.1	M00001384C:F12	39215
3233	1/28/98	182	RTA00000196AF.h.16.1	M00001384C:E03	39895
3234	1/28/98	105	RTA00000179AF.g.12.3	M00001398A:G03	36390
3235	1/28/98	252	RTA00000181AF.e.18.3	M00001448D:C09	8
3235	1/28/98	253	RTA00000181AF.e.17.3	M00001448D:C09	8
3236	1/28/98	301	RTA00000181AR.i.19.3	M00001452C:B06	16970
3236	1/28/98	295	RTA00000181AR.i.19.2	M00001452C:B06	16970
3237	1/28/98	288	RTA00000181AR.i.06.3	M00001452A:C07	19119
3237	2/24/98	198	RTA00000339R.l.14.1	M00001452A:C07	19119
3238	1/28/98	288	RTA00000181AR.i.06.3	M00001452A:C07	19119
3238	2/24/98	198	RTA00000339R.l.14.1	M00001452A:C07	19119
3239	1/28/98	109	RTA00000197AF.d.12.1	M00001451D:C10	39546
3240	1/28/98	149	RTA00000181AR.h.06.3	M00001450D:D04	87226
3241	1/28/98	75	RTA00000180AR.h.19.2	M00001428A:H10	84182
3242	1/28/98	21	RTA00000131A.g.19.2	M00001449A:G10	36535
3243	1/28/98	308	RTA00000178AF.j.20.1	M00001380C:E05	15066
3244	1/28/98	253	RTA00000181AF.e:17.3	M00001448D:C09	8
3244	1/28/98	252	RTA00000181AF.e.18.3	M00001448D:C09	8
3245	1/28/98	252	RTA00000181AF.e.18.3	M00001448D:C09	8
3245	1/28/98	253	RTA00000181AF.e.17.3	M00001448D:C09	8
3246	1/28/98	253	RTA00000181AF.e.17.3	M00001448D:C09	8
3246	1/28/98	252	RTA00000181AF.e.18.3	M00001448D:C09	8
3247	1/28/98	136	RTA00000197AF.c.10.1	M00001448B:F06	10400
3248	1/28/98	177	RTA00000197AF.c.3.1	M00001447C:C01	3145
3249	1/28/98	204	RTA00000180AR.o.5.2	M00001437D:C04	7848

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
3250	1/28/98	362	RTA00000197AR.c.24.1	M00001450A:B12	82498
3251	1/28/98	81	RTA00000196AF.b.15.1	M00001347B:E01	5102
3252	1/28/98	342	RTA00000196AF.d.10.1	M00001354C:B06	22256
3253	1/28/98	113	RTA00000196AF.d.09.1	M00001354B:B10	16934
3254	1/28/98	463	RTA00000177AR.k.23.4	M00001352D:D02	35550
3254	1/28/98	168	RTA00000177AR.k.23.1	M00001352D:D02	35550
3255	1/28/98	463	RTA00000177AR.k.23.4	M00001352D:D02	35550
3255	1/28/98	168	RTA00000177AR.k.23.1	M00001352D:D02	35550
3256	1/28/98	135	RTA00000196AF.c.22.1	M00001352D:C05	22548
3257	1/28/98	270	RTA00000178R.l.08.1	M00001383A:C03	39648
3258	1/28/98	359	RTA00000196AF.b.17.1	M00001348A:D04	12193
3259	1/28/98	493	RTA00000177AF.m.17.1	M00001355B:G10	14391
3259	1/28/98	337	RTA00000177AR.m.17.3	M00001355B:G10	14391
3259	1/28/98	330	RTA00000177AR.m.17.4	M00001355B:G10	14391
3260	1/28/98	361	RTA00000177AR.g.16.4	M00001347A:B10	13576
3261	1/28/98	265	RTA00000177AF.e.14.1	M00001343D:H07	23255
3262	1/28/98	56	RTA00000177AF.e.9.1	M00001343D:C04	37442
3263	1/28/98	48	RTA00000177AR.a.23.5	M00001339D:G02	6995
3264	2/24/98	308	RTA00000353R.d.11.1	M00004692A:H08	0
3265	1/28/98	164	RTA00000193AR.i.14.4	M00004307C:A06	9457
3266	1/28/98	283	RTA00000177AF.i.8.4	M00001350A:H01	7187
3267	1/28/98	15	RTA00000177AR.n.8.1	M00001356D:F06	4188
3267	1/28/98	89	RTA00000177AF.n.8.3	M00001356D:F06	4188
3268	1/28/98	383	RTA00000199F.f.20.2	M00003847B:G03	0
3269	1/28/98	132	RTA00000178AF.f.20.3	M00001372C:F07	39881
3270	1/28/98	296	RTA00000196AF.f.20.1	M00001371D:G01	22774
3271	1/28/98	297	RTA00000178AF.f.9.3	M00001371C:E09	7172
3272	1/28/98	240	RTA00000178AF.e.1.1	M00001369A:H12	2664
3273	1/28/98	16	RTA00000196AF.e.16.1	M00001363C:H02	39252
3274	1/28/98	112	RTA00000177AF.m.8.1	M00001354C:C10	8010
3275	1/28/98	154	RTA00000196F.e.7.1	M00001360D:E11	1039
3276	1/28/98	330	RTA00000177AR.m.17.4	M00001355B:G10	14391
3276	1/28/98	493	RTA00000177AF.m.17.1	M00001355B:G10	14391
3276	1/28/98	337	RTA00000177AR.m.17.3	M00001355B:G10	14391
3277	1/28/98	89	RTA00000177AF.n.8.3	M00001356D:F06	4188
3277	1/28/98	15	RTA00000177AR.n.8.1	M00001356D:F06	4188
3278	1/28/98	493	RTA00000177AF.m.17.1	M00001355B:G10	14391
3278	1/28/98	337	RTA00000177AR.m.17.3	M00001355B:G10	14391
3278	1/28/98	330	RTA00000177AR.m.17.4	M00001355B:G10	14391
3279	1/28/98	337	RTA00000177AR.m.17.3	M00001355B:G10	14391
3279	1/28/98	330	RTA00000177AR.m.17.4	M00001355B:G10	14391
3279	1/28/98	493	RTA00000177AF.m.17.1	M00001355B:G10	14391
3280	1/28/98	330	RTA00000177AR.m.17.4	M00001355B:G10	14391
3280	1/28/98	493	RTA00000177AF.m.17.1	M00001355B:G10	14391
3280	1/28/98	337	RTA00000177AR.m.17.3	M00001355B:G10	14391
3281	1/28/98	337	RTA00000177AR.m.17.3	M00001355B:G10	14391
3281	1/28/98	493	RTA00000177AF.m.17.1	M00001355B:G10	14391
3281	1/28/98	330	RTA00000177AR.m.17.4	M00001355B:G10	14391
3282	1/28/98	169	RTA00000196AF.g.24.1	M00001380C:F02	8685
3283	1/28/98	363	RTA00000196AF.e.14.1	M00001362C:A10	12850

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
3284	1/28/98	92	RTA00000198AF.j.18.1	M00001653B:G07	22759
3284	1/28/98	433	RTA00000198R.j.18.1	M00001653B:G07	22759
3285	1/28/98	537	RTA00000188AF.g.14.1	M00003774C:D02	0
3286	1/28/98	434	RTA00000187AR.d.2.2	M00001664C:H10	4892
3287	1/28/98	703	RTA00000198F.l.09.1	M00001664B:D06	3611
3288	1/28/98	430	RTA00000198R.k.23.1	M00001661B:C08	8995
3288	1/28/98	294	RTA00000198AF.k.23.1	M00001661B:C08	8995
3289	1/28/98	294	RTA00000198AF.k.23.1	M00001661B:C08	8995
3289	1/28/98	430	RTA00000198R.k.23.1	M00001661B:C08	8995
3290	1/28/98	754	RTA00000187AF.l.11.1	M00001681A:F03	4482
3291	1/28/98	732	RTA00000186AF.p.01.2	M00001654D:G11	40440
3292	1/28/98	475	RTA00000187AR.m.3.3	M00001682C:B12	17055
3293	1/28/98	433	RTA00000198R.j.18.1	M00001653B:G07	22759
3293	1/28/98	92	RTA00000198AF.j.18.1	M00001653B:G07	22759
3294	1/28/98	555	RTA00000198AF.j.08.1	M00001651B:A11	10983
3295	1/28/98	399	RTA00000186AF.m.15.2	M00001649C:B10	40122
3296	1/28/98	575	RTA00000186AF.l.12.2	M00001645A:C12	19267
3297	1/28/98	666	RTA00000198F.i.10.1	M00001640B:F03	12792
3298	1/28/98	654	RTA00000186AF.j.21.2	M00001639D:B07	22506
3299	1/28/98	670	RTA00000186AF.p.17.3	M00001656B:A07	38383
3300	1/28/98	393	RTA00000188AF.b.14.1	M00003754D:D02	0
3301	1/28/98	422	RTA00000189AF.b.12.1	M00003829B:G03	17233
3301	1/28/98	210	RTA00000189AR.b.12.1	M00003829B:G03	17233
3302	1/28/98	587	RTA00000199F.a.3.1	M00003772D:E10	16617
3303	1/28/98	394	RTA00000198AF.p.22.1	M00003771A:G10	0
3304	1/28/98	542	RTA00000198R.p.12.1	M00003763D:E10	8878
3304	1/28/98	64	RTA00000198AF.p.12.1	M00003763D:E10	8878
3305	1/28/98	64	RTA00000198AF.p.12.1	M00003763D:E10	8878
3305	1/28/98	542	RTA00000198R.p.12.1	M00003763D:E10	8878
3306	1/28/98	465	RTA00000187AF.k.20.1	M00001680B:C01	3648
3307	1/28/98	423	RTA00000188AR.b.17.1	M00003755A:B03	10662
3308	1/28/98	711	RTA00000198F.i.2.1	M00001637B:E07	8076
3309	1/28/98	497	RTA00000198AF.o.09.1	M00003751B:A05	4310
3309	1/28/98	506	RTA00000198R.o.09.1	M00003751B:A05	4310
3310	1/28/98	506	RTA00000198R.o.09.1	M00003751B:A05	4310
3310	1/28/98	497	RTA00000198AF.o.09.1	M00003751B:A05	4310
3311	1/28/98	432	RTA00000198AF.o.05.1	M00003750A:D01	26702
3311	1/28/98	49	RTA00000198R.o.05.1	M00003750A:D01	26702
3312	1/28/98	49	RTA00000198R.o.05.1	M00003750A:D01	26702
3312	1/28/98	432	RTA00000198AF.o.05.1	M00003750A:D01	26702
3313	1/28/98	585	RTA00000198AF.n.18.1	M00001771A:A07	16715
3314	1/28/98	527	RTA00000198R.m.23.1	M00001684B:G03	38469
3315	1/28/98	471	RTA00000188AF.e.2.1	M00003763B:H01	0
3316	1/28/98	171	RTA00000198R.c.07.1	M00001575D:G05	19181
3316	1/28/98	525	RTA00000198AF.c.7.1	M00001575D:G05	19181
3317	1/28/98	557	RTA00000198AF.d.9.1	M00001587D:A10	8841
3318	1/28/98	523	RTA00000198AF.d.4.1	M00001586D:E02	22435
3319	1/28/98	441	RTA00000185AF.e.6.1	M00001583B:E10	0
3320	1/28/98	439	RTA00000185AF.d.14.2	M00001579D:G07	8071
3321	1/28/98	561	RTA00000185AR.d.10.1	M00001579C:H10	0

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
3322	1/28/98	277	RTA00000198AR.i.08.1	M00001639A:F10	9807
3322	1/28/98	487	RTA00000198F.i.8.1	M00001639A:F10	9807
3323	1/28/98	525	RTA00000198AF.c.7.1	M00001575D:G05	19181
3323	1/28/98	171	RTA00000198R.c.07.1	M00001575D:G05	19181
3324	2/24/98	317	RTA00000195AF.b.21.1	M00001595B:A09	39055
3324	1/28/98	602	RTA00000195AF.b.21.1	M00001595B:A09	39055
3325	1/28/98	507	RTA00000198AF.c.5.1	M00001573D:F10	53802
3326	1/28/98	414	RTA00000185AR.b.15.1	M00001573D:F04	39813
3326	1/28/98	428	RTA00000185AF.b.15.2	M00001573D:F04	39813
3327	1/28/98	428	RTA00000185AF.b.15.2	M00001573D:F04	39813
3327	1/28/98	414	RTA00000185AR.b.15.1	M00001573D:F04	39813
3328	1/28/98	414	RTA00000185AR.b.15.1	M00001573D:F04	39813
3328	1/28/98	428	RTA00000185AF.b.15.2	M00001573D:F04	39813
3329	1/28/98	428	RTA00000185AF.b.15.2	M00001573D:F04	39813
3329	1/28/98	414	RTA00000185AR.b.15.1	M00001573D:F04	39813
3330	1/28/98	392	RTA00000185AF.b.11.2	M00001573C:D03	9024
3331	1/28/98	549	RTA00000198AF.c.16.1	M00001579C:B11	26801
3332	1/28/98	628	RTA00000198AF.g.16.1	M00001621D:D03	6602
3333	1/28/98	616	RTA00000188AF.m.07.1	M00003798D:E03	23183
3334	1/28/98	489	RTA00000186AF.h.22.1	M00001634B:C10	16485
3335	1/28/98	655	RTA00000186AF.g.8.2	M00001630B:A11	8065
3336	1/28/98	592	RTA00000186AF.e.18.1	M00001624C:A06	0
3337	1/28/98	713	RTA00000198AF.g.21.1	M00001624A:F09	6273
3338	1/28/98	554	RTA00000186AR.e.07.4	M00001623D:G03	4175
3338	1/28/98	400	RTA00000186AR.e.07.3	M00001623D:G03	4175
3339	1/28/98	467	RTA00000195AF.b.19.1	M00001589A:D12	77678
3340	1/28/98	646	RTA00000186AF.d.24.1	M00001623C:H07	3114
3341	1/28/98	740	RTA00000198AF.d.15.1	M00001590C:H08	5997
3342	1/28/98	504	RTA00000198AF.g.2.1	M00001615C:D02	16640
3343	1/28/98	470	RTA00000198AF.f.16.1	M00001614A:E06	0
3344	1/28/98	388	RTA00000185AF.n.17.1	M00001609B:A11	5336
3345	1/28/98	495	RTA00000185AF.j.21.1	M00001597A:E12	0
3346	2/24/98	317	RTA00000195AF.b.21.1	M00001595B:A09	39055
3346	1/28/98	602	RTA00000195AF.b.21.1	M00001595B:A09	39055
3347	1/28/98	487	RTA00000198F.i.8.1	M00001639A:F10	9807
3347	1/28/98	277	RTA00000198AR.i.08.1	M00001639A:F10	9807
3348	1/28/98	554	RTA00000186AR.e.07.4	M00001623D:G03	4175
3348	1/28/98	400	RTA00000186AR.e.07.3	M00001623D:G03	4175
3349	1/28/98	699	RTA00000178AF.a.12.1	M00001362B:H06	0
3350	1/28/98	416	RTA00000199F.a.5.1	M00003773B:G01	22134
3351	1/28/98	656	RTA00000178AR.h.22.3	M00001376B:A08	19230
3351	1/28/98	657	RTA00000178AR.h.22.2	M00001376B:A08	19230
3351	2/24/98	1137	RTA00000345F.d.03.1	M00001376B:A08	19230
3352	1/28/98	656	RTA00000178AR.h.22.3	M00001376B:A08	19230
3352	1/28/98	657	RTA00000178AR.h.22.2	M00001376B:A08	19230
3352	2/24/98	1137	RTA00000345F.d.03.1	M00001376B:A08	19230
3353	1/28/98	522	RTA00000178AR.h.17.2	M00001376A:C05	23824
3353	2/24/98	1095	RTA00000345F.c.12.1	M00001376A:C05	23824
3354	1/28/98	522	RTA00000178AR.h.17.2	M00001376A:C05	23824
3354	2/24/98	1095	RTA00000345F.c.12.1	M00001376A:C05	23824

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
3355	1/28/98	656	RTA00000178AR.h.22.3	M00001376B:A08	19230
3355	1/28/98	657	RTA00000178AR.h.22.2	M00001376B:A08	19230
3355	2/24/98	1137	RTA00000345F.d.03.1	M00001376B:A08	19230
3356	1/28/98	566	RTA00000195F.a.4.1	M00001372C:G12	20470
3357	1/28/98	657	RTA00000178AR.h.22.2	M00001376B:A08	19230
3357	1/28/98	656	RTA00000178AR.h.22.3	M00001376B:A08	19230
3357	2/24/98	1137	RTA00000345F.d.03.1	M00001376B:A08	19230
3358	1/28/98	605	RTA00000196F.e.9.1	M00001361A:H07	23300
3359	1/28/98	532	RTA00000177AF.o.4.1	M00001358C:C06	0
3360	1/28/98	493	RTA00000177AF.m.17.1	M00001355B:G10	14391
3360	1/28/98	330	RTA00000177AR.m.17.4	M00001355B:G10	14391
3360	1/28/98	337	RTA00000177AR.m.17.3	M00001355B:G10	14391
3361	1/28/98	330	RTA00000177AR.m.17.4	M00001355B:G10	14391
3361	1/28/98	493	RTA00000177AF.m.17.1	M00001355B:G10	14391
3361	1/28/98	337	RTA00000177AR.m.17.3	M00001355B:G10	14391
3362	1/28/98	337	RTA00000177AR.m.17.3	M00001355B:G10	14391
3362	1/28/98	493	RTA00000177AF.m.17.1	M00001355B:G10	14391
3362	1/28/98	330	RTA00000177AR.m.17.4	M00001355B:G10	14391
3363	1/28/98	742	RTA00000177AF.m.1.1	M00001353D:D10	14929
3364	1/28/98	547	RTA00000196AF.g.8.1	M00001375B:G12	39665
3365	1/28/98	510	RTA00000178AF.n.23.1	M00001387B:E02	3298
3366	1/28/98	606	RTA00000179AR.e.01.4	M00001395A:C09	2493
3367	2/24/98	1065	RTA00000195R.a.06.1	M00001394A:E04	35265
3367	1/28/98	595	RTA00000195R.a.06.1	M00001394A:E04	35265
3368	2/24/98	1065	RTA00000195R.a.06.1	M00001394A:E04	35265
3368	1/28/98	595	RTA00000195R.a.06.1	M00001394A:E04	35265
3369	1/28/98	370	RTA00000179AF.c.15.3	M00001392D:H06	2995
3369	1/28/98	460	RTA00000179AF.c.15.1	M00001392D:H06	2995
3370	1/28/98	370	RTA00000179AF.c.15.3	M00001392D:H06	2995
3370	1/28/98	460	RTA00000179AF.c.15.1	M00001392D:H06	2995
3371	1/28/98	657	RTA00000178AR.h.22.2	M00001376B:A08	19230
3371	1/28/98	656	RTA00000178AR.h.22.3	M00001376B:A08	19230
3371	2/24/98	1137	RTA00000345F.d.03.1	M00001376B:A08	19230
3372	1/28/98	675	RTA00000179AR.b.21.3	M00001392C:D05	4366
3372	2/24/98	1264	RTA00000345F.e.13.1	M00001392C:D05	4366
3373	1/28/98	168	RTA00000177AR.k.23.1	M00001352D:D02	35550
3373	1/28/98	463	RTA00000177AR.k.23.4	M00001352D:D02	35550
3374	1/28/98	652	RTA00000178AR.m.21.4	M00001385A:F12	7861
3374	1/28/98	653	RTA00000178AR.m.21.5	M00001385A:F12	7861
3375	1/28/98	653	RTA00000178AR.m.21.5	M00001385A:F12	7861
3375	1/28/98	652	RTA00000178AR.m.21.4	M00001385A:F12	7861
3376	1/28/98	672	RTA00000196AF.h.09.1	M00001382B:F12	8015
3377	1/28/98	668	RTA00000178AF.i.17.1	M00001377C:E12	0
3378	1/28/98	746	RTA00000178AF.i.01.2	M00001376B:F03	4
3379	1/28/98	656	RTA00000178AR.h.22.3	M00001376B:A08	19230
3379	1/28/98	657	RTA00000178AR.h.22.2	M00001376B:A08	19230
3379	2/24/98	1137	RTA00000345F.d.03.1	M00001376B:A08	19230
3380	1/28/98	675	RTA00000179AR.b.21.3	M00001392C:D05	4366
3380	2/24/98	1264	RTA00000345F.e.13.1	M00001392C:D05	4366
3381	1/28/98	651	RTA00000189AR.d.22.2	M00003844C:B11	6539

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
3382	1/28/98	444	RTA00000189AF.l.16.1	M00003879A:G05	0
3383	1/28/98	648	RTA00000199F.i.9.1	M00003878C:E04	7
3384	2/24/98	678	RTA00000195AF.c.24.1	M00003860D:H07	0
3384	1/28/98	412	RTA00000195AF.c.24.1	M00003860D:H07	0
3385	1/28/98	412	RTA00000195AF.c.24.1	M00003860D:H07	0
3385	2/24/98	678	RTA00000195AF.c.24.1	M00003860D:H07	0
3386	1/28/98	484	RTA00000199F.g.20.2	M00003860D:A01	15767
3387	1/28/98	398	RTA00000177AR.l.13.3	M00001353A:G12	8078
3388	1/28/98	556	RTA00000199F.f.17.2	M00003845D:B04	22905
3389	1/28/98	545	RTA00000196F.a.2.1	M00001338B:E02	3575
3390	1/28/98	406	RTA00000199F.f.09.2	M00003842B:D09	22907
3390	1/28/98	78	RTA00000199R.f.09.1	M00003842B:D09	22907
3391	1/28/98	78	RTA00000199R.f.09.1	M00003842B:D09	22907
3391	1/28/98	406	RTA00000199F.f.09.2	M00003842B:D09	22907
3392	1/28/98	692	RTA00000199F.e.4.1	M00003820B:C05	0
3393	1/28/98	458	RTA00000199R.d.16.1	M00003812C:A05	24191
3394	1/28/98	755	RTA00000199F.c.21.2	M00003803C:D09	5070
3395	1/28/98	505	RTA00000188AF.n.03.1	M00003801B:B10	9443
3396	1/28/98	714	RTA00000199R.g.07.1	M00003853D:D03	0
3397	1/28/98	724	RTA00000177AR.f.15.4	M00001345B:E10	9062
3398	1/28/98	623	RTA00000198R.b.24.1	M00001571D:B11	19047
3398	1/28/98	748	RTA00000198AF.b.24.1	M00001571D:B11	19047
3399	1/28/98	395	RTA00000196R.c.21.2	M00001352C:H10	0
3400	1/28/98	593	RTA00000196R.c.14.2	M00001352B:F04	23105
3400	1/28/98	485	RTA00000196AF.c.14.1	M00001352B:F04	23105
3401	1/28/98	485	RTA00000196AF.c.14.1	M00001352B:F04	23105
3401	1/28/98	593	RTA00000196R.c.14.2	M00001352B:F04	23105
3402	1/28/98	645	RTA00000177AF.k.9.1	M00001352A:E02	16245
3403	1/28/98	576	RTA00000196AF.c.7.1	M00001350B:G11	0
3404	1/28/98	737	RTA00000189AR.m.9.1	M00003880B:C08	2917
3405	1/28/98	728	RTA00000177AR.f.17.4	M00001345C:B01	8594
3406	1/28/98	453	RTA00000199AF.i.20.1	M00003881A:D09	9544
3407	1/28/98	440	RTA00000177AR.f.13.4	M00001345A:G11	10480
3408	1/28/98	680	RTA00000177AF.f.10.1	M00001345A:E01	6420
3409	1/28/98	573	RTA00000196AF.b.7.1	M00001344A:G07	7774
3410	1/28/98	402	RTA00000177AF.b.21.4	M00001341A:F12	4443
3411	1/28/98	702	RTA00000177AR.b.8.5	M00001340B:A06	17062
3412	1/28/98	463	RTA00000177AR.k.23.4	M00001352D:D02	35550
3412	1/28/98	168	RTA00000177AR.k.23.1	M00001352D:D02	35550
3413	1/28/98	600	RTA00000177AF.g.4.1	M00001346B:B07	4119
3414	1/28/98	280	RTA00000193AF.b.18.1	M00004233C:H09	7542
3415	1/28/98	748	RTA00000198AF.b.24.1	M00001571D:B11	19047
3415	1/28/98	623	RTA00000198R.b.24.1	M00001571D:B11	19047
3416	1/28/98	249	RTA00000200R.o.03.2	M00004257C:H06	22807
3416	1/28/98	178	RTA00000200F.o.03.1	M00004257C:H06	22807
3416	1/28/98	85	RTA00000200R.o.03.1	M00004257C:H06	22807
3417	1/28/98	282	RTA00000193AF.c.15.1	M00004248B:E08	3726
3418	1/28/98	307	RTA00000200F.n.05.2	M00004246C:A09	18989
3418	1/28/98	319	RTA00000200F.n.05.1	M00004246C:A09	18989
3419	1/28/98	319	RTA00000200F.n.05.1	M00004246C:A09	18989

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
3419	1/28/98	307	RTA00000200F.n.05.2	M00004246C:A09	18989
3420	1/28/98	85	RTA00000200R.o.03.1	M00004257C:H06	22807
3420	1/28/98	249	RTA00000200R.o.03.2	M00004257C:H06	22807
3420	1/28/98	178	RTA00000200F.o.03.1	M00004257C:H06	22807
3421	1/28/98	307	RTA00000200F.n.05.2	M00004246C:A09	18989
3421	1/28/98	319	RTA00000200F.n.05.1	M00004246C:A09	18989
3422	1/28/98	50	RTA00000201R.a.02.1	M00004295B:D02	35362
3422	1/28/98	235	RTA00000201AF.a.02.1	M00004295B:D02	35362
3423	1/28/98	251	RTA00000192AF.n.13.1	M00004197D:H01	8210
3424	1/28/98	47	RTA00000192AF.m.12.1	M00004191D:B11	0
3425	1/28/98	494	RTA00000200AF.k.1.1	M00004188C:A09	40049
3425	1/28/98	194	RTA00000200R.k.01.1	M00004188C:A09	40049
3426	1/28/98	494	RTA00000200AF.k.1.1	M00004188C:A09	40049
3426	1/28/98	194	RTA00000200R.k.01.1	M00004188C:A09	40049
3427	1/28/98	231	RTA00000192AF.l.13.2	M00004185C:C03	11443
3428	1/28/98	382	RTA00000200AF.j.6.1	M00004176B:E08	22902
3429	1/28/98	307	RTA00000200F.n.05.2	M00004246C:A09	18989
3429	1/28/98	319	RTA00000200F.n.05.1	M00004246C:A09	18989
3430	1/28/98	52	RTA00000201R.b.02.1	M00004319D:G09	22660
3431	1/28/98	271	RTA00000201F.d.02.1	M00004375A:H01	2599
3431	1/28/98	239	RTA00000201R.d.02.1	M00004375A:H01	2599
3431	1/28/98	227	RTA00000201R.d.02.2	M00004375A:H01	2599
3432	1/28/98	227	RTA00000201R.d.02.2	M00004375A:H01	2599
3432	1/28/98	239	RTA00000201R.d.02.1	M00004375A:H01	2599
3432	1/28/98	271	RTA00000201F.d.02.1	M00004375A:H01	2599
3433	1/28/98	227	RTA00000201R.d.02.2	M00004375A:H01	2599
3433	1/28/98	271	RTA00000201F.d.02.1	M00004375A:H01	2599
3433	1/28/98	239	RTA00000201R.d.02.1	M00004375A:H01	2599
3434	1/28/98	271	RTA00000201F.d.02.1	M00004375A:H01	2599
3434	1/28/98	239	RTA00000201R.d.02.1	M00004375A:H01	2599
3434	1/28/98	227	RTA00000201R.d.02.2	M00004375A:H01	2599
3435	1/28/98	227	RTA00000201R.d.02.2	M00004375A:H01	2599
3435	1/28/98	271	RTA00000201F.d.02.1	M00004375A:H01	2599
3435	1/28/98	239	RTA00000201R.d.02.1	M00004375A:H01	2599
3436	1/28/98	178	RTA00000200F.o.03.1	M00004257C:H06	22807
3436	1/28/98	249	RTA00000200R.o.03.2	M00004257C:H06	22807
3436	1/28/98	85	RTA00000200R.o.03.1	M00004257C:H06	22807
3437	1/28/98	273	RTA00000201F.c.08.1	M00004353C:H07	0
3438	1/28/98	328	RTA00000200AF.g.09.1	M00004131B:H09	22785
3438	1/28/98	26	RTA00000200R.g.09.1	M00004131B:H09	22785
3439	2/24/98	571	RTA00000355R.e.14.1	M00004314B:G07	16837
3439	1/28/98	343	RTA00000201F.a.18.1	M00004314B:G07	16837
3440	1/28/98	343	RTA00000201F.a.18.1	M00004314B:G07	16837
3440	2/24/98	571	RTA00000355R.e.14.1	M00004314B:G07	16837
3441	1/28/98	164	RTA00000193AR.i.14.4	M00004307C:A06	9457
3442	1/28/98	50	RTA00000201R.a.02.1	M00004295B:D02	35362
3442	1/28/98	235	RTA00000201AF.a.02.1	M00004295B:D02	35362
3443	1/28/98	235	RTA00000201AF.a.02.1	M00004295B:D02	35362
3443	1/28/98	50	RTA00000201R.a.02.1	M00004295B:D02	35362
3444	1/28/98	50	RTA00000201R.a.02.1	M00004295B:D02	35362

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
3444	1/28/98	235	RTA00000201AF.a.02.1	M00004295B:D02	35362
3445	1/28/98	227	RTA00000201R.d.02.2	M00004375A:H01	2599
3445	1/28/98	271	RTA00000201F.d.02.1	M00004375A:H01	2599
3445	1/28/98	239	RTA00000201R.d.02.1	M00004375A:H01	2599
3446	1/28/98	13	RTA00000190AF.i.5.1	M00003919A:A10	0
3447	1/28/98	72	RTA00000200F.a.6.1	M00004029B:F11	36952
3448	1/28/98	101	RTA00000191AF.d.08.2	M00003997B:G07	970
3449	1/28/98	79	RTA00000199AF.p.4.1	M00003985C:F01	10282
3450	1/28/98	121	RTA00000199AF.o.16.1	M00003979A:F03	16721
3451	1/28/98	193	RTA00000199AF.n.3.1	M00003946D:C11	0
3452	1/28/98	165	RTA00000192AF.g.23.1	M00004157C:A09	6455
3453	1/28/98	381	RTA00000199AF.m.14.1	M00003938A:B04	10580
3454	1/28/98	123	RTA00000191AF.k.6.1	M00004078B:A11	5451
3455	1/28/98	102	RTA00000199R.j.08.1	M00003884D:G07	37844
3456	1/28/98	86	RTA00000189AF.l.22.1	M00003879C:G10	33333
3457	1/28/98	148	RTA00000199F.h.17.2	M00003871A:A05	36254
3458	1/28/98	143	RTA00000199R.h.09.1	M00003867C:H09	76020
3459	1/28/98	266	RTA00000199F.f.21.2	M00003847C:E09	13344
3460	2/24/98	153	RTA00000422F.g.22.1	M00001585B:A06	22561
3461	1/28/98	292	RTA00000199AF.m.18.1	M00003939C:F04	0
3462	1/28/98	275	RTA00000191AF.o.17.2	M00004102A:H02	5957
3462	1/28/98	274	RTA00000191AF.o.17.1	M00004102A:H02	5957
3463	1/28/98	239	RTA00000201R.d.02.1	M00004375A:H01	2599
3463	1/28/98	271	RTA00000201F.d.02.1	M00004375A:H01	2599
3463	1/28/98	227	RTA00000201R.d.02.2	M00004375A:H01	2599
3464	1/28/98	328	RTA00000200AF.g.09.1	M00004131B:H09	22785
3464	1/28/98	26	RTA00000200R.g.09.1	M00004131B:H09	22785
3465	1/28/98	214	RTA00000200AF.f.22.1	M00004121C:F06	16521
3466	1/28/98	160	RTA00000192AF.b.20.1	M00004118D:E08	0
3467	1/28/98	98	RTA00000200AF.f.14.1	M00004115D:C08	22051
3467	1/28/98	100	RTA00000200R.f.14.1	M00004115D:C08	22051
3468	1/28/98	98	RTA00000200AF.f.14.1	M00004115D:C08	22051
3468	1/28/98	100	RTA00000200R.f.14.1	M00004115D:C08	22051
3469	1/28/98	305	RTA00000200AF.b.15.1	M00004040D:F01	10627
3470	1/28/98	98	RTA00000200AF.f.14.1	M00004115D:C08	22051
3470	1/28/98	100	RTA00000200R.f.14.1	M00004115D:C08	22051
3471	1/28/98	29	RTA00000200AF.b.19.1	M00004042D:H02	22847
3472	1/28/98	274	RTA00000191AF.o.17.1	M00004102A:H02	5957
3472	1/28/98	275	RTA00000191AF.o.17.2	M00004102A:H02	5957
3473	1/28/98	274	RTA00000191AF.o.17.1	M00004102A:H02	5957
3473	1/28/98	275	RTA00000191AF.o.17.2	M00004102A:H02	5957
3474	1/28/98	275	RTA00000191AF.o.17.2	M00004102A:H02	5957
3474	1/28/98	274	RTA00000191AF.o.17.1	M00004102A:H02	5957
3475	1/28/98	226	RTA00000191AR.o.09.4	M00004096A:G02	0
3476	1/28/98	40	RTA00000200AR.e.02.1	M00004090A:F09	36059
3477	1/28/98	175	RTA00000200F.i.5.1	M00004156B:A12	22892
3478	1/28/98	98	RTA00000200AF.f.14.1	M00004115D:C08	22051
3478	1/28/98	100	RTA00000200R.f.14.1	M00004115D:C08	22051
3479	1/28/98	643	RTA00000184AF.c.9.1	M00001546C:G10	16245
3480	1/28/98	615	RTA00000197R.p.20.1	M00001554B:B07	22795

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
3480	1/28/98	559	RTA00000197AF.p.20.1	M00001554B:B07	22795
3481	1/28/98	660	RTA00000197AF.p.16.1	M00001552D:G08	6013
3482	1/28/98	521	RTA00000197AF.p.12.1	M00001552B:G05	0
3483	1/28/98	403	RTA00000184AF.f.13.1	M00001550D:H02	3784
3484	1/28/98	517	RTA00000184AF.e.14.1	M00001549C:D02	16347
3485	1/28/98	676	RTA00000197AR.m.14.1	M00001531B:E09	14879
3486	1/28/98	596	RTA00000184AF.d.9.1	M00001548A:B11	6515
3487	1/28/98	559	RTA00000197AF.p.20.1	M00001554B:B07	22795
3487	1/28/98	615	RTA00000197R.p.20.1	M00001554B:B07	22795
3488	1/28/98	729	RTA00000184AF.a.19.1	M00001544C:C06	2628
3489	1/28/98	682	RTA00000125A.j.16.1	M00001544A:E06	0
3490	1/28/98	723	RTA00000183AF.p.24.1	M00001543C:F01	3116
3491	1/28/98	509	RTA00000183AF.p.17.1	M00001543A:H12	5158
3492	1/28/98	738	RTA00000183AF.o.8.1	M00001540C:B10	8927
3493	1/28/98	227	RTA00000201R.d.02.2	M00004375A:H01	2599
3493	1/28/98	271	RTA00000201F.d.02.1	M00004375A:H01	2599
3493	1/28/98	239	RTA00000201R.d.02.1	M00004375A:H01	2599
3494	1/28/98	502	RTA00000197AF.o.23.1	M00001549A:A09	12682
3495	1/28/98	468	RTA00000198AF.a.18.1	M00001561C:E11	0
3496	1/28/98	210	RTA00000189AR.b.12.1	M00003829B:G03	17233
3496	1/28/98	422	RTA00000189AF.b.12.1	M00003829B:G03	17233
3497	1/28/98	748	RTA00000198AF.b.24.1	M00001571D:B11	19047
3497	1/28/98	623	RTA00000198R.b.24.1	M00001571D:B11	19047
3498	1/28/98	397	RTA00000198AF.b.22.1	M00001571B:E03	38956
3499	1/28/98	571	RTA00000198AF.b.14.1	M00001569C:B06	801
3500	1/28/98	492	RTA00000198AF.b.8.1	M00001567C:H12	22636
3500	1/28/98	23	RTA00000198R.b.08.1	M00001567C:H12	22636
3501	1/28/98	492	RTA00000198AF.b.8.1	M00001567C:H12	22636
3501	1/28/98	23	RTA00000198R.b.08.1	M00001567C:H12	22636
3502	1/28/98	559	RTA00000197AF.p.20.1	M00001554B:B07	22795
3502	1/28/98	615	RTA00000197R.p.20.1	M00001554B:B07	22795
3503	1/28/98	727	RTA00000184AF.n.12.2	M00001561D:C11	3727
3504	1/28/98	559	RTA00000197AF.p.20.1	M00001554B:B07	22795
3504	1/28/98	615	RTA00000197R.p.20.1	M00001554B:B07	22795
3505	1/28/98	641	RTA00000198F.a.10.1	M00001558A:E11	6695
3506	1/28/98	731	RTA00000184F.k.02.1	M00001557B:H10	5192
3507	1/28/98	597	RTA00000198F.a.4.1	M00001557A:F01	9635
3508	1/28/98	560	RTA00000184AF.i.23.3	M00001556A:F11	1577
3509	1/28/98	601	RTA00000184AF.i.10.2	M00001555A:B01	3744
3510	1/28/98	700	RTA00000183AF.i.18.2	M00001529D:H02	40129
3511	1/28/98	437	RTA00000198R.a.23.1	M00001563B:D11	10700
3512	1/28/98	591	RTA00000197AF.h.1.1	M00001470A:H01	13075
3512	1/28/98	110	RTA00000197R.h.01.1	M00001470A:H01	13075
3513	1/28/98	259	RTA00000197AF.j.4.1	M00001492D:A11	17209
3513	1/28/98	386	RTA00000197AR.j.04.1	M00001492D:A11	17209
3514	1/28/98	386	RTA00000197AR.j.04.1	M00001492D:A11	17209
3514	1/28/98	259	RTA00000197AF.j.4.1	M00001492D:A11	17209
3515	1/28/98	644	RTA00000197F.i.12.1	M00001489B:A06	3605
3516	1/28/98	633	RTA00000197F.i.8.1	M00001488A:E01	6292
3517	1/28/98	546	RTA00000197F.i.6.1	M00001487C:D06	12149

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
3518	1/28/98	650	RTA00000183AR.n.17.1	M00001539B:H06	9800
3519	1/28/98	513	RTA00000197AF.h.14.1	M00001477B:F04	7045
3520	1/28/98	519	RTA00000183AF.a.24.2	M00001499B:A11	10539
3521	1/28/98	110	RTA00000197R.h.01.1	M00001470A:H01	13075
3521	1/28/98	591	RTA00000197AF.h.1.1	M00001470A:H01	13075
3522	1/28/98	446	RTA00000182AF.a.23.3	M00001463A:F06	9755
3523	1/28/98	739	RTA00000181AF.p.12.3	M00001460C:H02	22204
3524	1/28/98	635	RTA00000181AF.p.7.3	M00001460A:E01	38773
3525	1/28/98	720	RTA00000197AF.f.14.1	M00001459B:C09	3732
3526	1/28/98	623	RTA00000198R.b.24.1	M00001571D:B11	19047
3526	1/28/98	748	RTA00000198AF.b.24.1	M00001571D:B11	19047
3527	1/28/98	419	RTA00000182AF.j.20.1	M00001483B:D03	4769
3528	1/28/98	632	RTA00000183AR.g.03.1	M00001512D:G09	3956
3528	1/28/98	630	RTA00000183AR.g.03.2	M00001512D:G09	3956
3529	1/28/98	695	RTA00000197F.m.5.1	M00001528C:H04	10872
3530	1/28/98	479	RTA00000197R.l.22.1	M00001528A:C11	6962
3530	1/28/98	665	RTA00000197AF.l.22.1	M00001528A:C11	6962
3531	1/28/98	479	RTA00000197R.l.22.1	M00001528A:C11	6962
3531	1/28/98	665	RTA00000197AF.l.22.1	M00001528A:C11	6962
3532	1/28/98	479	RTA00000197R.l.22.1	M00001528A:C11	6962
3532	1/28/98	665	RTA00000197AF.l.22.1	M00001528A:C11	6962
3533	1/28/98	479	RTA00000197R.l.22.1	M00001528A:C11	6962
3533	1/28/98	665	RTA00000197AF.l.22.1	M00001528A:C11	6962
3534	1/28/98	550	RTA00000183AF.g.14.1	M00001513D:A03	0
3535	1/28/98	404	RTA00000195AF.b.6.1	M00001496C:G10	39490
3536	1/28/98	630	RTA00000183AR.g.03.2	M00001512D:G09	3956
3536	1/28/98	632	RTA00000183AR.g.03.1	M00001512D:G09	3956
3537	1/28/98	570	RTA00000183AF.a.19.2	M00001499A:A05	3788
3538	1/28/98	630	RTA00000183AR.g.03.2	M00001512D:G09	3956
3538	1/28/98	632	RTA00000183AR.g.03.1	M00001512D:G09	3956
3539	1/28/98	603	RTA00000183AR.d.11.3	M00001504D:G06	6420
3540	1/28/98	715	RTA00000197AR.k.11.1	M00001500D:E10	53758
3541	1/28/98	503	RTA00000197AF.k.9.1	M00001500C:C08	3138
3542	1/28/98	719	RTA00000183AF.b.12.1	M00001500A:B02	0
3543	1/28/98	271	RTA00000201F.d.02.1	M00004375A:H01	2599
3543	1/28/98	239	RTA00000201R.d.02.1	M00004375A:H01	2599
3543	1/28/98	227	RTA00000201R.d.02.2	M00004375A:H01	2599
3544	1/28/98	630	RTA00000183AR.g.03.2	M00001512D:G09	3956
3544	1/28/98	632	RTA00000183AR.g.03.1	M00001512D:G09	3956
3545	3/24/98	15	RTA00000425F.j.14.1	M00001639D:C12	73397
3546	3/24/98	111	RTA00000425F.d.08.1	M00001631A:F06	74350
3547	3/24/98	152	RTA00000425F.d.07.1	M00001631A:F12	43197
3548	3/24/98	147	RTA00000425F.d.21.1	M00001631B:H04	78920
3549	3/24/98	77	RTA00000425F.i.17.1	M00001633A:F11	43213
3550	3/24/98	418	RTA00000425F.i.18.1	M00001633A:G10	42255
3551	3/24/98	197	RTA00000425F.j.20.1	M00001633B:A12	26760
3552	3/24/98	143	RTA00000425F.j.22.1	M00001633B:E03	73882
3553	3/24/98	283	RTA00000425F.k.20.1	M00001633C:A08	74048
3554	3/24/98	139	RTA00000425F.k.22.1	M00001633C:E12	78123
3555	2/24/98	870	RTA00000418F.n.24.1	M00001659D:C09	73153

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
3556	3/24/98	403	RTA00000425F.n.17.1	M00001636A:H12	78304
3557	2/24/98	1109	RTA00000422F.f.22.1	M00001584A:G03	38703
3558	3/24/98	150	RTA00000424F.d.04.1	M00001478A:F12	76505
3558	3/24/98	149	RTA00000424F.d.04.3	M00001478A:F12	76505
3559	3/24/98	358	RTA00000425F.n.19.1	M00001638B:C08	78324
3560	3/24/98	165	RTA00000425F.e.21.1	M00001629D:D10	77203
3561	3/24/98	443	RTA00000425F.k.16.1	M00001640A:F05	75282
3562	3/24/98	252	RTA00000425F.m.03.1	M00001642D:G08	76045
3563	3/24/98	116	RTA00000425F.n.05.1	M00001647D:G07	73965
3564	3/24/98	425	RTA00000522F.i.07.2	M00001649A:E10	78377
3565	3/24/98	445	RTA00000522F.j.08.2	M00001650D:D10	76613
3566	3/24/98	371	RTA00000522F.j.09.2	M00001650D:F11	78522
3567	3/24/98	97	RTA00000522F.j.14.2	M00001651C:D11	73123
3568	3/24/98	69	RTA00000522F.j.15.2	M00001651C:G12	76535
3569	3/24/98	373	RTA00000522F.j.19.2	M00001652B:D06	76224
3570	3/24/98	93	RTA00000522F.k.14.1	M00001652D:G02	74280
3571	3/24/98	50	RTA00000522F.k.15.1	M00001652D:G06	76866
3572	3/24/98	141	RTA00000522F.k.19.1	M00001653A:A05	32625
3573	3/24/98	409	RTA00000425F.l.10.1	M00001638A:C08	26893
3574	2/24/98	443	RTA00000414F.f.15.1	M00005260A:A12	0
3575	2/24/98	886	RTA00000420F.m.15.1	M00005235B:F10	0
3576	2/24/98	260	RTA00000414F.e.08.1	M00005236A:E04	0
3577	2/24/98	734	RTA00000414F.e.09.1	M00005236A:G10	0
3578	2/24/98	1077	RTA00000414F.e.11.1	M00005236B:A12	0
3579	2/24/98	970	RTA00000414F.e.15.1	M00005236B:G03	0
3580	2/24/98	271	RTA00000414F.e.16.1	M00005236B:H10	0
3581	2/24/98	58	RTA00000420F.m.18.1	M00005254D:A10	0
3582	2/24/98	289	RTA00000420F.n.08.1	M00005257A:H11	0
3583	2/24/98	1033	RTA00000414F.e.19.1	M00005257C:E05	0
3584	2/24/98	793	RTA00000414F.e.21.1	M00005257C:G01	0
3585	2/24/98	36	RTA00000414F.e.22.1	M00005257D:A06	0
3586	2/24/98	852	RTA00000414F.f.03.1	M00005257D:G07	0
3587	3/24/98	341	RTA00000425F.d.06.1	M00001631A:D03	77660
3588	2/24/98	961	RTA00000420F.n.21.2	M00005259B:D12	0
3589	3/24/98	441	RTA00000528F.g.22.2	M00001630C:F09	920
3590	2/24/98	940	RTA00000414F.f.17.1	M00005260A:F04	0
3591	2/24/98	160	RTA00000414F.f.19.1	M00005260B:E11	0
3592	3/24/98	140	RTA00000424F.m.14.1	M00001612D:D12	77491
3593	3/24/98	34	RTA00000424F.m.15.1	M00001612D:F06	73759
3594	3/24/98	212	RTA00000424F.n.06.1	M00001613A:D02	74737
3595	3/24/98	308	RTA00000424F.k.23.1	M00001614A:B10	31061
3596	3/24/98	372	RTA00000424F.m.24.1	M00001614C:G07	77045
3597	3/24/98	396	RTA00000528F.g.05.2	M00001615C:E07	3770
3598	3/24/98	296	RTA00000425F.e.02.1	M00001625C:F10	76143
3599	3/24/98	99	RTA00000425F.c.20.1	M00001626D:A02	73581
3600	3/24/98	442	RTA00000425F.d.14.1	M00001629A:H09	13417
3601	3/24/98	357	RTA00000425F.e.19.1	M00001629D:B10	73409
3602	2/24/98	210	RTA00000419F.p.24.1	M00004039B:E12	63477
3603	2/24/98	501	RTA00000414F.f.05.1	M00005257D:H11	0
3604	2/24/98	561	RTA00000420F.e.10.1	M00004108D:G04	65899

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
3605	2/24/98	758	RTA00000407F.a.01.1	M00004039A:H11	12501
3606	2/24/98	688	RTA00000413F.d.23.1	M00004090B:H06	66030
3607	2/24/98	124	RTA00000420F.d.05.1	M00004092B:E05	64432
3608	2/24/98	329	RTA00000413F.e.16.1	M00004093C:C02	63836
3609	2/24/98	359	RTA00000420F.d.12.1	M00004096D:H03	64095
3610	2/24/98	429	RTA00000422F.c.17.1	M00004099D:F01	1360
3611	2/24/98	630	RTA00000413F.f.19.1	M00004100B:C07	65189
3612	2/24/98	439	RTA00000413F.g.23.1	M00004103B:E09	40700
3613	2/24/98	3	RTA00000420F.d.18.1	M00004105C:B05	63074
3614	2/24/98	1064	RTA00000420F.d.19.1	M00004105C:C08	43146
3615	2/24/98	671	RTA00000413F.h.12.1	M00004107A:A12	66929
3616	2/24/98	507	RTA00000420F.e.02.1	M00004107B:D07	40259
3617	2/24/98	319	RTA00000420F.b.21.1	M00004088D:B10	65057
3618	2/24/98	931	RTA00000420F.e.09.1	M00004108D:E07	66325
3619	2/24/98	840	RTA00000420F.b.20.1	M00004088D:B05	0
3620	2/24/98	545	RTA00000420F.e.15.1	M00004110A:A10	20190
3621	2/24/98	981	RTA00000420F.e.20.1	M00004110B:A07	64762
3622	3/24/98	370	RTA00000424F.d.19.3	M00001448B:A07	73180
3623	3/24/98	370	RTA00000424F.d.19.3	M00001448B:A07	73180
3624	3/24/98	189	RTA00000424F.d.22.3	M00001448B:G07	76189
3625	3/24/98	189	RTA00000424F.d.22.3	M00001448B:G07	76189
3626	3/24/98	92	RTA00000424F.a.24.4	M00001448D:E11	73951
3627	3/24/98	92	RTA00000424F.a.24.4	M00001448D:E11	73951
3628	3/24/98	279	RTA00000528F.b.03.1	M00001455A:D10	2078
3629	3/24/98	279	RTA00000528F.b.03.1	M00001455A:D10	2078
3630	3/24/98	480	RTA00000424F.d.17.3	M00001455A:E11	73958
3631	3/24/98	480	RTA00000424F.d.17.3	M00001455A:E11	73958
3632	2/24/98	583	RTA00000406F.i.17.1	M00003904B:C03	37902
3633	2/24/98	590	RTA00000407F.b.22.1	M00004108B:B02	37487
3634	2/24/98	1075	RTA00000413F.b.17.1	M00004078A:F07	21704
3635	2/24/98	544	RTA00000420F.l.21.2	M00005232A:H12	0
3636	1/28/98	684	RTA00000200AR.b.11.1	M00004040A:G12	12043
3636	2/24/98	1166	RTA00000347F.h.01.1	M00004040A:G12	12043
3637	1/28/98	684	RTA00000200AR.b.11.1	M00004040A:G12	12043
3637	2/24/98	1166	RTA00000347F.h.01.1	M00004040A:G12	12043
3638	2/24/98	1087	RTA00000401F.o.13.1	M00004040C:A01	3220
3639	2/24/98	114	RTA00000341F.m.21.1	M00004051D:E01	0
3640	2/24/98	811	RTA00000413F.a.12.1	M00004072D:F09	63403
3641	2/24/98	714	RTA00000420F.a.08.1	M00004073A:D10	19473
3642	1/28/98	387	RTA00000191AF.j.14.1	M00004073A:H12	1002
3642	2/24/98	632	RTA00000191AF.j.14.1	M00004073A:H12	1002
3643	1/28/98	387	RTA00000191AF.j.14.1	M00004073A:H12	1002
3643	2/24/98	632	RTA00000191AF.j.14.1	M00004073A:H12	1002
3644	2/24/98	964	RTA00000423F.l.15.1	M00004075B:G09	11219
3645	2/24/98	355	RTA00000420F.a.19.1	M00004076A:D12	34192
3646	2/24/98	745	RTA00000413F.b.04.1	M00004076D:H07	66427
3647	2/24/98	64	RTA00000413F.d.18.1	M00004090B:B04	65305
3648	2/24/98	698	RTA00000413F.b.16.1	M00004078A:E05	65126
3649	2/24/98	190	RTA00000419F.p.23.1	M00004039B:A05	64748
3650	2/24/98	903	RTA00000420F.a.21.1	M00004078B:C11	66241

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
3651	2/24/98	588	RTA00000420F.a.23.1	M00004078B:F12	42158
3652	2/24/98	1185	RTA00000413F.b.20.1	M00004079D:G08	66063
3653	2/24/98	619	RTA00000420F.b.04.1	M00004081A:E02	63820
3654	2/24/98	988	RTA00000407F.a.22.1	M00004081A:G01	15570
3655	2/24/98	705	RTA00000407F.a.23.1	M00004081C:A10	23489
3656	2/24/98	282	RTA00000407F.a.24.1	M00004083A:E08	37560
3657	2/24/98	835	RTA00000413F.c.10.1	M00004083B:C01	65600
3658	2/24/98	598	RTA00000420F.b.18.1	M00004086D:G08	66136
3659	2/24/98	335	RTA00000413F.d.02.1	M00004087B:A12	66172
3660	2/24/98	504	RTA00000413F.d.05.1	M00004087C:A01	64788
3661	2/24/98	76	RTA00000413F.d.16.1	M00004088C:F01	63331
3662	2/24/98	726	RTA00000420F.b.19.1	M00004088D:A11	36873
3663	2/24/98	521	RTA00000413F.b.14.1	M00004078A:C11	66591
3664	2/24/98	255	RTA00000419F.o.16.1	M00003989C:G05	62867
3665	2/24/98	665	RTA00000419F.p.20.1	M00004039A:C03	9458
3666	2/24/98	1234	RTA00000352R.c.20.1	M00003982A:B12	7339
3667	2/24/98	247	RTA00000412F.j.17.1	M00003982C:G04	64071
3668	2/24/98	1145	RTA00000423F.k.21.2	M00003984D:B08	37499
3669	2/24/98	993	RTA00000406F.o.05.1	M00003985B:G04	37894
3670	2/24/98	328	RTA00000423F.k.19.2	M00003985D:E10	17615
3671	2/24/98	254	RTA00000341F.l.15.1	M00003986B:A08	5294
3672	2/24/98	948	RTA00000419F.o.06.1	M00003986C:D09	64643
3673	2/24/98	661	RTA00000341F.l.16.1	M00003986D:C08	8479
3674	2/24/98	117	RTA00000341F.m.13.1	M00003987B:E12	26502
3675	2/24/98	1210	RTA00000419F.o.09.1	M00003987B:F08	66396
3676	2/24/98	460	RTA00000341F.j.12.1	M00003987C:G03	12195
3677	2/24/98	486	RTA00000346F.l.13.1	M00003980B:C11	7542
3678	2/24/98	723	RTA00000419F.o.15.1	M00003989C:D03	32487
3679	2/24/98	897	RTA00000419F.n.24.1	M00003980A:F04	65995
3680	2/24/98	92	RTA00000412F.l.04.1	M00003989D:F12	66372
3681	2/24/98	1014	RTA00000412F.l.14.1	M00004029B:F01	62792
3682	2/24/98	348	RTA00000412F.l.19.1	M00004029C:C05	65825
3683	2/24/98	284	RTA00000412F.l.21.1	M00004029C:G10	65183
3684	2/24/98	188	RTA00000406F.p.04.1	M00004030D:F11	37458
3685	2/24/98	812	RTA00000412F.o.05.1	M00004034A:A01	63575
3686	2/24/98	911	RTA00000406F.p.13.1	M00004034C:G02	8584
3687	2/24/98	230	RTA00000423F.k.01.1	M00004034D:E09	40426
3688	2/24/98	1076	RTA00000423F.k.09.1	M00004035B:H09	26630
3689	2/24/98	941	RTA00000419F.p.08.1	M00004036D:B04	65560
3690	2/24/98	1186	RTA00000419F.p.10.1	M00004036D:B09	41448
3691	2/24/98	42	RTA00000423F.k.17.2	M00004038A:F02	37512
3692	2/24/98	934	RTA00000414F.e.01.1	M00005233D:H07	0
3693	2/24/98	37	RTA00000406F.o.15.1	M00003988D:A08	37482
3694	2/24/98	1016	RTA00000406F.n.12.1	M00003960A:G07	37517
3695	1/28/98	584	RTA00000190AR.c.03.1	M00003904C:A08	0
3695	2/24/98	1069	RTA00000346F.k.05.1	M00003904C:A08	0
3696	1/28/98	584	RTA00000190AR.c.03.1	M00003904C:A08	0
3696	2/24/98	1069	RTA00000346F.k.05.1	M00003904C:A08	0
3697	2/24/98	489	RTA00000406F.j.19.1	M00003906A:F12	1685
3698	2/24/98	461	RTA00000412F.d.16.1	M00003906B:H06	26829

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
3699	2/24/98	558	RTA00000419F.m.04.1	M00003906C:C05	74367
3700	2/24/98	120	RTA00000401F.m.02.1	M00003907A:F01	1573
3701	2/24/98	628	RTA00000412F.d.19.1	M00003907B:C03	75743
3702	2/24/98	792	RTA00000406F.k.11.1	M00003907B:D05	38715
3703	2/24/98	292	RTA00000423F.i.18.1	M00003918A:D08	14996
3704	2/24/98	1192	RTA00000406F.m.17.1	M00003918A:F09	0
3705	2/24/98	9	RTA00000406F.n.02.1	M00003918C:H10	15051
3706	2/24/98	629	RTA00000352R.c.04.1	M00003924A:D08	71976
3707	2/24/98	438	RTA00000195R.d.09.1	M00003981C:B04	8537
3708	2/24/98	433	RTA00000419F.n.02.1	M00003958B:H08	65963
3709	2/24/98	147	RTA00000422F.c.02.1	M00004118B:A03	2902
3710	2/24/98	649	RTA00000412F.g.03.1	M00003971B:A10	64740
3711	2/24/98	1141	RTA00000347F.f.08.1	M00003972D:H02	5948
3712	2/24/98	252	RTA00000412F.g.24.1	M00003973C:C03	28741
3713	2/24/98	732	RTA00000412F.h.11.1	M00003974B:B11	63175
3714	2/24/98	181	RTA00000412F.h.21.1	M00003974D:F02	64348
3715	2/24/98	345	RTA00000412F.h.23.2	M00003974D:H04	65118
3716	2/24/98	148	RTA00000419F.n.04.1	M00003975C:F07	13102
3717	2/24/98	311	RTA00000419F.n.09.1	M00003977C:A06	66070
3718	2/24/98	1044	RTA00000419F.n.11.1	M00003977C:B03	66477
3719	2/24/98	652	RTA00000419F.n.12.1	M00003977D:A03	66086
3720	2/24/98	452	RTA00000419F.n.13.1	M00003977D:A06	66026
3721	2/24/98	796	RTA00000419F.n.15.1	M00003977D:D04	63484
3722	2/24/98	1249	RTA00000419F.n.17.1	M00003978D:G04	63186
3723	2/24/98	860	RTA00000419F.m.23.1	M00003958B:E11	64263
3724	2/24/98	713	RTA00000414F.b.10.1	M00005212D:D09	0
3725	2/24/98	1002	RTA00000419F.p.18.1	M00004038D:G06	63002
3726	2/24/98	1048	RTA00000413F.o.07.2	M00005100A:C01	0
3727	2/24/98	508	RTA00000420F.i.20.1	M00005101C:E12	0
3728	2/24/98	1001	RTA00000413F.p.07.2	M00005102C:D03	0
3729	2/24/98	88	RTA00000420F.i.24.1	M00005134B:E08	0
3730	2/24/98	93	RTA00000413F.p.24.1	M00005139A:H03	0
3731	2/24/98	142	RTA00000420F.j.19.1	M00005140C:B10	0
3732	2/24/98	833	RTA00000420F.j.20.1	M00005140D:C06	0
3733	2/24/98	316	RTA00000414F.a.02.1	M00005178D:H04	0
3734	2/24/98	1100	RTA00000414F.a.12.1	M00005210A:E06	0
3735	2/24/98	1175	RTA00000414F.b.04.1	M00005212B:E01	0
3736	2/24/98	1236	RTA00000414F.b.06.1	M00005212C:C03	0
3737	2/24/98	747	RTA00000413F.n.24.1	M00004960C:E10	0
3738	2/24/98	207	RTA00000414F.b.08.1	M00005212C:H02	0
3739	2/24/98	935	RTA00000420F.i.07.1	M00004960A:B08	0
3740	2/24/98	741	RTA00000414F.b.12.1	M00005212D:H01	0
3741	2/24/98	865	RTA00000414F.c.03.1	M00005216A:D09	0
3742	2/24/98	862	RTA00000414F.c.07.1	M00005216A:H01	0
3743	2/24/98	565	RTA00000420F.k.17.2	M00005217B:A06	0
3744	2/24/98	1226	RTA00000414F.c.12.1	M00005218A:F09	0
3745	2/24/98	512	RTA00000414F.c.16.1	M00005228A:B03	0
3746	2/24/98	817	RTA00000420F.l.08.2	M00005228C:C05	0
3747	2/24/98	573	RTA00000414F.c.23.1	M00005229B:G12	0
3748	2/24/98	1237	RTA00000414F.c.24.1	M00005229B:H04	0

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
3749	2/24/98	727	RTA00000414F.d.02.1	M00005229B:H06	0
3750	2/24/98	566	RTA00000414F.d.05.1	M00005229D:H03	0
3751	2/24/98	307	RTA00000420F.l.12.2	M00005230B:H09	0
3752	3/24/98	149	RTA00000424F.d.04.3	M00001478A:F12	76505
3752	3/24/98	150	RTA00000424F.d.04.1	M00001478A:F12	76505
3753	2/24/98	946	RTA00000414F.b.07.1	M00005212C:D02	0
3754	1/28/98	343	RTA00000201F.a.18.1	M00004314B:G07	16837
3754	2/24/98	571	RTA00000355R.e.14.1	M00004314B:G07	16837
3755	2/24/98	481	RTA00000413F.i.23.1	M00004118B:F01	63073
3756	2/24/98	1039	RTA00000407F.c.08.1	M00004118D:B05	37549
3757	2/24/98	824	RTA00000420F.f.07.1	M00004119A:C09	66312
3758	2/24/98	813	RTA00000346F.o.06.1	M00004136D:B02	4937
3759	2/24/98	1070	RTA00000346F.n.22.1	M00004137A:D06	0
3760	2/24/98	283	RTA00000346F.n.06.1	M00004139C:A12	12439
3761	2/24/98	368	RTA00000346F.o.08.1	M00004149C:B02	0
3762	2/24/98	704	RTA00000355R.a.12.1	M00004159C:F09	36756
3762	1/28/98	685	RTA00000200F.i.9.1	M00004159C:F09	36756
3763	1/28/98	685	RTA00000200F.i.9.1	M00004159C:F09	36756
3763	2/24/98	704	RTA00000355R.a.12.1	M00004159C:F09	36756
3764	2/24/98	1254	RTA00000341F.p.11.1	M00004159C:G12	0
3765	2/24/98	1188	RTA00000341F.o.18.1	M00004169D:B11	37189
3766	2/24/98	40	RTA00000352R.l.06.1	M00004187D:H06	40343
3767	2/24/98	456	RTA00000413F.o.06.1	M00005100A:B02	0
3768	2/24/98	882	RTA00000355R.c.03.1	M00004244C:G07	3986
3769	2/24/98	503	RTA00000420F.m.08.1	M00005233B:D04	0
3770	2/24/98	571	RTA00000355R.e.14.1	M00004314B:G07	16837
3770	1/28/98	343	RTA00000201F.a.18.1	M00004314B:G07	16837
3771	2/24/98	91	RTA00000355R.e.15.1	M00004316A:G09	22639
3771	1/28/98	410	RTA00000201F.a.20.1	M00004316A:G09	22639
3772	2/24/98	91	RTA00000355R.e.15.1	M00004316A:G09	22639
3772	1/28/98	410	RTA00000201F.a.20.1	M00004316A:G09	22639
3773	2/24/98	1135	RTA00000346F.o.16.1	M00004358D:C02	176
3774	2/24/98	220	RTA00000413F.k.02.1	M00004690A:G08	0
3775	2/24/98	487	RTA00000420F.g.05.1	M00004891B:D01	0
3776	2/24/98	102	RTA00000420F.g.06.1	M00004891C:D04	0
3777	2/24/98	1238	RTA00000420F.g.09.1	M00004895B:E12	0
3778	2/24/98	18	RTA00000420F.g.12.1	M00004895B:G04	0
3779	2/24/98	1196	RTA00000413F.l.18.1	M00004895D:G07	0
3780	2/24/98	579	RTA00000413F.m.16.1	M00004898C:F03	0
3781	2/24/98	143	RTA00000420F.h.13.1	M00004899D:G06	0
3782	2/24/98	909	RTA00000420F.i.04.1	M00004959D:H12	0
3783	2/24/98	709	RTA00000352R.p.09.1	M00004228C:H03	16915
3784	3/24/98	221	RTA00000427F.j.22.1	M00004097D:B05	66367
3785	3/24/98	188	RTA00000525F.c.15.1	M00004040A:A07	7692
3786	3/24/98	401	RTA00000525F.c.16.1	M00004040A:B04	38209
3787	3/24/98	53	RTA00000525F.c.17.1	M00004040A:C08	38160
3788	3/24/98	325	RTA00000525F.c.18.1	M00004040B:C05	24208
3789	3/24/98	159	RTA00000525F.c.19.1	M00004040B:F07	38159
3790	3/24/98	209	RTA00000427F.g.16.1	M00004069A:E12	63011
3791	3/24/98	123	RTA00000427F.g.05.1	M00004069C:C08	63138

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
3792	3/24/98	62	RTA00000427F.j.19.1	M00004077A:G12	41395
3793	3/24/98	265	RTA00000427F.h.02.1	M00004085B:G01	63652
3794	3/24/98	235	RTA00000427F.g.19.1	M00004087A:B05	64611
3795	3/24/98	333	RTA00000427F.k.21.1	M00004090D:F12	62880
3796	3/24/98	130	RTA00000427F.h.12.1	M00004092C:D08	36894
3797	3/24/98	243	RTA00000424F.c.15.3	M00001476D:F12	73533
3798	3/24/98	227	RTA00000427F.i.11.1	M00004097C:H08	26635
3799	3/24/98	456	RTA00000427F.a.10.1	M00004038B:D01	65370
3800	3/24/98	7	RTA00000523F.o.20.1	M00005177B:H02	0
3801	3/24/98	291	RTA00000523F.o.23.1	M00005177C:G04	0
3802	3/24/98	119	RTA00000523F.p.06.1	M00005177D:F09	0
3803	3/24/98	178	RTA00000428F.a.12.1	M00005179B:H02	0
3804	3/24/98	463	RTA00000523F.p.16.1	M00005179D:B03	0
3805	3/24/98	390	RTA00000524F.a.11.1	M00005210D:C09	0
3806	3/24/98	468	RTA00000524F.a.18.1	M00005211A:E09	0
3807	3/24/98	114	RTA00000524F.a.23.1	M00005211C:E09	0
3808	3/24/98	29	RTA00000524F.b.03.1	M00005212A:D10	0
3809	3/24/98	36	RTA00000428F.a.16.1	M00005212D:F08	0
3810	3/24/98	417	RTA00000524F.b.10.1	M00005213C:A01	0
3811	3/24/98	182	RTA00000524F.b.17.1	M00005214B:A06	0
3812	3/24/98	348	RTA00000427F.i.09.1	M00004097C:E03	65916
3813	3/24/98	384	RTA00000527F.p.03.1	M00004029B:A06	5940
3814	3/24/98	84	RTA00000527F.k.18.1	M00003982B:C10	11332
3815	3/24/98	48	RTA00000527F.k.21.1	M00003982B:H10	36051
3816	3/24/98	271	RTA00000527F.l.05.1	M00003983A:D02	13016
3817	3/24/98	246	RTA00000426F.m.21.1	M00003983A:F06	64915
3818	3/24/98	16	RTA00000426F.m.22.1	M00003983A:G02	30002
3819	3/24/98	367	RTA00000527F.l.19.1	M00003983D:E08	36856
3820	3/24/98	477	RTA00000527F.l.21.1	M00003983D:H02	36439
3821	3/24/98	126	RTA00000527F.m.05.1	M00003985A:C01	17240
3822	3/24/98	89	RTA00000527F.n.02.1	M00003986C:G11	24190
3823	3/24/98	263	RTA00000527F.n.07.1	M00003986D:H12	15939
3824	3/24/98	49	RTA00000527F.n.22.1	M00004027A:A08	24175
3825	3/24/98	449	RTA00000426F.m.04.1	M00004028A:B10	36865
3826	3/24/98	336	RTA00000426F.n.17.1	M00004039D:B10	66572
3827	3/24/98	27	RTA00000527F.p.02.1	M00004029B:A01	36844
3828	3/24/98	297	RTA00000525F.c.11.1	M00004039C:E02	37895
3829	3/24/98	17	RTA00000527F.p.06.1	M00004029B:G10	1292
3830	3/24/98	310	RTA00000527F.p.08.1	M00004029C:F02	36013
3831	3/24/98	478	RTA00000527F.p.09.1	M00004029C:F05	7694
3832	3/24/98	253	RTA00000426F.m.08.1	M00004030B:A12	63781
3833	3/24/98	414	RTA00000426F.m.12.1	M00004030B:D08	63740
3834	3/24/98	345	RTA00000426F.n.23.1	M00004030C:A08	18176
3835	3/24/98	98	RTA00000527F.p.16.1	M00004030C:C02	23798
3836	3/24/98	115	RTA00000525F.b.05.1	M00004034C:F05	21116
3837	3/24/98	444	RTA00000525F.b.09.1	M00004035B:F05	23472
3838	3/24/98	158	RTA00000427F.a.06.1	M00004036A:A11	66550
3839	3/24/98	376	RTA00000525F.b.21.1	M00004037C:D04	9486
3840	3/24/98	293	RTA00000525F.c.02.1	M00004038A:E05	14618
3841	3/24/98	138	RTA00000527F.c.22.1	M00003822B:G12	37496

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
3842	3/24/98	30	RTA00000426F.m.07.1	M00004028A:G03	63504
3843	3/24/98	322	RTA00000523F.i.17.1	M00003856B:A12	65779
3844	3/24/98	311	RTA00000428F.b.02.1	M00005214D:D10	0
3845	3/24/98	233	RTA00000426F.f.13.1	M00003851A:A06	65384
3846	3/24/98	274	RTA00000523F.h.06.1	M00003851B:D03	28745
3847	3/24/98	407	RTA00000523F.h.08.1	M00003851B:E01	62893
3848	3/24/98	82	RTA00000523F.h.15.1	M00003851C:F09	65137
3849	3/24/98	316	RTA00000523F.h.16.1	M00003851D:H11	66031
3850	3/24/98	232	RTA00000527F.i.13.2	M00003852B:G04	2924
3851	3/24/98	451	RTA00000527F.i.15.2	M00003852C:F07	14235
3852	3/24/98	249	RTA00000523F.h.21.1	M00003853B:C10	41440
3853	3/24/98	72	RTA00000426F.f.19.1	M00003854C:C09	66701
3854	3/24/98	60	RTA00000523F.i.06.1	M00003855A:A01	66341
3855	3/24/98	91	RTA00000527F.i.21.2	M00003855A:F01	37490
3856	3/24/98	137	RTA00000527F.h.17.1	M00003848D:G02	37799
3857	3/24/98	433	RTA00000527F.j.04.2	M00003856A:G04	11809
3858	3/24/98	157	RTA00000523F.g.10.1	M00003848B:E07	40694
3859	3/24/98	75	RTA00000523F.i.22.1	M00003857A:E12	64688
3860	3/24/98	481	RTA00000523F.j.02.1	M00003857A:H10	62853
3861	3/24/98	377	RTA00000527F.j.12.2	M00003857C:E05	37503
3862	3/24/98	286	RTA00000426F.g.19.1	M00003858B:G02	63672
3863	3/24/98	71	RTA00000527F.j.20.2	M00003860D:E06	37603
3864	3/24/98	205	RTA00000426F.h.12.1	M00003905C:F12	78093
3865	3/24/98	40	RTA00000426F.h.23.1	M00003911A:D12	75964
3866	3/24/98	369	RTA00000524F.c.08.1	M00005217C:C01	0
3867	3/24/98	234	RTA00000524F.c.16.1	M00005218D:G10	0
3868	3/24/98	8	RTA00000428F.b.06.1	M00005228A:A09	0
3869	3/24/98	193	RTA00000428F.b.12.1	M00005231C:B07	0
3870	3/24/98	419	RTA00000428F.b.22.1	M00005231D:B09	0
3871	2/24/98	486	RTA00000346F.l.13.1	M00003980B:C11	7542
3872	3/24/98	421	RTA00000523F.i.10.1	M00003855B:B09	64876
3873	3/24/98	10	RTA00000527F.f.12.1	M00003829D:D12	5945
3874	3/24/98	145	RTA00000426F.m.24.1	M00003981A:A07	63943
3875	3/24/98	39	RTA00000527F.c.23.1	M00003822C:A07	37742
3876	3/24/98	35	RTA00000426F.f.11.1	M00003823C:B01	63102
3877	3/24/98	385	RTA00000426F.f.12.1	M00003823C:C04	19096
3878	3/24/98	2	RTA00000523F.d.19.1	M00003824A:A06	26489
3879	3/24/98	225	RTA00000527F.d.09.1	M00003824A:G11	10848
3880	3/24/98	359	RTA00000523F.d.21.1	M00003824B:C09	33424
3881	3/24/98	330	RTA00000523F.d.23.1	M00003824C:A10	63633
3882	3/24/98	254	RTA00000523F.d.24.1	M00003824D:D08	64799
3883	3/24/98	74	RTA00000527F.d.19.1	M00003825B:F10	486
3884	3/24/98	67	RTA00000527F.e.03.1	M00003825D:F01	25560
3885	3/24/98	352	RTA00000527F.e.13.1	M00003826C:F05	37588
3886	3/24/98	185	RTA00000527F.h.21.1	M00003850C:G09	37630
3887	3/24/98	338	RTA00000523F.e.15.1	M00003829C:E08	7919
3888	3/24/98	284	RTA00000524F.b.19.1	M00005216B:D02	0
3889	3/24/98	242	RTA00000523F.e.20.1	M00003829D:F03	65164
3890	3/24/98	301	RTA00000527F.f.18.1	M00003830D:B11	37577
3891	3/24/98	259	RTA00000528F.m.04.1	M00003830D:H11	10815

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
3892	3/24/98	160	RTA00000523F.f.06.1	M00003833D:H08	62871
3893	3/24/98	166	RTA00000523F.f.07.1	M00003833D:H10	62799
3894	3/24/98	196	RTA00000523F.f.12.1	M00003840A:C10	63751
3895	3/24/98	447	RTA00000523F.f.19.1	M00003840B:F05	34169
3896	3/24/98	113	RTA00000527F.g.07.1	M00003840C:C02	37488
3897	3/24/98	45	RTA00000528F.m.12.1	M00003842D:F08	5768
3898	3/24/98	415	RTA00000527F.g.12.1	M00003845C:D04	37746
3899	3/24/98	1	RTA00000527F.g.13.1	M00003845D:A04	36035
3900	3/24/98	450	RTA00000527F.g.21.1	M00003846B:C05	36028
3901	3/24/98	144	RTA00000527F.g.23.1	M00003846C:F08	37538
3902	3/24/98	422	RTA00000527F.f.03.1	M00003829A:B08	17788
3903	3/24/98	176	RTA00000522F.g.15.1	M00001595B:G07	76536
3904	3/24/98	264	RTA00000425F.e.09.1	M00001608C:G04	75550
3905	3/24/98	32	RTA00000424F.n.14.1	M00001584D:C11	73008
3906	3/24/98	459	RTA00000425F.c.03.1	M00001585D:B12	74643
3907	3/24/98	124	RTA00000424F.m.12.1	M00001586C:H07	77675
3908	3/24/98	314	RTA00000522F.e.09.1	M00001589D:A01	32599
3909	3/24/98	262	RTA00000424F.k.03.1	M00001590D:B04	21289
3910	3/24/98	106	RTA00000424F.j.14.1	M00001592B:B02	74311
3911	3/24/98	424	RTA00000424F.k.10.1	M00001592D:H02	73232
3912	3/24/98	168	RTA00000424F.j.12.1	M00001594C:E05	73827
3913	3/24/98	420	RTA00000424F.j.13.1	M00001594C:H03	74485
3914	3/24/98	210	RTA00000522F.g.06.1	M00001594D:G11	78221
3915	3/24/98	439	RTA00000522F.g.10.1	M00001595A:C07	74294
3916	3/24/98	300	RTA00000424F.m.08.1	M00001584A:A07	19402
3917	3/24/98	355	RTA00000522F.g.12.1	M00001595A:E07	78783
3918	3/24/98	411	RTA00000424F.n.12.1	M00001582C:G02	41589
3919	3/24/98	238	RTA00000522F.g.17.1	M00001595B:G10	76486
3920	3/24/98	472	RTA00000522F.g.18.1	M00001595B:H11	73226
3921	3/24/98	102	RTA00000522F.g.19.1	M00001595C:A01	78119
3922	3/24/98	280	RTA00000522F.g.20.1	M00001595C:A05	77688
3923	3/24/98	191	RTA00000522F.g.22.1	M00001595C:B12	77504
3924	3/24/98	163	RTA00000522F.h.01.1	M00001595C:E05	75010
3925	3/24/98	438	RTA00000522F.h.02.1	M00001595C:E09	74947
3926	3/24/98	257	RTA00000522F.h.07.1	M00001595D:C11	75149
3927	3/24/98	389	RTA00000424F.i.15.1	M00001596A:A02	78043
3928	3/24/98	167	RTA00000424F.i.20.1	M00001596A:D01	44010
3929	3/24/98	374	RTA00000528F.f.10.1	M00001596C:G05	3600
3930	3/24/98	215	RTA00000425F.f.02.1	M00001607A:A01	76982
3931	3/24/98	22	RTA00000527F.k.15.1	M00003982A:G03	22688
3932	3/24/98	378	RTA00000522F.g.11.1	M00001595A:D12	75432
3933	3/24/98	63	RTA00000522F.b.01.1	M00001570C:B02	75691
3934	3/24/98	430	RTA00000424F.g.08.1	M00001482C:F09	74928
3935	3/24/98	340	RTA00000424F.h.06.1	M00001485C:D07	77552
3936	3/24/98	161	RTA00000424F.h.10.1	M00001485C:G06	72925
3937	3/24/98	368	RTA00000424F.i.11.1	M00001485D:A05	41569
3938	3/24/98	455	RTA00000424F.g.24.1	M00001487C:A11	79156
3939	3/24/98	211	RTA00000424F.h.03.1	M00001487C:G09	74447
3940	3/24/98	174	RTA00000424F.b.21.4	M00001530A:B02	24686
3941	3/24/98	383	RTA00000424F.b.23.4	M00001530A:H05	77322

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
3942	3/24/98	179	RTA00000424F.d.10.3	M00001530D:A11	73110
3943	3/24/98	393	RTA00000424F.b.15.4	M00001539B:B10	74958
3944	3/24/98	347	RTA00000522F.a.05.1	M00001567A:C04	32611
3945	3/24/98	303	RTA00000522F.a.06.1	M00001567A:C11	73662
3946	3/24/98	229	RTA00000424F.n.13.1	M00001584D:B06	74942
3947	3/24/98	392	RTA00000522F.a.20.1	M00001567C:E07	74070
3948	3/24/98	226	RTA00000425F.e.15.1	M00001608D:F11	75921
3949	3/24/98	285	RTA00000522F.b.07.1	M00001570D:E05	78634
3950	3/24/98	465	RTA00000528F.d.04.1	M00001570D:E07	2395
3951	3/24/98	404	RTA00000522F.b.18.1	M00001573B:A06	3460
3952	3/24/98	9	RTA00000522F.b.22.1	M00001573B:H12	75181
3953	3/24/98	109	RTA00000424F.a.01.4	M00001575A:D05	43214
3953	3/24/98	125	RTA00000424F.a.01.1	M00001575A:D05	43214
3954	3/24/98	125	RTA00000424F.a.01.1	M00001575A:D05	43214
3954	3/24/98	109	RTA00000424F.a.01.4	M00001575A:D05	43214
3955	3/24/98	294	RTA00000424F.a.05.1	M00001575B:C01	77976
3955	3/24/98	292	RTA00000424F.a.05.4	M00001575B:C01	77976
3956	3/24/98	292	RTA00000424F.a.05.4	M00001575B:C01	77976
3956	3/24/98	294	RTA00000424F.a.05.1	M00001575B:C01	77976
3957	3/24/98	434	RTA00000522F.c.11.1	M00001576C:H02	31064
3958	3/24/98	299	RTA00000522F.c.14.1	M00001577A:A03	75449
3959	3/24/98	110	RTA00000522F.d.08.1	M00001578B:A06	74284
3960	3/24/98	306	RTA00000522F.d.23.1	M00001579D:F02	73868
3961	3/24/98	350	RTA00000424F.n.11.1	M00001582C:C04	73874
3962	3/24/98	366	RTA00000522F.a.17.1	M00001567C:B08	79032
3963	3/24/98	239	RTA00000523F.j.17.1	M00003966B:A04	63610
3964	3/24/98	405	RTA00000425F.e.07.1	M00001608C:D02	75992
3965	3/24/98	231	RTA00000426F.e.17.1	M00003810C:B06	64089
3966	3/24/98	104	RTA00000527F.b.18.1	M00003810D:H09	37469
3967	3/24/98	312	RTA00000426F.f.17.1	M00003811C:C02	66334
3968	3/24/98	266	RTA00000426F.f.16.1	M00003813B:F02	65613
3969	3/24/98	183	RTA00000527F.c.04.1	M00003813C:H08	23090
3970	3/24/98	435	RTA00000523F.c.13.1	M00003813D:B12	40668
3971	3/24/98	255	RTA00000523F.c.14.1	M00003813D:C02	66015
3972	3/24/98	131	RTA00000523F.c.15.1	M00003813D:G06	36935
3973	3/24/98	270	RTA00000426F.g.16.1	M00003814B:C01	41446
3974	3/24/98	95	RTA00000523F.c.18.1	M00003817C:A10	66179
3975	3/24/98	329	RTA00000527F.c.09.1	M00003817C:G06	64859
3976	3/24/98	65	RTA00000523F.c.01.1	M00003810A:A02	65710
3977	3/24/98	398	RTA00000527F.c.16.1	M00003821A:H09	22908
3978	3/24/98	96	RTA00000523F.b.13.1	M00003809B:A03	66330
3979	3/24/98	313	RTA00000523F.j.21.1	M00003966C:A12	36925
3980	3/24/98	86	RTA00000523F.k.01.1	M00003966C:F03	41437
3981	3/24/98	26	RTA00000427F.b.23.1	M00003973D:F08	64297
3982	3/24/98	277	RTA00000427F.e.08.1	M00003974D:E01	47387
3983	3/24/98	397	RTA00000427F.e.10.1	M00003974D:H07	64599
3984	3/24/98	31	RTA00000427F.c.10.1	M00003976B:E06	65478
3985	3/24/98	151	RTA00000427F.c.12.1	M00003976B:H07	66995
3986	3/24/98	57	RTA00000427F.c.20.1	M00003978A:E01	26527
3987	3/24/98	213	RTA00000427F.c.22.1	M00003978A:E09	63990

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
3988	3/24/98	289	RTA00000427F.d.10.1	M00003978C:A12	40685
3989	3/24/98	28	RTA00000427F.d.08.1	M00003980C:E12	63967
3990	3/24/98	335	RTA00000427F.d.09.1	M00003980C:F12	66486
3991	3/24/98	267	RTA00000425F.i.21.1	M00001635B:B02	75305
3992	3/24/98	343	RTA00000527F.c.11.1	M00003817D:D12	37484
3993	3/24/98	251	RTA00000425F.f.24.1	M00001656D:C04	40841
3994	3/24/98	155	RTA00000424F.l.19.1	M00001609C:A12	75454
3995	3/24/98	321	RTA00000424F.m.04.1	M00001609C:G05	79017
3996	3/24/98	214	RTA00000424F.k.12.1	M00001610C:B07	77666
3997	3/24/98	446	RTA00000425F.f.20.1	M00001653D:H07	74071
3998	3/24/98	428	RTA00000522F.l.08.1	M00001654A:E08	78781
3999	3/24/98	295	RTA00000522F.l.15.1	M00001654B:A01	74691
4000	3/24/98	275	RTA00000522F.l.22.1	M00001654C:D10	75801
4001	3/24/98	223	RTA00000522F.m.02.1	M00001654C:G07	76834
4002	3/24/98	391	RTA00000522F.m.03.1	M00001654C:G09	79194
4003	3/24/98	346	RTA00000522F.m.19.1	M00001655C:C07	41544
4004	3/24/98	51	RTA00000522F.n.02.1	M00001655D:E08	74959
4005	3/24/98	94	RTA00000522F.n.05.1	M00001655D:H11	73260
4006	3/24/98	332	RTA00000523F.c.03.1	M00003810B:B11	36913
4007	3/24/98	172	RTA00000425F.f.11.1	M00001656C:C04	79275
4008	3/24/98	58	RTA00000527F.k.06.1	M00003981B:B12	12469
4009	3/24/98	240	RTA00000522F.n.14.1	M00001657C:C11	73410
4010	3/24/98	56	RTA00000522F.n.16.1	M00001657D:A10	26769
4011	3/24/98	20	RTA00000522F.o.06.1	M00001659D:A09	26860
4012	3/24/98	38	RTA00000528F.i.22.1	M00001661D:D05	2478
4013	3/24/98	413	RTA00000425F.i.10.1	M00001664B:E08	78736
4014	3/24/98	412	RTA00000425F.i.11.1	M00001664B:F06	21716
4015	3/24/98	202	RTA00000528F.j.11.1	M00001669B:C12	1070
4016	3/24/98	432	RTA00000522F.o.20.1	M00001669C:B09	74853
4017	3/24/98	245	RTA00000522F.p.09.1	M00001670A:F09	75204
4018	3/24/98	331	RTA00000528F.k.10.1	M00001678C:F09	1981
4019	3/24/98	356	RTA00000523F.a.07.1	M00001693A:H06	75804
4020	3/24/98	200	RTA00000527F.a.13.1	M00003805D:E06	37740
4021	3/24/98	14	RTA00000523F.b.02.1	M00003806C:A06	65163
4022	3/24/98	177	RTA00000522F.n.12.1	M00001656A:H12	74117
4023	2/24/98	1158	RTA00000405F.o.03.1	M00003829C:H05	37575
4024	2/24/98	1181	RTA00000346F.f.14.1	M00003800B:F03	16998
4025	2/24/98	610	RTA00000419F.d.07.1	M00003820B:D10	21421
4026	2/24/98	1227	RTA00000411F.g.05.1	M00003822D:B10	64664
4027	2/24/98	412	RTA00000411F.g.06.1	M00003822D:C06	66065
4028	2/24/98	21	RTA00000411F.g.08.1	M00003822D:D04	45815
4029	2/24/98	1208	RTA00000347F.e.24.1	M00003823B:F07	8188
4030	2/24/98	502	RTA00000341F.d.08.1	M00003824C:D07	0
4031	2/24/98	528	RTA00000405F.n.16.1	M00003825B:B10	21503
4032	2/24/98	15	RTA00000419F.c.19.1	M00003820A:A08	64346
4033	2/24/98	637	RTA00000419F.d.14.1	M00003828A:D05	64945
4034	2/24/98	81	RTA00000419F.c.16.1	M00003819D:B01	65254
4035	2/24/98	754	RTA00000419F.e.02.1	M00003830C:A03	65010
4036	2/24/98	430	RTA00000419F.e.04.1	M00003831C:G05	62963
4037	2/24/98	541	RTA00000411F.h.15.1	M00003832A:A09	65160

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
4038	2/24/98	1079	RTA00000419F.e.10.1	M00003833B:B03	63225
4039	2/24/98	577	RTA00000419F.e.11.1	M00003833B:C12	36780
4040	2/24/98	1220	RTA00000419F.e.23.1	M00003834B:G04	65772
4041	2/24/98	691	RTA00000354R.n.08.1	M00003835A:A09	8802
4042	2/24/98	536	RTA00000411F.i.02.1	M00003835B:H11	66975
4043	2/24/98	421	RTA00000419F.f.10.1	M00003835D:G06	66193
4044	2/24/98	1150	RTA00000411F.g.24.1	M00003825B:B11	65233
4045	2/24/98	533	RTA00000423F.e.11.1	M00003809B:E10	2566
4046	2/24/98	520	RTA00000406F.c.20.1	M00003871D:G06	38578
4047	2/24/98	41	RTA00000419F.b.12.1	M00003806B:C09	63148
4048	2/24/98	917	RTA00000423F.e.21.1	M00003806B:G05	66961
4049	2/24/98	326	RTA00000419F.b.15.1	M00003806D:D11	43969
4050	2/24/98	297	RTA00000419F.b.18.1	M00003808D:D08	67034
4051	2/24/98	139	RTA00000419F.b.19.1	M00003809A:C01	65534
4052	2/24/98	1021	RTA00000419F.b.21.1	M00003809A:F01	65366
4053	2/24/98	1152	RTA00000405F.m.07.1	M00003809B:B02	37733
4054	2/24/98	310	RTA00000419F.d.06.1	M00003820B:D07	65496
4055	2/24/98	120	RTA00000401F.m.02.1	M00003907A:F01	1573
4056	2/24/98	69	RTA00000405F.o.18.1	M00003839A:D07	11016
4057	2/24/98	482	RTA00000411F.e.24.1	M00003813A:B02	64781
4058	2/24/98	50	RTA00000411F.f.02.1	M00003813A:D08	63386
4059	2/24/98	602	RTA00000411F.f.06.1	M00003813B:E09	64186
4060	2/24/98	761	RTA00000411F.f.14.1	M00003814B:C12	62984
4061	2/24/98	674	RTA00000411F.f.17.1	M00003814B:F12	65661
4062	2/24/98	1164	RTA00000405F.m.21.1	M00003815C:C06	24218
4063	2/24/98	951	RTA00000419F.c.04.1	M00003815C:D12	63749
4064	2/24/98	471	RTA00000419F.c.11.1	M00003817B:C04	65504
4065	2/24/98	1047	RTA00000419F.c.14.1	M00003819B:G01	65727
4066	2/24/98	1178	RTA00000400F.f.11.1	M00001636A:E07	4088
4067	2/24/98	89	RTA00000406F.c.08.1	M00003870C:A10	22387
4068	2/24/98	94	RTA00000406F.a.23.1	M00003867B:D10	38712
4069	2/24/98	1038	RTA00000406F.b.01.1	M00003867B:G07	39006
4070	2/24/98	783	RTA00000406F.b.02.1	M00003867B:G08	38744
4071	2/24/98	563	RTA00000406F.b.08.1	M00003867D:A06	18258
4072	2/24/98	1072	RTA00000419F.j.03.1	M00003868B:G06	77578
4073	2/24/98	846	RTA00000419F.j.11.1	M00003868C:C07	73183
4074	2/24/98	17	RTA00000411F.m.15.1	M00003868D:B09	78014
4075	2/24/98	589	RTA00000411F.m.18.1	M00003868D:D09	75629
4076	2/24/98	971	RTA00000411F.i.11.1	M00003837C:E05	66849
4077	2/24/98	794	RTA00000406F.c.06.1	M00003870C:A01	37924
4078	2/24/98	788	RTA00000419F.i.04.1	M00003860B:F11	65791
4079	2/24/98	883	RTA00000406F.c.09.1	M00003870C:E10	5671
4080	2/24/98	918	RTA00000419F.j.22.1	M00003871A:A02	73525
4081	2/24/98	757	RTA00000423F.h.13.1	M00003871A:B09	14398
4082	2/24/98	208	RTA00000419F.j.23.1	M00003871A:C11	74470
4083	2/24/98	1127	RTA00000401F.g.22.1	M00003871A:G09	1147
4084	2/24/98	1205	RTA00000419F.k.05.1	M00003871C:E04	11757
4085	2/24/98	522	RTA00000406F.c.18.1	M00003871C:F12	14368
4086	2/24/98	459	RTA00000419F.k.06.1	M00003871D:A10	78493
4087	2/24/98	965	RTA00000411F.n.06.1	M00003871D:E11	73886

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
4088	2/24/98	457	RTA00000411F.m.19.1	M00003868D:D11	74924
4089	2/24/98	145	RTA00000419F.g.12.1	M00003842C:G03	66171
4090	2/24/98	633	RTA00000341F.d.02.1	M00003797A:G03	4706
4091	2/24/98	1026	RTA00000419F.f.18.1	M00003839D:E11	64047
4092	2/24/98	524	RTA00000419F.f.23.1	M00003840D:H10	65002
4093	2/24/98	204	RTA00000351R.k.19.1	M00003841B:E03	936
4094	2/24/98	968	RTA00000419F.f.24.1	M00003841B:E06	18717
4095	2/24/98	209	RTA00000411F.j.02.1	M00003841C:D07	65310
4096	2/24/98	1118	RTA00000411F.j.03.1	M00003841C:F01	66263
4097	2/24/98	470	RTA00000411F.j.06.1	M00003841C:H08	63545
4098	2/24/98	1153	RTA00000411F.j.07.1	M00003841C:H11	66963
4099	1/28/98	412	RTA00000195AF.c.24.1	M00003860D:H07	0
4099	2/24/98	678	RTA00000195AF.c.24.1	M00003860D:H07	0
4100	2/24/98	777	RTA00000419F.g.02.1	M00003842A:A03	62839
4101	2/24/98	678	RTA00000195AF.c.24.1	M00003860D:H07	0
4101	1/28/98	412	RTA00000195AF.c.24.1	M00003860D:H07	0
4102	2/24/98	799	RTA00000411F.j.15.1	M00003843A:E04	66871
4103	2/24/98	932	RTA00000405F.p.03.1	M00003844A:A11	11346
4104	2/24/98	266	RTA00000419F.g.15.1	M00003844D:A07	32519
4105	2/24/98	547	RTA00000419F.h.02.1	M00003845D:G08	63985
4106	2/24/98	290	RTA00000411F.k.16.1	M00003852C:B06	64759
4107	2/24/98	23	RTA00000411F.k.20.1	M00003854B:A07	64973
4108	2/24/98	1138	RTA00000411F.k.21.1	M00003854B:D04	65349
4109	2/24/98	1000	RTA00000351R.j.21.1	M00003859D:C05	31604
4110	2/24/98	980	RTA00000411F.i.13.1	M00003837C:F10	66138
4111	2/24/98	112	RTA00000422F.c.11.1	M00003841D:A04	2643
4112	2/24/98	905	RTA00000405F.g.21.2	M00001673B:F07	38966
4112	2/24/98	906	RTA00000405F.g.21.1	M00001673B:F07	38966
4113	2/24/98	294	RTA00000405F.l.17.1	M00003805A:F02	17225
4114	2/24/98	105	RTA00000346F.d.08.1	M00001671A:A10	39955
4115	2/24/98	1190	RTA00000405F.g.02.2	M00001671B:G05	10567
4116	2/24/98	280	RTA00000418F.p.15.1	M00001671C:C11	31066
4117	2/24/98	1151	RTA00000405F.g.18.2	M00001672D:E08	5255
4118	2/24/98	66	RTA00000405F.g.19.2	M00001673A:G08	37150
4119	2/24/98	1239	RTA00000340F.o.22.1	M00001673B:B07	7356
4120	2/24/98	906	RTA00000405F.g.21.1	M00001673B:F07	38966
4120	2/24/98	905	RTA00000405F.g.21.2	M00001673B:F07	38966
4121	2/24/98	893	RTA00000418F.p.10.1	M00001669D:F05	75323
4122	2/24/98	906	RTA00000405F.g.21.1	M00001673B:F07	38966
4122	2/24/98	905	RTA00000405F.g.21.2	M00001673B:F07	38966
4123	2/24/98	808	RTA00000418F.p.08.1	M00001669D:D06	73983
4124	2/24/98	469	RTA00000405F.g.24.1	M00001673D:D06	39076
4125	2/24/98	1094	RTA00000405F.h.03.2	M00001673D:F10	20633
4126	2/24/98	803	RTA00000405F.h.05.2	M00001674A:G07	75706
4127	2/24/98	667	RTA00000405F.h.07.2	M00001674A:G11	4984
4128	2/24/98	276	RTA00000423F.a.18.1	M00001675A:G10	26761
4129	2/24/98	1050	RTA00000405F.f.05.2	M00001669C:D09	14359
4129	2/24/98	1049	RTA00000405F.f.05.1	M00001669C:D09	14359
4130	2/24/98	1050	RTA00000405F.f.05.2	M00001669C:D09	14359
4130	2/24/98	1049	RTA00000405F.f.05.1	M00001669C:D09	14359

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
4131	2/24/98	104	RTA00000421F.n.03.1	M00001675C:A04	1638
4132	2/24/98	388	RTA00000411F.a.07.1	M00001675C:C03	74547
4133	2/24/98	906	RTA00000405F.g.21.1	M00001673B:F07	38966
4133	2/24/98	905	RTA00000405F.g.21.2	M00001673B:F07	38966
4134	2/24/98	222	RTA00000405F.e.09.1	M00001663C:F12	38978
4135	2/24/98	518	RTA00000410F.m.18.1	M00001660B:A09	76365
4136	2/24/98	218	RTA00000346F.e.13.1	M00001660B:D03	74653
4137	2/24/98	427	RTA00000410F.m.20.1	M00001660B:E03	74285
4138	2/24/98	1099	RTA00000400F.m.16.1	M00001660B:E04	3307
4139	2/24/98	775	RTA00000405F.c.22.1	M00001660C:B06	39053
4140	2/24/98	28	RTA00000422F.p.06.2	M00001661A:B11	39282
4141	2/24/98	108	RTA00000418F.o.18.1	M00001661B:F06	78676
4142	2/24/98	954	RTA00000410F.n.05.1	M00001662A:C07	77830
4143	2/24/98	1182	RTA00000346F.d.21.1	M00001670B:G12	6641
4144	2/24/98	1043	RTA00000423F.b.17.1	M00001662B:F06	8200
4145	2/24/98	447	RTA00000423F.b.04.3	M00001675D:E10	6311
4146	2/24/98	305	RTA00000418F.p.06.1	M00001664A:F08	32628
4147	2/24/98	1116	RTA00000410F.o.04.1	M00001664D:F04	79018
4148	2/24/98	320	RTA00000422F.p.07.2	M00001661A:E06	39024
4149	2/24/98	197	RTA00000410F.o.05.1	M00001669A:B02	75262
4150	2/24/98	738	RTA00000422F.n.20.1	M00001669B:B12	38676
4151	2/24/98	495	RTA00000400F.o.21.1	M00001669C:C08	16259
4152	2/24/98	1050	RTA00000405F.f.05.2	M00001669C:D09	14359
4152	2/24/98	1049	RTA00000405F.f.05.1	M00001669C:D09	14359
4153	2/24/98	1049	RTA00000405F.f.05.1	M00001669C:D09	14359
4153	2/24/98	1050	RTA00000405F.f.05.2	M00001669C:D09	14359
4154	2/24/98	492	RTA00000340F.o.18.1	M00001669D:C03	4261
4155	2/24/98	61	RTA00000410F.n.07.1	M00001662A:G01	78823
4156	2/24/98	299	RTA00000405F.l.15.1	M00001694A:E03	19575
4157	2/24/98	475	RTA00000411F.d.05.1	M00001681C:A08	75812
4158	2/24/98	692	RTA00000411F.d.10.1	M00001681D:C12	76445
4159	2/24/98	336	RTA00000340F.n.13.1	M00001688D:B10	17055
4160	2/24/98	270	RTA00000411F.d.15.1	M00001692A:B06	74890
4161	2/24/98	969	RTA00000411F.d.18.1	M00001692A:G06	76063
4162	2/24/98	927	RTA00000411F.d.21.1	M00001692B:E01	74794
4163	2/24/98	1133	RTA00000405F.l.03.1	M00001692D:B01	38580
4164	2/24/98	576	RTA00000401F.d.15.2	M00001693C:C12	5297
4165	2/24/98	1059	RTA00000405F.h.21.2	M00001675C:D12	39072
4166	2/24/98	780	RTA00000405F.l.11.1	M00001693D:E08	2055
4167	2/24/98	933	RTA00000419F.a.18.1	M00001680A:B02	78484
4168	2/24/98	631	RTA00000411F.e.03.1	M00001694D:C12	73648
4169	2/24/98	585	RTA00000340R.o.12.1	M00003746C:E02	53732
4170	2/24/98	604	RTA00000351R.c.13.1	M00003747D:C05	11476
4171	2/24/98	187	RTA00000351R.g.11.1	M00003779D:E08	3077
4172	2/24/98	1060	RTA00000346F.g.02.1	M00003792A:B10	6901
4173	2/24/98	690	RTA00000341F.b.05.1	M00003793D:A11	0
4174	2/24/98	86	RTA00000346F.g.22.1	M00003794D:G03	6371
4175	2/24/98	1051	RTA00000346F.h.24.1	M00003797A:C11	4379
4176	2/24/98	377	RTA00000346F.i.01.1	M00003797A:D06	22260
4177	2/24/98	963	RTA00000405F.l.07.1	M00001693C:E09	38636

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
4178	2/24/98	121	RTA00000418F.p.19.1	M00001677D:B01	78544
4179	2/24/98	781	RTA00000423F.f.09.1	M00003808C:A05	64823
4180	2/24/98	1028	RTA00000346F.d.12.1	M00001676B:B09	11777
4181	2/24/98	82	RTA00000411F.b.03.1	M00001676B:E01	23634
4182	2/24/98	465	RTA00000350R.p.18.1	M00001676B:F05	11460
4183	2/24/98	56	RTA00000411F.b.06.1	M00001676C:A04	77884
4184	2/24/98	789	RTA00000423F.b.13.1	M00001676C:E07	20619
4185	2/24/98	267	RTA00000423F.a.19.1	M00001676D:A02	21396
4186	2/24/98	836	RTA00000411F.b.17.1	M00001676D:B02	72893
4187	2/24/98	370	RTA00000405F.i.20.1	M00001677A:G11	38532
4188	2/24/98	39	RTA00000187AF.l.7.1	M00001680D:F08	10539
4189	2/24/98	389	RTA00000411F.c.02.1	M00001677B:B04	72852
4190	2/24/98	1004	RTA00000419F.a.24.1	M00001680B:D02	79290
4191	2/24/98	958	RTA00000195AF.c.8.1	M00001678B:H01	0
4191	1/28/98	520	RTA00000195AF.c.8.1	M00001678B:H01	0
4192	2/24/98	958	RTA00000195AF.c.8.1	M00001678B:H01	0
4192	1/28/98	520	RTA00000195AF.c.8.1	M00001678B:H01	0
4193	2/24/98	500	RTA00000411F.c.10.1	M00001678D:B11	73117
4194	2/24/98	323	RTA00000421F.n.19.1	M00001679A:D10	16409
4195	2/24/98	309	RTA00000340F.n.01.1	M00001679A:G06	39081
4196	2/24/98	337	RTA00000340F.p.04.1	M00001679D:B02	78533
4197	1/28/98	238	RTA00000187AR.k.12.1	M00001679D:F02	78415
4197	2/24/98	407	RTA00000340R.m.07.1	M00001679D:F02	78415
4198	1/28/98	238	RTA00000187AR.k.12.1	M00001679D:F02	78415
4198	2/24/98	407	RTA00000340R.m.07.1	M00001679D:F02	78415
4199	2/24/98	387	RTA00000411F.a.15.1	M00001675D:B08	73812
4200	2/24/98	48	RTA00000411F.b.24.1	M00001677B:A12	30041
4201	2/24/98	234	RTA00000195AF.d.4.1	M00003881D:D06	22766
4201	1/28/98	185	RTA00000195AF.d.4.1	M00003881D:D06	22766
4202	2/24/98	130	RTA00000406F.f.12.1	M00003879A:C11	21895
4203	2/24/98	953	RTA00000406F.f.05.1	M00003878C:F06	22961
4204	2/24/98	138	RTA00000406F.f.03.1	M00003878C:D08	38687
4205	2/24/98	673	RTA00000406F.d.09.1	M00003875B:F12	38591
4206	2/24/98	136	RTA00000419F.l.12.1	M00003901C:B01	75710
4207	2/24/98	300	RTA00000406F.g.17.1	M00003881B:F10	37979
4208	2/24/98	2	RTA00000406F.d.16.1	M00003875C:G02	15040
4209	2/24/98	1207	RTA00000401F.j.21.1	M00003901B:F10	0
4210	2/24/98	494	RTA00000419F.k.12.1	M00003876C:F02	0
4211	2/24/98	515	RTA00000419F.l.03.1	M00003879A:D02	79060
4212	2/24/98	26	RTA00000423F.h.18.1	M00003876C:D02	37972
4213	2/24/98	49	RTA00000406F.d.12.1	M00003875C:A01	38575
4214	2/24/98	986	RTA00000406F.d.24.1	M00003876B:C05	37997
4215	2/24/98	150	RTA00000419F.k.19.1	M00003877C:G12	75447
4216	2/24/98	538	RTA00000423F.g.04.1	M00003903D:C12	23012
4217	2/24/98	1046	RTA00000346F.j.06.1	M00003879A:A02	5767
4218	2/24/98	868	RTA00000406F.i.08.1	M00003903C:E12	37946
4219	2/24/98	409	RTA00000406F.f.11.1	M00003879A:B08	38601
4220	2/24/98	924	RTA00000354R.m.02.1	M00003890B:C08	12766
4221	2/24/98	543	RTA00000419F.k.24.1	M00003878C:G08	75596
4222	1/28/98	185	RTA00000195AF.d.4.1	M00003881D:D06	22766

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
4222	2/24/98	234	RTA00000195AF.d.4.1	M00003881D:D06	22766
4223	2/24/98	382	RTA00000341F.h.10.1	M00003901B:G11	0
4224	2/24/98	550	RTA00000411F.n.20.1	M00003875C:A09	75816
4225	2/24/98	614	RTA00000406F.i.13.1	M00003904A:C04	37904
4226	2/24/98	13	RTA00000406F.f.18.1	M00003879B:G02	38587
4227	2/24/98	1256	RTA00000401F.k.19.1	M00003903D:D10	799
4228	2/24/98	185	RTA00000423F.j.05.1	M00003903C:C05	37958
4229	2/24/98	177	RTA00000406F.i.12.1	M00003903D:H11	39080
4230	2/24/98	802	RTA00000406F.g.03.1	M00003880B:D11	38690
4231	2/24/98	34	RTA00000411F.n.11.1	M00003875A:B01	77276
4232	2/24/98	498	RTA00000406F.e.15.1	M00003877C:A11	39074
4233	2/24/98	929	RTA00000411F.n.09.1	M00003875A:A07	78962
4234	2/24/98	984	RTA00000406F.g.08.1	M00003880C:H03	37963
4235	2/24/98	818	RTA00000406F.h.05.1	M00003901B:C03	38542
4236	2/24/98	592	RTA00000421F.p.18.1	M00003877B:H10	750
4237	2/24/98	313	RTA00000406F.g.07.1	M00003880C:E11	37925
4238	1/28/98	324	RTA00000184F.j.06.1	M00001556B:G02	11294
4239	2/24/98	773	RTA00000406F.h.03.1	M00003901B:A09	38585
4240	3/24/98	244	RTA00000426F.p.09.1	M00004033D:B07	66665
4241	3/24/98	222	RTA00000426F.p.10.1	M00004033D:C05	65845
4242	1/28/98	181	RTA00000198AF.d.2.1	M00001585A:F07	0
4243	1/28/98	77	RTA00000197AF.n.2.1	M00001535A:D02	6229
4244	2/24/98	844	RTA00000411F.a.09.1	M00001675C:F01	78629
4245	2/24/98	352	RTA00000411F.a.10.1	M00001675C:G01	73073
4246	3/24/98	272	RTA00000426F.m.02.1	M00004034C:C06	66237
4247	3/24/98	429	RTA00000525F.a.14.1	M00004033B:C02	37566
4248	2/24/98	118	RTA00000408F.h.03.1	M00001479D:H03	78382
4249	3/24/98	156	RTA00000525F.b.22.1	M00004037C:D07	16679
4250	2/24/98	70	RTA00000409F.m.13.1	M00001618B:E05	0
4251	2/24/98	1198	RTA00000412F.f.10.2	M00003959A:A03	65405
4252	2/24/98	1139	RTA00000404F.h.20.1	M00001619B:A09	15564
4253	3/24/98	41	RTA00000525F.b.17.1	M00004037B:A04	24715
4254	3/24/98	452	RTA00000525F.a.22.1	M00004033D:G06	36848
4255	2/24/98	1019	RTA00000403F.g.03.1	M00001479D:G06	23537
4256	2/24/98	532	RTA00000403F.a.24.1	M00001455B:A09	24128
4257	3/24/98	5	RTA00000426F.p.04.1	M00004029B:H08	34149
4258	3/24/98	43	RTA00000527F.p.07.1	M00004029C:B03	23343
4259	2/24/98	562	RTA00000401F.j.17.1	M00003901B:C05	5483
4260	2/24/98	303	RTA00000130A.h.22.1	M00001617A:D06	80933
4261	2/24/98	1201	RTA00000409F.m.02.1	M00001616C:A11	9157
4262	3/24/98	241	RTA00000527F.o.12.1	M00004028B:G08	688
4263	2/24/98	1170	RTA00000409F.l.24.1	M00001616C:A02	73174
4264	2/24/98	176	RTA00000403F.b.10.1	M00001455C:G07	73268
4265	1/28/98	131	RTA00000185AF.d.11.2	M00001579D:C03	6539
4265	1/28/98	626	RTA00000185AR.d.11.1	M00001579D:C03	6539
4266	1/28/98	190	RTA00000134A.c.7.1	M00001528A:A01	5175
4266	1/28/98	176	RTA00000183AF.h.19.1	M00001528A:A01	5175
4267	3/24/98	90	RTA00000525F.a.03.1	M00004031D:F05	36786
4268	3/24/98	236	RTA00000527F.o.01.1	M00004027A:D06	19088
4269	3/24/98	339	RTA00000426F.m.03.1	M00004034C:E08	66480

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
4270	1/28/98	183	RTA00000198AF.c.17.1	M00001579C:E08	6923
4271	3/24/98	44	RTA00000527F.p.17.1	M00004030C:D12	17223
4272	3/24/98	129	RTA00000527F.p.18.1	M00004030D:B06	31635
4273	3/24/98	402	RTA00000527F.p.24.1	M00004031B:A06	36832
4274	3/24/98	118	RTA00000525F.a.02.1	M00004031C:H10	37454
4275	1/28/98	353	RTA00000198F.a.9.1	M00001557D:C08	0
4276	2/24/98	1250	RTA00000403F.f.15.1	M00001477D:F10	22768
4277	1/28/98	131	RTA00000185AF.d.11.2	M00001579D:C03	6539
4277	1/28/98	626	RTA00000185AR.d.11.1	M00001579D:C03	6539
4278	2/24/98	428	RTA00000422F.f.14.1	M00001478B:D07	2036
4279	1/28/98	209	RTA00000182AF.c.5.1	M00001464D:F06	6397
4279	1/28/98	304	RTA00000182AR.c.5.1	M00001464D:F06	6397
4280	2/24/98	205	RTA00000138A.n.4.1	M00001624A:G11	21920
4281	2/24/98	251	RTA00000119A.i.9.1	M00001457A:G03	0
4282	3/24/98	250	RTA00000427F.h.24.1	M00004091B:H09	65193
4283	1/28/98	61	RTA00000197AF.h.11.1	M00001476D:G03	22264
4284	3/24/98	216	RTA00000427F.h.11.1	M00004092C:B12	26494
4285	1/28/98	110	RTA00000197R.h.01.1	M00001470A:H01	13075
4285	1/28/98	591	RTA00000197AF.h.1.1	M00001470A:H01	13075
4286	1/28/98	110	RTA00000197R.h.01.1	M00001470A:H01	13075
4286	1/28/98	591	RTA00000197AF.h.1.1	M00001470A:H01	13075
4287	3/24/98	276	RTA00000427F.h.19.1	M00004092D:B11	63047
4288	1/28/98	335	RTA00000182AF.e.3.2	M00001468B:H06	0
4289	3/24/98	475	RTA00000427F.i.06.1	M00004097B:D03	41450
4290	2/24/98	286	RTA00000404F.i.19.1	M00001625B:C10	38698
4291	1/28/98	209	RTA00000182AF.c.5.1	M00001464D:F06	6397
4291	1/28/98	304	RTA00000182AR.c.5.1	M00001464D:F06	6397
4292	2/24/98	1165	RTA00000408F.c.08.1	M00001456D:G11	73473
4293	1/28/98	304	RTA00000182AR.c.5.1	M00001464D:F06	6397
4293	1/28/98	209	RTA00000182AF.c.5.1	M00001464D:F06	6397
4294	1/28/98	138	RTA00000182AF.a.3.3	M00001462B:A10	0
4295	1/28/98	36	RTA00000181AF.p.4.3	M00001460A:A03	40392
4296	2/24/98	523	RTA00000418F.j.09.1	M00001626C:D12	76352
4297	2/24/98	296	RTA00000347F.d.06.1	M00001457C:F02	39122
4298	1/28/98	390	RTA00000197AR.f.07.1	M00001457C:C11	19261
4298	1/28/98	184	RTA00000197AF.f.7.1	M00001457C:C11	19261
4299	1/28/98	184	RTA00000197AF.f.7.1	M00001457C:C11	19261
4299	1/28/98	390	RTA00000197AR.f.07.1	M00001457C:C11	19261
4300	1/28/98	133	RTA00000181AR.n.20.3	M00001457B:E03	0
4301	3/24/98	132	RTA00000427F.k.17.1	M00004101A:F07	64965
4302	3/24/98	218	RTA00000427F.i.19.1	M00004102C:D01	64206
4303	3/24/98	436	RTA00000427F.i.21.1	M00004102C:F03	65540
4304	1/28/98	209	RTA00000182AF.c.5.1	M00001464D:F06	6397
4304	1/28/98	304	RTA00000182AR.c.5.1	M00001464D:F06	6397
4305	1/28/98	176	RTA00000183AF.h.19.1	M00001528A:A01	5175
4305	1/28/98	190	RTA00000134A.c.7.1	M00001528A:A01	5175
4306	1/28/98	12	RTA00000183AF.i.15.2	M00001529B:C04	2642
4306	2/24/98	379	RTA00000349R.j.07.1	M00001529B:C04	2642
4307	2/24/98	1156	RTA00000408F.f.10.2	M00001476D:C05	75309
4308	2/24/98	366	RTA00000403F.c.10.1	M00001456D:F05	75261

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
4309	2/24/98	353	RTA00000409F.n.17.1	M00001621C:C10	76725
4310	2/24/98	526	RTA00000411F.a.05.1	M00001675B:H03	76699
4311	2/24/98	90	RTA00000411F.a.02.1	M00001675B:E02	78537
4312	2/24/98	952	RTA00000411F.a.01.1	M00001675B:D02	74524
4313	2/24/98	392	RTA00000410F.p.23.1	M00001675B:C01	73948
4314	2/24/98	238	RTA00000340F.j.12.1	M00001624A:B06	3277
4315	1/28/98	176	RTA00000183AF.h.19.1	M00001528A:A01	5175
4315	1/28/98	190	RTA00000134A.c.7.1	M00001528A:A01	5175
4316	2/24/98	298	RTA00000406F.h.07.1	M00003901B:H04	38003
4317	1/28/98	190	RTA00000134A.c.7.1	M00001528A:A01	5175
4317	1/28/98	176	RTA00000183AF.h.19.1	M00001528A:A01	5175
4318	1/28/98	12	RTA00000183AF.i.15.2	M00001529B:C04	2642
4318	2/24/98	379	RTA00000349R.j.07.1	M00001529B:C04	2642
4319	1/28/98	122	RTA00000197AF.l.15.1	M00001517B:G08	4947
4320	3/24/98	199	RTA00000427F.f.24.1	M00004076D:B09	64572
4321	1/28/98	161	RTA00000183AF.e.23.2	M00001506D:A09	0
4322	1/28/98	17	RTA00000183AR.e.14.2	M00001506B:D09	17437
4323	1/28/98	346	RTA00000197AR.k.22.1	M00001505C:H01	11394
4324	1/28/98	125	RTA00000197AF.k.15.1	M00001504D:D11	22750
4325	1/28/98	212	RTA00000197AF.j.9.1	M00001494B:C01	13236
4326	1/28/98	314	RTA00000182AF.o.5.1	M00001493B:D09	5007
4327	1/28/98	386	RTA00000197AR.j.04.1	M00001492D:A11	17209
4327	1/28/98	259	RTA00000197AF.j.4.1	M00001492D:A11	17209
4328	1/28/98	259	RTA00000197AF.j.4.1	M00001492D:A11	17209
4328	1/28/98	386	RTA00000197AR.j.04.1	M00001492D:A11	17209
4329	1/28/98	94	RTA00000195AF.b.4.1	M00001490C:D07	0
4330	1/28/98	336	RTA00000186AF.f.24.1	M00001629B:E06	0
4330	1/28/98	83	RTA00000186AF.f.24.2	M00001629B:E06	0
4331	2/24/98	1037	RTA00000339F.l.12.1	M00001450A:G11	7711
4332	1/28/98	432	RTA00000198AF.o.05.1	M00003750A:D01	26702
4332	1/28/98	49	RTA00000198R.o.05.1	M00003750A:D01	26702
4333	2/24/98	468	RTA00000423F.c.19.1	M00001680B:E10	40472
4334	2/24/98	1009	RTA00000399F.o.24.1	M00001607D:A11	2272
4335	1/28/98	281	RTA00000188AF.n.10.1	M00003802D:B11	10283
4336	1/28/98	157	RTA00000188AF.n.01.1	M00003801A:B10	36412
4337	2/24/98	842	RTA00000401F.n.23.1	M00003982A:B06	1552
4338	2/24/98	1216	RTA00000404F.e.07.1	M00001608A:D03	9034
4339	2/24/98	1045	RTA00000408F.j.05.2	M00001483C:G06	73878
4340	2/24/98	483	RTA00000406F.g.22.1	M00003881D:C12	38590
4341	1/28/98	310	RTA00000188AF.m.08.1	M00003798D:H08	22155
4342	1/28/98	118	RTA00000199F.b.24.2	M00003794A:B03	0
4343	1/28/98	218	RTA00000188AF.o.18.1	M00003811D:A12	13678
4344	3/24/98	380	RTA00000427F.e.13.1	M00003959D:A04	66080
4345	1/28/98	315	RTA00000199R.d.23.1	M00003815D:H09	37477
4346	1/28/98	140	RTA00000199F.a.2.1	M00003772A:D07	12674
4347	3/24/98	101	RTA00000523F.j.19.1	M00003966B:D02	65910
4348	1/28/98	278	RTA00000198AF.p.16.1	M00003768A:E02	71877
4349	2/24/98	514	RTA00000404F.e.13.1	M00001608D:E09	12046
4350	1/28/98	508	RTA00000187AF.i.14.2	M00001679B:H07	19406
4350	2/24/98	928	RTA00000340F.m.04.1	M00001679B:H07	19406

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
4351	1/28/98	317	RTA00000198AF.p.09.1	M00003761D:E02	10473
4351	1/28/98	186	RTA00000198R.p.09.1	M00003761D:E02	10473
4352	1/28/98	317	RTA00000198AF.p.09.1	M00003761D:E02	10473
4352	1/28/98	186	RTA00000198R.p.09.1	M00003761D:E02	10473
4353	3/24/98	66	RTA00000427F.b.15.1	M00003971C:F09	66891
4354	1/28/98	508	RTA00000187AF.i.14.2	M00001679B:H07	19406
4354	2/24/98	928	RTA00000340F.m.04.1	M00001679B:H07	19406
4355	1/28/98	144	RTA00000198AF.o.18.1	M00003755A:A09	13018
4356	3/24/98	248	RTA00000527F.l.14.1	M00003983D:A09	14935
4357	1/28/98	347	RTA00000199F.b.03.2	M00003779B:E12	38340
4358	1/28/98	272	RTA00000199F.g.08.2	M00003853D:G08	0
4359	1/28/98	263	RTA00000190AF.n.6.1	M00003965A:B11	0
4360	2/24/98	1183	RTA00000346F.j.21.1	M00003879D:A08	3095
4361	2/24/98	553	RTA00000408F.j.12.2	M00001485B:C03	18226
4362	3/24/98	181	RTA00000523F.b.06.1	M00003808A:F09	28736
4363	1/28/98	246	RTA00000199AF.l.4.1	M00003911D:B04	4410
4364	1/28/98	51	RTA00000199R.k.07.1	M00003901C:A03	12973
4365	1/28/98	62	RTA00000190AF.a.18.2	M00003900D:B10	0
4366	1/28/98	117	RTA00000199AF.j.18.1	M00003889D:B09	5140
4367	1/28/98	255	RTA00000199AF.j.17.1	M00003889A:D10	5121
4368	1/28/98	180	RTA00000199AF.j.12.1	M00003887A:A06	22461
4369	3/24/98	256	RTA00000523F.b.20.1	M00003809C:H07	66492
4370	2/24/98	603	RTA00000399F.o.19.1	M00001607A:F11	2594
4371	2/24/98	510	RTA00000131A.g.16.2	M00001449A:F01	0
4372	1/28/98	49	RTA00000198R.o.05.1	M00003750A:D01	26702
4372	1/28/98	432	RTA00000198AF.o.05.1	M00003750A:D01	26702
4373	2/24/98	424	RTA00000138A.e.13.1	M00001605A:E06	79608
4374	1/28/98	90	RTA00000199F.f.15.2	M00003845A:H12	8772
4375	1/28/98	244	RTA00000199F.f.12.2	M00003844C:A08	8131
4376	1/28/98	78	RTA00000199R.f.09.1	M00003842B:D09	22907
4376	1/28/98	406	RTA00000199F.f.09.2	M00003842B:D09	22907
4377	1/28/98	406	RTA00000199F.f.09.2	M00003842B:D09	22907
4377	1/28/98	78	RTA00000199R.f.09.1	M00003842B:D09	22907
4378	1/28/98	44	RTA00000199F.f.08.2	M00003841D:E03	12445
4379	1/28/98	39	RTA00000189AR.b.19.1	M00003832B:E01	5294
4379	2/24/98	239	RTA00000346F.j.02.1	M00003832B:E01	5294
4380	1/28/98	39	RTA00000189AR.b.19.1	M00003832B:E01	5294
4380	2/24/98	239	RTA00000346F.j.02.1	M00003832B:E01	5294
4381	2/24/98	1161	RTA00000346F.m.05.1	M00003983B:C08	5644
4382	2/24/98	887	RTA00000339F.p.06.1	M00001484A:A10	4880
4383	3/24/98	46	RTA00000523F.c.09.1	M00003813C:D08	47389
4384	2/24/98	1206	RTA00000418F.b.20.1	M00001484D:G05	73560
4385	1/28/98	336	RTA00000186AF.f.24.1	M00001629B:E06	0
4385	1/28/98	83	RTA00000186AF.f.24.2	M00001629B:E06	0
4386	1/28/98	111	RTA00000198AF.o.12.1	M00003751D:B02	22038
4387	3/24/98	365	RTA00000527F.k.16.1	M00003982B:B06	1015
4388	2/24/98	1113	RTA00000418F.p.21.1	M00001677D:F03	78068
4389	3/24/98	281	RTA00000527F.k.20.1	M00003982B:H07	17148
4390	1/28/98	360	RTA00000198F.i.5.1	M00001638A:D10	39989
4391	1/28/98	55	RTA00000186AF.i.21.1	M00001636C:H09	6033

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
4392	1/28/98	316	RTA00000198AF.h.24.1	M00001636C:C01	8390
4393	1/28/98	208	RTA00000198AF.h.22.1	M00001635C:A03	22366
4394	2/24/98	1031	RTA00000404F.g.08.1	M00001613D:H10	38980
4395	3/24/98	382	RTA00000427F.a.12.1	M00003982C:H10	63377
4396	2/24/98	916	RTA00000418F.p.20.1	M00001677D:B07	78023
4397	1/28/98	91	RTA00000198AF.j.19.1	M00001653C:F12	38914
4398	2/24/98	858	RTA00000341F.e.20.1	M00003891D:B10	67422
4399	1/28/98	354	RTA00000198R.k.03.1	M00001655A:F06	22765
4399	1/28/98	158	RTA00000198AF.k.03.1	M00001655A:F06	22765
4400	3/24/98	219	RTA00000427F.f.17.1	M00004115A:B12	63803
4401	3/24/98	153	RTA00000527F.l.13.1	M00003983C:F10	36904
4402	3/24/98	320	RTA00000427F.j.06.1	M00004102D:B05	63676
4403	2/24/98	762	RTA00000411F.c.04.1	M00001677B:E06	76858
4404	2/24/98	957	RTA00000411F.c.03.1	M00001677B:B06	79280
4405	3/24/98	479	RTA00000527F.l.23.1	M00003984A:B06	36018
4406	1/28/98	329	RTA00000186AF.b.9.1	M00001616C:F07	0
4407	2/24/98	1115	RTA00000340F.i.08.1	M00001615B:F07	12005
4408	2/24/98	1022	RTA00000401F.j.15.1	M00003901A:C09	3061
4409	1/28/98	4	RTA00000198R.f.04.1	M00001607D:F07	5023
4410	3/24/98	173	RTA00000426F.m.18.1	M00003986D:G07	62974
4411	2/24/98	616	RTA00000423F.c.11.1	M00001677D:B02	0
4412	1/28/98	345	RTA00000187AF.h.21.1	M00001679A:F01	39171
4413	2/24/98	621	RTA00000408F.i.18.2	M00001482C:D02	74410
4414	1/28/98	344	RTA00000198AF.o.02.1	M00003748A:B07	68756
4415	2/24/98	257	RTA00000411F.c.17.1	M00001678D:G03	77664
4416	2/24/98	944	RTA00000422F.k.24.1	M00001610C:E06	39118
4417	2/24/98	876	RTA00000423F.d.16.1	M00001678D:C11	39173
4418	2/24/98	1144	RTA00000345F.j.09.1	M00001451B:F01	13
4419	1/28/98	242	RTA00000198AF.m.17.1	M00001679D:F06	77992
4419	1/28/98	260	RTA00000198R.m.17.1	M00001679D:F06	77992
4420	1/28/98	260	RTA00000198R.m.17.1	M00001679D:F06	77992
4420	1/28/98	242	RTA00000198AF.m.17.1	M00001679D:F06	77992
4421	1/28/98	242	RTA00000198AF.m.17.1	M00001679D:F06	77992
4421	1/28/98	260	RTA00000198R.m.17.1	M00001679D:F06	77992
4422	1/28/98	260	RTA00000198R.m.17.1	M00001679D:F06	77992
4422	1/28/98	242	RTA00000198AF.m.17.1	M00001679D:F06	77992
4423	1/28/98	238	RTA00000187AR.k.12.1	M00001679D:F02	78415
4423	2/24/98	407	RTA00000340R.m.07.1	M00001679D:F02	78415
4424	1/28/98	276	RTA00000198AF.j.15.1	M00001653B:E09	4369
4425	1/28/98	65	RTA00000198AF.m.16.1	M00001679D:D05	51
4426	1/28/98	257	RTA00000198AF.e.20.1	M00001604C:E09	9810
4427	2/24/98	820	RTA00000423F.d.11.1	M00001678C:C06	38950
4428	3/24/98	466	RTA00000427F.d.06.1	M00003980B:C06	33446
4429	2/24/98	455	RTA00000399F.d.23.1	M00001481B:A07	3310
4430	2/24/98	851	RTA00000423F.d.07.1	M00001678B:B12	0
4431	1/28/98	142	RTA00000198AF.k.19.1	M00001660B:C04	75879
4432	2/24/98	485	RTA00000419F.a.02.1	M00001678A:F05	77993
4433	3/24/98	224	RTA00000527F.k.09.1	M00003981C:F05	213
4434	2/24/98	1032	RTA00000423F.c.13.1	M00001678A:A11	39059
4435	1/28/98	354	RTA00000198R.k.03.1	M00001655A:F06	22765

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
4435	1/28/98	158	RTA00000198AF.k.03.1	M00001655A:F06	22765
4436	1/28/98	354	RTA00000198R.k.03.1	M00001655A:F06	22765
4436	1/28/98	158	RTA00000198AF.k.03.1	M00001655A:F06	22765
4437	1/28/98	158	RTA00000198AF.k.03.1	M00001655A:F06	22765
4437	1/28/98	354	RTA00000198R.k.03.1	M00001655A:F06	22765
4438	1/28/98	238	RTA00000187AR.k.12.1	M00001679D:F02	78415
4438	2/24/98	407	RTA00000340R.m.07.1	M00001679D:F02	78415
4439	1/28/98	669	RTA00000192AF.c.2.1	M00004121B:G01	0
4440	3/24/98	394	RTA00000527F.g.14.1	M00003845D:B02	37532
4441	1/28/98	608	RTA00000192AF.p.8.1	M00004212B:C07	2379
4441	2/24/98	653	RTA00000352R.m.12.1	M00004212B:C07	2379
4442	1/28/98	608	RTA00000192AF.p.8.1	M00004212B:C07	2379
4442	2/24/98	653	RTA00000352R.m.12.1	M00004212B:C07	2379
4443	1/28/98	730	RTA00000192AF.o.11.1	M00004205D:F06	0
4444	2/24/98	1157	RTA00000422F.m.18.1	M00001647B:E04	23829
4445	2/24/98	1187	RTA00000120A.c.19.1	M00001464A:B03	81016
4446	2/24/98	913	RTA00000120A.c.20.1	M00001464A:B07	43235
4447	1/28/98	589	RTA00000192AF.l.1.1	M00004183C:D07	16392
4448	2/24/98	640	RTA00000405F.f.02.1	M00001669B:G02	38665
4449	1/28/98	27	RTA00000192AF.i.12.1	M00004169C:C12	5319
4450	2/24/98	681	RTA00000120A.c.24.1	M00001464A:D03	34278
4451	2/24/98	265	RTA00000340F.k.16.1	M00001647B:C09	13157
4452	1/28/98	70	RTA00000192AF.e.3.1	M00004138B:H02	13272
4453	3/24/98	171	RTA00000523F.e.10.1	M00003829A:F03	62878
4454	2/24/98	1134	RTA00000418F.m.02.1	M00001650A:A12	74550
4455	1/28/98	618	RTA00000192AF.a.14.1	M00004111D:A08	6874
4456	1/28/98	457	RTA00000191AR.l.7.2	M00004081C:D12	14391
4457	2/24/98	596	RTA00000351R.i.03.1	M00003846B:D06	6874
4458	3/24/98	460	RTA00000523F.f.16.1	M00003840B:E07	26522
4459	3/24/98	400	RTA00000523F.f.17.1	M00003840B:E08	63984
4460	2/24/98	1129	RTA00000401F.m.07.1	M00003907D:F11	2893
4461	2/24/98	132	RTA00000418F.m.05.1	M00001650B:C10	73600
4462	1/28/98	482	RTA00000187AF.j.7.1	M00001679C:F01	78091
4463	2/24/98	1107	RTA00000419F.l.22.1	M00003903D:C06	78444
4464	2/24/98	609	RTA00000404F.o.10.2	M00001651B:B12	16785
4465	1/28/98	376	RTA00000177AF.m.18.3	M00001355B:G11	0
4465	1/28/98	375	RTA00000177AF.m.18.1	M00001355B:G11	0
4466	2/24/98	186	RTA00000132A.k.6.1	M00001464A:E07	81284
4467	1/28/98	18	RTA00000196AF.c.17.1	M00001352C:F06	39602
4468	3/24/98	282	RTA00000427F.h.22.1	M00004108C:E01	64547
4469	2/24/98	859	RTA00000419F.m.22.1	M00003914A:G09	75600
4470	3/24/98	33	RTA00000524F.b.21.1	M00005216C:B09	0
4471	3/24/98	170	RTA00000523F.d.12.1	M00003822B:D08	64888
4472	3/24/98	117	RTA00000523F.d.18.1	M00003822B:G01	64072
4473	2/24/98	739	RTA00000423F.h.20.1	M00003914A:G06	38639
4474	2/24/98	527	RTA00000419F.m.21.1	M00003914A:E04	77947
4475	2/24/98	237	RTA00000119A.j.22.1	M00001460A:F07	80336
4476	2/24/98	349	RTA00000404F.m.10.2	M00001641D:E02	779
4477	2/24/98	462	RTA00000119A.j.23.1	M00001460A:G07	79835
4478	2/24/98	1263	RTA00000341F.i.22.1	M00003911A:F10	7825

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
4479	3/24/98	47	RTA00000523F.e.18.1	M00003829D:A11	62898
4480	1/28/98	152	RTA00000196AF.c.20.1	M00001352C:H02	8934
4481	3/24/98	13	RTA00000528F.m.16.1	M00003845D:C03	4468
4482	1/28/98	14	RTA00000196R.c.11.2	M00001352A:E12	13658
4483	2/24/98	641	RTA00000410F.j.20.1	M00001642D:G10	73601
4484	1/28/98	141	RTA00000196AF.c.6.1	M00001350A:D06	23148
4485	1/28/98	25	RTA00000196AF.c.1.1	M00001349C:C05	8171
4486	2/24/98	436	RTA00000119A.m.15.1	M00001461A:E05	80989
4487	1/28/98	9	RTA00000177AF.g.22.1	M00001347C:G08	7031
4488	2/24/98	162	RTA00000406F.l.08.1	M00003908D:D12	39016
4489	2/24/98	1056	RTA00000419F.m.18.1	M00003908C:G09	76014
4490	1/28/98	73	RTA00000177AF.e.21.3	M00001344A:H07	4306
4491	3/24/98	326	RTA00000527F.e.09.1	M00003826B:E11	37521
4492	2/24/98	900	RTA00000419F.m.13.1	M00003908A:F12	79052
4493	2/24/98	441	RTA00000404F.m.20.2	M00001647A:H08	39144
4494	2/24/98	1217	RTA00000410F.j.17.1	M00001642D:F02	72912
4495	3/24/98	309	RTA00000523F.j.10.1	M00003860B:G09	63384
4496	2/24/98	385	RTA00000418F.m.14.1	M00001651B:E06	75711
4497	2/24/98	1121	RTA00000120A.m.10.3	M00001467A:B03	81376
4498	1/28/98	617	RTA00000179AF.d.13.3	M00001394A:F01	6583
4499	2/24/98	1242	RTA00000405F.d.10.1	M00001661C:F11	39000
4500	3/24/98	19	RTA00000527F.j.02.2	M00003856A:B07	4896
4501	2/24/98	645	RTA00000422F.p.12.2	M00001661C:F10	9840
4502	3/24/98	142	RTA00000523F.i.18.1	M00003856B:C04	64463
4503	2/24/98	376	RTA00000400F.k.22.1	M00001656A:B07	2512
4504	1/28/98	532	RTA00000177AF.o.4.1	M00001358C:C06	0
4505	2/24/98	1128	RTA00000423F.a.02.3	M00001656B:A08	39210
4506	2/24/98	1143	RTA00000423F.a.03.1	M00001656B:D05	26796
4507	2/24/98	408	RTA00000405F.d.14.1	M00001662A:C12	35209
4508	3/24/98	360	RTA00000523F.j.03.1	M00003860A:A08	64535
4509	1/28/98	409	RTA00000180AF.d.1.3	M00001418D:B06	8526
4510	2/24/98	784	RTA00000418F.o.14.1	M00001661B:B05	33524
4511	3/24/98	120	RTA00000426F.h.09.1	M00003905B:G03	78797
4512	1/28/98	706	RTA00000177AF.i.6.4	M00001350A:B08	0
4513	3/24/98	4	RTA00000426F.h.11.1	M00003905B:H05	75479
4514	2/24/98	697	RTA00000412F.d.14.1	M00003905D:C08	76757
4515	2/24/98	908	RTA00000423F.g.03.1	M00003905C:G11	38007
4516	3/24/98	342	RTA00000427F.e.12.1	M00003959C:G06	62813
4517	2/24/98	97	RTA00000403F.e.01.1	M00001473A:C11	38965
4518	2/24/98	555	RTA00000133A.d.22.1	M00001469A:G11	11797
4519	2/24/98	454	RTA00000418F.n.19.1	M00001659C:F02	28761
4520	2/24/98	562	RTA00000401F.j.17.1	M00003901B:C05	5483
4521	2/24/98	1215	RTA00000422F.o.08.2	M00001659D:D03	26832
4522	2/24/98	635	RTA00000418F.o.17.1	M00001661B:F03	79069
4523	3/24/98	190	RTA00000523F.h.12.1	M00003851C:D07	65745
4524	1/28/98	267	RTA00000186AF.g.11.2	M00001630B:H09	5214
4525	2/24/98	238	RTA00000340F.j.12.1	M00001624A:B06	3277
4526	2/24/98	331	RTA00000404F.o.18.2	M00001651C:C05	39110
4527	1/28/98	626	RTA00000185AR.d.11.1	M00001579D:C03	6539
4527	1/28/98	131	RTA00000185AF.d.11.2	M00001579D:C03	6539

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
4528	1/28/98	626	RTA00000185AR.d.11.1	M00001579D:C03	6539
4528	1/28/98	131	RTA00000185AF.d.11.2	M00001579D:C03	6539
4529	1/28/98	147	RTA00000185AF.c.24.2	M00001578B:E04	23001
4530	2/24/98	164	RTA00000345F.k.06.1	M00001475A:A12	0
4531	2/24/98	611	RTA00000404F.p.02.2	M00001652D:A06	39097
4532	2/24/98	274	RTA00000405F.e.08.1	M00001663C:F10	37916
4533	2/24/98	755	RTA00000423F.d.17.1	M00001663A:C11	20630
4534	2/24/98	126	RTA00000422F.j.20.1	M00001653A:G07	22388
4535	3/24/98	195	RTA00000523F.i.08.1	M00003855A:C12	65099
4536	3/24/98	83	RTA00000527F.i.05.2	M00003851C:B06	37481
4537	1/28/98	375	RTA00000177AF.m.18.1	M00001355B:G11	0
4537	1/28/98	376	RTA00000177AF.m.18.3	M00001355B:G11	0
4538	2/24/98	763	RTA00000135A.m.18.1	M00001545A:C03	19255
4539	2/24/98	362	RTA00000418F.m.16.1	M00001653B:E06	74986
4540	2/24/98	287	RTA00000410F.n.09.1	M00001662C:A04	11736
4541	3/24/98	416	RTA00000527F.i.12.2	M00003852B:D11	0
4542	2/24/98	662	RTA00000339F.o.07.1	M00001473D:G01	2566
4543	2/24/98	949	RTA00000340R.j.07.1	M00001654C:D05	38954
4544	3/24/98	146	RTA00000527F.i.17.2	M00003853B:C08	37539
4545	2/24/98	939	RTA00000405F.a.03.1	M00001654C:E04	39065
4546	3/24/98	42	RTA00000527F.i.19.2	M00003853C:C06	38089
4547	3/24/98	381	RTA00000426F.f.18.1	M00003854C:C02	63271
4548	2/24/98	656	RTA00000403F.e.08.1	M00001473D:B11	19126
4549	3/24/98	37	RTA00000426F.f.20.1	M00003854C:F01	65134
4550	2/24/98	733	RTA00000405F.d.18.1	M00001662C:B02	10494
4551	1/28/98	334	RTA00000181AR.b.21.3	M00001444C:D05	3266
4551	1/28/98	321	RTA00000181AR.b.21.1	M00001444C:D05	3266
4552	3/24/98	198	RTA00000523F.o.05.1	M00005175B:H04	0
4553	3/24/98	302	RTA00000427F.p.04.2	M00005100B:H07	0
4554	3/24/98	203	RTA00000427F.p.10.2	M00005102C:F09	0
4555	1/28/98	331	RTA00000197AR.c.20.1	M00001449D:A06	16282
4556	3/24/98	6	RTA00000523F.l.10.1	M00005134B:E01	0
4557	1/28/98	174	RTA00000181AF.e.22.3	M00001448D:F09	3442
4558	3/24/98	79	RTA00000523F.l.15.1	M00005134C:E11	0
4559	3/24/98	386	RTA00000523F.l.16.1	M00005134C:G04	0
4560	3/24/98	76	RTA00000523F.l.18.1	M00005134D:A06	0
4561	3/24/98	192	RTA00000523F.m.02.1	M00005134D:H03	0
4562	3/24/98	290	RTA00000427F.l.03.1	M00005136D:B07	0
4563	3/24/98	269	RTA00000427F.p.02.2	M00005100B:D02	0
4564	1/28/98	321	RTA00000181AR.b.21.1	M00001444C:D05	3266
4564	1/28/98	334	RTA00000181AR.b.21.3	M00001444C:D05	3266
4565	3/24/98	334	RTA00000427F.n.11.1	M00004960B:A09	0
4566	1/28/98	334	RTA00000181AR.b.21.3	M00001444C:D05	3266
4566	1/28/98	321	RTA00000181AR.b.21.1	M00001444C:D05	3266
4567	1/28/98	334	RTA00000181AR.b.21.3	M00001444C:D05	3266
4567	1/28/98	321	RTA00000181AR.b.21.1	M00001444C:D05	3266
4568	3/24/98	328	RTA00000523F.n.01.1	M00005137A:E01	0
4569	1/28/98	356	RTA00000180AF.l.12.2	M00001433B:H11	0
4570	3/24/98	68	RTA00000523F.n.04.1	M00005138B:D12	0
4571	3/24/98	127	RTA00000523F.n.10.1	M00005140D:G09	0

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
4572	1/28/98	187	RTA00000180AR.j.04.4	M00001429C:G12	22300
4573	3/24/98	112	RTA00000523F.n.12.1	M00005173C:A02	0
4574	3/24/98	305	RTA00000523F.n.16.1	M00005173D:H02	0
4575	3/24/98	164	RTA00000523F.n.17.1	M00005174D:B02	0
4576	3/24/98	107	RTA00000523F.n.20.1	M00005174D:H02	0
4577	2/24/98	898	RTA00000418F.l.03.1	M00001641C:C06	79058
4578	3/24/98	288	RTA00000427F.l.04.1	M00005136D:C01	0
4579	3/24/98	462	RTA00000427F.p.13.2	M00004695B:E04	0
4580	1/28/98	137	RTA00000181AF.m.4.3	M00001455A:E09	13238
4581	1/28/98	20	RTA00000181AF.l.14.2	M00001454D:D06	2364
4582	3/24/98	105	RTA00000526F.d.01.1	M00004104B:A02	4468
4583	3/24/98	261	RTA00000427F.i.22.1	M00004104D:B05	63199
4584	3/24/98	81	RTA00000427F.j.07.1	M00004105A:B10	64819
4585	3/24/98	287	RTA00000525F.d.19.1	M00004114B:D09	36860
4586	1/28/98	311	RTA00000191AR.j.4.2	M00004071D:A10	5198
4587	3/24/98	337	RTA00000525F.e.08.1	M00004115C:H04	24193
4588	3/24/98	206	RTA00000525F.f.07.1	M00004119A:A06	37500
4589	3/24/98	461	RTA00000427F.f.15.1	M00004119D:A07	66734
4590	3/24/98	410	RTA00000427F.f.16.1	M00004119D:H06	64122
4591	3/24/98	307	RTA00000427F.p.03.2	M00005100B:G11	0
4592	3/24/98	180	RTA00000523F.k.02.1	M00004687A:C03	0
4593	1/28/98	115	RTA00000179AR.o.20.3	M00001409D:F11	2409
4594	3/24/98	315	RTA00000427F.n.19.1	M00004891D:E07	0
4595	3/24/98	375	RTA00000427F.p.19.2	M00004895C:G05	0
4596	3/24/98	470	RTA00000427F.p.24.2	M00004897D:F03	0
4597	1/28/98	155	RTA00000197F.e.8.1	M00001454A:C11	3135
4598	1/28/98	286	RTA00000181AR.k.2.3	M00001453C:A11	0
4598	1/28/98	389	RTA00000181AR.k.2.2	M00001453C:A11	0
4599	1/28/98	286	RTA00000181AR.k.2.3	M00001453C:A11	0
4599	1/28/98	389	RTA00000181AR.k.2.2	M00001453C:A11	0
4600	1/28/98	285	RTA00000181AR.j.14.3	M00001453B:E10	5399
4601	3/24/98	317	RTA00000428F.a.01.1	M00004897D:G05	0
4602	3/24/98	85	RTA00000427F.m.21.1	M00004900C:E11	0
4603	3/24/98	121	RTA00000427F.n.02.1	M00004900D:B10	0
4604	3/24/98	78	RTA00000427F.o.05.1	M00004958B:D01	0
4605	3/24/98	437	RTA00000427F.n.10.1	M00004960B:A08	0
4606	3/24/98	388	RTA00000526F.d.17.1	M00004235A:A12	2757
4607	1/28/98	299	RTA00000196AF.f.5.1	M00001366D:G02	11937
4608	1/28/98	369	RTA00000196F.m.3.1	M00001413A:F02	10453
4609	3/24/98	319	RTA00000523F.p.15.1	M00005178B:H01	0
4610	1/28/98	374	RTA00000178AF.l.11.1	M00001383A:G04	23286
4611	2/24/98	1090	RTA00000405F.g.22.1	M00001673C:A02	527
4612	1/28/98	127	RTA00000178AF.k.18.1	M00001382A:F04	9755
4613	1/28/98	104	RTA00000196R.h.03.1	M00001381A:D02	6636
4614	2/24/98	642	RTA00000341F.h.19.1	M00003916C:C05	0
4615	2/24/98	655	RTA00000351R.p.14.1	M00003915C:H04	13166
4616	1/28/98	145	RTA00000178AF.h.24.1	M00001376B:C06	6745
4617	2/24/98	224	RTA00000341F.g.21.1	M00003914C:F09	8823
4618	2/24/98	301	RTA00000401F.m.23.1	M00003914C:C02	2801
4619	2/24/98	133	RTA00000404F.l.20.1	M00001639B:H05	38638

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
4619	2/24/98	63	RTA00000404F.l.20.2	M00001639B:H05	38638
4620	2/24/98	542	RTA00000410F.i.19.1	M00001641B:C10	78988
4621	2/24/98	63	RTA00000404F.l.20.2	M00001639B:H05	38638
4621	2/24/98	133	RTA00000404F.l.20.1	M00001639B:H05	38638
4622	2/24/98	600	RTA00000406F.m.04.1	M00003914B:A11	14959
4623	1/28/98	33	RTA00000178AR.a.20.1	M00001362C:H11	945
4623	2/24/98	979	RTA00000345F.b.17.1	M00001362C:H11	945
4624	1/28/98	33	RTA00000178AR.a.20.1	M00001362C:H11	945
4624	2/24/98	979	RTA00000345F.b.17.1	M00001362C:H11	945
4625	3/24/98	73	RTA00000524F.b.12.1	M00005213C:G01	0
4626	1/28/98	373	RTA00000196F.e.12.1	M00001361C:H11	10147
4627	2/24/98	1233	RTA00000418F.l.02.1	M00001641C:C05	39316
4628	3/24/98	184	RTA00000524F.b.18.1	M00005214B:D11	0
4629	3/24/98	353	RTA00000428F.a.18.1	M00005214C:A09	0
4630	1/28/98	89	RTA00000177AF.n.8.3	M00001356D:F06	4188
4630	1/28/98	15	RTA00000177AR.n.8.1	M00001356D:F06	4188
4631	1/28/98	89	RTA00000177AF.n.8.3	M00001356D:F06	4188
4631	1/28/98	15	RTA00000177AR.n.8.1	M00001356D:F06	4188
4632	1/28/98	375	RTA00000177AF.m.18.1	M00001355B:G11	0
4632	1/28/98	376	RTA00000177AF.m.18.3	M00001355B:G11	0
4633	1/28/98	375	RTA00000177AF.m.18.1	M00001355B:G11	0
4633	1/28/98	376	RTA00000177AF.m.18.3	M00001355B:G11	0
4634	2/24/98	682	RTA00000410F.i.17.1	M00001641B:B01	78147
4635	1/28/98	367	RTA00000196F.i.24.1	M00001392C:D10	4233
4636	1/28/98	264	RTA00000179AF.k.3.3	M00001401A:H07	0
4637	1/28/98	333	RTA00000196F.k.15.1	M00001400A:F06	8320
4638	1/28/98	38	RTA00000196R.k.07.1	M00001399C:D09	22443
4638	1/28/98	289	RTA00000196F.k.07.1	M00001399C:D09	22443
4639	1/28/98	38	RTA00000196R.k.07.1	M00001399C:D09	22443
4639	1/28/98	289	RTA00000196F.k.07.1	M00001399C:D09	22443
4640	1/28/98	289	RTA00000196F.k.07.1	M00001399C:D09	22443
4640	1/28/98	38	RTA00000196R.k.07.1	M00001399C:D09	22443
4641	1/28/98	38	RTA00000196R.k.07.1	M00001399C:D09	22443
4641	1/28/98	289	RTA00000196F.k.07.1	M00001399C:D09	22443
4642	3/24/98	324	RTA00000523F.o.09.1	M00005176A:C12	0
4643	3/24/98	122	RTA00000523F.o.12.1	M00005177A:B06	0
4644	1/28/98	167	RTA00000179AF.d.22.3	M00001394C:C11	7955
4645	1/28/98	351	RTA00000179AF.c.22.1	M00001393B:B09	22515
4645	1/28/98	459	RTA00000179AF.c.22.3	M00001393B:B09	22515
4646	1/28/98	351	RTA00000179AF.c.22.1	M00001393B:B09	22515
4646	1/28/98	459	RTA00000179AF.c.22.3	M00001393B:B09	22515
4647	3/24/98	361	RTA00000523F.p.08.1	M00005178A:A07	0
4648	1/28/98	43	RTA00000179AF.c.14.3	M00001392D:H04	0
4649	3/24/98	268	RTA00000427F.k.19.1	M00004103B:B07	62851
4650	3/24/98	473	RTA00000523F.o.21.1	M00005177C:A01	0
4651	1/28/98	60	RTA00000196AR.i.12.3	M00001389D:G11	38800
4651	1/28/98	128	RTA00000196F.i.12.1	M00001389D:G11	38800
4652	1/28/98	128	RTA00000196F.i.12.1	M00001389D:G11	38800
4652	1/28/98	60	RTA00000196AR.i.12.3	M00001389D:G11	38800
4653	1/28/98	60	RTA00000196AR.i.12.3	M00001389D:G11	38800

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
4653	1/28/98	128	RTA00000196F.i.12.1	M00001389D:G11	38800
4654	1/28/98	60	RTA00000196AR.i.12.3	M00001389D:G11	38800
4654	1/28/98	128	RTA00000196F.i.12.1	M00001389D:G11	38800
4655	1/28/98	28	RTA00000178AR.o.01.5	M00001387B:H07	0
4656	1/28/98	279	RTA00000196AF.h.24.1	M00001386A:D11	7308
4657	1/28/98	130	RTA00000196AF.h.23.1	M00001386A:C02	13357
4658	1/28/98	254	RTA00000178AF.n.2.1	M00001385C:H11	17083
4659	1/28/98	74	RTA00000196AF.h.20.1	M00001385B:F10	0
4660	1/28/98	377	RTA00000178AF.m.19.1	M00001384D:H07	0
4660	1/28/98	120	RTA00000178AR.m.19.5	M00001384D:H07	0
4661	1/28/98	377	RTA00000178AF.m.19.1	M00001384D:H07	0
4661	1/28/98	120	RTA00000178AR.m.19.5	M00001384D:H07	0
4662	3/24/98	228	RTA00000523F.o.14.1	M00005177A:H09	0
4663	1/28/98	567	RTA00000177AR.m.13.1	M00001355A:C12	4175
4663	1/28/98	538	RTA00000177AR.m.13.3	M00001355A:C12	4175
4663	1/28/98	533	RTA00000177AR.m.13.4	M00001355A:C12	4175
4664	1/28/98	511	RTA00000196AF.g.10.1	M00001376B:A02	12498
4665	1/28/98	620	RTA00000201R.g.08.1	M00004692A:E07	0
4665	1/28/98	619	RTA00000201F.g.08.1	M00004692A:E07	0
4665	1/28/98	621	RTA00000201R.g.08.2	M00004692A:E07	0
4666	3/24/98	194	RTA00000522F.j.12.2	M00001651C:A04	74341
4667	2/24/98	79	RTA00000419F.g.08.1	M00003842C:D11	66700
4668	1/28/98	619	RTA00000201F.g.08.1	M00004692A:E07	0
4668	1/28/98	620	RTA00000201R.g.08.1	M00004692A:E07	0
4668	1/28/98	621	RTA00000201R.g.08.2	M00004692A:E07	0
4669	1/28/98	529	RTA00000178AF.b.13.1	M00001364A:E11	3114
4670	2/24/98	111	RTA00000128A.i.20.1	M00001560A:F03	9900
4671	3/24/98	379	RTA00000522F.k.02.2	M00001652C:B09	77622
4672	3/24/98	135	RTA00000522F.k.10.2	M00001652D:B09	77619
4673	2/24/98	1197	RTA00000128A.j.10.1	M00001560A:H06	80085
4674	2/24/98	140	RTA00000128A.j.6.2	M00001560A:H10	5316
4675	3/24/98	247	RTA00000425F.j.21.1	M00001633B:B11	77373
4676	1/28/98	538	RTA00000177AR.m.13.3	M00001355A:C12	4175
4676	1/28/98	567	RTA00000177AR.m.13.1	M00001355A:C12	4175
4676	1/28/98	533	RTA00000177AR.m.13.4	M00001355A:C12	4175
4677	2/24/98	729	RTA00000403F.m.20.1	M00001576A:F11	707
4677	2/24/98	437	RTA00000403F.m.20.2	M00001576A:F11	707
4678	1/28/98	533	RTA00000177AR.m.13.4	M00001355A:C12	4175
4678	1/28/98	538	RTA00000177AR.m.13.3	M00001355A:C12	4175
4678	1/28/98	567	RTA00000177AR.m.13.1	M00001355A:C12	4175
4679	1/28/98	533	RTA00000177AR.m.13.4	M00001355A:C12	4175
4679	1/28/98	538	RTA00000177AR.m.13.3	M00001355A:C12	4175
4679	1/28/98	567	RTA00000177AR.m.13.1	M00001355A:C12	4175
4680	1/28/98	538	RTA00000177AR.m.13.3	M00001355A:C12	4175
4680	1/28/98	567	RTA00000177AR.m.13.1	M00001355A:C12	4175
4680	1/28/98	533	RTA00000177AR.m.13.4	M00001355A:C12	4175
4681	1/28/98	533	RTA00000177AR.m.13.4	M00001355A:C12	4175
4681	1/28/98	538	RTA00000177AR.m.13.3	M00001355A:C12	4175
4681	1/28/98	567	RTA00000177AR.m.13.1	M00001355A:C12	4175
4682	1/28/98	620	RTA00000201R.g.08.1	M00004692A:E07	0

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
4682	1/28/98	621	RTA00000201R.g.08.2	M00004692A:E07	0
4682	1/28/98	619	RTA00000201F.g.08.1	M00004692A:E07	0
4683	2/24/98	845	RTA00000348R.b.04.1	M00001342B:E01	1890
4684	2/24/98	1088	RTA00000339R.b.02.1	M00001344B:F12	0
4684	2/24/98	1149	RTA00000339F.b.02.1	M00001344B:F12	0
4685	2/24/98	618	RTA00000423F.l.04.1	M00004039B:G08	14320
4686	2/24/98	1235	RTA00000411F.j.04.1	M00003841C:F03	66219
4687	2/24/98	415	RTA00000340R.f.05.1	M00001569B:G11	3202
4688	2/24/98	1088	RTA00000339R.b.02.1	M00001344B:F12	0
4688	2/24/98	1149	RTA00000339F.b.02.1	M00001344B:F12	0
4689	2/24/98	1067	RTA00000411F.j.11.1	M00003841D:F06	66154
4690	1/28/98	429	RTA00000196F.i.19.1	M00001390C:C11	39498
4690	2/24/98	925	RTA00000353R.h.10.1	M00001390C:C11	39498
4691	1/28/98	508	RTA00000187AF.i.14.2	M00001679B:H07	19406
4691	2/24/98	928	RTA00000340F.m.04.1	M00001679B:H07	19406
4692	2/24/98	10	RTA00000350R.c.12.1	M00001550D:A04	9728
4693	1/28/98	553	RTA00000201F.b.22.1	M00004344B:H04	35728
4694	1/28/98	459	RTA00000179AF.c.22.3	M00001393B:B09	22515
4694	1/28/98	351	RTA00000179AF.c.22.1	M00001393B:B09	22515
4695	1/28/98	351	RTA00000179AF.c.22.1	M00001393B:B09	22515
4695	1/28/98	459	RTA00000179AF.c.22.3	M00001393B:B09	22515
4696	2/24/98	235	RTA00000126A.o.23.1	M00001551A:B10	6268
4697	2/24/98	942	RTA00000126A.n.6.2	M00001551A:D04	79917
4698	2/24/98	228	RTA00000411F.k.19.1	M00003852D:E08	64200
4699	1/28/98	638	RTA00000193AF.l.05.2	M00004348A:A02	2815
4700	3/24/98	431	RTA00000425F.l.09.1	M00001638A:B04	75251
4701	1/28/98	540	RTA00000179AF.b.10.3	M00001391D:D10	0
4702	2/24/98	390	RTA00000355R.a.14.1	M00004187D:G09	10207
4703	1/28/98	429	RTA00000196F.i.19.1	M00001390C:C11	39498
4703	2/24/98	925	RTA00000353R.h.10.1	M00001390C:C11	39498
4704	2/24/98	930	RTA00000127A.h.22.2	M00001554A:E04	13155
4705	2/24/98	1193	RTA00000411F.k.14.1	M00003851A:C10	63987
4706	1/28/98	694	RTA00000201R.c.19.1	M00004370A:G05	22357
4707	3/24/98	80	RTA00000425F.p.12.1	M00001638C:G01	73219
4708	3/24/98	344	RTA00000425F.p.15.1	M00001638C:H07	31680
4709	1/28/98	743	RTA00000178AF.k.9.1	M00001381B:F06	16342
4710	2/24/98	202	RTA00000419F.g.22.1	M00003845D:A09	64515
4711	1/28/98	749	RTA00000178AR.i.13.4	M00001377B:H01	0
4712	3/24/98	217	RTA00000425F.j.16.1	M00001639D:F02	75631
4713	3/24/98	448	RTA00000425F.j.18.1	M00001639D:G12	75561
4714	1/28/98	385	RTA00000201F.c.24.1	M00004374D:E10	35731
4715	2/24/98	904	RTA00000127A.e.6.1	M00001553A:E07	5885
4716	2/24/98	620	RTA00000420F.a.07.1	M00004072C:F08	63405
4717	1/28/98	396	RTA00000179AR.b.02.3	M00001391B:G12	0
4718	2/24/98	463	RTA00000403F.o.22.1	M00001583A:D01	25076
4718	2/24/98	1084	RTA00000403F.o.22.2	M00001583A:D01	25076
4719	2/24/98	1225	RTA00000346F.j.13.1	M00003841C:E04	5337
4720	2/24/98	1221	RTA00000403F.o.17.1	M00001582D:A02	23085
4721	2/24/98	878	RTA00000413F.c.12.1	M00004083B:G03	65334
4722	2/24/98	764	RTA00000413F.c.17.1	M00004085B:B05	36831

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
4723	2/24/98	398	RTA00000407F.b.04.1	M00004086D:B09	63221
4724	2/24/98	1179	RTA00000341F.o.12.1	M00004144A:F04	2883
4725	2/24/98	7	RTA00000413F.d.12.1	M00004088C:A12	66467
4726	2/24/98	881	RTA00000413F.d.15.1	M00004088C:E04	64943
4727	2/24/98	463	RTA00000403F.o.22.1	M00001583A:D01	25076
4727	2/24/98	1084	RTA00000403F.o.22.2	M00001583A:D01	25076
4728	2/24/98	1084	RTA00000403F.o.22.2	M00001583A:D01	25076
4728	2/24/98	463	RTA00000403F.o.22.1	M00001583A:D01	25076
4729	1/28/98	506	RTA00000198R.o.09.1	M00003751B:A05	4310
4729	1/28/98	497	RTA00000198AF.o.09.1	M00003751B:A05	4310
4730	2/24/98	1015	RTA00000129A.b.6.2	M00001582A:H01	39111
4731	2/24/98	866	RTA00000407F.b.08.1	M00004088D:B03	37513
4732	2/24/98	943	RTA00000413F.c.03.1	M00004081D:H09	64527
4733	2/24/98	463	RTA00000403F.o.22.1	M00001583A:D01	25076
4733	2/24/98	1084	RTA00000403F.o.22.2	M00001583A:D01	25076
4734	1/28/98	490	RTA00000198AF.n.05.1	M00001687A:G01	24157
4735	2/24/98	798	RTA00000420F.c.04.1	M00004089A:B08	65007
4736	2/24/98	850	RTA00000420F.c.07.1	M00004089A:E02	65555
4737	2/24/98	199	RTA00000403F.m.13.2	M00001575D:A10	39077
4738	1/28/98	424	RTA00000187AR.j.24.1	M00001679D:B05	78356
4738	1/28/98	418	RTA00000187AR.k.01.1	M00001679D:B05	78356
4739	1/28/98	424	RTA00000187AR.j.24.1	M00001679D:B05	78356
4739	1/28/98	418	RTA00000187AR.k.01.1	M00001679D:B05	78356
4740	1/28/98	418	RTA00000187AR.k.01.1	M00001679D:B05	78356
4740	1/28/98	424	RTA00000187AR.j.24.1	M00001679D:B05	78356
4741	1/28/98	424	RTA00000187AR.j.24.1	M00001679D:B05	78356
4741	1/28/98	418	RTA00000187AR.k.01.1	M00001679D:B05	78356
4742	1/28/98	482	RTA00000187AF.j.7.1	M00001679C:F01	78091
4743	1/28/98	693	RTA00000198F.m.12.1	M00001679C:D05	4
4744	3/24/98	23	RTA00000522F.p.07.1	M00001670A:C11	76888
4745	1/28/98	497	RTA00000198AF.o.09.1	M00003751B:A05	4310
4745	1/28/98	506	RTA00000198R.o.09.1	M00003751B:A05	4310
4746	1/28/98	642	RTA00000189AF.i.14.1	M00003868B:G11	0
4747	2/24/98	1119	RTA00000126A.k.24.1	M00001550A:F07	39428
4748	2/24/98	654	RTA00000421F.a.05.1	M00001570C:G06	5278
4749	2/24/98	1146	RTA00000347F.h.02.1	M00004072D:H12	562
4750	2/24/98	137	RTA00000339R.a.06.1	M00001346A:E04	58694
4751	2/24/98	729	RTA00000403F.m.20.1	M00001576A:F11	707
4751	2/24/98	437	RTA00000403F.m.20.2	M00001576A:F11	707
4752	2/24/98	627	RTA00000408F.p.21.1	M00001579A:C03	77930
4753	2/24/98	735	RTA00000420F.a.11.1	M00004073C:D04	66460
4754	2/24/98	525	RTA00000348R.d.24.1	M00001349B:G05	5774
4755	2/24/98	624	RTA00000420F.a.16.1	M00004075D:C10	63345
4756	2/24/98	437	RTA00000403F.m.20.2	M00001576A:F11	707
4756	2/24/98	729	RTA00000403F.m.20.1	M00001576A:F11	707
4757	2/24/98	437	RTA00000403F.m.20.2	M00001576A:F11	707
4757	2/24/98	729	RTA00000403F.m.20.1	M00001576A:F11	707
4758	1/28/98	499	RTA00000199F.b.22.2	M00003791C:E09	17018
4759	2/24/98	843	RTA00000418F.g.03.1	M00001579C:E06	78737
4760	2/24/98	956	RTA00000423F.l.06.1	M00004062A:H06	38136

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
4761	2/24/98	826	RTA00000422F.e.07.1	M00001579C:G05	38964
4761	2/24/98	832	RTA00000403F.o.10.2	M00001579C:G05	38964
4762	2/24/98	826	RTA00000422F.e.07.1	M00001579C:G05	38964
4762	2/24/98	832	RTA00000403F.o.10.2	M00001579C:G05	38964
4763	2/24/98	826	RTA00000422F.e.07.1	M00001579C:G05	38964
4763	2/24/98	832	RTA00000403F.o.10.2	M00001579C:G05	38964
4764	2/24/98	826	RTA00000422F.e.07.1	M00001579C:G05	38964
4764	2/24/98	832	RTA00000403F.o.10.2	M00001579C:G05	38964
4765	2/24/98	1159	RTA00000413F.b.18.1	M00004078C:F04	39873
4766	2/24/98	1122	RTA00000419F.f.16.1	M00003839D:E02	64679
4767	2/24/98	1053	RTA00000413F.b.24.1	M00004080A:F01	65117
4768	2/24/98	1052	RTA00000420F.b.02.1	M00004081A:A08	64013
4769	2/24/98	157	RTA00000339F.a.23.1	M00001361B:C07	4022
4770	1/28/98	452	RTA00000199F.d.19.2	M00003813D:H12	6707
4771	2/24/98	480	RTA00000411F.i.15.1	M00003837C:G08	31612
4772	2/24/98	125	RTA00000403F.m.18.1	M00001576A:B09	39185
4773	2/24/98	548	RTA00000413F.b.12.1	M00004077B:H11	64932
4774	2/24/98	814	RTA00000408F.l.24.1	M00001530B:G09	34263
4775	1/28/98	688	RTA00000193AF.g.3.1	M00004050D:A06	5567
4776	1/28/98	451	RTA00000200AF.b.20.1	M00004043A:D02	40403
4777	1/28/98	456	RTA00000200AF.b.12.1	M00004040B:F10	22053
4778	2/24/98	849	RTA00000122A.n.16.1	M00001517A:G08	80553
4779	1/28/98	12	RTA00000183AF.i.15.2	M00001529B:C04	2642
4779	2/24/98	379	RTA00000349R.j.07.1	M00001529B:C04	2642
4780	1/28/98	12	RTA00000183AF.i.15.2	M00001529B:C04	2642
4780	2/24/98	379	RTA00000349R.j.07.1	M00001529B:C04	2642
4781	1/28/98	512	RTA00000191AF.c.3.1	M00003987D:D06	3549
4782	2/24/98	431	RTA00000399F.j.15.1	M00001578C:G06	1261
4783	1/28/98	586	RTA00000199R.o.11.1	M00003976C:A10	23172
4784	1/28/98	496	RTA00000190AF.p.3.1	M00003975B:F03	2378
4785	2/24/98	340	RTA00000408F.l.13.1	M00001530A:B12	4423
4786	1/28/98	617	RTA00000179AF.d.13.3	M00001394A:F01	6583
4787	2/24/98	779	RTA00000408F.l.16.1	M00001530A:F12	73468
4788	1/28/98	387	RTA00000191AF.j.14.1	M00004073A:H12	1002
4788	2/24/98	632	RTA00000191AF.j.14.1	M00004073A:H12	1002
4789	1/28/98	464	RTA00000199AF.l.14.1	M00003917A:D02	22865
4790	2/24/98	668	RTA00000408F.m.05.2	M00001530C:G10	23384
4791	2/24/98	1066	RTA00000123A.f.2.1	M00001531A:H03	80379
4792	2/24/98	213	RTA00000123A.f.3.1	M00001531A:H07	44017
4793	2/24/98	43	RTA00000420F.g.04.1	M00004891B:B12	0
4794	2/24/98	302	RTA00000356R.f.18.1	M00004692A:H10	0
4795	2/24/98	308	RTA00000353R.d.11.1	M00004692A:H08	0
4796	2/24/98	975	RTA00000411F.n.02.1	M00003870B:F04	78049
4797	1/28/98	722	RTA00000199R.j.24.1	M00003895C:A10	0
4798	2/24/98	643	RTA00000420F.l.14.2	M00005230D:F06	0
4799	1/28/98	480	RTA00000181AF.o.08.2	M00001457C:H12	849
4800	1/28/98	518	RTA00000199AF.n.22.1	M00003971A:A06	23064
4801	1/28/98	618	RTA00000192AF.a.14.1	M00004111D:A08	6874
4802	2/24/98	937	RTA00000121A.n.15.1	M00001511A:G08	40849
4803	2/24/98	821	RTA00000420F.h.16.1	M00004927A:E06	0

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
4804	2/24/98	658	RTA00000121A.n.2.1	M00001511A:A05	33585
4805	2/24/98	551	RTA00000340F.b.05.1	M00001513A:G07	0
4806	2/24/98	172	RTA00000420F.i.17.1	M00005101C:B09	0
4807	2/24/98	1224	RTA00000122A.h.24.1	M00001514A:A12	48
4808	1/28/98	631	RTA00000200AF.h.19.2	M00004151D:E03	0
4809	2/24/98	80	RTA00000122A.g.16.1	M00001514A:B04	81366
4810	2/24/98	809	RTA00000420F.i.23.1	M00005134A:D11	0
4811	2/24/98	650	RTA00000122A.g.17.1	M00001514A:B08	32655
4812	2/24/98	73	RTA00000413F.p.15.2	M00005136D:D06	0
4813	1/28/98	425	RTA00000200AF.c.16.1	M00004064D:A11	23433
4814	2/24/98	60	RTA00000413F.p.17.2	M00005136D:G06	0
4815	1/28/98	387	RTA00000191AF.j.14.1	M00004073A:H12	1002
4815	2/24/98	632	RTA00000191AF.j.14.1	M00004073A:H12	1002
4816	2/24/98	837	RTA00000420F.h.01.1	M00004897C:D06	0
4817	2/24/98	123	RTA00000122A.j.18.1	M00001516A:D05	81317
4818	2/24/98	77	RTA00000420F.j.22.1	M00005173B:F01	0
4819	1/28/98	734	RTA00000200AF.d.21.1	M00004087C:D03	0
4820	1/28/98	733	RTA00000200AF.d.20.1	M00004087A:G08	26600
4821	2/24/98	1003	RTA00000420F.k.08.2	M00005176C:C09	0
4822	1/28/98	442	RTA00000191AF.l.9.1	M00004081C:H06	0
4823	1/28/98	457	RTA00000191AR.l.7.2	M00004081C:D12	14391
4824	2/24/98	552	RTA00000411F.n.12.1	M00003875A:C04	73308
4825	2/24/98	782	RTA00000419F.k.03.1	M00003871C:B05	40822
4826	2/24/98	839	RTA00000414F.b.01.1	M00005212B:A02	0
4827	1/28/98	674	RTA00000197AR.e.24.1	M00001456B:F10	39250
4827	1/28/98	3	RTA00000197AF.e.24.1	M00001456B:F10	39250
4828	1/28/98	669	RTA00000192AF.c.2.1	M00004121B:G01	0
4829	1/28/98	718	RTA00000196F.l.14.2	M00001408B:G06	23144
4830	2/24/98	1259	RTA00000420F.l.19.2	M00005231A:H04	0
4831	1/28/98	717	RTA00000200F.o.10.2	M00004269B:C08	36432
4832	2/24/98	107	RTA00000125A.g.16.1	M00001544A:C09	21497
4833	1/28/98	697	RTA00000193AF.e.21.1	M00004271B:B06	0
4834	2/24/98	829	RTA00000411F.m.11.1	M00003867A:D12	73196
4835	1/28/98	409	RTA00000180AF.d.1.3	M00001418D:B06	8526
4836	3/24/98	426	RTA00000424F.k.21.1	M00001614A:A04	73197
4837	2/24/98	874	RTA00000346F.o.22.1	M00004300C:H09	7381
4838	3/24/98	136	RTA00000424F.m.22.1	M00001614C:E11	72943
4839	2/24/98	636	RTA00000418F.e.21.1	M00001577B:A03	74773
4840	2/24/98	1202	RTA00000347F.h.10.1	M00004206A:E02	22779
4841	2/24/98	1030	RTA00000125A.c.17.1	M00001542A:E04	80619
4842	2/24/98	753	RTA00000345F.o.13.1	M00001546B:F12	11500
4843	2/24/98	221	RTA00000414F.f.13.1	M00005259D:H08	0
4844	2/24/98	193	RTA00000347F.b.10.1	M00001546C:C07	8044
4845	2/24/98	1104	RTA00000126A.b.10.1	M00001547A:F06	0
4846	2/24/98	1177	RTA00000126A.b.9.1	M00001547A:F11	81279
4847	2/24/98	923	RTA00000126A.d.19.1	M00001548A:G01	79474
4848	2/24/98	98	RTA00000411F.l.03.1	M00003854D:A12	62702
4849	2/24/98	625	RTA00000126A.h.22.2	M00001549A:F01	0
4850	1/28/98	710	RTA00000196AF.l.3.1	M00001405B:D07	20864
4851	2/24/98	1102	RTA00000126A.j.15.2	M00001549A:H11	40425

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
4852	3/24/98	467	RTA00000528F.h.02.2	M00001632C:D08	1701
4853	1/28/98	411	RTA00000179AF.j.13.3	M00001400B:H06	0
4854	2/24/98	1126	RTA00000136A.h.6.1	M00001550A:D09	81620
4855	1/28/98	712	RTA00000201F.b.21.1	M00004341B:G03	9071
4856	2/24/98	1257	RTA00000419F.h.21.1	M00003856C:B08	64828
4857	2/24/98	194	RTA00000124A.k.5.1	M00001538A:F12	80252
4858	1/28/98	508	RTA00000187AF.i.14.2	M00001679B:H07	19406
4858	2/24/98	928	RTA00000340F.m.04.1	M00001679B:H07	19406
4859	1/28/98	3	RTA00000197AF.e.24.1	M00001456B:F10	39250
4859	1/28/98	674	RTA00000197AR.e.24.1	M00001456B:F10	39250
4860	2/24/98	606	RTA00000420F.l.20.2	M00005232A:C10	0
4861	2/24/98	30	RTA00000411F.m.24.1	M00003870B:B08	77568
4862	2/24/98	31	RTA00000134A.j.10.1	M00001534A:G06	81383
4863	2/24/98	1136	RTA00000406F.c.05.1	M00003870A:H01	22077
4864	2/24/98	411	RTA00000420F.m.12.1	M00005234D:B04	0
4865	2/24/98	1086	RTA00000403F.n.22.2	M00001578B:B05	26775
4865	2/24/98	1085	RTA00000403F.n.22.1	M00001578B:B05	26775
4866	2/24/98	1018	RTA00000413F.j.21.1	M00004688A:A02	0
4867	2/24/98	657	RTA00000124A.k.20.1	M00001538A:C08	80913
4868	2/24/98	718	RTA00000124A.k.23.1	M00001538A:D03	81350
4869	2/24/98	1092	RTA00000125A.c.2.1	M00001542A:F06	40148
4870	2/24/98	615	RTA00000135A.b.23.1	M00001538A:D12	35241
4871	2/24/98	639	RTA00000414F.d.09.1	M00005231C:B01	0
4872	2/24/98	1086	RTA00000403F.n.22.2	M00001578B:B05	26775
4872	2/24/98	1085	RTA00000403F.n.22.1	M00001578B:B05	26775
4873	2/24/98	99	RTA00000420F.m.19.1	M00005254D:B08	0
4874	2/24/98	1085	RTA00000403F.n.22.1	M00001578B:B05	26775
4874	2/24/98	1086	RTA00000403F.n.22.2	M00001578B:B05	26775
4875	2/24/98	1086	RTA00000403F.n.22.2	M00001578B:B05	26775
4875	2/24/98	1085	RTA00000403F.n.22.1	M00001578B:B05	26775
4876	1/28/98	725	RTA00000197AF.b.1.1	M00001441D:E04	12134
4877	2/24/98	215	RTA00000403F.j.18.1	M00001539D:E10	5790
4878	2/24/98	1010	RTA00000408F.n.16.2	M00001540C:B03	73720
4879	2/24/98	1074	RTA00000423F.h.11.1	M00003867C:E11	38977
4880	2/24/98	27	RTA00000420F.n.19.2	M00005259B:C01	0
4881	1/28/98	578	RTA00000180AF.g.17.1	M00001426A:A09	16653
4882	2/24/98	1172	RTA00000423F.h.03.1	M00003875D:D09	37903
4883	2/24/98	1008	RTA00000414F.f.07.1	M00005259C:B05	0
4884	2/24/98	582	RTA00000414F.e.14.1	M00005236B:F10	0
4885	1/28/98	178	RTA00000200F.o.03.1	M00004257C:H06	22807
4885	1/28/98	249	RTA00000200R.o.03.2	M00004257C:H06	22807
4885	1/28/98	85	RTA00000200R.o.03.1	M00004257C:H06	22807
4886	2/24/98	1223	RTA00000347F.a.14.1	M00001429D:F11	7421
4887	2/24/98	488	RTA00000339F.k.23.1	M00001429D:H12	0
4888	3/24/98	100	RTA00000424F.i.21.1	M00001596A:E07	73482
4889	3/24/98	64	RTA00000424F.i.24.1	M00001596A:G06	79101
4890	3/24/98	207	RTA00000424F.j.07.1	M00001596B:C11	79211
4891	3/24/98	327	RTA00000424F.j.08.1	M00001596B:D09	73972
4892	3/24/98	349	RTA00000424F.j.09.1	M00001596B:H05	74387
4893	3/24/98	154	RTA00000522F.h.13.1	M00001596C:F09	40823

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
4894	2/24/98	1252	RTA00000400F.g.08.1	M00001639A:C11	1275
4895	2/24/98	261	RTA00000341F.b.06.1	M00003794A:E12	17008
4896	1/28/98	312	RTA00000193AF.h.2.1	M00004290A:B03	3273
4897	1/28/98	590	RTA00000190AF.d.2.1	M00003906B:F12	2444
4898	1/28/98	213	RTA00000200F.o.04.1	M00004260D:C12	12514
4899	2/24/98	333	RTA00000399F.f.11.1	M00001487C:F01	40167
4900	1/28/98	249	RTA00000200R.o.03.2	M00004257C:H06	22807
4900	1/28/98	178	RTA00000200F.o.03.1	M00004257C:H06	22807
4900	1/28/98	85	RTA00000200R.o.03.1	M00004257C:H06	22807
4901	1/28/98	85	RTA00000200R.o.03.1	M00004257C:H06	22807
4901	1/28/98	178	RTA00000200F.o.03.1	M00004257C:H06	22807
4901	1/28/98	249	RTA00000200R.o.03.2	M00004257C:H06	22807
4902	1/28/98	85	RTA00000200R.o.03.1	M00004257C:H06	22807
4902	1/28/98	249	RTA00000200R.o.03.2	M00004257C:H06	22807
4902	1/28/98	178	RTA00000200F.o.03.1	M00004257C:H06	22807
4903	1/28/98	249	RTA00000200R.o.03.2	M00004257C:H06	22807
4903	1/28/98	85	RTA00000200R.o.03.1	M00004257C:H06	22807
4903	1/28/98	178	RTA00000200F.o.03.1	M00004257C:H06	22807
4904	1/28/98	249	RTA00000200R.o.03.2	M00004257C:H06	22807
4904	1/28/98	85	RTA00000200R.o.03.1	M00004257C:H06	22807
4904	1/28/98	178	RTA00000200F.o.03.1	M00004257C:H06	22807
4905	3/24/98	133	RTA00000425F.f.04.1	M00001607A:B06	24633
4906	3/24/98	169	RTA00000425F.f.05.1	M00001607A:D10	24090
4907	2/24/98	44	RTA00000418F.k.14.1	M00001639A:H06	76133
4908	2/24/98	1204	RTA00000419F.l.02.1	M00003879A:C01	75736
4909	2/24/98	748	RTA00000346F.f.11.1	M00003793C:D09	38528
4910	2/24/98	4	RTA00000339F.i.20.1	M00001438D:C06	4356
4911	1/28/98	93	RTA00000200F.o.11.1	M00004270A:F11	0
4912	1/28/98	435	RTA00000182AR.c.22.1	M00001467A:D08	16283
4913	1/28/98	683	RTA00000187AR.j.01.1	M00001679C:D01	79028
4914	3/24/98	469	RTA00000522F.e.20.1	M00001590B:H10	26770
4915	1/28/98	172	RTA00000186AF.p.09.2	M00001655C:E04	6879
4916	2/24/98	806	RTA00000345F.f.08.1	M00001413B:H09	0
4917	1/28/98	677	RTA00000197AF.i.19.1	M00001490B:H11	39554
4918	1/28/98	443	RTA00000197AR.i.17.1	M00001490A:E11	3516
4919	2/24/98	863	RTA00000406F.p.08.1	M00004032C:B02	37573
4920	3/24/98	55	RTA00000528F.e.23.1	M00001593B:D10	19242
4921	2/24/98	1211	RTA00000399F.f.14.1	M00001487D:C11	11483
4922	1/28/98	609	RTA00000196AF.n.05.1	M00001418B:F07	12531
4922	2/24/98	1120	RTA00000353R.l.23.1	M00001418B:F07	12531
4923	1/28/98	609	RTA00000196AF.n.05.1	M00001418B:F07	12531
4923	2/24/98	1120	RTA00000353R.l.23.1	M00001418B:F07	12531
4924	3/24/98	474	RTA00000522F.h.05.1	M00001595C:H11	73358
4925	1/28/98	284	RTA00000199F.d.10.2	M00003808C:B05	22049
4925	2/24/98	816	RTA00000354R.n.04.1	M00003808C:B05	22049
4926	2/24/98	1112	RTA00000418F.c.05.1	M00001487B:F02	76475
4927	1/28/98	687	RTA00000197AF.g.4.1	M00001464B:B03	8821
4928	2/24/98	990	RTA00000121A.h.19.1	M00001471A:D04	80334
4929	1/28/98	696	RTA00000180AR.d.16.3	M00001419D:C10	11393
4929	2/24/98	1184	RTA00000345F.h.08.1	M00001419D:C10	11393

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
4930	1/28/98	751	RTA00000179AF.c.4.3	M00001392D:B11	0
4931	1/28/98	696	RTA00000180AR.d.16.3	M00001419D:C10	11393
4931	2/24/98	1184	RTA00000345F.h.08.1	M00001419D:C10	11393
4932	1/28/98	162	RTA00000201F.e.15.1	M00004444B:D11	9960
4933	1/28/98	126	RTA00000201F.d.16.1	M00004388B:A08	0
4934	1/28/98	332	RTA00000193AR.n.04.3	M00004375C:D01	9850
4935	2/24/98	838	RTA00000408F.k.19.1	M00001487C:G03	77593
4936	2/24/98	113	RTA00000401F.e.02.1	M00003805B:C04	0
4937	3/24/98	278	RTA00000522F.g.21.1	M00001595C:A09	77310
4938	3/24/98	54	RTA00000425F.f.19.1	M00001653D:G07	32635
4939	2/24/98	976	RTA00000419F.b.17.1	M00003808D:D04	63261
4940	2/24/98	59	RTA00000346F.j.08.1	M00003879B:A06	39951
4941	2/24/98	151	RTA00000341F.c.21.1	M00003789C:F06	7899
4942	1/28/98	67	RTA00000200AF.g.07.1	M00004128B:G01	0
4943	2/24/98	324	RTA00000340F.p.17.1	M00003750C:H05	0
4944	2/24/98	476	RTA00000345F.h.01.1	M00001441B:D11	10834
4945	2/24/98	245	RTA00000195AF.d.20.1	M00004117A:D11	37574
4945	1/28/98	87	RTA00000195AF.d.20.1	M00004117A:D11	37574
4946	2/24/98	245	RTA00000195AF.d.20.1	M00004117A:D11	37574
4946	1/28/98	87	RTA00000195AF.d.20.1	M00004117A:D11	37574
4947	2/24/98	991	RTA00000419F.b.10.1	M00001694C:G04	78566
4948	2/24/98	14	RTA00000419F.b.09.1	M00001694C:F12	78128
4949	1/28/98	261	RTA00000192AF.a.24.1	M00004114C:F11	13183
4950	1/28/98	24	RTA00000200AF.f.11.1	M00004111D:D11	0
4951	3/24/98	408	RTA00000522F.o.10.1	M00001660D:E05	78798
4952	1/28/98	328	RTA00000200AF.g.09.1	M00004131B:H09	22785
4952	1/28/98	26	RTA00000200R.g.09.1	M00004131B:H09	22785
4953	2/24/98	861	RTA00000419F.b.06.1	M00001694B:B08	76728
4954	3/24/98	24	RTA00000522F.n.08.1	M00001656A:D10	76343
4955	2/24/98	760	RTA00000423F.d.04.1	M00001694A:B12	11307
4956	3/24/98	220	RTA00000522F.o.18.1	M00001669B:H06	76366
4957	2/24/98	279	RTA00000418F.i.21.1	M00001596D:E10	78728
4958	1/28/98	84	RTA00000191AF.h.14.1	M00004056B:D09	13553
4959	1/28/98	284	RTA00000199F.d.10.2	M00003808C:B05	22049
4959	2/24/98	816	RTA00000354R.n.04.1	M00003808C:B05	22049
4960	2/24/98	217	RTA00000399F.o.17.1	M00001599D:A09	1106
4961	1/28/98	287	RTA00000200AF.b.07.1	M00004039C:C01	17125
4961	1/28/98	173	RTA00000200AR.b.07.1	M00004039C:C01	17125
4962	1/28/98	287	RTA00000200AF.b.07.1	M00004039C:C01	17125
4962	1/28/98	173	RTA00000200AR.b.07.1	M00004039C:C01	17125
4963	1/28/98	287	RTA00000200AF.b.07.1	M00004039C:C01	17125
4963	1/28/98	173	RTA00000200AR.b.07.1	M00004039C:C01	17125
4964	1/28/98	287	RTA00000200AF.b.07.1	M00004039C:C01	17125
4964	1/28/98	173	RTA00000200AR.b.07.1	M00004039C:C01	17125
4965	3/24/98	464	RTA00000522F.p.18.1	M00001671A:H06	76376
4966	3/24/98	453	RTA00000522F.p.22.1	M00001671B:F02	73322
4967	2/24/98	54	RTA00000399F.o.01.1	M00001595C:E01	3055
4968	2/24/98	1219	RTA00000347F.e.20.1	M00003771B:E05	39911
4969	2/24/98	825	RTA00000404F.k.22.2	M00001635D:C12	39084
4969	2/24/98	364	RTA00000404F.k.22.1	M00001635D:C12	39084

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
4970	1/28/98	241	RTA00000200AF.l.17.1	M00004217C:D03	12771
4970	1/28/98	151	RTA00000200R.l.17.1	M00004217C:D03	12771
4970	1/28/98	202	RTA00000200R.l.17.2	M00004217C:D03	12771
4971	1/28/98	241	RTA00000200AF.l.17.1	M00004217C:D03	12771
4971	1/28/98	151	RTA00000200R.l.17.1	M00004217C:D03	12771
4971	1/28/98	202	RTA00000200R.l.17.2	M00004217C:D03	12771
4972	1/28/98	241	RTA00000200AF.l.17.1	M00004217C:D03	12771
4972	1/28/98	202	RTA00000200R.l.17.2	M00004217C:D03	12771
4972	1/28/98	151	RTA00000200R.l.17.1	M00004217C:D03	12771
4973	1/28/98	241	RTA00000200AF.l.17.1	M00004217C:D03	12771
4973	1/28/98	202	RTA00000200R.l.17.2	M00004217C:D03	12771
4973	1/28/98	151	RTA00000200R.l.17.1	M00004217C:D03	12771
4974	1/28/98	241	RTA00000200AF.l.17.1	M00004217C:D03	12771
4974	1/28/98	202	RTA00000200R.l.17.2	M00004217C:D03	12771
4974	1/28/98	151	RTA00000200R.l.17.1	M00004217C:D03	12771
4975	1/28/98	241	RTA00000200AF.l.17.1	M00004217C:D03	12771
4975	1/28/98	151	RTA00000200R.l.17.1	M00004217C:D03	12771
4975	1/28/98	202	RTA00000200R.l.17.2	M00004217C:D03	12771
4976	1/28/98	241	RTA00000200AF.l.17.1	M00004217C:D03	12771
4976	1/28/98	151	RTA00000200R.l.17.1	M00004217C:D03	12771
4976	1/28/98	202	RTA00000200R.l.17.2	M00004217C:D03	12771
4977	1/28/98	241	RTA00000200AF.l.17.1	M00004217C:D03	12771
4977	1/28/98	151	RTA00000200R.l.17.1	M00004217C:D03	12771
4977	1/28/98	202	RTA00000200R.l.17.2	M00004217C:D03	12771
4978	1/28/98	241	RTA00000200AF.l.17.1	M00004217C:D03	12771
4978	1/28/98	151	RTA00000200R.l.17.1	M00004217C:D03	12771
4978	1/28/98	202	RTA00000200R.l.17.2	M00004217C:D03	12771
4979	1/28/98	366	RTA00000192AF.o.19.1	M00004208D:H08	3549
4980	1/28/98	328	RTA00000200AF.g.09.1	M00004131B:H09	22785
4980	1/28/98	26	RTA00000200R.g.09.1	M00004131B:H09	22785
4981	1/28/98	245	RTA00000200AF.k.7.1	M00004193C:G11	0
4982	2/24/98	1036	RTA00000339F.k.08.1	M00001439B:A10	8133
4983	2/24/98	72	RTA00000347F.a.08.1	M00001592C:G04	3135
4984	2/24/98	1163	RTA00000341F.b.14.1	M00003763A:C01	5992
4985	2/24/98	278	RTA00000404F.c.10.1	M00001593B:E11	23534
4986	1/28/98	250	RTA00000192AF.j.21.1	M00004176D:B12	2289
4987	2/24/98	511	RTA00000341F.b.13.1	M00003762B:H09	0
4988	1/28/98	27	RTA00000192AF.i.12.1	M00004169C:C12	5319
4989	2/24/98	416	RTA00000404F.c.19.1	M00001594A:D06	39026
4990	2/24/98	351	RTA00000340F.p.20.1	M00003752B:C02	17008
4991	1/28/98	215	RTA00000192AR.e.14.3	M00004142A:D08	3300
4992	1/28/98	163	RTA00000192AR.e.13.3	M00004142A:B12	9457
4993	1/28/98	318	RTA00000200AF.g.17.1	M00004138A:H09	0
4994	2/24/98	1105	RTA00000340F.p.18.1	M00003751C:A04	287
4995	2/24/98	1080	RTA00000351R.g.06.1	M00003771D:G05	0
4996	2/24/98	478	RTA00000418F.h.08.1	M00001589B:E07	76401
4997	2/24/98	584	RTA00000418F.d.22.1	M00001573B:C06	75324
4998	2/24/98	493	RTA00000129A.d.1.2	M00001587A:F05	80058
4999	2/24/98	402	RTA00000420F.e.16.1	M00004110A:E04	63639
5000	2/24/98	1006	RTA00000129A.e.14.1	M00001587A:F08	80053

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
5001	2/24/98	285	RTA00000413F.i.02.1	M00004110D:A10	65857
5002	1/28/98	659	RTA00000185AR.k.23.2	M00001601A:E09	0
5003	2/24/98	122	RTA00000420F.f.06.1	M00004115D:D08	64812
5004	2/24/98	245	RTA00000195AF.d.20.1	M00004117A:D11	37574
5004	1/28/98	87	RTA00000195AF.d.20.1	M00004117A:D11	37574
5005	1/28/98	87	RTA00000195AF.d.20.1	M00004117A:D11	37574
5005	2/24/98	245	RTA00000195AF.d.20.1	M00004117A:D11	37574
5006	2/24/98	720	RTA00000129A.d.2.4	M00001587A:G06	80119
5007	2/24/98	687	RTA00000350R.g.10.1	M00001587C:C10	9026
5008	3/24/98	18	RTA00000522F.e.16.1	M00001590A:C08	75283
5009	1/28/98	447	RTA00000198AF.d.8.1	M00001587A:H03	0
5010	1/28/98	554	RTA00000186AR.e.07.4	M00001623D:G03	4175
5010	1/28/98	400	RTA00000186AR.e.07.3	M00001623D:G03	4175
5011	1/28/98	526	RTA00000185AF.e.20.1	M00001585A:D06	5865
5012	2/24/98	1	RTA00000404F.a.02.1	M00001589B:E12	9738
5013	1/28/98	530	RTA00000185AF.d.24.2	M00001582D:F05	0
5014	2/24/98	1096	RTA00000421F.a.06.1	M00001589C:A11	2385
5015	1/28/98	131	RTA00000185AF.d.11.2	M00001579D:C03	6539
5015	1/28/98	626	RTA00000185AR.d.11.1	M00001579D:C03	6539
5016	1/28/98	626	RTA00000185AR.d.11.1	M00001579D:C03	6539
5016	1/28/98	131	RTA00000185AF.d.11.2	M00001579D:C03	6539
5017	2/24/98	1020	RTA00000412F.p.06.1	M00004038B:H10	65485
5018	1/28/98	671	RTA00000185AR.d.08.1	M00001579C:E09	6562
5019	2/24/98	1240	RTA00000404F.a.18.1	M00001590B:B02	36267
5020	2/24/98	115	RTA00000418F.h.19.1	M00001590B:C05	0
5021	2/24/98	211	RTA00000404F.a.19.1	M00001590B:C07	38624
5022	1/28/98	455	RTA00000198AF.d.12.1	M00001589A:C01	21142
5023	1/28/98	622	RTA00000186AR.m.14.2	M00001649B:G12	9800
5024	2/24/98	958	RTA00000195AF.c.8.1	M00001678B:H01	0
5024	1/28/98	520	RTA00000195AF.c.8.1	M00001678B:H01	0
5025	1/28/98	520	RTA00000195AF.c.8.1	M00001678B:H01	0
5025	2/24/98	958	RTA00000195AF.c.8.1	M00001678B:H01	0
5026	1/28/98	690	RTA00000198R.l.21.1	M00001673A:A04	19194
5027	2/24/98	772	RTA00000413F.e.04.1	M00004090C:C07	64176
5028	2/24/98	834	RTA00000407F.b.11.1	M00004090C:C10	0
5029	2/24/98	1154	RTA00000403F.m.09.2	M00001575B:G01	26814
5030	2/24/98	1203	RTA00000413F.e.10.1	M00004092C:B03	31033
5031	2/24/98	12	RTA00000339F.b.17.1	M00001366D:E12	10020
5032	2/24/98	947	RTA00000347F.g.08.1	M00004096B:F05	23121
5033	1/28/98	39	RTA00000189AR.b.19.1	M00003832B:E01	5294
5033	2/24/98	239	RTA00000346F.j.02.1	M00003832B:E01	5294
5034	1/28/98	39	RTA00000189AR.b.19.1	M00003832B:E01	5294
5034	2/24/98	239	RTA00000346F.j.02.1	M00003832B:E01	5294
5035	2/24/98	560	RTA00000419F.d.16.1	M00003828B:E07	64357
5036	2/24/98	568	RTA00000403F.m.03.1	M00001573D:D10	39179
5037	2/24/98	191	RTA00000419F.d.17.1	M00003828B:F09	64353
5038	2/24/98	607	RTA00000420F.d.16.1	M00004103D:F10	64485
5039	2/24/98	1130	RTA00000354R.p.01.1	M00004104C:H12	0
5040	2/24/98	710	RTA00000413F.g.24.1	M00004104D:A04	65481
5041	2/24/98	24	RTA00000423F.l.09.1	M00004118A:H08	9752

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
5042	2/24/98	896	RTA00000423F.l.20.1	M00004105C:E09	12580
5043	2/24/98	1078	RTA00000423F.f.03.1	M00003829C:D10	63852
5044	1/28/98	558	RTA00000186AR.h.14.1	M00001632D:H07	0
5045	2/24/98	155	RTA00000413F.h.13.1	M00004107A:D01	65190
5046	2/24/98	926	RTA00000399F.k.20.1	M00001585C:D10	3003
5047	2/24/98	1194	RTA00000420F.e.05.1	M00004107D:E12	63908
5048	1/28/98	400	RTA00000186AR.e.07.3	M00001623D:G03	4175
5048	1/28/98	554	RTA00000186AR.e.07.4	M00001623D:G03	4175
5049	2/24/98	570	RTA00000405F.n.13.1	M00003824A:G10	23810
5050	2/24/98	334	RTA00000408F.p.05.1	M00001575B:B02	9649
5051	2/24/98	1029	RTA00000411F.f.04.1	M00003813A:G04	64526
5052	3/24/98	134	RTA00000424F.c.14.3	M00001476D:A09	76614
5053	2/24/98	396	RTA00000406F.e.21.1	M00003877D:G05	9090
5054	3/24/98	230	RTA00000424F.g.14.1	M00001572A:B06	74879
5055	2/24/98	617	RTA00000423F.f.23.1	M00003816C:E09	15390
5056	2/24/98	5	RTA00000408F.o.12.2	M00001572A:A10	78578
5057	2/24/98	689	RTA00000419F.p.03.1	M00004035A:G10	1937
5058	3/24/98	273	RTA00000424F.a.02.4	M00001575A:D06	78806
5059	2/24/98	241	RTA00000339F.d.13.1	M00001395C:F11	0
5060	3/24/98	237	RTA00000522F.c.01.1	M00001576A:C11	74938
5061	1/28/98	745	RTA00000183AF.m.11.1	M00001536D:G02	8927
5062	1/28/98	408	RTA00000183AR.l.15.1	M00001535C:E01	39383
5063	2/24/98	464	RTA00000195AF.c.12.1	M00003818B:G12	37582
5063	1/28/98	300	RTA00000195AF.c.12.1	M00003818B:G12	37582
5064	1/28/98	647	RTA00000197F.m.11.1	M00001530B:D10	16488
5065	2/24/98	464	RTA00000195AF.c.12.1	M00003818B:G12	37582
5065	1/28/98	300	RTA00000195AF.c.12.1	M00003818B:G12	37582
5066	3/24/98	395	RTA00000522F.d.06.1	M00001578B:A02	74809
5067	2/24/98	516	RTA00000339F.f.20.1	M00001399A:C03	6494
5068	2/24/98	890	RTA00000418F.j.19.1	M00001634D:D02	78399
5069	2/24/98	435	RTA00000340F.b.02.1	M00001503C:G05	10185
5070	3/24/98	175	RTA00000528F.d.18.1	M00001582C:E01	2684
5071	2/24/98	168	RTA00000411F.e.22.1	M00003812B:D07	63638
5072	2/24/98	1071	RTA00000404F.k.18.2	M00001635A:C06	5475
5073	2/24/98	189	RTA00000347F.a.13.1	M00001402D:F02	22446
5074	2/24/98	825	RTA00000404F.k.22.2	M00001635D:C12	39084
5074	2/24/98	364	RTA00000404F.k.22.1	M00001635D:C12	39084
5075	3/24/98	25	RTA00000425F.c.06.1	M00001585D:D11	78041
5076	3/24/98	186	RTA00000425F.c.07.1	M00001585D:F03	76042
5077	3/24/98	208	RTA00000424F.m.10.1	M00001586C:E06	34251
5078	2/24/98	420	RTA00000422F.b.16.1	M00003813B:A11	17045
5079	3/24/98	103	RTA00000424F.b.22.1	M00001530A:F11	72971
5079	3/24/98	88	RTA00000424F.b.22.4	M00001530A:F11	72971
5080	3/24/98	318	RTA00000523F.a.01.1	M00001671C:F11	74923
5081	2/24/98	676	RTA00000411F.g.21.1	M00003823D:G05	64500
5082	3/24/98	3	RTA00000528F.b.23.1	M00001479C:F10	1605
5083	2/24/98	1244	RTA00000418F.h.23.1	M00001591A:B08	75153
5084	2/24/98	321	RTA00000339F.c.21.1	M00001389C:A08	5325
5085	1/28/98	429	RTA00000196F.i.19.1	M00001390C:C11	39498
5085	2/24/98	925	RTA00000353R.h.10.1	M00001390C:C11	39498

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
5086	1/28/98	429	RTA00000196F.i.19.1	M00001390C:C11	39498
5086	2/24/98	925	RTA00000353R.h.10.1	M00001390C:C11	39498
5087	3/24/98	471	RTA00000528F.c.11.1	M00001486D:D12	1701
5088	2/24/98	103	RTA00000418F.j.12.1	M00001626C:G08	73316
5089	2/24/98	1148	RTA00000345F.d.23.1	M00001390D:E03	5862
5090	2/24/98	87	RTA00000403F.l.20.1	M00001573A:A06	18267
5091	3/24/98	427	RTA00000522F.b.08.1	M00001570D:E06	26915
5092	1/28/98	661	RTA00000198R.b.04.1	M00001565A:H09	0
5093	2/24/98	200	RTA00000339F.c.02.1	M00001381C:B08	12975
5094	2/24/98	1243	RTA00000404F.j.19.1	M00001630D:H10	0
5095	1/28/98	750	RTA00000198AF.a.19.1	M00001561D:C05	0
5096	2/24/98	418	RTA00000410F.a.01.1	M00001631D:B10	73354
5097	3/24/98	458	RTA00000424F.d.12.3	M00001530D:E06	74342
5097	3/24/98	454	RTA00000424F.d.12.2	M00001530D:E06	74342
5098	3/24/98	458	RTA00000424F.d.12.3	M00001530D:E06	74342
5098	3/24/98	454	RTA00000424F.d.12.2	M00001530D:E06	74342
5099	2/24/98	159	RTA00000348R.j.17.1	M00001391D:C06	2641
5100	2/24/98	539	RTA00000346F.m.15.1	M00004037B:C04	13553
5101	2/24/98	170	RTA00000422F.n.08.1	M00001632B:E05	38655
5102	3/24/98	162	RTA00000522F.a.12.1	M00001567A:H05	33515
5103	2/24/98	315	RTA00000419F.p.12.1	M00004037A:E04	13767
5104	2/24/98	119	RTA00000423F.k.05.1	M00004036D:F02	37472
5105	3/24/98	12	RTA00000522F.a.23.1	M00001570C:A05	38613
5106	3/24/98	103	RTA00000424F.b.22.1	M00001530A:F11	72971
5106	3/24/98	88	RTA00000424F.b.22.4	M00001530A:F11	72971
5107	2/24/98	21	RTA00000411F.g.08.1	M00003822D:D04	45815
5108	1/28/98	35	RTA00000191AF.n.17.1	M00004091B:D11	7848
5109	3/24/98	39	RTA00000527F.c.23.1	M00003822C:A07	37742
5110	1/28/98	43	RTA00000179AF.c.14.3	M00001392D:H04	0
5111	2/24/98	54	RTA00000399F.o.01.1	M00001595C:E01	3055
5112	2/24/98	63	RTA00000404F.l.20.2	M00001639B:H05	38638
5113	1/28/98	82	RTA00000183AF.l.18.1	M00001535D:C01	3484
5114	3/24/98	84	RTA00000527F.k.18.1	M00003982B:C10	11332
5115	1/28/98	99	RTA00000184AF.d.8.1	M00001548A:A08	4393
5116	2/24/98	99	RTA00000420F.m.19.1	M00005254D:B08	0
5117	2/24/98	100	RTA00000339F.o.23.1	M00001473C:D09	7801
5118	2/24/98	104	RTA00000421F.n.03.1	M00001675C:A04	1638
5119	2/24/98	105	RTA00000346F.d.08.1	M00001671A:A10	39955
5120	2/24/98	114	RTA00000341F.m.21.1	M00004051D:E01	0
5121	1/28/98	137	RTA00000181AF.m.4.3	M00001455A:E09	13238
5122	1/28/98	162	RTA00000201F.e.15.1	M00004444B:D11	9960
5123	1/28/98	170	RTA00000197AF.d.23.1	M00001453A:E11	16130
5124	1/28/98	206	RTA00000181AF.o.04.2	M00001457C:C12	22205
5125	1/28/98	209	RTA00000182AF.c.5.1	M00001464D:F06	6397
5126	2/24/98	215	RTA00000403F.j.18.1	M00001539D:E10	5790
5127	2/24/98	219	RTA00000419F.c.18.1	M00003819D:B11	41394
5128	1/28/98	229	RTA00000198AF.g.3.1	M00001615C:F03	0
5129	1/28/98	230	RTA00000185AR.b.18.1	M00001575B:C09	12171
5130	3/24/98	245	RTA00000522F.p.09.1	M00001670A:F09	75204
5131	2/24/98	258	RTA00000406F.k.15.1	M00003907C:C04	38549

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5132	1/28/98	262	RTA00000186AF.c.17.1	M00001619D:G05	8551
5133	1/28/98	269	RTA00000183AF.k.13.1	M00001534B:C12	0
5134	1/28/98	276	RTA00000198AF.j.15.1	M00001653B:E09	4369
5135	2/24/98	281	RTA00000411F.l.13.1	M00003857C:C09	43114
5136	1/28/98	284	RTA00000199F.d.10.2	M00003808C:B05	22049
5137	1/28/98	292	RTA00000199AF.m.18.1	M00003939C:F04	0
5138	1/28/98	297	RTA00000178AF.f.9.3	M00001371C:E09	7172
5139	2/24/98	301	RTA00000401F.m.23.1	M00003914C:C02	2801
5140	1/28/98	302	RTA00000186AF.d.1.2	M00001621C:C08	40044
5141	1/28/98	315	RTA00000199R.d.23.1	M00003815D:H09	37477
5142	2/24/98	315	RTA00000419F.p.12.1	M00004037A:E04	13767
5143	1/28/98	321	RTA00000181AR.b.21.1	M00001444C:D05	3266
5144	3/24/98	323	RTA00000524F.c.12.1	M00005218B:D09	0
5145	1/28/98	329	RTA00000186AF.b.9.1	M00001616C:F07	0
5146	1/28/98	334	RTA00000181AR.b.21.3	M00001444C:D05	3266
5147	2/24/98	334	RTA00000408F.p.05.1	M00001575B:B02	9649
5148	1/28/98	335	RTA00000182AF.e.3.2	M00001468B:H06	0
5149	1/28/98	336	RTA00000186AF.f.24.1	M00001629B:E06	0
5150	2/24/98	341	RTA00000412F.g.20.2	M00003972C:F08	25018
5151	2/24/98	343	RTA00000422F.g.21.1	M00001583A:F07	17232
5152	1/28/98	347	RTA00000199F.b.03.2	M00003779B:E12	38340
5153	2/24/98	354	RTA00000404F.c.03.2	M00001592C:F11	39198
5154	1/28/98	361	RTA00000177AR.g.16.4	M00001347A:B10	13576
5155	1/28/98	364	RTA00000187AF.g.13.1	M00001676C:C11	2991
5156	2/24/98	377	RTA00000346F.i.01.1	M00003797A:D06	22260
5157	2/24/98	389	RTA00000411F.c.02.1	M00001677B:B04	72852
5158	2/24/98	403	RTA00000403F.d.22.1	M00001473A:A07	10692
5159	1/28/98	407	RTA00000178AF.e.20.1	M00001370D:E12	3135
5160	1/28/98	422	RTA00000189AF.b.12.1	M00003829B:G03	17233
5161	2/24/98	429	RTA00000422F.c.17.1	M00004099D:F01	1360
5162	2/24/98	431	RTA00000399F.j.15.1	M00001578C:G06	1261
5163	1/28/98	439	RTA00000185AF.d.14.2	M00001579D:G07	8071
5164	2/24/98	448	RTA00000127A.a.3.1	M00001552A:H10	13232
5165	2/24/98	450	RTA00000118A.a.23.1	M00001395A:H02	3500
5166	1/28/98	451	RTA00000200AF.b.20.1	M00004043A:D02	40403
5167	2/24/98	455	RTA00000399F.d.23.1	M00001481B:A07	3310
5168	1/28/98	475	RTA00000187AR.m.3.3	M00001682C:B12	17055
5169	3/24/98	475	RTA00000427F.i.06.1	M00004097B:D03	41450
5170	3/24/98	477	RTA00000527F.l.21.1	M00003983D:H02	36439
5171	1/28/98	480	RTA00000181AF.o.08.2	M00001457C:H12	849
5172	3/24/98	480	RTA00000424F.d.17.3	M00001455A:E11	73958
5173	3/24/98	481	RTA00000523F.j.02.1	M00003857A:H10	62853
5174	1/28/98	483	RTA00000192AF.h.19.1	M00004162C:A07	4642
5175	2/24/98	489	RTA00000406F.j.19.1	M00003906A:F12	1685
5176	1/28/98	501	RTA00000200R.k.11.1	M00004197C:F03	9796
5177	2/24/98	502	RTA00000341F.d.08.1	M00003824C:D07	0
5178	2/24/98	508	RTA00000420F.i.20.1	M00005101C:E12	0
5179	1/28/98	510	RTA00000178AF.n.23.1	M00001387B:E02	3298
5180	1/28/98	511	RTA00000196AF.g.10.1	M00001376B:A02	12498
5181	2/24/98	519	RTA00000404F.l.10.1	M00001638B:F10	23136

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
5182	2/24/98	524	RTA00000419F.f.23.1	M00003840D:H10	65002
5183	1/28/98	525	RTA00000198AF.c.7.1	M00001575D:G05	19181
5184	1/28/98	526	RTA00000185AF.e.20.1	M00001585A:D06	5865
5185	1/28/98	527	RTA00000198R.m.23.1	M00001684B:G03	38469
5186	1/28/98	529	RTA00000178AF.b.13.1	M00001364A:E11	3114
5187	1/28/98	530	RTA00000185AF.d.24.2	M00001582D:F05	0
5188	1/28/98	540	RTA00000179AF.b.10.3	M00001391D:D10	0
5189	1/28/98	541	RTA00000197AR.b.16.1	M00001445C:A08	0
5190	1/28/98	545	RTA00000196F.a.2.1	M00001338B:E02	3575
5191	2/24/98	547	RTA00000419F.h.02.1	M00003845D:G08	63985
5192	1/28/98	548	RTA00000179AF.f.23.3	M00001397B:G03	35258
5193	1/28/98	550	RTA00000183AF.g.14.1	M00001513D:A03	0
5194	2/24/98	555	RTA00000133A.d.22.1	M00001469A:G11	11797
5195	1/28/98	569	RTA00000196AF.l.23.1	M00001412A:E04	12052
5196	1/28/98	570	RTA00000183AF.a.19.2	M00001499A:A05	3788
5197	1/28/98	574	RTA00000192AF.f.3.1	M00004146C:C11	5257
5198	1/28/98	575	RTA00000186AF.l.12.2	M00001645A:C12	19267
5199	1/28/98	576	RTA00000196AF.c.7.1	M00001350B:G11	0
5200	2/24/98	579	RTA00000413F.m.16.1	M00004898C:F03	0
5201	1/28/98	580	RTA00000197F.a.12.1	M00001438B:B09	7895
5202	2/24/98	580	RTA00000403F.o.07.1	M00001579C:A01	39037
5203	2/24/98	584	RTA00000418F.d.22.1	M00001573B:C06	75324
5204	1/28/98	585	RTA00000198AF.n.18.1	M00001771A:A07	16715
5205	1/28/98	601	RTA00000184AF.i.10.2	M00001555A:B01	3744
5206	1/28/98	607	RTA00000200AF.k.12.1	M00004198B:D02	7359
5207	1/28/98	613	RTA00000177AF.k.18.4	M00001352C:A05	53729
5208	1/28/98	640	RTA00000190AF.f.5.1	M00003909A:H04	5015
5209	2/24/98	645	RTA00000422F.p.12.2	M00001661C:F10	9840
5210	1/28/98	654	RTA00000186AF.j.21.2	M00001639D:B07	22506
5211	1/28/98	680	RTA00000177AF.f.10.1	M00001345A:E01	6420
5212	1/28/98	699	RTA00000178AF.a.12.1	M00001362B:H06	0
5213	1/28/98	703	RTA00000198F.l.09.1	M00001664B:D06	3611
5214	1/28/98	704	RTA00000190AF.o.12.1	M00003972D:C09	3438
5215	1/28/98	723	RTA00000183AF.p.24.1	M00001543C:F01	3116
5216	2/24/98	733	RTA00000405F.d.18.1	M00001662C:B02	10494
5217	1/28/98	739	RTA00000181AF.p.12.3	M00001460C:H02	22204
5218	1/28/98	742	RTA00000177AF.m.1.1	M00001353D:D10	14929
5219	2/24/98	774	RTA00000403F.e.24.1	M00001476B:D10	16432
5220	2/24/98	775	RTA00000405F.c.22.1	M00001660C:B06	39053
5221	2/24/98	790	RTA00000345F.n.08.1	M00001517A:B11	0
5222	2/24/98	816	RTA00000354R.n.04.1	M00003808C:B05	22049
5223	2/24/98	829	RTA00000411F.m.11.1	M00003867A:D12	73196
5224	2/24/98	851	RTA00000423F.d.07.1	M00001678B:B12	0
5225	2/24/98	871	RTA00000403F.f.23.1	M00001479C:E01	39223
5226	2/24/98	877	RTA00000418F.m.22.1	M00001654D:E12	74567
5227	2/24/98	914	RTA00000138A.m.15.1	M00001624A:A03	41603
5228	2/24/98	923	RTA00000126A.d.19.1	M00001548A:G01	79474
5229	2/24/98	924	RTA00000354R.m.02.1	M00003890B:C08	12766
5230	2/24/98	940	RTA00000414F.f.17.1	M00005260A:F04	0
5231	2/24/98	1005	RTA00000339F.e.17.1	M00001397D:G08	7568

SEQ ID NO:	Filing Date of Priority Appln	SEQ ID NO: in Priority Appln	Sequence Name	Clone Name	Cluster ID
5232	2/24/98	1013	RTA00000404F.b.18.1	M00001592A:H05	13669
5233	2/24/98	1037	RTA00000339F.l.12.1	M00001450A:G11	7711
5234	2/24/98	1055	RTA00000346F.a.04.1	M00001607B:C05	5382
5235	2/24/98	1070	RTA00000346F.n.22.1	M00004137A:D06	0
5236	2/24/98	1096	RTA00000421F.a.06.1	M00001589C:A11	2385
5237	2/24/98	1125	RTA00000118A.n.5.1	M00001451A:C10	0
5238	2/24/98	1128	RTA00000423F.a.02.3	M00001656B:A08	39210
5239	2/24/98	1129	RTA00000401F.m.07.1	M00003907D:F11	2893
5240	2/24/98	1136	RTA00000406F.c.05.1	M00003870A:H01	22077
5241	2/24/98	1142	RTA00000418F.i.06.1	M00001591B:B06	75151
5242	2/24/98	1145	RTA00000423F.k.21.2	M00003984D:B08	37499
5243	2/24/98	1149	RTA00000339F.b.02.1	M00001344B:F12	0
5244	2/24/98	1166	RTA00000347F.h.01.1	M00004040A:G12	12043
5245	2/24/98	1177	RTA00000126A.b.9.1	M00001547A:F11	81279
5246	2/24/98	1187	RTA00000120A.c.19.1	M00001464A:B03	81016
5247	2/24/98	1203	RTA00000413F.e.10.1	M00004092C:B03	31033
5248	2/24/98	1205	RTA00000419F.k.05.1	M00003871C:E04	11757
5249	2/24/98	1230	RTA00000399F.j.14.1	M00001578C:F05	16942
5250	2/24/98	1233	RTA00000418F.l.02.1	M00001641C:C05	39316
5251	2/24/98	1248	RTA00000419F.o.07.1	M00003986C:E09	14059
5252	2/24/98	1261	RTA00000404F.m.17.2	M00001643B:E05	0

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
2503	AB011149	Homo sapiens mRNA for KIAA0577 protein, complete cds	0	3043678	(AB011149) KIAA0577 protein [Homo sapiens]	1e-096
2504	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
2505	Z59973	H.sapiens CpG DNA, clone 184b10, forward read cpg184b10.ft1a .	1e-009	<NONE>	<NONE>	<NONE>
2506	AJ000742	Homo Sapiens hisH1 gene, 5' UTR	2e-016	<NONE>	<NONE>	<NONE>
2507	U10324	Human nuclear factor NF90 mRNA, complete cds.	3e-009	1729881	TETRACYCLINE RESISTANCE PROTEIN, CLASS H (TETA(H)) >gi|392873 (U00792) tetracycline resistance protein [Pasteurella multocida]	9.3
2508	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	3e-010	1890128	(U89949) folate binding protein [Sus scrofa]	7.3
2509	M15657	Human aldolase B (ALDOB) gene, exons 2 through 6.	0.002	<NONE>	<NONE>	<NONE>
2510	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	8e-008	<NONE>	<NONE>	<NONE>
2511	U39722	Mycoplasma genitalium section 44 of 51 of the complete genome	0.043	2773162	(AF039595) sulfonylurea receptor 1B [Rattus norvegicus]	10
2512	AB012174	Homo sapiens DNA, anonymous heat-stable fragment RP7-1B	7e-017	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
2513	AB012174	Homo sapiens DNA, anonymous heat-stable fragment RP7-1B	7e-017	<NONE>	<NONE>	<NONE>
2514	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	7e-007	2984585	(AC004472) P1.11659_4 [Homo sapiens]	1e-013
2515	AF061016	Homo sapiens UDP-glucose dehydrogenase (UGDH) mRNA, complete cds	0	3127127	(AF061016) UDP-glucose dehydrogenase [Homo sapiens] dehydrogenase [Homo sapiens]	7e-035
2516	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	6e-005	2983872	(AE000742) putative protein [Aquifex aeolicus]	1.5
2517	X13293	Human mRNA for B-myb gene	3e-019	127584	MYB-RELATED PROTEIN B (B-MYB) human >gi|29472 (X13293) B-myb protein (AA 1-700) [Homo sapiens]	0.0002
2518	Y10183	H.sapiens mRNA for MEMD protein	0	3882036	(AJ010405) hypothetical protein	2.5
2519	M90297	Human glucokinase (GCK) gene, exon 1 and 5' flanking region.	4e-023	2851668	HYPOTHETICAL OUTER MEMBRANE USHER PROTEIN IN RIBB-GLGS INTERGENIC REGION PRECURSOR	7.8
2520	V00436	Gallus gallus fragment of gene X of ovalbumin family coding for the first leader exon.	4.4	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
2521	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	6e-006	3800811	(AF072251) methyl-CpG binding protein 2 [Mus musculus]	6.9
2522	Y09540	H.sapiens AHSG gene, partial	2e-007	2135357	HLA class I alpha chain - human (fragment) sapiens]	3.1
2523	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	3e-007	<NONE>	<NONE>	<NONE>
2524	D87438	Human mRNA for KIAA0251 gene, partial cds	1e-011	<NONE>	<NONE>	<NONE>
2525	AE001203	Treponema pallidum section 19 of 87 of the complete genome	0.42	<NONE>	<NONE>	<NONE>
2526	U47322	Cloning vector DNA, complete sequence.	2e-036	987050	(X65335) lacZ gene product [unidentified cloning vector]	4e-008
2527	M97287	Human MAR/SAR DNA binding protein (SATB1) mRNA, complete cds. > :: gb|I58691|I58691 Sequence 1 from patent US 5652340	0	417747	DNA-BINDING PROTEIN SATB1 (SPECIAL AT-RICH SEQUENCE BINDING PROTEIN 1) protein SATB1 - human >gi|337811 (M97287) putative [Homo sapiens]	2e-009
2528	AF005355	Oryctolagus cuniculus translation initiation factor eIF2C mRNA, complete cds	1e-094	3253159	(AF005355) translation initiation factor eIF2C	2e-084
2529	L16978	Anadara trapezia beta globin gene, complete cds.	0.11	<NONE>	<NONE>	<NONE>
2530	M24191	Human beta globulin pseudogene, clone 46B	0.013	3878519	(Z92806) K10G4.7 [Caenorhabditis elegans]	0.6

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
2531	AF047611	Euroglyphus maynei group 1 allergen Eur m 1 0102	0.12	<NONE>	<NONE>	<NONE>
2532	AE001372	Plasmodium falciparum chromosome 2, section 9 of 73 of the complete sequence	0.002	<NONE>	<NONE>	<NONE>
2533	J04700	Homo sapiens calcium-dependent protease large subunit (CANPmL) gene, promoter region and exon 1.	0.014	<NONE>	<NONE>	<NONE>
2534	AF038958	Homo sapiens synaptic glycoprotein SC2 spliced variant mRNA, complete cds	4e-086	2144098	SC2 - rat >gi|256994|bbs|115268 (S45663) SC2=synaptic glycoprotein [rats, brain, Peptide, 308 aa]	1e-033
2535	L13434	Human chromosome 3p21.1 gene sequence, complete cds.	8e-008	1085432	mucin (clone PGM-2A) - pig	4.3
2536	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	1e-011	3873713	(Z74026) cDNA EST yk452h4.3 comes from this gene; cDNA EST yk452h4.5 comes from this gene	4e-010
2537	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	1e-011	<NONE>	<NONE>	<NONE>
2538	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	2e-006	386644	type Ia hair keratin a3 [human, Peptide, 404 aa] >gi|3724101|gnl|PID|e1330425 (Y16788) keratin, type I [Homo sapiens]	1.9

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
2539	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	0.0005	<NONE>	<NONE>	<NONE>
2540	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
2541	U79248	Human clone 23826 mRNA sequence	6e-005	<NONE>	<NONE>	<NONE>
2542	D44598	Saccharomyces cerevisiae chromosome VI phage 4121	1e-010	2828280	(AL021687) putative protein [Arabidopsis thaliana] >gi|2832633|gnl|PID|e1249651 (AL021711) putative protein [Arabidopsis thaliana]	6e-060
2543	X64037	H.sapiens mRNA for RNA polymerase II associated protein RAP74	0	35871	(X64002) RAP74 [Homo sapiens] >gi|228483|prf||1804353A transcription factor RAP74 [Homo sapiens]	4e-049
2544	M18857	A.californica nuclear polyhedrosis virus ORFs encoding a delayed early protein and two late protein, complete cds.	0.38	3169096	(AL023706) hypothetical protein	3e-029
2545	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	7e-006	<NONE>	<NONE>	<NONE>
2546	L22403	Homo sapiens DNA sequence, repeat region.	1e-020	<NONE>	<NONE>	<NONE>
2547	L22403	Homo sapiens DNA sequence, repeat region.	1e-020	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
2548	D38417	Mouse mRNA for arylhydrocarbon receptor, complete cds	3e-028	<NONE>	<NONE>	<NONE>
2549	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	2e-006	<NONE>	<NONE>	<NONE>
2550	X04754	Drosophila yolk polypeptide gene YP3	1e-012	2500649	PROBABLE RNA 3'-TERMINAL PHOSPHATE CYCLASE (RNA-3'-PHOSPHATE CYCLASE) (RNA CYCLASE)	1e-022
2551	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	3e-011	<NONE>	<NONE>	<NONE>
2552	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	2e-006	<NONE>	<NONE>	<NONE>
2553	U49169	Dictyostelium discoideum V-ATPase A subunit (vatA) mRNA, complete cds	0.13	586429	VERY HYPOTHETICAL 13.2 KD PROTEIN IN PTC3-SAS3 INTERGENIC REGION >gi|626813|pir||S45788 probable membrane protein YBL053w - yeast (Saccharomyces cerevisiae) >gi|536079 (Z35814) ORF YBL053w	1.1
2554	M22462	Chicken protein p54 (ets-1) mRNA, complete cds.	1.1	2078531	(U89506) Mlark [Mus musculus]	5.6

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
2555	U73664	Human t(11;14)(q13;q32) breakpoint junction sequence	0.37	2909381	(Y16569) ORF [Mycobacterium tuberculosis]	3.3
2556	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	6e-006	3025166	PUTATIVE NUCLEOSIDE TRANSPORTER YEGT >gi|1736823|gnl|PID|d1016692 (D90848) Nucleoside permease NupG (Nucleoside-transport system protein NupG). [Escherichia coli] >gi|1788415 (AE000299) putative nucleoside permease protein [Escherichia coli]	1.4
2557	U09210	Human vesicular acetylcholine transporter mRNA, complete cds.	0.041	3176395	(AB015041) PIF1 [Caenorhabditis elegans]	1e-006
2558	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	0.002	540271	(U14635) similar to GABA and glycine receptors	1e-020
2559	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	7e-007	<NONE>	<NONE>	<NONE>
2560	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	1e-010	<NONE>	<NONE>	<NONE>
2561	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	3e-009	1788739	(AE000327) orf, hypothetical protein [Escherichia coli]	6.8

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
2562	AF073710	Homo sapiens regulator of G-protein signaling 9 mRNA, complete cds	1e-013	728831	!!!! ALU SUBFAMILY J WARNING ENTRY	0.38
2563	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	1e-011	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	5.1
2564	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	6e-007	<NONE>	<NONE>	<NONE>
2565	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	5e-015	<NONE>	<NONE>	<NONE>
2566	M98502	Mus musculus protein encoding twelve zinc finger proteins (pMLZ-4) mRNA, complete cds.	2e-017	2370153	(Y13374) putative prenylated protein prenylated protein [Homo sapiens] >gi|3360403 (AF052096) putative prenylated protein [Homo sapiens]	7.3
2567	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	1e-009	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	2.5
2568	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	3e-008	2580433	(D76414) ppGpp hydrolase [Staphylococcus aureus]	2.4
2569	X82206	H.sapiens mRNA for alpha-centractin	4e-085	2909479	(AL021930) hypothetical protein Rv0290	1.4
2570	Z68758	Human DNA sequence from cosmid cN85E10 on chromosome 22q11.2-qter	8e-009	1082778	secretory phospholipase A2 receptor precursor, transmembrane form - human >gi|862375	7.1

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
2571	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.0005	2583019	(AF022724) ARIX homeodomain protein [Homo sapiens]	0.64
2572	L19637	Arabidopsis thaliana adenine phosphoribosyltransferase (apt) gene, complete cds.	0.12	<NONE>	<NONE>	<NONE>
2573	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	2e-008	388057	(L22982) merozoite surface protein-1 [Plasmodium chabaudi]	6.9
2574	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	0.0005	3913436	PROBABLE ATP-DEPENDENT RNA HELICASE A (NUCLEAR DNA HELICASE II) (NDH II)	9.5
2575	AJ005698	Homo sapiens mRNA for poly(A)-specific ribonuclease	3e-011	3776076	(AJ005698) poly(A)-specific ribonuclease [Homo sapiens]	0.28
2576	Z96602	H.sapiens telomeric DNA sequence, clone 3QTEL015, read 3QTELOO015.seq	2e-006	2407641	(AF018956) neuropilin [Homo sapiens]	1.4
2577	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	4e-012	3880672	(AL032633) cDNA EST EMBL:T00127 comes from this gene; cDNA EST EMBL:T01189 comes from this gene [Caenorhabditis elegans]	0.82
2578	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	4e-012	2088843	(AF003386) F59E12.9 gene product [Caenorhabditis elegans]	3.5

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
2579	U95315	Mycobacterium gordonae IS1511 transposase and Tn554 tpna transposase homolog genes, complete cds	3.8	<NONE>	<NONE>	<NONE>
2580	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	6e-012	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	9.6
2581	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	2e-013	<NONE>	<NONE>	<NONE>
2582	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	3e-008	<NONE>	<NONE>	<NONE>
2583	U85193	Human nuclear factor I-B2 (NFIB2) mRNA, complete cds	2e-038	<NONE>	<NONE>	<NONE>
2584	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	3e-009	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	5.2
2585	U67532	Methanococcus jannaschii section 74 of 150 of the complete genome	0.005	1938410	(U97000) No definition line found [Caenorhabditis elegans]	4.5
2586	X65319	Cloning vector pCAT-Enhancer	3e-081	987050	(X65335) lacZ gene product [unidentified cloning vector]	3e-015
2587	AB006534	Homo sapiens mRNA for hepatocyte growth factor activator inhibitor type 2, complete cds	e-103	2065529	(U78095) bikunin [Homo sapiens]	3e-025

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
2588	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	6e-006	3152559	(AC002986) Similarity to A. thaliana gene product F21M12.20, gb|AC000132. EST gb|Z25651 comes from this gene. [Arabidopsis thaliana]	6e-008
2589	X82829	B.taurus mRNA for nuclear DNA helicase II	9e-009	1353239	(U10245) putative RNA helicase A [Arabidopsis thaliana]	3e-017
2590	AE001366	Plasmodium falciparum chromosome 2, section 3 of 73 of the complete sequence	0.047	<NONE>	<NONE>	<NONE>
2591	D78572	House mouse; Musculus domesticus mRNA for membrane glycoprotein, complete cds > :: dbj|E12950|E12950 cDNA GA3-43 encoding novel polypeptide which appear when differentiate from embryo-tumor cell P19 to nerve cell	1e-041	1545807	(D78572) membrane glycoprotein [Mus musculus]	1e-026
2592	M77130	H.sapiens (clone B7) hY4 Ro RNA pseudogene.	4e-011	629174	cellulose 1,4-beta-cellobiosidase (EC 3.2.1.91) - Clostridium thermocellum >gi|530014 (X80993) cellulose 1,4-beta-cellobiosidase [Clostridium thermocellum]	1.5

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
2593	M34661	Human chaperonin (HSP60) non-functional pseudogene 3.	1	<NONE>	<NONE>	<NONE>
2594	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	6e-006	1723894	HYPOTHETICAL GTP-BINDING PROTEIN IN SEH1-PRP20 INTERGENIC REGION >gi|2131584|pir||S64106 hypothetical protein YGL099w - yeast (Saccharomyces cerevisiae) >gi|1322637|gnl|PID|e243302 (Z72621) ORF YGL099w [Saccharomyces cerevisiae]	9e-015
2595	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	9e-010	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	0.16
2596	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	1e-010	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	3.4
2597	U57715	Rattus norvegicus FGF receptor activating protein FRAG1 (FRAG1) mRNA, complete cds	0	1518609	(U57715) FGF receptor activating protein FRAG1 [Rattus norvegicus]	2e-088
2598	Z64776	H.sapiens CpG DNA, clone 167d8, forward read cpg167d8.ft1b .	0.0002	1777782	(U52513) ISG family member [Homo sapiens]	2.4

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
2599	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	3e-008	<NONE>	<NONE>	<NONE>
2600	AF022158	Homo sapiens KRAB domain zinc finger protein	3e-010	2507553	ZINC FINGER PROTEIN 33A (ZINC FINGER PROTEIN KOX31) (KIAA0065) (HA0946) Kruppel-related. [Homo sapiens]	1e-016
2601	Y07660	M.tuberculosis accBC gene	2e-068	465847	HYPOTHETICAL 66.5 KD PROTEIN F02A9.5 IN CHROMOSOME III >gi|280542|pir||S28313 hypothetical protein F02A9.5 - Caenorhabditis elegans Genefinder; similar to Propionyl-CoA carboxylase beta chain; cDNA EST EMBL:M89018 comes from this gene; cDNA EST EMBL:D2806	8e-075
2602	S51858	MO25 gene [mice, embryos, mRNA, 2322 nt]	0	547911	MO25 PROTEIN >gi|2143483|pir||I57997 hypothetical calcium-binding protein - mouse protein [mice, embryos, Peptide, 341 aa] [Mus sp.]	e-119
2603	AB018345	Homo sapiens mRNA for KIAA0802 protein, partial cds	e-131	3882325	(AB018345) KIAA0802 protein [Homo sapiens]	3e-053

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
2604	L41560	Homo sapiens (clones HGPCD2 and HGPCD15) pterin-4a-carbinolamine dehydratase (PCBD) gene, complete cds.	2e-005	<NONE>	<NONE>	<NONE>
2605	AJ000041	Homo sapiens mRNA for HOXC11	e-180	987050	(X65335) lacZ gene product [unidentified cloning vector]	0.001
2606	U55939	Expression vector pVP-Nco, complete sequence.	4e-043	987050	(X65335) lacZ gene product [unidentified cloning vector]	9e-009
2607	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	2e-014	124139	TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 >gi|73901|pir||WZBE61 gene 61 protein - human herpesvirus 3 >gi|60050 (X04370) ORF 61 (AA1-467) [Human herpesvirus 3] >gi|228664|prf||1808271A gene 61 protein	0.48
2608	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	3e-009	<NONE>	<NONE>	<NONE>
2609	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	1e-013	3878130	(Z83112) predicted using Genefinder	9
2610	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	3e-010	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	5.3

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
2611	D14965	C.elegans gene for alpha-2 tubulin, complete cds	3.7	<NONE>	<NONE>	<NONE>
2612	Z61840	H.sapiens CpG DNA, clone 59g12, forward read cpg59g12.ft1a .	2e-080	3581872	(AL031541) putative integral membrane protein [Streptomyces coelicolor]	1.4
2613	U59924	Sus scrofa nitric oxide synthase (NOS) mRNA, complete cds	1.1	<NONE>	<NONE>	<NONE>
2614	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	2e-006	<NONE>	<NONE>	<NONE>
2615	AF054625	Reporter vector pSRF-Luc, complete sequence	4e-065	987050	(X65335) lacZ gene product [unidentified cloning vector]	3e-015
2616	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	1e-011	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	3.1
2617	AF031924	Homo sapiens homeobox transcription factor barx2	e-161	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	5.5
2618	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	4e-012	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	5.6
2619	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	1e-009	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	5.6
2620	AF053461	Reporter vector pCRE-Luc, complete sequence	1e-013	1065484	(U40415) similar to S. cerevisiae LAG1 (SP:P38703)	0.49
2621	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete	1e-009	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		cds				
2622	AF013758	Homo sapiens polyadenylate binding protein-interacting protein-1 (PAIP1) mRNA, complete cds	0	3046900	(AF013758) polyadenylate binding protein-interacting protein-1 [Homo sapiens]	3e-072
2623	D29808	Human mRNA for T-cell acute lymphoblastic leukemia associated antigen 1 (TALLA-1), complete cds	0.014	<NONE>	<NONE>	<NONE>
2624	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	5e-013	2690005	(AE000794) B. burgdorferi predicted coding region BBF30	7.6
2625	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.041	<NONE>	<NONE>	<NONE>
2626	Z12112	pWE15A cosmid vector DNA	2e-067	987050	(X65335) lacZ gene product [unidentified cloning vector]	3e-008
2627	AB018326	Homo sapiens mRNA for KIAA0783 protein, complete cds	0	3882287	(AB018326) KIAA0783 protein [Homo sapiens]	1e-073
2628	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	1e-011	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	5.4
2629	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	2e-016	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	5.4

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
2630	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	2e-006	1001632	(D64002) hypothetical protein	3.2
2631	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	3e-010	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	0.29
2632	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	2e-006	<NONE>	<NONE>	<NONE>
2633	X05167	Barley gene for thiol protease aleurain	0.13	1065515	(U40420) weak similarity to procollagen alpha chain 1(V) chain [Caenorhabditis elegans]	9e-018
2634	Z96177	H.sapiens telomeric DNA sequence, clone 10QTEL040, read 10QTELOO040.seq	2e-060	987050	(X65335) lacZ gene product [unidentified cloning vector]	5e-010
2635	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	2e-006	123432	ZERKNUELLT PROTEIN 1 (ZEN-1)	3.4
2636	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	2e-006	123432	ZERKNUELLT PROTEIN 1 (ZEN-1)	3.4
2637	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	5e-013	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	1.5
2638	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	5e-013	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	1.5

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
2639	AF103734	Sindbis-like virus YN87448, complete genome	3.5	<NONE>	<NONE>	<NONE>
2640	M27280	H.influenzae lic-1 operon licA, licB, licC and licD genes, encoding outer membrane lipopolysaccharide phase variation, complete cds.	3.4	2529686	(AC002535) putative G-beta-repeat containing protein, 5' partial [Arabidopsis thaliana]	6e-018
2641	AF103734	Sindbis-like virus YN87448, complete genome	3.5	<NONE>	<NONE>	<NONE>
2642	X05167	Barley gene for thiol protease aleurain	0.13	1065515	(U40420) weak similarity to procollagen alpha chain 1(V) chain [Caenorhabditis elegans]	9e-018
2643	L76159	Homo sapiens FRG1 mRNA, complete cds.	4e-032	1246233	(L76159) FRG1 gene product [Homo sapiens]	1e-005
2644	AF086047	Homo sapiens full length insert cDNA clone YX84A05	3e-008	628916	Delta-12 desaturases - Anabaena variabilis desaturase [Anabaena variabilis]	6
2645	AF086136	Homo sapiens full length insert cDNA clone ZA89C06	4e-021	3849864	(AJ007629) pall protein [Emericella nidulans]	4.6
2646	AB004818	Homo sapiens mRNA for ENX-2, complete cds	1e-011	<NONE>	<NONE>	<NONE>
2647	D87686	Homo sapiens mRNA for KIAA0017 protein, complete cds	e-165	3540219	(D87686) KIAA0017 protein [Homo sapiens]	5e-054
2648	Z49218	S.cerevisiae chromosome XIII cosmid 7056	0.002	2984715	(AF053957) dynamin associated protein isoform Dap160-1	0.33

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
2649	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	1e-009	868241	(U29488) C56C10.3 gene product [Caenorhabditis elegans]	7e-030
2650	D38417	Mouse mRNA for arylhydrocarbon receptor, complete cds	3e-028	<NONE>	<NONE>	<NONE>
2651	L29252	Human (clone D13-2) L-iditol-2 dehydrogenase gene, exon 4, exon 5, exon 6 and exon 7.	0.35	<NONE>	<NONE>	<NONE>
2652	U29171	Human casein kinase I delta mRNA, complete cds >	3e-063	1176666	HYPOTHETICAL 139.1 KD PROTEIN C08B11.3 IN CHROMOSOME II >gi|3874171|gnl|PID|e1343795 proteins; cDNA EST EMBL:T01154 comes from this gene; cDNA EST EMBL:T02016 comes from this gene; cDNA EST EMBL:D34307 comes from this gene; cDNA EST EMBL:D37339 comes from	6.8
2653	U63648	Mus musculus p160 myb-binding protein (P160) mRNA, complete cds	6e-058	2645205	(U63648) p160 myb-binding protein [Mus musculus]	2e-038
2654	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	3e-010	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	5.9
2655	Y11740	H.sapiens whn gene, exon 1a and 1b	0.12	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
2656	D26179	Rat mRNA for V-1 protein, complete cds	2e-005	3879121	(Z70310) predicted using Genefinder; Similarity to Mouse ankyrin (PIR Acc. No. S37771); cDNA EST EMBL:T01923 comes from this gene; cDNA EST EMBL:D32335 comes from this gene; cDNA EST EMBL:D32723 comes from this gene; cDNA ES... Genefinder; Similarity to M	8e-087
2657	U67518	Methanococcus jannaschii section 60 of 150 of the complete genome	1.2	3876465	(Z81071) predicted using Genefinder; Similarity to Human small nuclear ribonucleoprotein E cDNA EST yk375g7.5 comes from this gene; cDNA EST yk435f5.3 comes from this gen...	6e-011
2658	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	3e-008	<NONE>	<NONE>	<NONE>
2659	U83176	Mus musculus ROSA 26 transcription AS ROSA26AS mRNA, complete cds	0	1778861	(U83176) ROSA26AS [Mus musculus]	e-101
2660	AB018374	Mus musculus GARP34 mRNA, complete cds	2e-065	3724364	(AB018374) GARP34 [Mus musculus]	7e-010
2661	AB018374	Mus musculus GARP34 mRNA, complete cds	2e-065	3724364	(AB018374) GARP34 [Mus musculus]	7e-010

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
2662	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	4e-011	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	4.6
2663	AL022168	Human DNA sequence from clone U247E12 on chromosome Xq22-23, complete sequence [Homo sapiens]	8e-008	<NONE>	<NONE>	<NONE>
2664	M10277	Human cytoplasmic beta-actin gene, complete cds.	5e-063	<NONE>	<NONE>	<NONE>
2665	D83769	Homo sapiens DNA, corresponding sequence for DHFR	5e-014	763429	(U22961) putative ORF; similar in part to the product encoded by human glycerol-3-phosphate dehydrogenase mRNA, GenBank Accession Number L34041; Method: conceptual translation supplied by author [Homo sapiens]	5.9
2666	U15426	Human anonymous mRNA sequence with CCA repeat region.	3e-071	1065484	(U40415) similar to S. cerevisiae LAG1 (SP:P38703)	3e-015
2667	AF032900	Homo sapiens timing protein CLK-1 mRNA, complete cds	0	3811295	(AF032900) timing protein CLK-1; ubiquinone biosynthesis protein COQ7 [Homo sapiens]	3e-061
2668	L39210	Homo sapiens inosine monophosphate dehydrogenase type II gene, complete cds	e-111	2887425	(AB007885) KIAA0425 [Homo sapiens]	3e-036

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
2669	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	7.00E-07	<NONE>	<NONE>	<NONE>
2670	X93016	S.scrofa mRNA for cytosolic malic enzyme NADP-dependent	5e-045	101706	hypothetical protein 2 - yeast (Saccharomyces kluyveri) plasmid pSKL >gi|4870 (X54850) ORF 2, has similarity to DNA polymerase [Saccharomyces kluyveri]	7.7
2671	J03068	Human DNF1552 (lung) mRNA, complete cds.	0.041	2414623	(Z99259) putative phosphotransferase	7e-021
2672	X81372	H.sapiens mRNA for biphenyl hydrolase-related protein	2e-016	728831	!!!! ALU SUBFAMILY J WARNING ENTRY	0.0001
2673	AB012130	Homo sapiens SBC2 mRNA for sodium bicarbonate cotransporter2, complete cds	0.00E+00	3097316	(AB012130) sodium bicarbonate cotransporter2 [Homo sapiens]	3e-045
2674	D83769	Homo sapiens DNA, corresponding sequence for DHFR	5e-014	763429	(U22961) putative ORF; similar in part to the product encoded by human glycerol-3-phosphate dehydrogenase mRNA, GenBank Accession Number L34041; Method: conceptual translation supplied by author [Homo sapiens]	5.9
2675	D38522	Human mRNA for KIAA0080 gene, partial cds	1e-022	728831	!!!! ALU SUBFAMILY J WARNING ENTRY	0.002
2676	D38522	Human mRNA for KIAA0080 gene, partial cds	1e-022	728831	!!!! ALU SUBFAMILY J WARNING	0.002

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					ENTRY	
2677	AF072810	Homo sapiens transcription factor WSTF mRNA, complete cds	0	4049922	(AF072810) transcription factor WSTF [Homo sapiens]	1e-070
2678	U41767	Human metargidin precursor mRNA, complete cds	e-130	1235674	(U41767) metargidin precursor [Homo sapiens]	1.00E-02
2679	L81613	Homo sapiens (subclone 4_c7 from P1 H17) DNA sequence	0.38	<NONE>	<NONE>	<NONE>
2680	M68841	Human L1 repetitive sequence with a region homologous to a mouse ORF.	9.00E-30	106322	hypothetical protein (L1H 3' region) - human	8e-008
2681	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	0.0005	<NONE>	<NONE>	<NONE>
2682	D87973	Mus musculus Impact mRNA, complete cds	0	4038076	(D87973) Impact [Mus musculus]	1e-095
2683	M69175	Human H-protein mRNA, complete cds.	2e-017	<NONE>	<NONE>	<NONE>
2684	Z80361	H.sapiens HLA-DRB pseudogene, repeat region;	1e-082	1706108	MITOCHONDRIAL CARNITINE O-PALMITOYLTRANSFERASE I, LIVER ISOFORM (CPT I) (CPTI-L) carnitine palmitoyltransferase I [Homo sapiens] I [Homo sapiens]	0.67

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
2685	AF017044	Dictyostelium discoideum LTR-retrotransposon Skipper, partial genomic sequence, 3' end	0.014	<NONE>	<NONE>	<NONE>
2686	U40825	Mus musculus WW-domain binding protein 1 mRNA, complete cds	e-118	1777577	(U40825) WW-domain binding protein 1 [Mus musculus]	2.00E-29
2687	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	2e-005	2281149	(U58553) maturase [Carum carvi]	4.6
2688	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	8e-008	3328840	(AE001314) Putative outer membrane protein A [Chlamydia trachomatis]	5.8
2689	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
2690	AB012130	Homo sapiens SBC2 mRNA for sodium bicarbonate cotransporter2, complete cds	0.00E+00	3097316	(AB012130) sodium bicarbonate cotransporter2 [Homo sapiens]	3e-045
2691	X69516	H.sapiens gene for folate receptor	3e-008	<NONE>	<NONE>	<NONE>
2692	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	5.00E-04	1203965	(L42379) bone-derived growth factor [Homo sapiens]	0.17
2693	Z15027	H.sapiens HLA class III DNA	3.00E-07	728836	!!!! ALU SUBFAMILY SP WARNING ENTRY	3.6
2694	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	2e-006	<NONE>	<NONE>	<NONE>
2695	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	2e-006	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
2696	X77775	G.gallus Gal beta 1, 3 GalNAc-specific GalNAc alpha 2, 6-sialyltransferase mRNA.	1e-022	3873839	(Z81029) W05H12.2 [Caenorhabditis elegans] >gi|3880545|gnl|PID|e1350077 (Z82072) W05H12.2	5.9
2697	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	2e-005	2281149	(U58553) maturase [Carum carvi]	4.6
2698	U33005	Mus musculus tbc1 mRNA, complete cds. > :: gb|I86429|I86429 Sequence 1 from patent US 5700927	3e-093	3893077	(Y17923) lyncein [Bos taurus]	1e-040
2699	U74651	Human DNA polymerase gamma (polg) gene, promoter region and partial cds	1e-022	113667	!!!! ALU CLASS B WARNING ENTRY !!!!	0.002
2700	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	9e-009	3064257	(AF043899) amphiphysin IIc1 [Homo sapiens]	0.87
2701	U43893	Mus musculus ATP synthase gamma-subunit gene, nuclear gene encoding a mitochondrial protein, partial cds	0.005	3929529	(AF034611) intrinsic factor-B12 receptor precursor; cubilin [Homo sapiens]	0.67
2702	U43893	Mus musculus ATP synthase gamma-subunit gene, nuclear gene encoding a mitochondrial protein, partial cds	0.005	3929529	(AF034611) intrinsic factor-B12 receptor precursor; cubilin [Homo sapiens]	0.67

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
2703	M30704	Human amphiregulin (AR) mRNA, complete cds, clones lambda-AR1 and lambda-AR2.	0	113754	AMPHIREGULIN PRECURSOR (AR)	4e-041
2704	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	9e-010	<NONE>	<NONE>	<NONE>
2705	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	3e-011	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	5.2
2706	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	1e-009	2832664	(AL021710) pollen-specific protein - like [Arabidopsis thaliana]	8e-020
2707	U00684	Human unknown mRNA.	2e-038	2500412	30S RIBOSOMAL PROTEIN S6 Mycoplasma pneumoniae (SGC3) (ATCC 29342) >gi|1674305 similar to Swiss-Prot Accession Number P02358, from E. coli [Mycoplasma pneumoniae]	1.3
2708	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	5e-015	108693	glutamic acid-rich protein, retinal - bovine taurus]	0.067
2709	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	1e-011	79703	hypothetical 32K protein (frxC 5' region) - Synechocystis sp. (PCC 6803) >gi|217091|gnl|PID|d1001745	0.8

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
2710	AF083395	Homo sapiens phospholipase A2-activating protein mRNA, complete cds	e-175	4106818	(AF083395) phospholipase A2-activating protein [Homo sapiens]	4e-039
2711	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	3e-011	<NONE>	<NONE>	<NONE>
2712	AB019488	Homo sapiens DNA for TRKA, exon 17 and complete cds	0	37403	(X03541) trk gene product (aa 1-641) [Homo sapiens]	1e-032
2713	X62570	H.sapiens mRNA for IFP53	e-105	32709	(X62570) IFP53 [Homo sapiens]	6e-033
2714	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.005	1170056	GENERAL SECRETION PATHWAY PROTEIN F	4.3
2715	AF031924	Homo sapiens homeobox transcription factor barx2	e-161	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	5.5
2716	AF031924	Homo sapiens homeobox transcription factor barx2	e-161	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	5.5
2717	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	9e-010	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	5.4
2718	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	9e-010	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	5.4
2719	L20826	Human I-plastin mRNA, complete cds.	e-163	2493466	I-PLASTIN (INTESTINE-SPECIFIC PLASTIN) >gi|1362892|pir||A 56536 plastin, intestine-specific - human >gi|405230 (L20826) I-plastin	6e-069

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
2720	Z54386	H.sapiens CpG DNA, clone 10g3, forward read cpg10g3.ft1a .	7e-059	1788180	(AE000281) biotin sulfoxide reductase 2 [Escherichia coli]	5.8
2721	AF086201	Homo sapiens full length insert cDNA clone ZC42G09	1e-085	2564332	(AB006630) KIAA0292 [Homo sapiens]	5.4
2722	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	4e-012	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	0.12
2723	AJ006267	Homo sapiens mRNA for ClpX-like protein	0	3688380	(AJ006267) ClpX-like protein [Homo sapiens]	1e-091
2724	AF064801	Homo sapiens multiple membrane spanning receptor TRC8 (TRC8) mRNA, complete cds	0	3395787	(AF064801) multiple membrane spanning receptor TRC8	e-123
2725	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	2e-006	2599526	(AF029331) immunoglobulin heavy chain V region [Homo sapiens]	4.2
2726	Y08013	S.salar DNA segment containing GT repeat	0.006	<NONE>	<NONE>	<NONE>
2727	Y08013	S.salar DNA segment containing GT repeat	0.006	<NONE>	<NONE>	<NONE>
2728	AE000971	Archaeoglobus fulgidus section 136 of 172 of the complete genome	0.041	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
2729	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	7e-007	1170586	RAS GTPASE-ACTIVATING-LIKE PROTEIN IQGAP1 (P195) (KIAA0051) >gi|627594|pir||A54854 Ras GTPase activating-related protein - human sapiens] >gi|536844 (L33075) ras GTPase-activating-like protein [Homo sapiens]	9e-011
2730	M60858	Human nucleolin gene, complete cds.	e-129	<NONE>	<NONE>	<NONE>
2731	M85145	Human tumor necrosis factor receptor, 3' flank.	2e-007	<NONE>	<NONE>	<NONE>
2732	M85145	Human tumor necrosis factor receptor, 3' flank.	2e-007	<NONE>	<NONE>	<NONE>
2733	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	4e-013	<NONE>	<NONE>	<NONE>
2734	L07063	Mus musculus FKBP65 binding protein mRNA, complete cds	6e-089	2137294	FKBP65 binding protein - mouse >gi|894162	6e-024
2735	X63432	H.sapiens ACTB mRNA for mutant beta-actin	e-112	987050	(X65335) lacZ gene product [unidentified cloning vector]	3e-014
2736	AF083395	Homo sapiens phospholipase A2-activating protein mRNA, complete cds	0	4106818	(AF083395) phospholipase A2-activating protein [Homo sapiens]	1e-094
2737	AJ012449	Homo sapiens mRNA for NS1-binding protein	3e-009	3165570	(AF067946) similar to Drosophila ring canal protein	4e-032

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
2738	M27878	Human DNA binding protein (HPF2) mRNA, complete cds.	3e-063	3702137	(AL031393) dJ733D15.1 (Zinc-finger protein) [Homo sapiens]	1e-040
2739	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
2740	Y15230	Homo sapiens pygl gene, exon 5 and partial intron 4 and 5	e-166	3170407	(AF046798) glycogen phosphorylase [Homo sapiens]	1e-044
2741	Z96177	H.sapiens telomeric DNA sequence, clone 10QTEL040, read 10QTELOO040.seq	1e-053	987050	(X65335) lacZ gene product [unidentified cloning vector]	2e-005
2742	M90058	Human serglycin gene, exons 1,2, and 3.	3e-010	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	8.8
2743	X69878	H.sapiens Flt4 mRNA for transmembrane tyrosine kinase	2e-088	<NONE>	<NONE>	<NONE>
2744	X69878	H.sapiens Flt4 mRNA for transmembrane tyrosine kinase	2e-088	<NONE>	<NONE>	<NONE>
2745	AB007923	Homo sapiens mRNA for KIAA0454 protein, partial cds	0	3413870	(AB007923) KIAA0454 protein [Homo sapiens]	1e-098
2746	AF042181	Homo sapiens testis-specific Y-encoded-like protein (TSPYL) mRNA, partial cds	2e-047	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	3
2747	AL021173	Caenorhabditis elegans cosmid VK10D6R, complete sequence [Caenorhabditis elegans]	1.2	<NONE>	<NONE>	<NONE>
2748	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	4e-012	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	0.12

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
2749	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	2e-008	<NONE>	<NONE>	<NONE>
2750	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	2e-008	<NONE>	<NONE>	<NONE>
2751	M22970	Human pancreatic phospholipase A-2 (PLA-2) gene, exons 1 to 3.	1e-032	113671	!!!! ALU CLASS F WARNING ENTRY !!!!	3e-006
2752	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	1e-011	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	5.2
2753	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	3e-011	3219914	HYPOTHETICAL 16.8 KD PROTEIN C30D10.04 IN CHROMOSOME II >gi|2276353|gnl|PID|e330328 pombe]	1e-011
2754	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	1e-011	3875246	(Z81490) similar to WD domain, G-beta repeats (2 domains); cDNA EST EMBL:T00482 comes from this gene; cDNA EST EMBL:T00923 comes from this gene; cDNA EST yk449d4.3 comes from this gene; cDNA EST yk449d4.5 comes from this gen...	6e-078

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
2755	D79205	Human mRNA for ribosomal protein L39, complete cds	1e-086	1173044	60S RIBOSOMAL PROTEIN L39 norvegicus] >gi|1373419 (U57846) ribosomal protein L39 ribosomal protein L39 [Homo sapiens]	4e-009
2756	AB014591	Homo sapiens mRNA for KIAA0691 protein, complete cds	0	3327196	(AB014591) KIAA0691 protein [Homo sapiens]	1e-047
2757	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	1e-012	115409	CUTICLE COLLAGEN ROL-6 elegans] >gi|3879235|gnl|PID|e1348932 (Z66499) similar to cuticle collagen ROL-6; cDNA EST cm10c4 comes from this gene; cDNA EST EMBL:M88874 comes from this gene; cDNA EST yk265e2.3 comes from this gene; cDNA EST yk265e2.5 comes fro	0.031
2758	U78096	Human macrophage colony stimulating factor receptor (c-fms) gene, exon 1A, 2 and partial cds	4e-012	126296	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG protein [Nycticebus coucang]	0.0005
2759	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	3e-010	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
2760	M27878	Human DNA binding protein (HPF2) mRNA, complete cds.	3e-063	3702137	(AL031393) dJ733D15.1 (Zinc-finger protein) [Homo sapiens]	1e-040
2761	U43076	Mus musculus cdc37 homolog mRNA, complete cds	2e-017	755484	(U20281) cell division cycle control protein 37 [Gallus gallus]	8e-022
2762	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	1e-011	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	5.2
2763	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	2e-005	1171883	SODIUM-INDEPENDENT ORGANIC ANION TRANSPORTER (ORGANIC ANION TRANSPORTING POLYPEPTIDE) anion - rat >gi|410311 (L19031) oatp [Rattus norvegicus]	2e-036
2764	X54452	D.discoideum culmination spiA (Dd31) gene	3.3	<NONE>	<NONE>	<NONE>
2765	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	4e-012	<NONE>	<NONE>	<NONE>
2766	AF053698	Reporter vector pAP1-Luc, complete sequence	3e-019	987050	(X65335) lacZ gene product [unidentified cloning vector]	0.2
2767	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	1e-012	3582428	(AB017257) glycocyamine kinase beta chain [Neanthes diversicolor]	4.3
2768	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
2769	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial	6e-006	3511122	(AF060503) zinc finger protein [Homo sapiens]	5.3

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		cds				
2770	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	1e-012	<NONE>	<NONE>	<NONE>
2771	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	1e-012	<NONE>	<NONE>	<NONE>
2772	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	2e-006	<NONE>	<NONE>	<NONE>
2773	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	1e-013	804788	(M13002) 2855 is the position of the first start codon in ORF 2; putative [Mus musculus]	0.64
2774	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	8e-008	<NONE>	<NONE>	<NONE>
2775	M86526	Rat proline-rich protein (PRP) gene, 5' end, and containing several Alu-like repetitive elements.	0.37	<NONE>	<NONE>	<NONE>
2776	Z22923	M.musculus alpha2 (IX) collagen gene, complete CDS.	0.002	<NONE>	<NONE>	<NONE>
2777	Z22923	M.musculus alpha2 (IX) collagen gene, complete CDS.	0.002	<NONE>	<NONE>	<NONE>
2778	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	1e-012	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	5.4

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
2779	Z74035	Caenorhabditis elegans cosmid F47G9, complete sequence [Caenorhabditis elegans]	3.4	2879805	(AL021813) hypothetical protein	5.7
2780	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	1e-012	<NONE>	<NONE>	<NONE>
2781	AG001356	Homo sapiens genomic DNA, 21q region, clone: 9H11BG25	2e-015	<NONE>	<NONE>	<NONE>
2782	D83006	Saccharomyces cerevisiae MNN4 gene, complete cds	1.2	<NONE>	<NONE>	<NONE>
2783	Z59640	H.sapiens CpG DNA, clone 167g11, forward read cpg167g11.ft1b .	0.12	<NONE>	<NONE>	<NONE>
2784	AF049069	Pinus radiata PRE87 mRNA, complete cds	1.1	1518141	(U66568) myocyte enhancer factor 2A MEF2A [Danio rerio]	3.1
2785	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	4e-012	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	5.4
2786	AF031931	Hydra oligactis cyclic GMP-dependent protein kinase (hyGK) mRNA, complete cds	0.13	<NONE>	<NONE>	<NONE>
2787	Z96177	H.sapiens telomeric DNA sequence, clone 10QTEL040, read 10QTELOO040.seq	3e-041	987050	(X65335) lacZ gene product [unidentified cloning vector]	0.015

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
2788	L48716	Homo sapiens galactose-1-phosphate uridyl transferase (GALT) mutant F117S gene, exons 3 and 4	1.1	77657	hypothetical 30.1K protein - Pseudomonas aeruginosa	0.095
2789	U73902	Mus musculus emerin (Sta) mRNA, complete cds	0.37	529773	(U06752) Heterodimeric complex composed of a mucin subunit, ASGP-1, which is predominantly O-glycosylated, and a cysteine-rich transmembrane subunit, ASGP-2, which is predominantly N-glycosylated [Rattus norvegicus]	0.009
2790	X54171	H.sapiens NG2-6 DNA	4e-021	<NONE>	<NONE>	<NONE>
2791	M30519	Mouse mammary tumor virus gag gene, 3' end, pol gene, 5' end.	0.12	1262926	(U51903) RasGAP-related protein [Homo sapiens]	4.3
2792	AJ223355	Rattus norvegicus mRNA for mitochondrial dicarboxylate carrier	0.38	128059	NEGATIVE FACTOR (F-PROTEIN) (27 KD PROTEIN) (3'ORF) >gi|77283|pir||S07993 nef protein - simian immunodeficiency virus SIVsm (isolate F236) immunodeficiency virus]	2
2793	AF086022	Homo sapiens full length insert cDNA clone YW23E02	6e-005	3402679	(AC004697) unknown protein [Arabidopsis thaliana]	9e-016
2794	U47322	Cloning vector DNA, complete sequence.	9e-010	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
2795	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	6e-006	3873667	(Z71178) similar to collagen	0.093
2796	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	3e-009	2745961	(U51869) Bcd orf2 [Homo sapiens]	0.47
2797	AF041209	Homo sapiens midline 1 fetal kidney isoform 2	0.0002	<NONE>	<NONE>	<NONE>
2798	AF092564	Homo sapiens chromosome-associated protein-C	5e-056	4092846	(AB019987) chromosome-associated polypeptide-C [Homo sapiens]	3e-017
2799	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	6e-006	<NONE>	<NONE>	<NONE>
2800	M95623	Homo sapiens hydroxymethylbilane synthase gene, complete cds.	0.005	4007760	(AL034433) importin alpha subunit	4.2
2801	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	7e-007	<NONE>	<NONE>	<NONE>
2802	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	6e-006	1065945	(U40799) coded for by C. elegans cDNA yk28f2.3; coded for by C. elegans cDNA yk12c10.3; coded for by C. elegans cDNA yk5a12.3; coded for by C. elegans cDNA yk49a8.3; coded for by C. elegans cDNA yk12c10.5; coded for by C. elegans cDNA yk28f2...	0.12

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
2803	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	0.04	<NONE>	<NONE>	<NONE>
2804	M74558	Human SIL mRNA, complete cds. > :: gb|G28581|G28581 human STS SHGC-35335.	e-126	<NONE>	<NONE>	<NONE>
2805	M72885	Human GOS2 gene, 5' flank and cds.	0.36	3873821	(Z68213) cDNA EST yk266c4.5 comes from this gene; cDNA EST yk266c4.3 comes from this gene	1.8
2806	U27341	Bos taurus endothelin converting enzyme-2 Sequence 1 from patent US 5736376	6e-078	2136744	endothelin converting enzyme-2 - bovine	3e-028
2807	U36756	Mus musculus thrombin receptor (Cf2r) gene, exon 1	0.013	<NONE>	<NONE>	<NONE>
2808	AJ003209	Human immunodeficiency virus type 1 mRNA for reverse transcriptase, isolate H-20, partial	0.12	<NONE>	<NONE>	<NONE>
2809	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	1e-010	<NONE>	<NONE>	<NONE>
2810	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	8e-009	1272701	(L11900) cytochrome b [Cratogeomys bulleri]	9.3

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
2811	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	3e-009	<NONE>	<NONE>	<NONE>
2812	AB006572	Homo sapiens RMP mRNA for RPB5 meidating protein, complete cds	0	3970833	(AB006572) RPB5 meidating protein [Homo sapiens]	5e-037
2813	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	2e-006	1109865	(U41540) coded for by C. elegans cDNA yk42d12.5; coded for by C. elegans cDNA yk27e10.5; coded for by C. elegans cDNA cm08h6; coded for by C. elegans cDNA yk88e12.5; coded for by C. elegans cDNA yk42d12.3; coded for by C. elegans cDNA yk27e1...	2e-009
2814	Z26259	H.sapiens isoform 1 gene for L-type calcium channel, exon 4	3e-029	3426264	(AF037269) cell division protein [Mycobacterium smegmatis]	0.47
2815	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.0002	2358285	(AF010403) ALR [Homo sapiens]	0.27
2816	AC004498	Homo sapiens chromosome 5, P1 clone 1209C1 (LBNL H104), complete sequence [Homo sapiens]	2e-006	<NONE>	<NONE>	<NONE>
2817	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	3e-010	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	3.1

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
2818	U43626	Human chromosome 15q11-q13 putative DNA replication origin in the g-aminobutyric acid receptor b3 and a5 gene cluster	2e-018	2197085	(AF003535) ORF2-like protein [Homo sapiens]	0.0002
2819	Z96402	H.sapiens telomeric DNA sequence, clone 18QTEL022, read 18QTELOO022.seq	0.001	386792	(M32334) intercellular adhesion molecule 2 (ICAM-2) [Homo sapiens]	9.2
2820	U43626	Human chromosome 15q11-q13 putative DNA replication origin in the g-aminobutyric acid receptor b3 and a5 gene cluster	2e-018	2197085	(AF003535) ORF2-like protein [Homo sapiens]	0.0002
2821	U66534	Human beta4-integrin (ITGB4) gene, exon 14,15,16,17 and 18	0.12	<NONE>	<NONE>	<NONE>
2822	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	3e-009	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	3.2
2823	AC001462	Homo sapiens (subclone 2_h10 from BAC H107) DNA sequence	3e-011	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	7.1
2824	AE000464	Escherichia coli K-12 MG1655 section 354 of 400 of the complete genome	6e-005	3879850	(Z81592) predicted using Genefinder	2e-039
2825	AB018304	Homo sapiens mRNA for KIAA0761 protein, partial cds	3e-009	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
2826	AL008982	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-52, complete sequence	3.2	3880930	(AL021481) similar to Phosphoglucomutase and phosphomannomutase phosphoserine; cDNA EST EMBL:D36168 comes from this gene; cDNA EST EMBL:D70697 comes from this gene; cDNA EST yk373h9.5 comes from this gene; cDNA EST EMBL:T008...	5e-053
2827	Z54196	S.cereale DNA for repeat unit (D1100 family)	0.36	2500714	HYPOTHETICAL 35.0 KD PROTEIN F48E8.1 IN CHROMOSOME III >gi|746485 (U23514) similar to antigen domain of venom allergen (SP:VA52_DOLMA, P10736) and to antigen 5 (PIR:A37329) [Caenorhabditis elegans]	4.1
2828	Z95979	Homo sapiens hRED1 gene, exons 7, 8, 9 and 10	7e-017	113668	!!!! ALU CLASS C WARNING ENTRY !!!!	0.002
2829	Z15030	H.sapiens gene for ventricular myosin light chain 2 > :: gb|L01652|HUMVMLC Human ventricular myosin light chain 2 gene, seven exons.	5e-024	565265	(M76741) biliary glycoprotein [Homo sapiens]	9.2
2830	U56440	Human His-1 gene sequence	8e-007	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
2831	AF009941	Tomocichla tuba cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, complete cds	1.2	<NONE>	<NONE>	<NONE>
2832	X68011	H.sapiens ZNF81 gene	3e-030	1731442	ZINC FINGER PROTEIN 81 human (fragment) >gi|454325 (X68011) ZNF81 gene product	1e-020
2833	U36499	Human lymphoid-specific SP100 homolog (LYSP100-A) mRNA, complete cds	1e-020	<NONE>	<NONE>	<NONE>
2834	Z60692	H.sapiens CpG DNA, clone 31f7, reverse read cpg31f7.rt1a .	3e-059	<NONE>	<NONE>	<NONE>
2835	X92485	P.vivax pval gene	0.0002	<NONE>	<NONE>	<NONE>
2836	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.0005	576257	Prostatic Acid Phosphatase (E.C.3.1.3.2) Complexed With Tartaric Acid >gi|576258|pdb|1RPT| Prostatic Acid Phosphatase (E.C.3.1.3.2) Complexed With Vanadate	3e-009

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
2837	U72372	Scandia geniculata 18S ribosomal RNA and 25S ribosomal RNA genes, partial sequence, and internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence	0.12	<NONE>	<NONE>	<NONE>
2838	D49425	Anabaena variabilis rbpD gene for RNA-binding protein, complete cds	3.2	<NONE>	<NONE>	<NONE>
2839	X95844	S.cerevisiae POP3 gene	3.5	<NONE>	<NONE>	<NONE>
2840	AE001425	Plasmodium falciparum chromosome 2, section 62 of 73 of the complete sequence	0.041	3880909	(AL032636) Y40B1B.3 [Caenorhabditis elegans]	5.5
2841	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	2e-007	<NONE>	<NONE>	<NONE>
2842	X69064	M.musculus Ank-1 mRNA for erythroid ankyrin	1.3	<NONE>	<NONE>	<NONE>
2843	U61950	Caenorhabditis elegans cosmid C45E5	0.13	<NONE>	<NONE>	<NONE>
2844	U73332	Human non-coding genomic sequence upstream from unique L0 sequence in the alpha-globin gene cluster	1e-010	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
2845	U21051	Human G protein-coupled receptor (GPR4) gene, complete cds.	0.13	<NONE>	<NONE>	<NONE>
2846	X57921	O.sativa random single-copy DNA fragment 12RG214R	4.1	<NONE>	<NONE>	<NONE>
2847	AF037219	Homo sapiens PIX1 mRNA sequence	0.043	<NONE>	<NONE>	<NONE>
2848	M55124	Human cystic fibrosis transmembrane conductance regulator (CFTR) gene, exon 17b	0.005	<NONE>	<NONE>	<NONE>
2849	AF035527	Mus musculus EHF (Ehf) mRNA, complete cds	e-164	3138930	(AF035527) EHF [Mus musculus]	5e-084
2850	AF052695	Rattus norvegicus cell cycle protein p55CDC gene, complete cds	3.7	2894379	(Y14573) ring finger protein [Hordeum vulgare]	8.2
2851	<NONE>	<NONE>	<NONE>	3327112	(AB014549) KIAA0649 protein [Homo sapiens]	3.8
2852	M34664	Human chaperonin (HSP60) mRNA, complete cds.	0	2501737	TRANSCRIPTIONAL ACTIVATOR PROTEIN ACU-15 >gi|1922895|gnl|PID|e308394 (Y11565) transcriptional activator protein [Neurospora crassa]	4.4
2853	D49701	Aspergillus oryzae niaD gene for nitrate reductase, complete cds	0.042	3879556	(Z70756) T06E4.11 [Caenorhabditis elegans]	0.5

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
2854	AF016266	Homo sapiens TRAIL receptor 2 mRNA, complete cds	1e-010	134846	SMALL PROLINE-RICH PROTEIN II rich protein [Homo sapiens]	1.5
2855	U44862	Human Down Syndrome region of chromosome 21, clone A11E6-2B6.	1.2	<NONE>	<NONE>	<NONE>
2856	X14503	Chlamydomonas eugametos petD gene for cytochrome b6/f complex subunit IV	0.13	<NONE>	<NONE>	<NONE>
2857	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	2e-006	3228515	(U70256) SomA [Synechococcus PCC6301]	4.6
2858	M25534	Chicken actin-capping protein (CapZ 36/32) alpha subunit mRNA, complete cds.	0.41	<NONE>	<NONE>	<NONE>
2859	X84372	D.melanogaster lethal(3)73Ah gene	1.1	<NONE>	<NONE>	<NONE>
2860	AF053551	Homo sapiens metaxin 2 (MTX2) mRNA, nuclear gene encoding mitochondrial protein, complete cds	0	3283049	(AF053551) metaxin 2 [Homo sapiens]	2e-089
2861	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	6e-005	3877358	(Z66520) similar to RBB3 like protein; cDNA EST EMBL:C08891 comes from this gene; cDNA EST EMBL:C09371 comes from this gene; cDNA EST yk468f10.5 comes	3e-005

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					from this gene [Caenorhabditis elegans]	
2862	AB002450	Homo sapiens mRNA from chromosome 5q21-22, clone:A3-A	2e-014	3790760	(AF099922) No definition line found [Caenorhabditis elegans]	2.5
2863	AF053698	Reporter vector pAP1-Luc, complete sequence	1e-009	<NONE>	<NONE>	<NONE>
2864	AF045086	Drosophila prosaltans 14045-0901.4 cytochrome oxidase II (COII) gene, mitochondrial gene encoding mitochondrial protein, complete cds	0.005	<NONE>	<NONE>	<NONE>
2865	Y09312	C.botulinum HA-70 gene (partial) and HA-17 gene	0.002	1171601	(X95276) rps8 [Plasmodium falciparum]	5.7
2866	AJ001597	Homo sapiens gene encoding cAMP-dependent protein kinase gamma isoform	0.005	1869883	(Z86099) RS1 [human herpesvirus 2] herpesvirus 2]	0.52
2867	AF022962	Mus musculus Sec8 mRNA, complete cds	1.1	<NONE>	<NONE>	<NONE>
2868	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.0005	2499622	PROBABLE SERINE/THREONINE-PROTEIN KINASE YOL113W (PROTEIN KINASE 75490	3.5

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					D)	
2869	AJ005262	Dictyostelium discoideum gene encoding a novel glycoprotein	0.12	<NONE>	<NONE>	<NONE>
2870	U08214	Rattus sp. DNA binding protein (URE-B1) mRNA, complete cds.	0.12	4033834	(AJ009556) cytoskeleton assembly control protein Sla2p [Candida albicans]	0.13
2871	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
2872	M31061	Human ornithine decarboxylase gene, complete cds.	2e-015	3808095	(Y08560) SCO-spondin [Bos taurus]	0.098
2873	U21914	Human duplicate spinal muscular atrophy mRNA, clone 5G7, partial cds.	0.002	<NONE>	<NONE>	<NONE>
2874	<NONE>	<NONE>	<NONE>	1228047	(D83782) the KIAA0199 gene is expressed ubiquitously.; the KIAA0199 protein shows similarity to sea urchin hydroxymethylglutalyl-CoA reductase, and retains 8 hydrophobic domains. [Homo sapiens]	2.5
2875	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.0002	4105505	(AF046914) multiple inositol polyphosphate phosphatase	5.6
2876	Z96210	H.sapiens telomeric DNA sequence, clone 12PTEL057, read 12PTELOO057.seq	0.014	2347056	(AJ000085) Nedd4 protein [Xenopus laevis]	5.8

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
2877	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	5e-013	2133693	masquerade precursor - fruit fly (Drosophila melanogaster) >gi|665545 (U18130) masquerade [Drosophila melanogaster] >gi|1095942|prf||2110286A masquerade gene	1.2
2878	X54252	C. elegans complete mitochondrial genome	0.38	<NONE>	<NONE>	<NONE>
2879	S81913	adrenocorticotropin receptor [Papio anubis=baboons, adrenal, mRNA Partial, 426 nt]	1.2	<NONE>	<NONE>	<NONE>
2880	X65997	M.musculus c-kit mRNA for truncated tyrosine-kinase	0.13	<NONE>	<NONE>	<NONE>
2881	AE000588	Helicobacter pylori section 66 of 134 of the complete genome	1.1	<NONE>	<NONE>	<NONE>
2882	U64861	Caenorhabditis elegans cosmid C47D2.	0.12	<NONE>	<NONE>	<NONE>
2883	U23173	Caenorhabditis elegans cosmid K07E1	0.37	2854192	(AF045645) contains similarity to microsomal triglyceride transfer proteins [Caenorhabditis elegans]	7.2
2884	AB014579	Homo sapiens mRNA for KIAA0679 protein, partial cds	0	3327172	(AB014579) KIAA0679 protein [Homo sapiens]	2e-053

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
2885	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	3e-009	1707032	(U80445) coded for by C. elegans cDNA yk13g5.3; coded for by C. elegans cDNA yk21g6.3; coded for by C. elegans cDNA CEMSE18F; coded for by C. elegans cDNA yk126b1.3; coded for by C. elegans cDNA yk65h8.3; coded for by C. elegans cDNA yk65h8....	0.17
2886	Z22795	H.sapiens microsatellite repeat.	6e-005	<NONE>	<NONE>	<NONE>
2887	AE001061	Archaeoglobus fulgidus section 46 of 172 of the complete genome	1.1	3738162	(AL031856) putative involvement in protein glycosylation in the golgi [Schizosaccharomyces pombe]	2.4
2888	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	6e-006	<NONE>	<NONE>	<NONE>
2889	Z96643	H.sapiens telomeric DNA sequence, clone 5QTEL064, read 5QTELOO064.seq	0.0005	1363732	probable membrane protein YLR454w - yeast	4
2890	Z96643	H.sapiens telomeric DNA sequence, clone 5QTEL064, read 5QTELOO064.seq	0.0005	1363732	probable membrane protein YLR454w - yeast	4

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
2891	X80169	M.musculus mRNA for 200 kD protein	e-177	1717793	PROTEIN TSG24 (MEIOTIC CHECK POINT REGULATOR) >gi|1083553|pir||A 55117 tsg24 protein - mouse	5e-069
2892	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	9e-009	3832555	(AF077439) immunoglobulin heavy chain variable region	4.4
2893	AC002359	Homo sapiens Xp22 Cosmid U239B3 (from Lawrence Livermore X library) complete sequence [Homo sapiens]	2e-007	3599342	(AF081112) ORF2 [Mus musculus domesticus]	0.61
2894	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	4e-011	3123058	HYPOTHETICAL WD-REPEAT PROTEIN SLL0163 >gi|1001440|gnl|PI D|d1010715 (D63999) beta transducin-like protein [Synechocystis sp.]	0.001
2895	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	9e-010	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	5.2
2896	Z46940	H.sapiens PRM1 gene, PRM2 gene and TNP2 gene	0.013	<NONE>	<NONE>	<NONE>
2897	Z47735	H.sapiens NFKB1 gene, exons 11 & 12	2e-008	<NONE>	<NONE>	<NONE>
2898	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	0.004	2224611	(AB002333) KIAA0335 [Homo sapiens]	4

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
2899	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	0.0002	<NONE>	<NONE>	<NONE>
2900	X00367	Chlamydomonas chloroplast DNA region with ARS element 03 (ARS = autonomously replicating sequence)	0.12	<NONE>	<NONE>	<NONE>
2901	U41222	Dictyostelium discoideum RacE (racE) gene, complete cds	0.35	<NONE>	<NONE>	<NONE>
2902	AB007504	Triticum aestivum TaMADS#11 mRNA for MADS box transcription factor, complete cds	0.042	<NONE>	<NONE>	<NONE>
2903	X65319	Cloning vector pCAT-Enhancer	7e-069	987050	(X65335) lacZ gene product [unidentified cloning vector]	7e-011
2904	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	0.0005	3924670	(AC004990) supported by Genscan and several ESTs: C83049	6e-042
2905	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	0.041	2132051	hypothetical protein YOR083w - yeast	3.3
2906	Z12112	pWE15A cosmid vector DNA	6e-068	987050	(X65335) lacZ gene product [unidentified cloning vector]	2e-009
2907	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	2e-006	2995374	(AL022245) hypothetical protein	5e-005

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
2908	U47322	Cloning vector DNA, complete sequence.	3e-009	<NONE>	<NONE>	<NONE>
2909	X71623	H.sapiens ZNF74-1 mRNA > :: gb|G27154|G27154 human STS SHGC-31580.	4e-012	113669	!!!! ALU CLASS D WARNING ENTRY !!!!	4.1
2910	U43626	Human chromosome 15q11-q13 putative DNA replication origin in the g-aminobutyric acid receptor b3 and a5 gene cluster	7e-007	2394501	(AF024503) No definition line found [Caenorhabditis elegans]	9.6
2911	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	5e-014	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	5.3
2912	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	1e-012	2688749	(AE001179) conserved hypothetical protein [Borrelia burgdorferi]	2.3
2913	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	4e-013	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	3.9
2914	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	4e-013	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	4
2915	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	0.0002	<NONE>	<NONE>	<NONE>
2916	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	0.004	1209842	(U45423) minus strand repeat motif-containing gene	0.092

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
2917	X80283	P.polycephalum genomic DNA containing Taq I repetitive element	3.3	<NONE>	<NONE>	<NONE>
2918	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	6e-006	<NONE>	<NONE>	<NONE>
2919	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	6e-006	<NONE>	<NONE>	<NONE>
2920	Z97333	Homo sapiens RHCE gene	9e-020	113667	!!!! ALU CLASS B WARNING ENTRY !!!!	4e-005
2921	AF082350	Homo sapiens bone morphogenetic protein 15 precursor (BMP15) gene, exon 2 and complete cds	1	<NONE>	<NONE>	<NONE>
2922	L14684	Rattus norvegicus nuclear-encoded mitochondrial elongation factor G mRNA, complete cds.	0	585084	ELONGATION FACTOR G, MITOCHONDRIAL PRECURSOR (MEF-G) >gi|543383|pir||S40780 translation elongation factor G, mitochondrial - rat >gi|310102	9e-089
2923	D78335	Human mRNA for 5'-terminal region of UMK, complete cds	e-163	1718058	URIDINE KINASE (URIDINE MONOPHOSPHO KINASE) >gi|471981 (L31783) uridine kinase	7e-072
2924	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	2e-007	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
2925	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	1e-013	1351922	AMINE OXIDASE PRECURSOR (MONAMINE OXIDASE) (TYRAMINE OXIDASE) >gi|419575|pir||B41836 amine oxidase (flavin-containing) (EC 1.4.3.4) precursor - Klebsiella pneumoniae >gi|216723|gnl|PID|d1001529	5.6
2926	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	9e-009	<NONE>	<NONE>	<NONE>
2927	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	1e-013	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	9.7
2928	AB018285	Homo sapiens mRNA for KIAA0742 protein, partial cds	0	3882205	(AB018285) KIAA0742 protein [Homo sapiens]	2e-093
2929	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	6e-006	3882183	(AB018274) KIAA0731 protein [Homo sapiens]	4e-049
2930	X94762	H.sapiens DNA for Ki-67 antigen 5'-region (exon 1 & 2)	2e-068	631020	Kallmann syndrome protein homolog - chicken	5.6
2931	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	2e-007	3522948	(AC004411) hypothetical protein [Arabidopsis thaliana]	2e-026
2932	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete	4e-011	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	6.5

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		cds				
2933	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	9e-008	<NONE>	<NONE>	<NONE>
2934	M18795	Gorilla pseudo-beta- and delta-globin gene intergenic region with 2 Alu repeats.	7e-028	<NONE>	<NONE>	<NONE>
2935	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.0005	<NONE>	<NONE>	<NONE>
2936	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	3e-007	<NONE>	<NONE>	<NONE>
2937	U09874	Mus musculus SKD3 mRNA, complete cds.	2e-086	2493735	SKD3 PROTEIN SKD3 [Mus musculus]	6e-036
2938	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	1e-012	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	5.6
2939	D38417	Mouse mRNA for arylhydrocarbon receptor, complete cds	e-154	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	3.4
2940	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	3e-008	3879062	(Z81576) predicted using Genefinder	9.2
2941	AE001368	Plasmodium falciparum chromosome 2, section 5 of 73 of the complete sequence	0.014	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
2942	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	2e-005	<NONE>	<NONE>	<NONE>
2943	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	7e-007	<NONE>	<NONE>	<NONE>
2944	AF083322	Homo sapiens centriole associated protein CEP110 mRNA, complete cds	e-133	3435244	(AF083322) centriole associated protein CEP110 [Homo sapiens]	9e-015
2945	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.014	<NONE>	<NONE>	<NONE>
2946	L07040	pFNeo eukaryotic expression vector, complete sequence.	2e-038	987050	(X65335) lacZ gene product [unidentified cloning vector]	4e-005
2947	X65319	Cloning vector pCAT-Enhancer	2e-078	987050	(X65335) lacZ gene product [unidentified cloning vector]	1e-013
2948	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	3e-008	<NONE>	<NONE>	<NONE>
2949	AL031844	Human DNA sequence from clone 361H15 on chromosome 22q13.2-13.33, complete sequence [Homo sapiens]	3.2	<NONE>	<NONE>	<NONE>
2950	AC002186	Homo sapiens (subclone 1_f12 from P1 H115) DNA sequence	2e-037	2072966	(U93570) p40 [Homo sapiens]	4e-013

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
2951	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	6e-005	4105414	(AF045593) ETS DNA binding protein Yan [Drosophila virilis]	1.4
2952	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	3e-008	629692	hypothetical protein - common tobacco tabacum]	4.3
2953	S60885	LYAR=cell growth regulating nucleolar protein [mice, EL4 cells, mRNA, 1474 nt]	5e-035	2498524	CELL GROWTH REGULATING NUCLEOLAR PROTEIN >gi|423488|pir||A40683 cell growth regulating nucleolar protein LYAR - mouse >gi|300372|bbs|131782	5e-014
2954	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	1e-012	<NONE>	<NONE>	<NONE>
2955	Z23090	H.sapiens mRNA for 28 kDa heat shock protein.	1e-063	1709972	60S RIBOSOMAL PROTEIN L10A (CSA-19)	3e-020
2956	X87817	M.musculus mRNA for Ulip protein	0.0005	<NONE>	<NONE>	<NONE>
2957	U87997	Enterococcus faecium enterocin B (entB) gene, complete cds	1.2	<NONE>	<NONE>	<NONE>
2958	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	0.001	<NONE>	<NONE>	<NONE>
2959	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	1e-011	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
2960	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	3e-009	<NONE>	<NONE>	<NONE>
2961	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	3e-009	<NONE>	<NONE>	<NONE>
2962	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	1e-009	<NONE>	<NONE>	<NONE>
2963	X62025	H.sapiens rod cG-PDE G gene for 3', 5'-cyclic nucleotide phosphodiesterase	4e-034	728838	!!!! ALU SUBFAMILY SX WARNING ENTRY	9e-006
2964	AJ223364	Homo sapiens germ-line DNA upstream of Jkappa locus	1e-023	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	4.2
2965	Z47046	Human cosmid QLL2C9 from Xq28	3e-020	804808	(M13100) unknown protein [Rattus norvegicus]	7e-005
2966	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	0.0002	<NONE>	<NONE>	<NONE>
2967	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	9e-009	464502	PEROXISOMAL TARGETING SIGNAL RECEPTOR (PEROXISOMAL PROTEIN PAS10) (PEROXIN-5) (PTS1 RECEPTOR) >gi|1078412|pir||A49403 tetratricopeptide-repeat protein PAS10 - yeast tetratricopeptide-	9.5

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					repeat protein [Saccharomyces cerevisiae] >gi|817830 (Z49701) Pas10p [Sa	
2968	AF035940	Homo sapiens MAGOH mRNA, complete cds	3e-050	2306969	(AF007860) xl-Mago [Xenopus laevis]	1e-041
2969	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
2970	X66297	H.sapiens Alu repeat (terminator 3)	5e-014	<NONE>	<NONE>	<NONE>
2971	AB007934	Homo sapiens mRNA for KIAA0465 protein, partial cds	0	3413892	(AB007934) KIAA0465 protein [Homo sapiens]	e-118
2972	X15982	Ascobolus immersus DNA of linear mitochondrial plasmid pAI2 with virus like replication	0.042	<NONE>	<NONE>	<NONE>
2973	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	4e-012	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
2974	AC002181	Homo sapiens (subclone 2_a12 from BAC H111) DNA sequence	2e-014	3879351	(Z35663) Short region of similarity with glucose-6-phosphate 1-dehydrogenase from Plasmodium falciparum; cDNA EST EMBL:C12945 comes from this gene; cDNA EST yk251d3.3 comes from this gene; cDNA EST yk251d3.5 comes from this ...	0.69
2975	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	0.002	<NONE>	<NONE>	<NONE>
2976	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	5e-013	3334221	4-HYDROXYPHENYLPYRUVATE DIOXYGENASE 4-hydroxyphenylpyruvate dioxygenase [Mycosphaerella graminicola]	2e-012
2977	S60885	LYAR=cell growth regulating nucleolar protein	8e-028	2498524	CELL GROWTH REGULATING NUCLEOLAR PROTEIN >gi|423488|pir||A40683 cell growth regulating nucleolar protein LYAR - mouse >gi|300372|bbs|131782	0.72
2978	U43958	Cloning vector pRcCMV-luc luciferase gene, complete cds	1e-010	335109	(M24873) major structural protein [Rhesus macaque polyomavirus]	1.1

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
2979	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	2e-014	399294	CYTOCHROME P450 XXIA3 (STEROID 21-HYDROXYLASE) (P450-C21) >gi|2117374|pir||A 32525 steroid 21-monooxygenase (EC 1.14.99.10) cytochrome P450 21A1 - pig >gi|164560 (M83939) steroid 21-hydroxylase	3.5
2980	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.0002	1169449	PROBABLE EARLY E4 33 KD PROTEIN	1.9
2981	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	4e-011	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	3.2
2982	Z11711	H.sapiens gene for alpha-2 macroglobulin, exon 1	2e-014	728835	!!!! ALU SUBFAMILY SC WARNING ENTRY	4.2
2983	M76363	Human (Papua New Guinean) Mitochondrial DNA control region, sequence 130.	1e-053	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	5.9
2984	U21228	Promoter-probe vector pCG1408, complete sequence.	3e-049	<NONE>	<NONE>	<NONE>
2985	X52994	Sheep mRNA for CD3 gamma subunit (partial)	0.005	1084987	cryptogene protein G4 - Sauroleishmania tarentolae (strain LEM125)	2.6
2986	X52994	Sheep mRNA for CD3 gamma subunit (partial)	0.005	1084987	cryptogene protein G4 - Sauroleishmania tarentolae (strain LEM125)	2.6
2987	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
2988	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
2989	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	3e-009	123398	OCTAMER-BINDING TRANSCRIPTION FACTOR 1 (OTF-1) (NF-A1) >gi|104811|pir||A34873 transcription factor Oct-1, octamer-binding - chicken >gi|212467	3.2
2990	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	1e-010	3881655	(Z82090) similar to Alpha-2-macroglobulin family (3 domains); cDNA EST EMBL:D67694 comes from this gene [Caenorhabditis elegans]	6e-019
2991	AB018270	Homo sapiens mRNA for KIAA0727 protein, partial cds	0	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	2.5
2992	U58745	Caenorhabditis elegans cosmid C10G6.	1.2	2677839	(AF023476) meltrin-L precursor [Homo sapiens]	0.24
2993	X17051	E.gracilis DNA for ribosomal protein operon	0.13	<NONE>	<NONE>	<NONE>
2994	Z14974	D.melanogaster Cpo 61.1 gene for couch potato protein.	1.1	3021409	(Y12781) transducin (beta) like 1 protein [Homo sapiens]	6e-017
2995	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	8e-008	417442	PARA-AMINOBENZOATE SYNTHASE Streptomyces griseus >gi|388263 (M93058) p-aminobenzoic acid synthase [Streptomyces griseus]	4.2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
2996	U11270	Human antithrombin III gene, exon 1 and partial cds.	9e-020	113670	!!!! ALU CLASS E WARNING ENTRY !!!!	0.16
2997	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	1e-010	3024528	RAS-RELATED PROTEIN RAB2BV	1.1
2998	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	4e-012	728831	!!!! ALU SUBFAMILY J WARNING ENTRY	0.17
2999	U51670	Barbus barbus x Barbus meridionalis microsatellite clone no.77	0.13	<NONE>	<NONE>	<NONE>
3000	U79776	Mus musculus ajuba (Ajuba) mRNA, complete cds	4e-094	1710382	(U79776) ajuba; jub [Mus musculus]	8e-037
3001	U79776	Mus musculus ajuba (Ajuba) mRNA, complete cds	4e-094	1710382	(U79776) ajuba; jub [Mus musculus]	8e-037
3002	U79776	Mus musculus ajuba (Ajuba) mRNA, complete cds	e-100	1710382	(U79776) ajuba; jub [Mus musculus]	8e-019
3003	U79776	Mus musculus ajuba (Ajuba) mRNA, complete cds	e-100	1710382	(U79776) ajuba; jub [Mus musculus]	8e-019
3004	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.0005	482227	hypothetical protein T07C4.9 - Caenorhabditis elegans >gi|3879509|gnl|PID|e1349070 (Z29443) similar to Annexin; cDNA EST EMBL:C10640 comes from this gene; cDNA EST EMBL:C12433 comes from this	0.64

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					gene; cDNA EST yk192f7.5 comes from this gene; cDNA EST yk318c1	
3005	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	5e-013	1944590	(Z94121) hypothetical protein Rv3899c	7.8
3006	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
3007	U40603	Rattus norvegicus rat-slowpoke-alpha mRNA, complete cds	0.12	1082665	oligodendrocyte-specific proline-rich protein 2 - human >gi|1408050|gnl|PID|d1006205 (D28114) MOBP [Homo sapiens]	0.22
3008	AF044081	Rattus norvegicus steroidogenic acute regulatory protein (StAR) mRNA, complete cds	1.1	2213519	(Z97050) sigG [Mycobacterium tuberculosis]	3.1
3009	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	7e-007	<NONE>	<NONE>	<NONE>
3010	X13345	Human gene for plasminogen activator inhibitor 1	1e-009	<NONE>	<NONE>	<NONE>
3011	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	4e-012	395338	(X66924) helix-loop-helix protein [Homo sapiens]	0.85

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3012	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	1e-011	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	5.6
3013	D78335	Human mRNA for 5'-terminal region of UMK, complete cds	e-101	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	3.2
3014	U03887	Human BXP20 gene.	6e-005	<NONE>	<NONE>	<NONE>
3015	U43194	Mus musculus rhophilin mRNA, complete cds	4e-044	1176422	(U43194) rhophilin [Mus musculus]	7e-020
3016	AC004507	Homo sapiens chromosome 5, P1 clone 798F12 (LBNL H82), complete sequence [Homo sapiens]	1.2	<NONE>	<NONE>	<NONE>
3017	X63436	B.taurus mRNA for poly(A) polymerase	0	464345	POLY(A) POLYMERASE (PAP) polynucleotide adenylyltransferase [Bos taurus]	6e-065
3018	M98512	Human NFG genomic fragment.	1e-021	728831	!!!! ALU SUBFAMILY J WARNING ENTRY	0.095
3019	AJ005016	Homo sapiens mRNA for putative ABC transporter, partial	e-159	3005931	(AJ005016) ABC transporter [Homo sapiens]	2e-039
3020	AJ006778	Homo sapiens mRNA for DRIM protein	1e-053	<NONE>	<NONE>	<NONE>
3021	X65319	Cloning vector pCAT-Enhancer	3e-081	987050	(X65335) lacZ gene product [unidentified cloning vector]	3e-015
3022	U14698	Human Alu-Sb2 repeat, clone HSB-8P.	1e-040	728834	!!!! ALU SUBFAMILY SB2 WARNING ENTRY	0.0001

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3023	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	1e-010	3218396	(AL023860) hypothetical protein	0.0003
3024	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	1.20E-01	<NONE>	<NONE>	<NONE>
3025	Z59351	H.sapiens CpG DNA, clone 151a12, reverse read cpg151a12.rt1a .	3e-020	1079063	deep orange protein - fruit fly (Drosophila melanogaster) >gi|798832 (X86683) deep orange (dor)	9.90E-02
3026	AB014564	Homo sapiens mRNA for KIAA0664 protein, partial cds	e-164	2498095	5E5 ANTIGEN >gi|1085558|pir||JC4163 DNA-binding protein 5E5 - rat norvegicus] >gi|1581020|prf||2116328A DNA-binding protein 5E5 [Rattus norvegicus]	3.2
3027	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	1e-010	<NONE>	<NONE>	<NONE>
3028	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	1e-010	<NONE>	<NONE>	<NONE>
3029	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	1e-010	<NONE>	<NONE>	<NONE>
3030	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	4.00E-12	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	5.6

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3031	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	1.20E-01	<NONE>	<NONE>	<NONE>
3032	AF070523	Homo sapiens JWA protein mRNA, complete cds	0.00E+00	<NONE>	<NONE>	<NONE>
3033	Z19055	B.aphidicola tryptophan operon	0.41	<NONE>	<NONE>	<NONE>
3034	Z19055	B.aphidicola tryptophan operon	0.41	<NONE>	<NONE>	<NONE>
3035	Z19055	B.aphidicola tryptophan operon	0.41	<NONE>	<NONE>	<NONE>
3036	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	7.00E-07	<NONE>	<NONE>	<NONE>
3037	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	3e-009	<NONE>	<NONE>	<NONE>
3038	AF064482	Homo sapiens natural resistance-associated macrophage protein 2 (NRAMP2) gene, exons 16 and 16A, alternatively spliced IRE form, complete cds	0	<NONE>	<NONE>	<NONE>
3039	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	1.20E-01	<NONE>	<NONE>	<NONE>
3041	U28153	Caenorhabditis elegans UNC-76 (unc-76) gene, complete cds.	0.38	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3042	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	5.00E-03	1079063	deep orange protein - fruit fly (Drosophila melanogaster) >gi|798832 (X86683) deep orange (dor)	0.23
3043	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	5.00E-03	1079063	deep orange protein - fruit fly (Drosophila melanogaster) >gi|798832 (X86683) deep orange (dor)	0.23
3044	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	2.00E-05	<NONE>	<NONE>	<NONE>
3045	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	3e-009	<NONE>	<NONE>	<NONE>
3046	U63810	Homo sapiens WD40 protein Ciao 1 mRNA, complete cds	0.00E+00	3219331	(AC004020) Unknown gene product [Homo sapiens]	2e-097
3047	M21533	Human MHC class I lymphocyte antigen (HLA-E)	2e-005	120467	V-FOS/FOX TRANSFORMIN G PROTEIN murine osteosarcoma virus (provirus) (fragment)	9.9
3048	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	6e-006	462702	NEUROFILAME NT TRIPLET H PROTEIN (200 KD NEUROFILAME NT PROTEIN) (NF-H)	2.6
3049	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	1e-010	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3050	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	4e-011	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	3.6
3051	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	5.00E-04	3116127	(AL023287) hypothetical protein	6.9
3052	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	7.00E-06	586875	HYPOTHETICAL 29.2 KD PROTEIN IN METS-KSGA INTERGENIC REGION >gi|2127033|pir||S 66068 hypothetical protein - Bacillus subtilis subtilis] >gi|2632306|gnl|PI D|e1181972 (Z99104) similar to hypothetical proteins [Bacillus subtilis]	2e-014
3053	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	1e-010	1326350	(U58748) similar to potential transmembrane domains in S. cerevisiae nulcear division RFT1 protein (SP:P38206)	0.035
3054	Y10938	Homo sapiens retroviral-like sequence S71, 5LTR and env-like sequence	6e-016	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	4.4
3055	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	2.00E-05	<NONE>	<NONE>	<NONE>
3056	AE000723	Aquifex aeolicus section 55 of 109 of the complete genome	1.20E+00	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3057	U18055	Lycopersicon esculentum 1-aminocyclopropane-1-carboxylate synthase (LE-ACS3) DNA, partial cds	1.10E+00	<NONE>	<NONE>	<NONE>
3058	AJ006025	Cicer arietinum mRNA for acyl-coA synthetase, partial	0.38	<NONE>	<NONE>	<NONE>
3059	AJ006025	Cicer arietinum mRNA for acyl-coA synthetase, partial	0.38	<NONE>	<NONE>	<NONE>
3060	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.014	<NONE>	<NONE>	<NONE>
3061	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.014	<NONE>	<NONE>	<NONE>
3062	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	3.00E-10	3880303	(Z54238) T28C6.1 [Caenorhabditis elegans]	4.10E-02
3063	AE000723	Aquifex aeolicus section 55 of 109 of the complete genome	1.20E+00	<NONE>	<NONE>	<NONE>
3064	Y14352	Gallus gallus gene encoding neurofascin, exons 31 & 31	0.042	995644	(Z54206) UL38 [Bovine herpesvirus 1] >gi|1149580 (Z49078) UL38 [Bovine herpesvirus 1] >gi|2653309|gnl|PID|e1187305	1.9
3065	AE000723	Aquifex aeolicus section 55 of 109 of the complete genome	1.20E+00	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3066	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	2.00E-03	<NONE>	<NONE>	<NONE>
3067	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	2.00E-03	<NONE>	<NONE>	<NONE>
3068	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	2.00E-03	<NONE>	<NONE>	<NONE>
3069	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	0.38	1395143	(D86080) aniline dioxygenase reductase component [Acinetobacter sp.] dioxygenase reductase component [Acinetobacter sp.]	9.00E-05
3070	AE001398	Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence	0.0005	<NONE>	<NONE>	<NONE>
3071	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.014	<NONE>	<NONE>	<NONE>
3072	D16902	Human HepG2 3' region cDNA, clone hmd2h10	2.00E-49	<NONE>	<NONE>	<NONE>
3073	Z26494	S.cerevisiae genes for histone H2A and H2B, trehalase, and hexaprenyl pyrophosphate synthetase	1.1	3581891	(AL031540) hypothetical wtf3 protein	9.70E+00

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3074	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	2.00E-05	2224921	(AF000606) insect intestinal mucin IIM22 [Trichoplusia ni]	1e-005
3075	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	0.37	<NONE>	<NONE>	<NONE>
3076	U18157	Human HLA class I genomic survey sequence.	2.00E-05	<NONE>	<NONE>	<NONE>
3077	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	4.20E-02	2622750	(AE000921) DNA topoisomerase I [Methanobacterium thermoautotrophicum]	2.5
3078	AF022789	Homo sapiens ubiquitin hydrolyzing enzyme I	0.00E+00	<NONE>	<NONE>	<NONE>
3079	U18055	Lycopersicon esculentum 1-aminocyclopropane-1-carboxylate synthase (LE-ACS3) DNA, partial cds	1.10E+00	<NONE>	<NONE>	<NONE>
3080	AF022388	Caenorhabditis elegans putative transcription factor MAB-3 (mab-3) gene, complete cds	1.40E-02	3747107	(AF095741) unknown [Rattus norvegicus]	6e-012
3081	AF084594	Plasmodium falciparum erythrocyte membrane protein 1 type w (var) gene, partial cds	1.20E+00	3132802	(AF063223) pol protein [Human immunodeficiency virus type 1]	1.2
3082	D16902	Human HepG2 3' region cDNA, clone hmd2h10	2.00E-49	<NONE>	<NONE>	<NONE>
3083	X65709	A.carrageenovora gene for arylsulfatase	0.014	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3084	AF060246	Mus musculus strain C57BL/6 zinc finger protein 106 (Zfp106) mRNA, H3a-a allele, complete cds	2e-078	3372657	(AF060246) zinc finger protein 106 [Mus musculus]	1e-031
3085	AF037332	Homo sapiens Eph-like receptor tyrosine kinase hEphB1b (EphB1) mRNA, complete cds	3.70E-01	<NONE>	<NONE>	<NONE>
3086	U17579	Human growth hormone-releasing hormone receptor gene, alternatively spliced forms a, b, and c, partial cds	0.053	<NONE>	<NONE>	<NONE>
3087	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.39	2950453	(AL022071) beta-transducin	2.00E-05
3088	U67479	Methanococcus jannaschii section 21 of 150 of the complete genome	0.005	<NONE>	<NONE>	<NONE>
3089	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	9e-010	3283350	(AF062378) calmodulin-binding protein SHA1 [Mus musculus]	3e-006
3090	Z59351	H.sapiens CpG DNA, clone 151a12, reverse read cpg151a12.rt1a .	3e-020	1079063	deep orange protein - fruit fly (Drosophila melanogaster) >gi|798832 (X86683) deep orange (dor)	9.90E-02

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3091	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	2e-005	1125753	(U42833) coded for by C. elegans cDNA CEESN37F; Similar to ammonium transport protein. [Caenorhabditis elegans]	1.00E-17
3092	AF021834	Homo sapiens tissue factor pathway inhibitor beta (TFPIbeta) mRNA, complete cds	e-172	125932	TISSUE FACTOR PATHWAY INHIBITOR PRECURSOR (TFPI) (LIPOPROTEIN-ASSOCIATED COAGULATION INHIBITOR) (LACI) (EXTRINSIC PATHWAY INHIBITOR) (EPI) precursor - human >gi|180546 (J03225) lipoprotein-associated coagulation inhibitor precursor associated coagulation	9e-032
3093	AJ006778	Homo sapiens mRNA for DRIM protein	0.00E+00	3242214	(AJ006778) DRIM protein [Homo sapiens]	3e-095
3094	AJ006778	Homo sapiens mRNA for DRIM protein	0.00E+00	3242214	(AJ006778) DRIM protein [Homo sapiens]	3e-095
3095	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	6e-005	<NONE>	<NONE>	<NONE>
3096	AJ006778	Homo sapiens mRNA for DRIM protein	0	3242214	(AJ006778) DRIM protein [Homo sapiens]	8.00E-93
3097	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete	2e-005	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		cds				
3098	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	3.00E-09	1850115	(Z86089) fadD2 [Mycobacterium tuberculosis]	1.4
3099	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	1e-009	<NONE>	<NONE>	<NONE>
3100	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	1e-009	<NONE>	<NONE>	<NONE>
3101	U67986	Bacillus megaterium anthranilate synthase (trpD) gene, partial cds, indole glycerol phosphate synthetase N-phosphoribosylan thranilate isomerase (trpF) gene partial cds	1.1	2102696	(U72761) karyopherin beta 3 [Homo sapiens]	1.90E+00
3102	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	3e-010	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	5.5

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3103	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	1.00E-10	135554	TETRACYCLINE RESISTANCE PROTEIN Bacillus cereus plasmid pBC16 >gi|72838|pir||YTSOG tetracycline resistance protein - Streptococcus agalactiae plasmid pMV158 >gi|80428|pir||JQ1211 tetracycline resistance protein - Bacillus sp. plasmid pTB19 >gi|151696 (M63	1.4
3104	AJ006778	Homo sapiens mRNA for DRIM protein	0	3242214	(AJ006778) DRIM protein [Homo sapiens]	8.00E-93
3105	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.002	<NONE>	<NONE>	<NONE>
3106	M60562	Mus musculus Mhc class II A beta polypeptide, partial cds (exons 3 and 4)	1.10E+00	<NONE>	<NONE>	<NONE>
3107	U91985	Human DNA fragmentation factor-45 mRNA, complete cds	e-133	2810997	DNA FRAGMENTATION FACTOR-45 factor-45 [Homo sapiens]	7e-013
3108	Y11455	S.salar microsatellite DNA, CA-repeat (AC)11.5	3.50E-01	3879530	(Z49130) cDNA EST yk486b9.3 comes from this gene; cDNA EST yk486b9.5 comes from this gene	0.0001
3109	Y11455	S.salar microsatellite DNA, CA-repeat (AC)11.5	3.50E-01	3879530	(Z49130) cDNA EST yk486b9.3 comes from this gene; cDNA EST yk486b9.5 comes from this gene	0.0001

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3110	AF052135	Homo sapiens clone 23625 mRNA sequence	4e-033	4098124	(U73522) STAM SH3 domain associating molecule [Homo sapiens]	5e-033
3111	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	6e-005	<NONE>	<NONE>	<NONE>
3112	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	9e-009	1351538	HYPOTHETICAL PROTEIN MG306 Mycoplasma genitalium (SGC3) >gi|3844885 (U39711) conserved hypothetical protein [Mycoplasma genitalium]	1.4
3113	L78777	Homo sapiens (subclone 2_b8 from P1 H49) DNA sequence	1.30E-01	<NONE>	<NONE>	<NONE>
3114	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.002	<NONE>	<NONE>	<NONE>
3115	U29917	Human AMP deaminase (AMPD3) gene, exon 8 and 9.	3.00E-10	<NONE>	<NONE>	<NONE>
3116	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	9e-009	<NONE>	<NONE>	<NONE>
3117	AE001038	Archaeoglobus fulgidus section 69 of 172 of the complete genome	0.14	<NONE>	<NONE>	<NONE>
3118	AF042378	Homo sapiens spindle pole body protein spc98 homolog GCP3 mRNA, complete cds	0	2801699	(AF042378) spindle pole body protein spc98 homolog GCP3	4e-080

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3119	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	2e-005	<NONE>	<NONE>	<NONE>
3120	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	9e-009	1351538	HYPOTHETICAL PROTEIN MG306 Mycoplasma genitalium (SGC3) >gi|3844885 (U39711) conserved hypothetical protein [Mycoplasma genitalium]	1.4
3121	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	7.00E-07	133361	DNA-DIRECTED RNA POLYMERASE III 128 KD POLYPEPTIDE (RNA POLYMERASE III SUBUNIT 2) 2.7.7.6) III second-largest chain - fruit fly polymerase III second-largest subunit [Drosophila melanogaster]	4.40E+00
3122	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	2.00E-05	<NONE>	<NONE>	<NONE>
3123	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	2.00E-05	<NONE>	<NONE>	<NONE>
3124	AJ011981	Homo sapiens mRNA sequence, IMAGE clone 417820	2.00E-69	461950	DPY-19 PROTEIN elegans >gi|156300 (L12018) putative [Caenorhabditis elegans]	2e-026

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3125	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	2e-005	<NONE>	<NONE>	<NONE>
3126	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	4e-011	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	3.60E+00
3127	M26216	Rat (lambda 20BH0.1) L-type 6-phosphofructo-2-kinase/fructose-2, 6-bisphosphatase	4.10E-02	205752	(M94288) Nopp140 [Rattus norvegicus]	1.1
3128	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	5.00E-03	<NONE>	<NONE>	<NONE>
3129	<NONE>	<NONE>	<NONE>	730888	OCTAPEPTIDE-REPEAT PROTEIN T2 >gi|296382	5.2
3130	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	5.00E-03	<NONE>	<NONE>	<NONE>
3131	X65446	H.sapiens gene locus DXS278 (S232-RU2) DNA	6e-011	119110	EBNA-1 NUCLEAR PROTEIN herpesvirus 4 (strain B95-8) >gi|1334880 (V01555) BKRF1 encodes EBNA-1 protein, latent cycle gene. [Human herpesvirus 4]	1e-005

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3132	X65446	H.sapiens gene locus DXS278 (S232-RU2) DNA	6e-011	119110	EBNA-1 NUCLEAR PROTEIN herpesvirus 4 (strain B95-8) >gi|1334880 (V01555) BKRF1 encodes EBNA-1 protein, latent cycle gene. [Human herpesvirus 4]	1e-005
3133	X72219	C.pasteurianum gap gene	0.015	<NONE>	<NONE>	<NONE>
3134	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	2e-006	<NONE>	<NONE>	<NONE>
3135	Z26494	S.cerevisiae genes for histone H2A and H2B, trehalase, and hexaprenyl pyrophosphate synthetase	1.1	3581891	(AL031540) hypothetical wtf3 protein	9.70E+00
3136	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	4e-011	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	3.60E+00
3137	AL010234	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-55, complete sequence	0.37	1213606	(X95910) ftsA [Campylobacter jejuni]	4.2
3138	U28153	Caenorhabditis elegans UNC-76 (unc-76) gene, complete cds.	0.39	<NONE>	<NONE>	<NONE>
3139	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	8.00E-07	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3140	J05073	Human phosphoglycerate mutase (PGAM-M) gene, complete cds.	1.00E-13	281501	phenylalanine--tRNA ligase (EC 6.1.1.20) beta chain - Thermus aquaticus	7
3141	M90656	Human gamma-glutamylcysteine synthetase (GCS) mRNA, complete cds.	0	1346190	GLUTAMATE--CYSTEINE LIGASE CATALYTIC SUBUNIT (GAMMA-GLUTAMYLCYSTEINE SYNTHETASE) glutamate--cysteine ligase (EC 6.3.2.2) heavy chain - human >gi|183039 (M90656) gamma-glutamylcysteine synthetase [Homo sapiens]	2.00E-71
3142	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	8e-006	951325	(U31517) nuclear receptor XR78E/F [Drosophila melanogaster]	9.4
3143	AF053551	Homo sapiens metaxin 2 (MTX2) mRNA, nuclear gene encoding mitochondrial protein, complete cds	0.00E+00	3283049	(AF053551) metaxin 2 [Homo sapiens]	1.00E-79
3144	AF088034	Homo sapiens full length insert cDNA clone ZC24F03	e-125	1353059	HYPOTHETICAL 27.4 KD PROTEIN IN MER2-BNA1 INTERGENIC REGION >gi|1077874|pir||S57042 hypothetical protein YJR024c - yeast (Saccharomyces cerevisiae)	9e-023

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					>gi|1015663 (Z49524) ORF YJR024c gene product [Saccharomyces cerevisiae]	
3145	AF087973	Homo sapiens full length insert cDNA clone YU79H10	1e-033	<NONE>	<NONE>	<NONE>
3146	AF032456	Homo sapiens ubiquitin conjugating enzyme G2	8.00E-07	<NONE>	<NONE>	<NONE>
3147	Y12259	R.norvegicus mRNA for Kir3.1 protein	6e-058	<NONE>	<NONE>	<NONE>
3148	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	2.00E-07	<NONE>	<NONE>	<NONE>
3149	X97154	D.willistoni mitochondrial 12S rRNA gene	1.20E+00	3875246	(Z81490) similar to WD domain, G-beta repeats (2 domains); cDNA EST EMBL:T00482 comes from this gene; cDNA EST EMBL:T00923 comes from this gene; cDNA EST yk449d4.3 comes from this gene; cDNA EST yk449d4.5 comes from this gen...	7e-016
3150	U17247	Saccharomyces cerevisiae chromosome XII cosmid L2142	1.20E-01	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3151	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	2e-005	172012	(M12087) thr-tRNA-synthetase [Saccharomyces cerevisiae]	0.21
3152	L78777	Homo sapiens (subclone 2_b8 from P1 H49) DNA sequence	1.30E-01	<NONE>	<NONE>	<NONE>
3153	AF053551	Homo sapiens metaxin 2 (MTX2) mRNA, nuclear gene encoding mitochondrial protein, complete cds	0.00E+00	3283049	(AF053551) metaxin 2 [Homo sapiens]	1.00E-79
3154	X53616	C.domesticus calnexin (pp90) mRNA	1.1	<NONE>	<NONE>	<NONE>
3155	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	0.043	<NONE>	<NONE>	<NONE>
3156	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	0.002	3327080	(AB014533) KIAA0633 protein [Homo sapiens]	4.2
3157	U60337	Homo sapiens beta-mannosidase mRNA, complete cds	0	3024091	BETA-MANNOSIDASE PRECURSOR beta-mannosidase [Homo sapiens]	4e-068
3158	U32790	Haemophilus influenzae Rd section 105 of 163 of the complete genome	1.1	<NONE>	<NONE>	<NONE>
3159	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	0.12	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3160	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	7e-007	1351696	HYPOTHETICAL 30.4 KD PROTEIN C3H1.13 IN CHROMOSOME I >gi|1103514 (Z68144) unknown	1.5
3161	U50535	Human BRCA2 region, mRNA sequence CG006	4e-012	728831	!!!! ALU SUBFAMILY J WARNING ENTRY	4.5
3162	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	3e-009	2132302	hypothetical protein YPR144c - yeast similarity near C-terminus to RNA Polymerase beta subunit (Swiss Prot. accession number P11213) and CCAAT-binding transcription factor (PIR accession number A36368) [Saccharomyces cerevisiae]	4e-022
3163	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
3164	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	3e-008	3123086	HYPOTHETICAL PROTEIN MJ1050 Methanococcus jannaschii >gi|1499895 (U67548) conserved hypothetical protein [Methanococcus jannaschii]	1.3
3165	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	0.005	<NONE>	<NONE>	<NONE>
3166	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial	0.005	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		cds				
3167	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	0.005	<NONE>	<NONE>	<NONE>
3168	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	1e-011	833783	(X14338) NADH:ubiquinone oxidoreductase (428 AA) [Bos taurus]	0.17
3169	M20918	C.thummi piger haemoglobin (Hb) gene DNA, complete cds.	0.12	2496813	HYPOTHETICAL 59.9 KD PROTEIN B0304.5 IN CHROMOSOME II >gi|1041884 (U39472) B0304.5 gene product [Caenorhabditis elegans]	0.12
3170	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	1e-011	100827	NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4 - wheat mitochondrion	4.1
3171	U28153	Caenorhabditis elegans UNC-76 (unc-76) gene, complete cds.	0.38	<NONE>	<NONE>	<NONE>
3172	AJ008065	Chrysolina bankii 16S rRNA gene, mitotype B2	0.045	<NONE>	<NONE>	<NONE>
3173	AB014591	Homo sapiens mRNA for KIAA0691 protein, complete cds	7e-057	3327196	(AB014591) KIAA0691 protein [Homo sapiens]	8e-007
3174	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	2e-007	3184082	(AL023781) N-terminal acetyltransferase 1 [Schizosaccharomyces pombe]	1e-036

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3175	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	3e-009	3219914	HYPOTHETICAL 16.8 KD PROTEIN C30D10.04 IN CHROMOSOME II >gi|2276353|gnl|PID|e330328 pombe]	2e-011
3176	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	0.002	133361	DNA-DIRECTED RNA POLYMERASE III 128 KD POLYPEPTIDE (RNA POLYMERASE III SUBUNIT 2) 2.7.7.6) III second-largest chain - fruit fly polymerase III second-largest subunit [Drosophila melanogaster]	4.3
3177	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	2e-006	2429362	(AF020261) proline rich protein [Santalum album]	0.033
3178	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	7e-007	3641258	(AF064554) ventral anterior homeobox-containing protein 1 [Mus musculus]	0.68
3179	AB018323	Homo sapiens mRNA for KIAA0780 protein, partial cds	3e-041	3327168	(AB014577) KIAA0677 protein [Homo sapiens]	2e-021
3180	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.002	<NONE>	<NONE>	<NONE>
3181	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	1e-011	3283350	(AF062378) calmodulin-binding protein SHA1 [Mus musculus]	5e-006

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3182	Z96207	H.sapiens telomeric DNA sequence, clone 12PTEL049, read 12PTELOO049.seq	8e-008	<NONE>	<NONE>	<NONE>
3183	AB017026	Mus musculus mRNA for oxysterol-binding protein, complete cds	0	3882265	(AB018315) KIAA0772 protein [Homo sapiens]	2e-091
3184	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	9e-009	<NONE>	<NONE>	<NONE>
3185	X05283	Drosophila melanogaster PKCG7 gene exons 7-14 for protein kinase C	4.6	<NONE>	<NONE>	<NONE>
3186	AF026069	Homo sapiens phosphomevalonate kinase (HUMPMKI) gene, partial cds	0.42	<NONE>	<NONE>	<NONE>
3187	AF052573	Homo sapiens DNA polymerase eta (POLH) mRNA, complete cds	0	3510695	(AF052573) DNA polymerase eta [Homo sapiens]	4e-011
3188	M80198	Human FKBP-12 pseudogene, clone lambda-512, 5' flank and complete cds.	5e-014	2315521	(AF016452) similar to the beta transducin family	4e-027
3189	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	8e-008	<NONE>	<NONE>	<NONE>
3190	AJ001296	Notophthalmus viridescens mRNA for cytokeratin 8	0.38	1175412	HYPOTHETICAL 24.2 KD PROTEIN C13A11.03 IN CHROMOSOME I >gi|984224 (Z54096) unknown	2e-020

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3191	Z60048	H.sapiens CpG DNA, clone 187a9, reverse read cpg187a9.rt1a .	4e-054	547662	HEPATOCYTE NUCLEAR FACTOR 3-BETA HNF-3 beta - mouse >gi|402191 (X74937) HNF-3beta [Mus musculus]	1e-020
3192	U95760	Drosophila melanogaster strawberry notch (sno) mRNA, complete cds	3e-071	2078282	(U95760) Sno [Drosophila melanogaster]	3e-068
3193	L09604	Homo sapiens differentiation-dependent A4 protein mRNA, complete cds.	2e-035	<NONE>	<NONE>	<NONE>
3194	AF054994	Homo sapiens clone 23832 mRNA sequence	0.12	<NONE>	<NONE>	<NONE>
3195	AF026069	Homo sapiens phosphomevalonate kinase (HUMPMKI) gene, partial cds	0.42	<NONE>	<NONE>	<NONE>
3196	AF026069	Homo sapiens phosphomevalonate kinase (HUMPMKI) gene, partial cds	0.42	<NONE>	<NONE>	<NONE>
3197	AB007918	Homo sapiens mRNA for KIAA0449 protein, partial cds	0.015	138240	GLYCOPROTEIN E PRECURSOR 1 >gi|59566|gnl|PID|e312380 (X14112) virion glycoprotein E [human herpesvirus 1] >gi|59882 (X02138) glycoprotein gE (Us8) [Human herpesvirus 1] >gi|291496 (L00036) gE protein [Human herpesvirus 1]	8.3

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3198	L07040	pFNeo eukaryotic expression vector, complete sequence.	1e-052	2072972	(U93572) putative p150 [Homo sapiens]	1e-019
3199	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	0.002	<NONE>	<NONE>	<NONE>
3200	M98502	Mus musculus protein encoding twelve zinc finger proteins (pMLZ-4) mRNA, complete cds.	5e-014	<NONE>	<NONE>	<NONE>
3201	M95098	Bos taurus lysozyme gene (cow 2), complete cds	1.1	3882205	(AB018285) KIAA0742 protein [Homo sapiens]	2e-034
3202	U49169	Dictyostelium discoideum V-ATPase A subunit (vatA) mRNA, complete cds	0.12	2126116	cymH protein - Klebsiella oxytoca >gi|854235	4.2
3203	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	2e-006	2911548	(Y15173) E2 protein [Human papillomavirus type 75]	0.39
3204	Z57610	H.sapiens CpG DNA, clone 187a10, reverse read cpg187a10.rt1a .	7e-090	417134	HEPATOCYTE NUCLEAR FACTOR 3-BETA norvegicus]	5e-019
3205	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	6e-006	4104093	(AF031642) urea transporter UT4 [Rattus norvegicus]	0.51
3206	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	0.0002	<NONE>	<NONE>	<NONE>
3207	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
3208	<NONE>	<NONE>	<NONE>	2252814	(AF006492) FOG [Mus musculus]	3.4

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3209	AF035940	Homo sapiens MAGOH mRNA, complete cds	e-131	2330011	(AF007862) mm-Mago [Mus musculus] >gi|2909828 (AF035939) similar to mago nashi [Mus musculus] >gi|2909830	4e-044
3210	U49169	Dictyostelium discoideum V-ATPase A subunit (vatA) mRNA, complete cds	0.12	1942101	Porcine Ribonuclease Inhibitor Complexed With Ribonuclease A	1.1
3211	AF054994	Homo sapiens clone 23832 mRNA sequence	0.12	<NONE>	<NONE>	<NONE>
3212	AF068627	Mus musculus DNA cytosine-5 methyltransferase 3B2 (Dnmt3b) mRNA, alternatively spliced, complete cds	0.0005	1869835	(Z86099) protein kinase [human herpesvirus 2]	0.86
3213	X68553	C.elegans repetitive DNA sequence	0.41	854065	(X83413) U88 [Human herpesvirus 6]	7e-007
3214	X68553	C.elegans repetitive DNA sequence	0.41	854065	(X83413) U88 [Human herpesvirus 6]	7e-007
3215	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	6e-005	<NONE>	<NONE>	<NONE>
3216	AF054994	Homo sapiens clone 23832 mRNA sequence	0.12	<NONE>	<NONE>	<NONE>
3217	U95760	Drosophila melanogaster strawberry notch (sno) mRNA, complete cds	3e-071	2078282	(U95760) Sno [Drosophila melanogaster]	3e-068
3218	X96400	P.tetraurelia alpha-51D gene	0.38	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3219	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	0.0002	<NONE>	<NONE>	<NONE>
3220	AF067212	Caenorhabditis elegans cosmid F37F2	0.005	<NONE>	<NONE>	<NONE>
3221	Y08844	L.esculentum PR1a2 gene	1.1	<NONE>	<NONE>	<NONE>
3222	Y08844	L.esculentum PR1a2 gene	1.1	<NONE>	<NONE>	<NONE>
3223	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	6.00E-05	<NONE>	<NONE>	<NONE>
3224	U08214	Rattus sp. DNA binding protein (URE-B1) mRNA, complete cds.	1.1	477513	mesoderm development regulatory protein Sna - mouse >gi|54121 (X67253) sna [Mus musculus]	1.1
3225	L19713	Human dematin (HRD1) mRNA, complete cds.	0.051	<NONE>	<NONE>	<NONE>
3226	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	0.043	2645389	(U83858) NADH dehydrogenase subunit 4 [Onychomys leucogaster]	7.5
3227	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	5.00E-03	2662477	(AF034804) LACK [Leishmania major]	3e-011
3228	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	0.0002	<NONE>	<NONE>	<NONE>
3229	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	4e-012	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	6.20E+00

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3230	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	0.0005	<NONE>	<NONE>	<NONE>
3231	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	0.0005	<NONE>	<NONE>	<NONE>
3232	AF036685	Caenorhabditis elegans cosmid C05B10	0.38	<NONE>	<NONE>	<NONE>
3233	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
3234	AL010153	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-80, complete sequence	6e-005	<NONE>	<NONE>	<NONE>
3235	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	5.00E-04	<NONE>	<NONE>	<NONE>
3236	U28153	Caenorhabditis elegans UNC-76 (unc-76) gene, complete cds.	0.39	<NONE>	<NONE>	<NONE>
3237	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	1e-009	<NONE>	<NONE>	<NONE>
3238	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	1e-009	<NONE>	<NONE>	<NONE>
3239	X65319	Cloning vector pCAT-Enhancer	5.00E-77	987050	(X65335) lacZ gene product [unidentified cloning vector]	3e-015

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3240	AG000140	Homo sapiens genomic DNA, 21q region, clone: T171X2	1.60E-01	2494505	HEPATOCYTE NUCLEAR FACTOR 3 FORKHEAD HOMOLOG 4 (HFH-4) >gi|2137385|pir||I49734 HNF-3/fork-head homolog-4 - mouse >gi|550488 (L13204) HNF-3/fork-head homolog-4 [Mus musculus]	7.5
3241	L77886	Human protein tyrosine phosphatase mRNA, complete cds	1.00E-21	139560	SATELLITE RNA 48 KD PROTEIN	5.9
3242	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	8e-008	3879988	(Z68318) T21B10.4 [Caenorhabditis elegans]	7.9
3243	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	7e-007	3184286	(AC004136) hypothetical protein [Arabidopsis thaliana]	7.7
3244	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	5.00E-04	<NONE>	<NONE>	<NONE>
3245	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	0.005	<NONE>	<NONE>	<NONE>
3246	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	0.005	<NONE>	<NONE>	<NONE>
3247	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	2.00E-05	1050849	(X83742) MAP kinase phosphatase [Xenopus laevis]	4.5

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3248	AF084186	Rattus norvegicus alpha-fodrin (A2A) mRNA, complete cds	0.39	3123155	HYPOTHETICAL 49.0 KD TRP-ASP REPEATS CONTAINING PROTEIN F55F8.5 IN CHROMOSOME I family [Caenorhabditis elegans]	5.00E-29
3249	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	5.00E-04	3293508	(AF069188) NADH dehydrogenase 1 [Ephedrus laevicollis]	0.3
3250	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	3e-009	3243110	(AF034976) unknown [Pilayella littoralis]	4.6
3251	M77812	Rabbit myosin heavy chain mRNA, complete cds.	0.58	3876408	(Z81069) Similarity to Yeast hypothetical 65.2 KD protein (SW:P36076); cDNA EST yk393e9.3 comes from this gene; cDNA EST yk393e9.5 comes from this gene [Caenorhabditis elegans]	3.1
3252	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.0002	<NONE>	<NONE>	<NONE>
3253	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	7e-007	1351841	ISOCITRATE LYASE (ISOCITRASE) lyase [Lycopersicon esculentum]	6.00E+00
3254	Z50144	R.norvegicus mRNA for kynurenine/alpha-aminoadipate aminotransferase	2.00E-76	1050752	(Z50144) kynurenine/alpha-aminoadipate aminotransferase	6e-033

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3255	Z50144	R.norvegicus mRNA for kynurenine/alpha-aminoadipate aminotransferase	2.00E-76	1050752	(Z50144) kynurenine/alpha-aminoadipate aminotransferase	6e-033
3256	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.043	109340	pepsin (EC 3.4.23.-) II-2/3 precursor - rabbit	4.5
3257	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	3e-007	3875769	(Z35662) similar to Approximately 25 cadherin-repeats, 3 EGF domains and one Laminin G domain; cDNA EST EMBL:D27303 comes from this gene; cDNA EST EMBL:D27305 comes from this gene; cDNA EST EMBL:D27304 comes from this gene; ... >gi|3876224|gnl|PID|e134589	4.20E-01
3258	AF041059	Homo sapiens WSCR4 gene, exon 7 and partial cds	5.90E-02	<NONE>	<NONE>	<NONE>
3259	AF054994	Homo sapiens clone 23832 mRNA sequence	0.13	<NONE>	<NONE>	<NONE>
3260	U87266	Arabidopsis thaliana 2,3-oxidosqualene-triterpenoid cyclase mRNA, complete cds	5.60E-01	1175412	HYPOTHETICAL 24.2 KD PROTEIN C13A11.03 IN CHROMOSOME I >gi|984224 (Z54096) unknown	2e-009

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3261	AL010240	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-64, complete sequence	1.3	3882205	(AB018285) KIAA0742 protein [Homo sapiens]	5.00E-10
3262	L20566	Aspergillus niger acid phospatase complete cds.	3.9	3777583	(AF084481) transmembrane protein [Homo sapiens]	5.00E+00
3263	U12202	Human ribosomal protein S24 (rps24) gene, complete cds	3.80E+00	<NONE>	<NONE>	<NONE>
3264	U70139	Mus musculus putative CCR4 protein mRNA, partial cds	0	2251234	(U70139) putative CCR4 protein [Mus musculus]	6e-093
3265	AF055666	Mus musculus kinesin light chain 2 (Klc2) mRNA, complete cds	0.53	3387889	(AF070532) emb-5 [Homo sapiens]	0.56
3266	AF077618	Homo sapiens p73 gene, exon 3	0.4	127709	MYOBLAST DETERMINATIO N PROTEIN 1	7.8
3267	AF072250	Homo sapiens methyl-CpG binding protein MBD4	e-161	3800809	(AF072250) methyl-CpG binding protein MBD4 [Homo sapiens]	2.00E-47
3268	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	8e-009	886048	(U25686) E93 [Drosophila melanogaster]	1.8
3269	AG001313	Homo sapiens genomic DNA, 21q region, clone: 125H6N26	0.0005	<NONE>	<NONE>	<NONE>
3270	U25846	Homarus americanus clone LOB5 farnesoic acid o-methyltransferase mRNA, complete cds.	1.40E-02	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3271	AF068627	Mus musculus DNA cytosine-5 methyltransferase 3B2 (Dnmt3b) mRNA, alternatively spliced, complete cds	0.0005	1698496	(U53444) LW-amid and MW-amid-containing preprohormone	4.40E+00
3272	U60022	Mus musculus antigen processing-associated transporter TAP1-k mRNA, complete cds	3.50E+00	2498941	SPLICEOSOME ASSOCIATED PROTEIN 62 spliceosome-associated protein SAP 62 - human >gi|409219	0.23
3273	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	7e-005	<NONE>	<NONE>	<NONE>
3274	U24676	Drosophila melanogaster twinstar (tsr) gene, complete cds	1.20E+00	<NONE>	<NONE>	<NONE>
3275	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	1.50E-02	<NONE>	<NONE>	<NONE>
3276	AF054994	Homo sapiens clone 23832 mRNA sequence	0.13	<NONE>	<NONE>	<NONE>
3277	AF072250	Homo sapiens methyl-CpG binding protein MBD4	e-161	3800809	(AF072250) methyl-CpG binding protein MBD4 [Homo sapiens]	2.00E-47
3278	AF054994	Homo sapiens clone 23832 mRNA sequence	0.13	<NONE>	<NONE>	<NONE>
3279	AF054994	Homo sapiens clone 23832 mRNA sequence	0.13	<NONE>	<NONE>	<NONE>
3280	AF054994	Homo sapiens clone 23832 mRNA sequence	0.13	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3281	AF054994	Homo sapiens clone 23832 mRNA sequence	0.13	<NONE>	<NONE>	<NONE>
3282	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	2e-005	<NONE>	<NONE>	<NONE>
3283	U20281	Gallus gallus clone pNG13 cell division cycle control protein 37 (cdc37) mRNA, complete cds.	0.017	2642625	(AF032118) intersectin [Xenopus laevis]	1.40E+00
3284	X65279	pWE15 cosmid vector DNA	2e-059	987050	(X65335) lacZ gene product [unidentified cloning vector]	3e-015
3285	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	4e-012	<NONE>	<NONE>	<NONE>
3286	D80005	Human mRNA for KIAA0183 gene, partial cds	0	<NONE>	<NONE>	<NONE>
3287	U27341	Bos taurus endothelin converting enzyme-2 Sequence 1 from patent US 5736376	1e-096	2136744	endothelin converting enzyme-2 - bovine	2e-047
3288	M58417	Drosophila melanogaster laminin B2 gene, complete cds.	0.35	1142698	(U26463) NADPH-dependent aldehyde reductase	6.8
3289	M58417	Drosophila melanogaster laminin B2 gene, complete cds.	0.35	1142698	(U26463) NADPH-dependent aldehyde reductase	6.8
3290	AF020043	Homo sapiens chromosome-associated polypeptide	0	1785540	(U82626) basement membrane-associated chondroitin proteoglycan Bamacan [Rattus norvegicus]	e-112

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3291	U57368	Mus musculus EGF repeat transmembrane protein mRNA, complete cds.	0	1336628	(U57368) EGF repeat transmembrane protein [Mus musculus]	e-101
3292	AB018323	Homo sapiens mRNA for KIAA0780 protein, partial cds	3e-041	3327168	(AB014577) KIAA0677 protein [Homo sapiens]	1e-021
3293	X65279	pWE15 cosmid vector DNA	2e-059	987050	(X65335) lacZ gene product [unidentified cloning vector]	3e-015
3294	X71642	M.musculus GEG-154 mRNA	3e-092	<NONE>	<NONE>	<NONE>
3295	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	1e-009	3879362	(Z81113) similar to DnaJ, prokaryotic heat shock protein, Zinc finger, C2H2 type; cDNA EST yk290e12.5 comes from this gene; cDNA EST yk290e12.3 comes from this gene; cDNA EST yk447h4.5 comes from this gene; cDNA EST yk474e4....	3e-005
3296	AB017026	Mus musculus mRNA for oxysterol-binding protein, complete cds	0	3551523	(AB017026) oxysterol-binding protein	e-103
3297	U43431	Human DNA topoisomerase III mRNA, complete cds.	0	2501242	DNA TOPOISOMERASE III >gi|1292912	6e-069
3298	M35296	Human tyrosine kinase arg gene mRNA.	1.1	2135080	epithelial microtubule-associated protein, 115K - human >gi|414115 (X73882) microtubule associated protein	1.8

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					[Homo sapiens]	
3299	D50646	Mouse mRNA for SDF2, complete cds	1e-031	2136205	stromal cell-derived factor 2 - human sapiens]	4e-014
3300	L34732	Homo sapiens T-cell receptor beta (TCRB) mRNA	0.35	3875664	(Z83104) predicted using Genefinder	3e-005
3301	AF030558	Rattus norvegicus phosphatidylinositol 5-phosphate 4-kinase gamma mRNA, complete cds	1e-013	<NONE>	<NONE>	<NONE>
3302	X03100	Human HLA-SB(DP) alpha gene	2e-018	<NONE>	<NONE>	<NONE>
3303	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	2e-006	2950243	(Z98204) extensin [Hordeum vulgare]	2e-005
3304	Y13631	Clostridium botulinum P-21, P-47 ntnh, bonT genes	1	<NONE>	<NONE>	<NONE>
3305	Y13631	Clostridium botulinum P-21, P-47 ntnh, bonT genes	1	<NONE>	<NONE>	<NONE>
3306	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	3e-011	1655830	(U59446) myrosinase-binding protein related protein	0.01
3307	X17538	Butyrivibrio fibrisolvens end1 gene for endoglucanase	0.12	1001811	(D64005) hypothetical protein	5.2
3308	D42053	Human mRNA for KIAA0091 gene, complete cds	0	577309	(D42053) KIAA0091 gene product is related to subtilisin. [Homo sapiens]	e-127

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3309	L81800	Homo sapiens (subclone 2_g9 from P1 H31) DNA sequence	2e-006	<NONE>	<NONE>	<NONE>
3310	L81800	Homo sapiens (subclone 2_g9 from P1 H31) DNA sequence	2e-006	<NONE>	<NONE>	<NONE>
3311	K01641	Mouse Ig kappa active V-region from 70Z/3 cells.	3.1	<NONE>	<NONE>	<NONE>
3312	K01641	Mouse Ig kappa active V-region from 70Z/3 cells.	3.1	<NONE>	<NONE>	<NONE>
3313	U09954	Human ribosomal protein L9 gene, 5' region and complete cds.	e-114	2136121	ribosomal protein L9 - human >gi|607793	3e-027
3314	M19735	Homo sapiens beta-hexosaminidase beta chain mRNA, complete cds.	0	179462	(M13519) N-acetyl-beta-glucosaminidase prepro-polypeptide	4e-075
3315	M31760	Human chromosome 9 t(9;22) breakpoint DNA.	2e-016	2981631	(AB012223) ORF2 [Canis familiaris]	0.018
3316	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	4e-013	495696	(U00067) C. elegans PAR-3 cell polarity protein	2.5
3317	U61084	Human phorbolin 3 mRNA, complete cds	0	4097433	(U61084) phorbolin 3 [Homo sapiens]	7e-099
3318	X95161	H.sapiens brca2 gene exon 11 > :: emb|A62786|A62786 Sequence 27 from Patent WO9719110	5e-024	244126	uroporphyrinogen III synthase, UROIIIS [human, Peptide Mutant, 265 aa]	0.12
3319	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	2e-013	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	3.9

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3320	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	8e-008	2143490	LGL-1 - mouse >gi|1041889|bbs|169033 267 aa] [Mus sp.]	7.2
3321	U76112	Mus musculus translation repressor NAT1 mRNA, complete cds	1e-013	729818	EUKARYOTIC INITIATION FACTOR 4F SUBUNIT P130 (EIF-4F) (MRNA CAP-BINDING PROTEIN COMPLEX SUBUNIT P130) >gi|539297|pir||B48086 translation initiation factor eIF-4F TIF4632 - yeast (Saccharomyces cerevisiae) >gi|295677 (L16924) p130 [Saccharomyces cerevisiae	1.9
3322	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	3e-009	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	5.2
3323	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	4e-013	495696	(U00067) C. elegans PAR-3 cell polarity protein	2.5
3324	U43626	Human chromosome 15q11-q13 putative DNA replication origin in the g-aminobutyric acid receptor b3 and a5 gene cluster	2e-018	2197085	(AF003535) ORF2-like protein [Homo sapiens]	0.0002
3325	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	2e-010	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3326	Z48561	E.coli perA, perB, perC and perD genes	0.38	2576325	(Y12239) env [porcine endogenous retrovirus]	7.4
3327	Z48561	E.coli perA, perB, perC and perD genes	0.38	2576325	(Y12239) env [porcine endogenous retrovirus]	7.4
3328	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.002	2576325	(Y12239) env [porcine endogenous retrovirus]	7.4
3329	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.002	2576325	(Y12239) env [porcine endogenous retrovirus]	7.4
3330	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	1e-010	1362915	protein-tyrosine kinase (EC 2.7.1.112) STK-1 precursor - human	0.5
3331	X65319	Cloning vector pCAT-Enhancer	3e-081	987050	(X65335) lacZ gene product [unidentified cloning vector]	3e-015
3332	AB018304	Homo sapiens mRNA for KIAA0761 protein, partial cds	0	3882243	(AB018304) KIAA0761 protein [Homo sapiens]	8e-098
3333	Y08460	Mus musculus mRNA for Mdes transmembrane protein	1e-085	2225941	(Y08460) Mdes protein [Mus musculus]	8e-071
3334	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	8e-009	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	5.1
3335	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
3336	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	2e-007	2687928	(AE001118) P115 protein [Borrelia burgdorferi]	5.2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3337	U94831	Homo sapiens multispanning membrane protein mRNA, complete cds	0	2276460	(U94831) multispanning membrane protein [Homo sapiens]	5e-087
3338	U14972	Human ribosomal protein S10 mRNA, complete cds.	2e-059	133715	40S RIBOSOMAL PROTEIN S10	0.0002
3339	K01254	Human gastrin gene, complete cds.	5e-005	<NONE>	<NONE>	<NONE>
3340	U08469	Glycine max 3-methylcrotonyl-CoA carboxylase mRNA, biotin-carrier domain, partial cds.	3e-051	3876562	(Z81074) Similarity to Soybean 3-methylcrotonyl-CoA carboxylase (TR:Q42777); cDNA EST EMBL:M75819 comes from this gene; cDNA EST EMBL:M89099 comes from this gene; cDNA EST EMBL:D32737 comes from this gene; cDNA EST EMBL:D327...	1e-073
3341	AB011139	Homo sapiens mRNA for KIAA0567 protein, partial cds	0	3043658	(AB011139) KIAA0567 protein [Homo sapiens]	e-123
3342	U07615	Rattus norvegicus mucin mRNA, partial cds.	2e-006	2506877	MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2) >gi|454154 (L21998) mucin [Homo sapiens]	0.0007
3343	AF061749	Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds	e-154	3372677	(AF061749) tumorous imaginal discs protein Tid56 homolog	4e-060

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3344	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	0.001	2984587	(AC004472) P1.11659_3 [Homo sapiens]	3e-008
3345	U45998	Onchocerca volvulus MRS3/MRS4 class mitochondrial solute carrier mRNA, complete cds	2e-008	3880433	(Z66521) similar to mitochondrial RNA splicing MSR4 like protein; cDNA EST EMBL:C09217 comes from this gene [Caenorhabditis elegans]	2e-051
3346	U43626	Human chromosome 15q11-q13 putative DNA replication origin in the g-aminobutyric acid receptor b3 and a5 gene cluster	2e-018	2197085	(AF003535) ORF2-like protein [Homo sapiens]	0.0002
3347	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	3e-009	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	5.2
3348	U14972	Human ribosomal protein S10 mRNA, complete cds.	2e-059	133715	40S RIBOSOMAL PROTEIN S10	0.0002
3349	M80198	Human FKBP-12 pseudogene, clone lambda-512, 5' flank and complete cds.	1.00E-10	2315521	(AF016452) similar to the beta transducin family	1e-022
3350	AB011180	Homo sapiens mRNA for KIAA0608 protein, partial cds	5e-077	3043740	(AB011180) KIAA0608 protein [Homo sapiens]	8e-071
3351	U45858	Zea mays glyceraldehyde-3-phosphate dehydrogenase	4.2	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3352	U45858	Zea mays glyceraldehyde-3-phosphate dehydrogenase	4.2	<NONE>	<NONE>	<NONE>
3353	AF035940	Homo sapiens MAGOH mRNA, complete cds	e-141	2330011	(AF007862) mm-Mago [Mus musculus] >gi|2909828 (AF035939) similar to mago nashi [Mus musculus] >gi|2909830	1e-075
3354	AF035940	Homo sapiens MAGOH mRNA, complete cds	e-141	2330011	(AF007862) mm-Mago [Mus musculus] >gi|2909828 (AF035939) similar to mago nashi [Mus musculus] >gi|2909830	1e-075
3355	M24486	Human prolyl 4-hydroxylase alpha subunit mRNA, complete cds, clone PA-11.	e-147	3876769	(Z69637) Similarity to Human Prolyl 4-hydroxylase alpha subunit (SW:P4HA_HUMAN); cDNA EST yk219g12.5 comes from this gene; cDNA EST yk319d8.5 comes from this gene; cDNA EST yk339d11.5 comes from this gene; cDNA EST yk371c9.3...	4e-012
3356	Z50144	R.norvegicus mRNA for kynurenine/alpha-aminoadipate aminotransferase	3.00E-93	1050752	(Z50144) kynurenine/alpha-aminoadipate aminotransferase	2e-043

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3357	M24486	Human prolyl 4-hydroxylase alpha subunit mRNA, complete cds, clone PA-11.	e-147	3876769	(Z69637) Similarity to Human Prolyl 4-hydroxylase alpha subunit (SW:P4HA_HUMAN); cDNA EST yk219g12.5 comes from this gene; cDNA EST yk319d8.5 comes from this gene; cDNA EST yk339d11.5 comes from this gene; cDNA EST yk371c9.3...	4e-012
3358	U83981	Homo sapiens apoptosis associated protein (GADD34) mRNA, complete cds	0	3258618	(U83981) apoptosis associated protein [Homo sapiens]	8.00E-24
3359	U30817	Bos taurus very-long-chain acyl-CoA dehydrogenase mRNA, nuclear gene encoding mitochondrial protein, complete cds.	1e-010	2765125	(Y11770) very-long-chain acyl-CoA dehydrogenase [Mus musculus]	4e-013
3360	Z35094	H.sapiens mRNA for SURF-2	5e-097	2498974	SURFEIT LOCUS PROTEIN 2	4e-046
3361	Z35094	H.sapiens mRNA for SURF-2	5e-097	2498974	SURFEIT LOCUS PROTEIN 2	4e-046
3362	Z35094	H.sapiens mRNA for SURF-2	5e-097	2498974	SURFEIT LOCUS PROTEIN 2	4e-046
3363	Z63829	H.sapiens CpG DNA, clone 90h2, forward read cpg90h2.ft1a .	5e-022	1050411	(L43146) nuclear factor I-B1 [Xenopus laevis]	5.4
3364	AF052573	Homo sapiens DNA polymerase eta (POLH) mRNA, complete cds	0	3510695	(AF052573) DNA polymerase eta [Homo sapiens]	4e-011

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3365	AF092564	Homo sapiens chromosome-associated protein-C	0	3851586	(AF092564) chromosome-associated protein-C [Homo sapiens]	6e-052
3366	AF031924	Homo sapiens homeobox transcription factor barx2	2.00E-90	<NONE>	<NONE>	<NONE>
3367	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	4e-011	419712	probable transposase (insertion sequence IS1138) - Mycoplasma pulmonis (SGC3)	2.6
3368	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	4e-011	419712	probable transposase (insertion sequence IS1138) - Mycoplasma pulmonis (SGC3)	2.6
3369	M24487	Human prolyl 4-hydroxylase alpha subunit mRNA, complete cds, clone PA-15.	e-125	2507090	PROLYL 4-HYDROXYLASE ALPHA SUBUNIT PRECURSOR >gi|66338|pir||DAHUA2 procollagen-proline dioxygenase (EC 1.14.11.2) alpha chain precursor, splice form 2 - human >gi|602675 (U14620) alpha-subunit of prolyl 4-hydroxylase [Homo sapiens]	1e-007

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3370	M24487	Human prolyl 4-hydroxylase alpha subunit mRNA, complete cds, clone PA-15.	e-125	2507090	PROLYL 4-HYDROXYLASE ALPHA SUBUNIT PRECURSOR >gi|66338|pir||DAHUA2 procollagen-proline dioxygenase (EC 1.14.11.2) alpha chain precursor, splice form 2 - human >gi|602675 (U14620) alpha-subunit of prolyl 4-hydroxylase [Homo sapiens]	1e-007
3371	U45858	Zea mays glyceraldehyde-3-phosphate dehydrogenase	4.2	<NONE>	<NONE>	<NONE>
3372	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	7e-006	<NONE>	<NONE>	<NONE>
3373	D50930	Human mRNA for KIAA0140 gene, complete cds	2e-046	<NONE>	<NONE>	<NONE>
3374	X06461	Herpes simplex virus type I immediate early (IE) gene 3 for transcriptional activator IE175 (= ICP 4)	3.00E-04	2924449	(AL022022) PE_PGRS [Mycobacterium tuberculosis]	4.00E-05
3375	X06461	Herpes simplex virus type I immediate early (IE) gene 3 for transcriptional activator IE175 (= ICP 4)	3.00E-04	2924449	(AL022022) PE_PGRS [Mycobacterium tuberculosis]	4.00E-05

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3376	X85753	Homo sapiens mRNA for CDK8 protein kinase > :: emb|A61243|A61243 Sequence 1 from Patent WO9709432	7e-059	<NONE>	<NONE>	<NONE>
3377	X76192	Mycoplasma sp. munIM, munIC and munIR genes.	1.2	<NONE>	<NONE>	<NONE>
3378	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.0002	<NONE>	<NONE>	<NONE>
3379	M24486	Human prolyl 4-hydroxylase alpha subunit mRNA, complete cds, clone PA-11.	e-147	3876769	(Z69637) Similarity to Human Prolyl 4-hydroxylase alpha subunit (SW:P4HA_HUMAN); cDNA EST yk219g12.5 comes from this gene; cDNA EST yk319d8.5 comes from this gene; cDNA EST yk339d11.5 comes from this gene; cDNA EST yk371c9.3...	4e-012
3380	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	7e-006	<NONE>	<NONE>	<NONE>
3381	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	1e-010	2119163	collagen alpha 1(III) chain precursor - mouse	0.005
3382	AB009357	Homo sapiens mRNA for TGF-beta activated kinase 1b, complete cds	0	1167506	(D76446) TAK1 (TGF-beta-activated kinase) [Mus musculus]	2e-033

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3383	D38112	Human mitochondrial DNA, complete sequence	5e-052	14016	(X55654) cytochrome C oxidase II subunit [Homo sapiens]	1e-014
3384	Z96177	H.sapiens telomeric DNA sequence, clone 10QTEL040, read 10QTELOO040.seq	7e-038	987050	(X65335) lacZ gene product [unidentified cloning vector]	0.035
3385	Z96177	H.sapiens telomeric DNA sequence, clone 10QTEL040, read 10QTELOO040.seq	7e-038	987050	(X65335) lacZ gene product [unidentified cloning vector]	0.035
3386	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	4e-011	2384956	(AF022985) No definition line found [Caenorhabditis elegans]	6e-029
3387	AF010484	Homo sapiens ICI YAC 9IA12, right end sequence	3e-010	<NONE>	<NONE>	<NONE>
3388	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	5e-013	113667	!!!! ALU CLASS B WARNING ENTRY !!!!	0.68
3389	AJ009761	Homo sapiens mRNA for putative dimethyladenosine transferase, partial	0	4050050	(AF102147) putative dimethyladenosine transferase [Homo sapiens]	4.00E-46
3390	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.048	<NONE>	<NONE>	<NONE>
3391	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.048	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3392	AL022579	Homo sapiens DNA sequence from clone 47K8 on chromosome Xp11.21-11.23, complete sequence [Homo sapiens]	1e-070	<NONE>	<NONE>	<NONE>
3393	U37454	Human Down Syndrome region of chromosome 21 genomic sequence, clone A31D6-1H7.	0.12	<NONE>	<NONE>	<NONE>
3394	AF058954	Homo sapiens GTP-specific succinyl-CoA synthetase beta subunit (SCS) mRNA, partial cds	0	3766199	(AF058954) GTP-specific succinyl-CoA synthetase beta subunit [Homo sapiens]	e-122
3395	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	3e-009	3043582	(AB011101) KIAA0529 protein [Homo sapiens]	2e-012
3396	Z23090	H.sapiens mRNA for 28 kDa heat shock protein.	3e-079	1709972	60S RIBOSOMAL PROTEIN L10A (CSA-19)	2e-025
3397	D14657	Human mRNA for KIAA0101 gene, complete cds	0	3183216	HYPOTHETICAL PROTEIN KIAA0101 sapiens]	2e-026
3398	D17577	Mouse mRNA for kinesin-like protein (Kif1b), complete cds	e-121	2497524	KINESIN-LIKE PROTEIN KIF1B mouse >gi|407339|gnl|PID|d1005029 (D17577) Kif1b [Mus musculus]	1e-048
3399	AF091078	Homo sapiens clone 559 unknown mRNA, complete sequence	0	4050050	(AF102147) putative dimethyladenosine transferase [Homo sapiens]	1e-048

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3400	AC000043	Homo sapiens Chromosome 22q13 Cosmid Clone p74a8, complete sequence [Homo sapiens]	7e-006	<NONE>	<NONE>	<NONE>
3401	AC000043	Homo sapiens Chromosome 22q13 Cosmid Clone p74a8, complete sequence [Homo sapiens]	7e-006	<NONE>	<NONE>	<NONE>
3402	AF031924	Homo sapiens homeobox transcription factor barx2	e-156	<NONE>	<NONE>	<NONE>
3403	AF031924	Homo sapiens homeobox transcription factor barx2	e-157	3882305	(AB018335) KIAA0792 protein [Homo sapiens]	4.5
3404	L22473	Human Bax alpha mRNA, complete cds.	0	728945	APOPTOSIS REGULATOR BAX, MEMBRANE ISOFORM ALPHA >gi|539664|pir||A47538 bcl-2-associated protein bax alpha splice form - human >gi|388166	9e-075
3405	U04709	Human adenine phosphoribosyltransferase (APRT) gene, 3' flanking region	e-151	113668	!!!! ALU CLASS C WARNING ENTRY !!!!	0.91
3406	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	3e-008	3064146	(AF036408) mucin-like protein [Trypanosoma cruzi]	7.6
3407	AF093268	Rattus norvegicus homer-1c mRNA, complete cds	e-171	1913909	(U92079) GLGF-domain protein Homer [Rattus norvegicus]	4e-046

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3408	U47322	Cloning vector DNA, complete sequence.	2.00E-38	987050	(X65335) lacZ gene product [unidentified cloning vector]	3.00E-03
3409	U78109	Mus musculus prepro-neurturin mRNA, complete cds	1.2	2506998	STANNIOCALCIN (STC) (CORPUSCLES OF STANNIUS PROTEIN) (CS) (HYPOCALCIN) (TELEOCALCIN)	1.2
3410	Z96177	H.sapiens telomeric DNA sequence, clone 10QTEL040, read 10QTELOO040.seq	5e-013	<NONE>	<NONE>	<NONE>
3411	D50930	Human mRNA for KIAA0140 gene, complete cds	0.00E+00	1235974	(X96713) collagen [Globodera pallida]	5.8
3412	D50930	Human mRNA for KIAA0140 gene, complete cds	2e-046	<NONE>	<NONE>	<NONE>
3413	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	1e-010	<NONE>	<NONE>	<NONE>
3414	L01777	Yersinia pseudotuberculosis (group IIA) rfb gene cluster	1.20E-01	<NONE>	<NONE>	<NONE>
3415	D17577	Mouse mRNA for kinesin-like protein (Kif1b), complete cds	e-130	2497524	KINESIN-LIKE PROTEIN KIF1B mouse >gi|407339|gnl|PID|d1005029 (D17577) Kif1b [Mus musculus]	1e-049
3416	AB014597	Homo sapiens mRNA for KIAA0697 protein, partial cds	2e-067	3327208	(AB014597) KIAA0697 protein [Homo sapiens]	6e-050

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3417	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	1.00E-11	<NONE>	<NONE>	<NONE>
3418	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.0002	<NONE>	<NONE>	<NONE>
3419	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.0002	<NONE>	<NONE>	<NONE>
3420	AB014597	Homo sapiens mRNA for KIAA0697 protein, partial cds	2e-067	3327208	(AB014597) KIAA0697 protein [Homo sapiens]	6e-050
3421	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	5e-014	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	5.5
3422	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	8.00E-08	1176456	(S79774) bile salt-dependent lipase, BSDL {EC 3.1.1.-} [human, fetal pancreas, Peptide Partial, 720 aa] [Homo sapiens]	9.4
3423	AF100661	Caenorhabditis elegans cosmid H20E11	0.39	<NONE>	<NONE>	<NONE>
3424	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	2.00E-04	<NONE>	<NONE>	<NONE>
3425	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	9.00E-10	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3426	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	9.00E-10	<NONE>	<NONE>	<NONE>
3427	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	2.00E-05	3056592	(AC004255) T1F9.13 [Arabidopsis thaliana]	10
3428	U89676	Candida albicans putative membrane protein (CSP37) gene, complete cds	0.12	<NONE>	<NONE>	<NONE>
3429	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	5e-014	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	5.5
3430	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
3431	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	2.00E-07	<NONE>	<NONE>	<NONE>
3432	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	2.00E-07	<NONE>	<NONE>	<NONE>
3433	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	2.00E-07	<NONE>	<NONE>	<NONE>
3434	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	4.00E-13	<NONE>	<NONE>	<NONE>
3435	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	4.00E-13	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3436	AB014597	Homo sapiens mRNA for KIAA0697 protein, partial cds	2e-067	3327208	(AB014597) KIAA0697 protein [Homo sapiens]	6e-050
3437	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	2.00E-06	1360669	collagen alpha 1(V) chain precursor - human sapiens]	1.8
3438	U65297	Geomys breviceps cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, complete cds	3.50E+00	<NONE>	<NONE>	<NONE>
3439	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	2.00E-06	3914965	TOXIN BMK-X PRECURSOR (BMK10) (BMK M10) (NEUROTOXIN M10) >gi|3138981 (AF062563) neurotoxin M10 precursor [Mesobuthus martensii]	4
3440	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	2.00E-06	3914965	TOXIN BMK-X PRECURSOR (BMK10) (BMK M10) (NEUROTOXIN M10) >gi|3138981 (AF062563) neurotoxin M10 precursor [Mesobuthus martensii]	4
3441	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	3e-011	3413900	(AB007938) KIAA0469 protein [Homo sapiens]	1.40E-02

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3442	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	1.00E-11	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	4.20E+00
3443	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	1.00E-11	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	4.20E+00
3444	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	8.00E-08	1176456	(S79774) bile salt-dependent lipase, BSDL {EC 3.1.1.-} [human, fetal pancreas, Peptide Partial, 720 aa] [Homo sapiens]	9.4
3445	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	4.00E-13	<NONE>	<NONE>	<NONE>
3446	U91543	Homo sapiens zinc-finger helicase (hZFH) mRNA, complete cds	1.00E-61	2961557	(AF050199) putative peroxisome microbody protein 175.1	3.70E+00
3447	X75258	H.sapiens DNA from recombination area	1.40E-02	1143020	(U28974) ORF1 [Spiroplasma virus]	9.5
3448	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	8.00E-08	<NONE>	<NONE>	<NONE>
3449	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	2.00E-07	631089	bat2 protein - human	0.055

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3450	AL022321	Homo sapiens DNA sequence from PAC 20O8 on chromosome 22q12.1-12.3. Contains exons 13 and 14 of the SLC5A1 (SGLT1) gene for solute carrier family 5 Sodium-Glucose Cot...	1.10E+00	3063453	(AC003981) F22O13.15 [Arabidopsis thaliana]	7.2
3451	AF060798	Homo sapiens myristilated and palmitylated serine-threonine kinase MPSK (MPSK1) mRNA, complete cds	0.00E+00	3372666	(AF060798) myristilated and palmitylated serine-threonine kinase MPSK [Homo sapiens]	2e-067
3452	AF080399	Drosophila melanogaster mitotic checkpoint control protein kinase BUB1 (Bub1) mRNA, complete cds	1.1	3184082	(AL023781) N-terminal acetyltransferase 1 [Schizosaccharomyces pombe]	1e-033
3453	AF041259	Homo sapiens breast cancer putative transcription factor (ZABC1) mRNA, complete cds	0.00E+00	3879065	(Z81576) R10E8.3 [Caenorhabditis elegans]	9.7
3454	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	3.70E-01	549359	MINOR CAPSID PROTEIN L2 type 26 >gi|396962 (X74472) late protein [Human papillomavirus type 26]	0.097
3455	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	2.00E-06	2746890	(AF040655) No definition line found [Caenorhabditis elegans]	9.1

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3456	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	2e-005	3874316	(Z81470) predicted using Genefinder	6.8
3457	V01399	Defective Semliki forest virus RNA. Derived by serial undiluted passaging of the virus in baby hamster kidney cells > :: gb|L00017|SFVD IB semliki forest virus defective interfering (18s di) rna di309.	0.98	2496616	HYPOTHETICAL 38.5 KD PROTEIN Y4EE	2.1
3458	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	4.60E-02	<NONE>	<NONE>	<NONE>
3459	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	6.00E-06	<NONE>	<NONE>	<NONE>
3460	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.014	630844	NADH dehydrogenase chain 2 - fruit fly dehydrogenase subunit 2 [Drosophila erecta]	7.3
3461	L49035	Gorilla gorilla ABC-transporter (TAP2) mRNA, complete cds	4.70E-01	2058691	(U94836) ERPROT 213-21 [Homo sapiens]	4.3
3462	U67524	Methanococcus jannaschii section 66 of 150 of the complete genome	4.10E-02	140229	HYPOTHETICAL 82 KD AVIRULENCE PROTEIN IN AVRBS3 REGION >gi|77844|pir||JQ0317 hypothetical 82K protein - Xanthomonas	7.3

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					campestris pv. vesicatoria	
3463	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	4.00E-12	<NONE>	<NONE>	<NONE>
3464	U65297	Geomys breviceps cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, complete cds	3.50E+00	<NONE>	<NONE>	<NONE>
3465	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
3466	U36266	Human beta-prime-adaptin (BAM22) gene, exons 18 and 19	1.20E+00	<NONE>	<NONE>	<NONE>
3467	AB018327	Homo sapiens mRNA for KIAA0784 protein, partial cds	0	3882289	(AB018327) KIAA0784 protein [Homo sapiens]	e-103
3468	AB018327	Homo sapiens mRNA for KIAA0784 protein, partial cds	0	3882289	(AB018327) KIAA0784 protein [Homo sapiens]	e-103
3469	U66789	Human laminin alpha 2 chain (LAMA2) gene, exon 57	4.80E-02	3873753	(Z66519) similar to phytoene synthase precursor; cDNA EST yk340f7.3 comes from this gene; cDNA EST yk340f7.5 comes from this gene [Caenorhabditis elegans]	3e-006

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3470	AB018327	Homo sapiens mRNA for KIAA0784 protein, partial cds	9.00E-88	3882289	(AB018327) KIAA0784 protein [Homo sapiens]	9e-022
3471	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	0.0002	<NONE>	<NONE>	<NONE>
3472	U67524	Methanococcus jannaschii section 66 of 150 of the complete genome	4.10E-02	140229	HYPOTHETICAL 82 KD AVIRULENCE PROTEIN IN AVRBS3 REGION >gi|77844|pir||JQ0317 hypothetical 82K protein - Xanthomonas campestris pv. vesicatoria	7.3
3473	L13972	Homo sapiens beta-galactoside alpha-2,3-sialyltransferase (SIAT4A) mRNA, complete cds	0.005	<NONE>	<NONE>	<NONE>
3474	L13972	Homo sapiens beta-galactoside alpha-2,3-sialyltransferase (SIAT4A) mRNA, complete cds	0.005	<NONE>	<NONE>	<NONE>
3475	AL031222	Caenorhabditis elegans cosmid 6R55, complete sequence [Caenorhabditis elegans]	1.10E-01	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3476	AF070529	Homo sapiens clone 24525 mRNA sequence	0	3879532	(Z49130) cDNA EST EMBL:D74028 comes from this gene; cDNA EST EMBL:D71354 comes from this gene; cDNA EST EMBL:D76320 comes from this gene; cDNA EST yk486c7.3 comes from this gene; cDNA EST yk486c7.5 comes from this gene; cDNA...	1.50E+00
3477	U02567	Mus musculus BALB/c T-cell antigen 4-1BB gene, complete cds.	1.30E-01	2414601	(Z99295) phosphatidyl synthase	5e-005
3478	AB018327	Homo sapiens mRNA for KIAA0784 protein, partial cds	9.00E-88	3882289	(AB018327) KIAA0784 protein [Homo sapiens]	9e-022
3479	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	1e-011	2315521	(AF016452) similar to the beta transducin family	2e-006
3480	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	9e-010	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	5.5
3481	Y09077	H.sapiens mRNA for atr gene > :: gb|U76308|HSU76308 Human protein kinase ATR mRNA, complete cds > :: emb|A61385|A61385 Sequence 1 from Patent WO9709433	0	1235902	(U49844) FRAP-related protein [Homo sapiens]	3e-051

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3482	Z48633	H.sapiens mRNA for retrotransposon.	e-165	1177607	(X92485) pva1 [Plasmodium vivax]	1.9
3483	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	5e-013	111978	mucin - rat	2.6
3484	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	3e-010	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	5.4
3485	X77335	A.thaliana gene for methyltransferase	0.13	1401051	(U24160) similar to Dvl-1 product encoded by GenBank Accession Number U10115; dishevelled segment polarity protein homolog [Mus musculus]	3.5
3486	AF038660	Homo sapiens chromosome 1p33-p34 beta-1,4-galactosyltransferase mRNA, complete cds	e-144	2995442	(Y12510) UDPGal:GlcNAc b1,4 galactosyltransferase [Homo sapiens]	9e-005
3487	U65960	Human kinase substrate HASPP28 gene, 5' flanking region and partial cds	1e-021	2120084	reverse transcriptase - mouse >gi|558908	9.7
3488	AF058907	Homo sapiens pleiotrophin (PTN) gene, exons UV3, UV2 and UV1	8e-060	120806	GAG POLYPROTEIN (CONTAINS: CORE PROTEIN P15; INNER COAT PROTEIN P12; CORE SHELL PROTEIN P30) >gi|74562|pir||FO VDA gag polyprotein - avian spleen necrosis virus (fragment)	5e-005

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					>gi|61758 (V01200) reading frame (gag?) [Spleen necrosis virus]	
3489	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	4e-011	3123086	HYPOTHETICAL PROTEIN MJ1050 Methanococcus jannaschii >gi|1499895 (U67548) conserved hypothetical protein [Methanococcus jannaschii]	2.5
3490	AF035940	Homo sapiens MAGOH mRNA, complete cds	5e-096	3879018	(Z81108) similar to MAGO NASHI PROTEIN; cDNA EST yk415g7.3 comes from this gene; cDNA EST yk425g2.3 comes from this gene; cDNA EST yk425g2.5 comes from this gene; cDNA EST yk415g7.5 comes from this gene; cDNA EST yk376g9.3 c...	5e-027
3491	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	5e-013	3201662	(AF042191) paraxial protocadherin; PAPC [Danio rerio]	3.5

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3492	S80107	membrane-associated diazepam binding inhibitor	e-113	244503	(S80107) membrane-associated diazepam binding inhibitor, MA-DBI [cattle, brain, Peptide, 552 aa] [Bos taurus]	2e-030
3493	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	4.00E-12	<NONE>	<NONE>	<NONE>
3494	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	6e-015	728834	!!!! ALU SUBFAMILY SB2 WARNING ENTRY	0.29
3495	U32794	Haemophilus influenzae Rd section 109 of 163 of the complete genome	1.3	2369865	(Y14131) RNA polymerase [grapevine leafroll-associated virus 2]	5.1
3496	AF030558	Rattus norvegicus phosphatidylinositol 5-phosphate 4-kinase gamma mRNA, complete cds	1e-013	<NONE>	<NONE>	<NONE>
3497	D17577	Mouse mRNA for kinesin-like protein (Kif1b), complete cds	e-121	2497524	KINESIN-LIKE PROTEIN KIF1B mouse >gi|407339|gnl|PID|d1005029 (D17577) Kif1b [Mus musculus]	1e-048
3498	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	6e-005	3881824	(Z73899) ZK829.5 [Caenorhabditis elegans]	1.5
3499	L35657	Homo sapiens (subclone H8 5_a10 from P1 35 H5 C8) DNA sequence.	2e-018	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	3.2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3500	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	1e-009	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	5.6
3501	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	1e-009	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	5.6
3502	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	9e-010	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	5.5
3503	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	2e-006	2661842	(Y15732) DNA polymerase beta [Xenopus laevis]	4e-016
3504	U65960	Human kinase substrate HASPP28 gene, 5' flanking region and partial cds	1e-021	2120084	reverse transcriptase - mouse >gi|558908	9.7
3505	L19031	Rattus norvegicus organic anion transporter	3e-030	1171883	SODIUM-INDEPENDENT ORGANIC ANION TRANSPORTER (ORGANIC ANION TRANSPORTING POLYPEPTIDE) anion - rat >gi|410311 (L19031) oatp [Rattus norvegicus]	2e-025
3506	U60337	Homo sapiens beta-mannosidase mRNA, complete cds	0	3024091	BETA-MANNOSIDASE PRECURSOR beta-mannosidase [Homo sapiens]	2e-085
3507	X92841	H.sapiens MICA gene	1e-055	106322	hypothetical protein (L1H 3' region) - human	1e-009

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3508	U50535	Human BRCA2 region, mRNA sequence CG006	4e-012	728831	!!!! ALU SUBFAMILY J WARNING ENTRY	4.2
3509	AF029984	Lycopersicon esculentum COP1 homolog (COP1) mRNA, complete cds	5e-035	3121867	COP1 REGULATORY PROTEIN sativum]	9e-052
3510	Z59258	H.sapiens CpG DNA, clone 13d2, reverse read cpg13d2.rt1c .	2e-046	3219914	HYPOTHETICAL 16.8 KD PROTEIN C30D10.04 IN CHROMOSOME II >gi|2276353|gnl|PID|e330328 pombe]	2e-009
3511	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	3e-008	<NONE>	<NONE>	<NONE>
3512	AF004161	Oryctolagus cuniculus peroxisomal Ca-dependent solute carrier mRNA, complete cds	9e-030	2352427	(AF004161) peroxisomal Ca-dependent solute carrier	1e-025
3513	U15643	Drosophila melanogaster ribosomal protein DL11 mRNA, complete cds	0.13	<NONE>	<NONE>	<NONE>
3514	U15643	Drosophila melanogaster ribosomal protein DL11 mRNA, complete cds	0.13	<NONE>	<NONE>	<NONE>
3515	X87212	H.sapiens mRNA for cathepsin C	e-103	1705632	DIPEPTIDYL-PEPTIDASE I PRECURSOR TRANSFERASE) >gi|2146949|pir||S66504 dipeptidyl-peptidase I (EC 3.4.14.1) precursor - human sapiens]	3e-034

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3516	U28789	Mus musculus p53-associated cellular protein PACT mRNA, partial cds	e-101	<NONE>	<NONE>	<NONE>
3517	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	1e-009	127112	MAK16 PROTEIN >gi|73269|pir||BV BYK6 MAK16 protein - yeast (Saccharomyces cerevisiae) cerevisiae] >gi|595561 (U12980) Mak16p: putative nuclear protein [Saccharomyces cerevisiae]	5e-022
3518	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	9e-009	<NONE>	<NONE>	<NONE>
3519	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	3e-010	2650142	(AE001070) A. fulgidus predicted coding region AF0495	0.38
3520	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	1e-012	2500418	40S RIBOSOMAL PROTEIN S5 >gi|1203905	1.6
3521	AF004161	Oryctolagus cuniculus peroxisomal Ca-dependent solute carrier mRNA, complete cds	9e-030	2352427	(AF004161) peroxisomal Ca-dependent solute carrier	1e-025

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3522	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.002	121743	GTPASE-ACTIVATING PROTEIN (GAP) (RAS P21 PROTEIN ACTIVATOR) (P120GAP) (RASGAP) human >gi|182972 (M23379) GTPase-activating protein activating protein [Homo sapiens]	2.8
3523	Z46372	R.norvegicus RNA for DNA topoisomerase II.	e-131	3876360	(Z68315) Similarity to Human MAP kinase phosphatase-1 (SW:PTN7_HUMAN) [Caenorhabditis elegans]	3e-011
3524	X85060	B.taurus cosmid-derived microsatellite DNA	1e-051	2072972	(U93572) putative p150 [Homo sapiens]	1e-019
3525	D86407	Homo sapiens DNA for apoER2, complete cds, and exon 19	0	3322933	(AE001238) DNA ligase (lig) [Treponema pallidum]	7.5
3526	D17577	Mouse mRNA for kinesin-like protein (Kif1b), complete cds	e-130	2497524	KINESIN-LIKE PROTEIN KIF1B mouse >gi|407339|gnl|PID|d1005029 (D17577) Kif1b [Mus musculus]	1e-049
3527	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	2e-007	2414623	(Z99259) putative phosphotransferase	4e-009
3528	U95760	Drosophila melanogaster strawberry notch (sno) mRNA, complete cds	1e-075	2076895	(AF002197) F20H11.2 gene product [Caenorhabditis elegans]	8e-057

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3529	X54326	H.sapiens mRNA for glutaminyl-tRNA synthetase	0	135104	MULTIFUNCTIONAL AMINOACYL-TRNA SYNTHETASE (CONTAINS: GLUTAMYL-TRNA SYNTHETASE glutamyl-prolyl-tRNA synthetase - human >gi|31958	3e-032
3530	Z73360	Human DNA sequence from cosmid 92M18, BRCA2 gene region chromosome 13q12-13.	3e-039	2072955	(U93566) p40 [Homo sapiens]	7.8
3531	Z73360	Human DNA sequence from cosmid 92M18, BRCA2 gene region chromosome 13q12-13.	3e-039	2072955	(U93566) p40 [Homo sapiens]	7.8
3532	Z73360	Human DNA sequence from cosmid 92M18, BRCA2 gene region chromosome 13q12-13.	1e-040	2072955	(U93566) p40 [Homo sapiens]	0.012
3533	Z73360	Human DNA sequence from cosmid 92M18, BRCA2 gene region chromosome 13q12-13.	1e-040	2072955	(U93566) p40 [Homo sapiens]	0.012
3534	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	1e-009	3808228	(AF039080) RNA dependent RNA polymerase [Sphaeropsis sapinea RNA virus 2]	1.5

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3535	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	2e-005	<NONE>	<NONE>	<NONE>
3536	U95760	Drosophila melanogaster strawberry notch (sno) mRNA, complete cds	3e-060	2078282	(U95760) Sno [Drosophila melanogaster]	1e-042
3537	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	0.13	2832777	(AL021086) 1-evidence=predicted by match; 1-match_accession=AA202870; 1-match_description=LD03215.5prime LD Drosophila melanogaster embryo BlueScript Drosophila melanogaster cDNA clone LD03215 5prime.; 1-match_species=Drosop...	4e-018
3538	U95760	Drosophila melanogaster strawberry notch (sno) mRNA, complete cds	1e-075	2076895	(AF002197) F20H11.2 gene product [Caenorhabditis elegans]	8e-057
3539	Z57610	H.sapiens CpG DNA, clone 187a10, reverse read cpg187a10.rt1a .	9e-061	913042	hepatocyte nuclear factor 3 beta, HNF3 beta	2e-014
3540	X83416	H.sapiens PrP gene, exon 2	e-169	1172651	PROTEASE PRTH >gi|440338 (L27483) neutral protease large subunit [Porphyromonas gingivalis]	6.2
3541	AF061016	Homo sapiens UDP-glucose dehydrogenase (UGDH) mRNA, complete cds	0	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	3.4

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3542	X07290	Human HF.12 gene mRNA	7e-080	1127843	(U41164) Cys2/His2 zinc finger protein [Rattus norvegicus]	1e-034
3543	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	4.00E-12	<NONE>	<NONE>	<NONE>
3544	U95760	Drosophila melanogaster strawberry notch (sno) mRNA, complete cds	3e-060	2078282	(U95760) Sno [Drosophila melanogaster]	1e-042
3546	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	0.002	1255409	(U53153) similar to mouse bullous pemphigoid antigen, BPAG2 (PIR:A46053) [Caenorhabditis elegans]	7.3
3547	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	8e-008	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	9.9
3548	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	2e-005	<NONE>	<NONE>	<NONE>
3549	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	0.0002	84605	glycine-rich protein GRP33 - brine shrimp	4.4
3550	X83212	H.sapiens tryptophan hydroxylase gene, promoter region	5e-013	807677	(M13101) unknown protein [Rattus norvegicus]	0.39
3551	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.005	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3552	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	4e-012	310622	(L20249) homologous to Saccharopolyspora erythraea beta-ketoacyl synthase [Streptomyces coriofaciens]	0.4
3553	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	7e-007	<NONE>	<NONE>	<NONE>
3554	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	8e-007	2996640	(AC004500) GDF-9 [Homo sapiens]	8.2
3555	Z35928	S.cerevisiae chromosome II reading frame ORF YBR059c	0.043	2384728	(AF015883) hydroxyproline-rich glycoprotein gas28p precursor [Chlamydomonas reinhardtii]	0.23
3556	Z30174	M.domesticus (C57Bl/6J) mRNA for zinc finger protein 30	2e-037	543345	zinc finger protein 30 - mouse domesticus]	1e-020
3557	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.002	<NONE>	<NONE>	<NONE>
3558	M36072	Human ribosomal protein L7a (surf 3) large subunit mRNA, complete cds.	1e-054	133014	60S RIBOSOMAL PROTEIN L7A (PLA-X POLYPEPTIDE) (SURF-3) >gi|71116|pir||R5HU7A ribosomal protein L7a - human >gi|71117|pir||R5RT7A ribosomal protein L7a - rat >gi|34203 (X52138) L7a protein [Homo sapiens] >gi|35512	0.019

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					(X06705) PLA-X polypeptide [Homo sapiens]	
3559	U84720	Homo sapiens mRNA export protein (RAE1) mRNA, complete cds	2e-037	<NONE>	<NONE>	<NONE>
3560	AE001054	Archaeoglobus fulgidus section 53 of 172 of the complete genome	1.2	<NONE>	<NONE>	<NONE>
3561	U34683	Human glutathione synthetase mRNA, complete cds	3e-052	1346191	GLUTATHIONE SYNTHETASE (GLUTATHIONE SYNTHASE) (GSH SYNTHETASE) (GSH-S) sapiens] >gi|1236350 (U34683) glutathione synthetase	1e-014
3562	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	6e-015	1825695	(U88180) similar to molybdenum cofactor biosynthesis protein E [Caenorhabditis elegans]	4e-012
3563	AE001421	Plasmodium falciparum chromosome 2, section 58 of 73 of the complete sequence	0.005	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3564	D10871	Human h NAT allele 2-2 gene for arylamine N-acetyltransferase	5e-016	3915580	ZINC FINGER PROTEIN 186 finger protein [Homo sapiens]	0.96
3565	M32251	Cat LINE-1 DNA sequence region 1.	2e-026	87765	hypothetical L1 protein (third intron of gene TS) - human >gi|364964|prf||1510254A L1 repetitive element ORF [Homo sapiens]	2e-011
3566	Y12773	H.sapiens TRIDENT/HFH1 1 gene, promoter sequence	3e-008	<NONE>	<NONE>	<NONE>
3567	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	3e-010	<NONE>	<NONE>	<NONE>
3568	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	1e-010	<NONE>	<NONE>	<NONE>
3569	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	9e-009	136821	HYPOTHETICAL PROTEIN UL13 precursor - human cytomegalovirus (strain AD169)	6
3570	AF039210	Homo sapiens caspase-activated nuclease mRNA, complete cds	e-104	3347857	(AF064019) DNA fragmentation factor 40 kDa subunit [Homo sapiens] >gi|3410909|gnl|PID|d1033212 (AB013918) CAD	1e-024
3571	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	4e-012	2132458	probable membrane protein YDL211c - yeast	7.5
3572	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete	4e-011	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	0.39

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		cds				
3573	U22233	Human methylthioadenosine phosphorylase (MTAP) mRNA, complete cds.	2e-015	2494053	5'-METHYLTHIOADENOSINE PHOSPHORYLASE (MTA PHOSPHORYLASE) (MTAPASE) phosphorylase (EC 2.4.2.28) - human >gi|847724 (U22233) methylthioadenosine phosphorylase [Homo sapiens]	0.02
3574	X76122	A.majus cyclin-1 mRNA.	3.2	2135633	MHC cell surface glycoprotein - human sapiens]	9
3575	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	1e-009	699508	(U20542) lethal(1)1Bi protein [Drosophila melanogaster]	0.64
3576	D13391	Human CYP19 gene for aromatase cytochrome P-450, promoter region (containing two cis-acting transcriptional regulatory elements)	2e-018	<NONE>	<NONE>	<NONE>
3577	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.0002	532806	(U13875) C26E6.5 gene product [Caenorhabditis elegans]	5e-045
3578	X63735	H.sapiens TRE5 and TRE18 sequence of the tre oncogene	4e-033	728831	!!!! ALU SUBFAMILY J WARNING ENTRY	9e-006
3579	AC004497	Homo sapiens chromosome 21, P1 clone	0.0005	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		LBNL#6				
3580	AB003095	Fruitfly strain SI259 mitochondrial DNA, A+T-rich region, partial sequence	0.12	<NONE>	<NONE>	<NONE>
3581	Z36019	S.cerevisiae chromosome II reading frame ORF YBR150c	3.2	4107113	(AB007462) Pax-2/5/8 [Ephydatia fluviatilis]	5.3
3582	Z56421	H.sapiens CpG DNA, clone 117c7, reverse read cpg117c7.rt1a .	1e-033	3876101	(Z75536) similar to DnaJ domain; cDNA EST yk398h12.5 comes from this gene; cDNA EST yk250d6.5 comes from this gene [Caenorhabditis elegans]	1e-040
3583	U36499	Human lymphoid-specific SP100 homolog (LYSP100-A) mRNA, complete cds	5e-015	1362890	phosphoprotein 75 - human >gi|402148	1e-008
3584	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	5e-005	<NONE>	<NONE>	<NONE>
3585	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.002	1045228	(X92429) Synthetase [Streptomyces anulatus]	0.84
3586	D86963	Human mRNA for KIAA0208 gene, complete cds	0.04	<NONE>	<NONE>	<NONE>
3587	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	1e-012	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3588	AB012113	Homo sapiens gene for CC chemokine PARC precursor, complete cds	0.0002	1723187	112.3 KD PROTEIN IN PYK1-SNC1 INTERGENIC REGION >gi|2131258|pir||S 70292 FUN12 protein Fun12p: 97kDa protein, function unknown [Saccharomyces cerevisiae]	4.2
3589	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	3e-007	<NONE>	<NONE>	<NONE>
3590	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	0.002	<NONE>	<NONE>	<NONE>
3591	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	6e-005	<NONE>	<NONE>	<NONE>
3592	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	1e-009	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	2.8
3593	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	3e-006	<NONE>	<NONE>	<NONE>
3594	M80938	Oryza sativa 16.9 kDa heat shock protein gene, complete cds.	1.5	<NONE>	<NONE>	<NONE>
3595	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	5e-014	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3596	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	1e-012	<NONE>	<NONE>	<NONE>
3597	X67813	C.familiaris SRP72 mRNA for signal recognition particle	4e-083	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	6.2
3598	AB007930	Homo sapiens mRNA for KIAA0461 perotein, partial cds	3e-038	3413884	(AB007930) KIAA0461 perotein [Homo sapiens]	3e-016
3599	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	8e-007	3093586	(AF018165) amyloid precursor protein [Tetraodon fluviatilis]	2.7
3600	Z35102	H.sapiens mRNA for Ndr protein kinase > :: emb|A52140|A52140 Sequence 6 from Patent WO9619579	e-126	2135799	Ndr protein kinase - human >gi|854170	9e-086
3601	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	2e-005	<NONE>	<NONE>	<NONE>
3602	X51544	Synthetic hamster-human hybrid cell (HCH-1) HSAG-2 gene Alu repeat region.	0.13	1706266	SULFATE ADENYLATE TRANSFERASE SUBUNIT 2 (ATP-SULFURYLASE) >gi|1322409|gnl|PID|e243270	5.8
3603	Z98237	H.sapiens DNA for exon trapped sequence	3e-051	3979947	(AL034393) Y18D10A.15 [Caenorhabditis elegans]	6e-005
3604	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	7e-005	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3605	M57465	N.crassa phytoene dehydrogenase (al-1) gene, complete cds.	0.29	<NONE>	<NONE>	<NONE>
3606	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.0002	<NONE>	<NONE>	<NONE>
3607	S71335	Aox1=alternative oxidase {alternative pathway} suspension cells, mRNA, 1408 nt]	1.1	<NONE>	<NONE>	<NONE>
3608	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	0.005	2621440	(AE000823) O-antigen transporter related protein	5.7
3609	U36199	Caenorhabditis elegans CeMef-2 (mef-2) gene, complete cds.	1.1	259519	(S48091) NSM [tomato spotted wilt virus TSWV, Peptide, 302 aa] [Tomato spotted wilt virus]	4.1
3610	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.35	3399767	(U76298) uclacyanin I [Arabidopsis thaliana] >gi|3831466	0.35
3611	AF000590	Homo sapiens chromosome 21q11-q21 genomic clone SA-292	7e-026	<NONE>	<NONE>	<NONE>
3612	U64195	HIV-1 isolate ZP36 from Australia, reverse transcriptase (pol) gene, partial cds.	1.2	<NONE>	<NONE>	<NONE>
3613	AB015331	Homo sapiens HRIHFB2017 mRNA, partial cds	1e-094	3970852	(AB015331) HRIHFB2017 [Homo sapiens]	0.0001
3614	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3615	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	1e-009	1743885	(U79716) Human Reelin [Homo sapiens]	9.5
3616	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	3e-006	<NONE>	<NONE>	<NONE>
3617	<NONE>	<NONE>	<NONE>	2338034	(AF005370) putative immediate early protein [Alcelaphine herpesvirus 1]	2e-008
3618	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	0.006	2707286	(AF036316) cyclin [Prorocentrum minimum]	1.2
3619	X79810	R.norvegicus CYP2C13 gene	0.049	2916892	(AL022004) PE_PGRS [Mycobacterium tuberculosis]	1
3620	AJ224516	Gallus gallus IL-2 gene	1.4	<NONE>	<NONE>	<NONE>
3621	Z79044	H.sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA21C9	0.42	<NONE>	<NONE>	<NONE>
3622	U39357	Ovis aries beta actin mRNA, complete cds	2e-024	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	1.3
3623	U39357	Ovis aries beta actin mRNA, complete cds	1e-043	940346	(U20963) ORF1; late mRNA [Suid herpesvirus 1]	5.6
3624	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	3e-008	2702361	(AF036706) No definition line found [Caenorhabditis elegans]	0.22
3625	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	0.041	244874	Glvr-1 product [mice, Peptide, 681 aa]	1.9

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3626	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	0.002	<NONE>	<NONE>	<NONE>
3627	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	0.002	1730141	FRAGILE X MENTAL RETARDATION SYNDROME RELATED PROTEIN 2 >gi|2135129|pir||S 60173 fragile X mental retardation syndrome related protein - human >gi|1098637 (U31501) fragile X mental retardation syndrome related protein [Homo sapiens]	9.4
3628	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	8e-008	<NONE>	<NONE>	<NONE>
3629	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	6e-006	<NONE>	<NONE>	<NONE>
3630	D87671	Rat mRNA for TIP120, complete cds	0	1799570	(D87671) TIP120 [Rattus norvegicus]	e-112
3631	D87671	Rat mRNA for TIP120, complete cds	0	1799570	(D87671) TIP120 [Rattus norvegicus]	e-110
3632	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3633	D88349	Chicken mRNA for tyrosinase, complete cds	0.12	2144081	luteinizing hormone/chorionic gonadotropin receptor - rat >gi|252167|bbs|109910 (S40803) luteinizing hormone/chorionic gonadotropin receptor, LH/CG receptor {alternatively spliced, clone rLHR1834}	9.3
3634	X17206	Human mRNA for LLRep3	3e-025	2920827	(U92697) ribosomal protein S2 [Rattus norvegicus]	0.0003
3635	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	4e-011	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	3.3
3636	X69878	H.sapiens Flt4 mRNA for transmembrane tyrosine kinase	2e-088	<NONE>	<NONE>	<NONE>
3637	X69878	H.sapiens Flt4 mRNA for transmembrane tyrosine kinase	2e-088	<NONE>	<NONE>	<NONE>
3638	X15509	Human gene for thymidine kinase, 5' region (EC 2.7.1.21)	4e-011	<NONE>	<NONE>	<NONE>
3639	U89744	Rattus norvegicus putative cell surface antigen mRNA, complete cds	0.39	1085432	mucin (clone PGM-2A) - pig	0.0006
3640	L29252	Human (clone D13-2) L-iditol-2 dehydrogenase gene, exon 4, exon 5, exon 6 and exon 7.	3e-006	83981	NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4 - Sauroleishmania tarentolae mitochondrion	2.4

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3641	Z35286	H.sapiens MDR3 gene, exon1, exon2	0.016	<NONE>	<NONE>	<NONE>
3642	M11373	Simian T-cell leukemia virus, pol-env-pX-3' LTR region.	0.39	2773324	(AF040381) carbonic anhydrase [Erwinia carotovora]	5.9
3643	M11373	Simian T-cell leukemia virus, pol-env-pX-3' LTR region.	0.39	2773324	(AF040381) carbonic anhydrase [Erwinia carotovora]	5.9
3644	Z11763	O.granulifera gene for alpha-tubulin	0.39	2138321	(U89012) dentin matrix acidic phosphoprotein 1 [Homo sapiens]	2.6
3645	<NONE>	<NONE>	<NONE>	1352944	HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR YJR151c - yeast (Saccharomyces cerevisiae) >gi|1015903	3.9
3646	U18351	Drosophila melanogaster insulin receptor gene, complete cds	0.005	1468983	(U64830) protein tyrosine kinase [Dictyostelium discoideum]	4e-012
3647	M28458	Human growth hormone receptor gene, exon 2.	1.2	2648877	(AE000987) A. fulgidus predicted coding region AF1681	8.1

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3648	AF069139	HIV-1 isolate DH12 clone 5 from the USA, vpr protein (vpr) gene, partial cds; tat protein (tat) and rev protein (rev) genes, complete cds; vpu pseudogene, complete sequence; envelope glycoprotein (env) and nef protein (n...	0.13	<NONE>	<NONE>	<NONE>
3649	U42627	Rattus norvegicus tyrosine phosphatase mRNA, complete cds.	0.41	1070602	collagen alpha 1(II) chain precursor - human	0.55
3650	Y12851	Homo sapiens P2X7 gene, exon 1 and joined CDS	0.005	<NONE>	<NONE>	<NONE>
3651	U39706	Mycoplasma genitalium section 28 of 51 of the complete genome	0.39	465542	HYPOTHETICAL 20.0 KD PROTEIN IN TRNP 5'REGION (ORF160) >gi|625956|pir||S38599 hypothetical protein 160 (rpl20 5' region) - euglenid (Astasia longa) plastid	2
3652	Z80361	H.sapiens HLA-DRB pseudogene, repeat region;	2e-048	<NONE>	<NONE>	<NONE>
3653	U12171	Oryza sativa IR54 anther specific (RTS2) gene, complete cds.	3.5	<NONE>	<NONE>	<NONE>
3654	AG001163	Homo sapiens genomic DNA, 21q region, clone: Q94A10X26	5e-014	728831	!!!! ALU SUBFAMILY J WARNING ENTRY	0.004
3655	X04780	Human tRNA-Tyr-pseudogene (clone pHtT2)	4.6	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3656	AF086264	Homo sapiens full length insert cDNA clone ZD43A10	0.002	<NONE>	<NONE>	<NONE>
3657	AB011118	Homo sapiens mRNA for KIAA0546 protein, partial cds	0.002	1588661	tryptase [Bos taurus]	1.3
3658	Z46379	Homo sapiens mRNA for anti-Sm antibody VH chain	0.13	<NONE>	<NONE>	<NONE>
3659	Y12930	H.rustica CHD-W gene, intron	0.39	3861232	(AJ235272) PROBABLE TRANSPORT ATP-BINDING PROTEIN MSBA (msbA2) [Rickettsia prowazekii]	1.2
3660	AF093267	Rattus norvegicus homer-1b mRNA, complete cds	0.005	<NONE>	<NONE>	<NONE>
3661	M34057	Human transforming growth factor-beta 1 binding protein mRNA, complete cds.	0.043	<NONE>	<NONE>	<NONE>
3662	X75418	H.sapiens TCR V Beta 13.2 gene (allele a).	0.4	<NONE>	<NONE>	<NONE>
3663	Z68758	Human DNA sequence from cosmid cN85E10 on chromosome 22q11.2-qter	2e-025	3399771	(AF041839) Smad6 [Xenopus laevis]	0.39
3664	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	2e-005	2078282	(U95760) Sno [Drosophila melanogaster]	0.0006
3665	Z75032	S.cerevisiae chromosome XV reading frame ORF YOR124c	0.14	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3666	U28831	Human protein immuno-reactive with anti-PTH polyclonal antibodies mRNA, partial cds. > :: gb|I40055|I40055 Sequence 1 from patent US 5618695	0	896065	(U28831) protein that is immuno-reactive with anti-PTH polyclonal antibodies [Homo sapiens]	e-100
3667	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	0.04	<NONE>	<NONE>	<NONE>
3668	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
3669	Z96359	H.sapiens telomeric DNA sequence, clone 17QTEL013, read 17QTELOO013.seq	7e-006	2921609	(AF039037) 980219 -this used to be part of R02C2.4 but was split into two genes based on protein similarities	7.7
3670	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	8e-008	3342730	(AC005331) R31341_1 [Homo sapiens]	2e-019
3671	U22460	Ictalurus punctatus heat shock protein 70 (CF Hsp70) mRNA, complete cds.	1.2	2143951	Ras-related protein - rat >gi|498257	5e-009
3672	Y12259	R.norvegicus mRNA for Kir3.1 protein	0.005	135213	TYPE IIS RESTRICTION ENZYME ECO57I METHYLTRANSFERASE ACTIVITY >gi|281976|pir||S26426 type II site-specific deoxyribonuclease (EC 3.1.21.4) Eco57I endonuclease	9.9

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					[Escherichia coli]	
3673	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	8e-008	3006154	(AL022299) putative cytochrome c1, heme protein precursor [Schizosaccharomyces pombe]	4.5
3674	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	6e-006	3915503	HYPOTHETICAL OXIDOREDUCTASE IN CHEV-MOBA INTERGENIC REGION >gi|2632227|gnl|PID|e1181911 1-dehydrogenase [Bacillus subtilis]	2e-021
3675	U71363	Human zinc finger protein zfp6 (ZF6) mRNA, partial cds	3e-070	2689441	(AC003682) F18547_1 [Homo sapiens]	4e-029
3676	AF042275	Oryza sativa anther-specific protein gene, complete cds	0.39	<NONE>	<NONE>	<NONE>
3677	M34601	P.berghei telomeric repeat region subfragment alpha DNA.	0.13	<NONE>	<NONE>	<NONE>
3678	U09368	Human zinc finger protein ZNF140	6e-047	3445181	(AC005498) R31665_2 [Homo sapiens]	4e-027
3679	D90345	Rat t complex polypeptide 1 (Tcp-1) mRNA	0.13	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3680	AE000758	Aquifex aeolicus section 90 of 109 of the complete genome	0.38	134134	RYANODINE RECEPTOR, SKELETAL MUSCLE muscle - rabbit >gi|1710 (X15750) ryanodine receptor (AA 1-5037) [Oryctolagus cuniculus] >gi|1714 (X15209) ryanodine receptor [Oryctolagus cuniculus]	9.8
3681	X60280	Vector plasmid pLTRpoly DNA	3e-040	2981631	(AB012223) ORF2 [Canis familiaris]	0.87
3682	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	3e-010	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	5.8
3683	L81683	Homo sapiens (subclone 1_d11 from P1 H54) DNA sequence	3e-019	113668	!!!! ALU CLASS C WARNING ENTRY !!!!	2
3684	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	1e-012	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	9.7
3685	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	2e-012	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	6.8
3686	X78261	H.sapiens mRNA for TRE17 5' extremity and unnamed adjacent to TRE17, locus tre-1.	3e-010	728836	!!!! ALU SUBFAMILY SP WARNING ENTRY	4.4
3687	AF093204	Gallus gallus clone Ocyal unknown mRNA	1e-011	3694883	(AF093204) unknown [Gallus gallus]	0.097
3688	L35664	Homo sapiens (subclone H8 8_f5 from P1 35 H5 C8) DNA	3e-031	2072966	(U93570) p40 [Homo sapiens]	8e-006

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		sequence.				
3689	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
3690	L10111	Octopus dofleini beta-tubulin mRNA, complete cds.	0.14	<NONE>	<NONE>	<NONE>
3691	S83333	CYP27=sterol 27-hydroxylase/cerebrotendinous xanthomatosis candidate gene {3' region, intron 6 to intron 8} [human, Genomic, 1725 nt, segment 4 of 4]	3.5	<NONE>	<NONE>	<NONE>
3692	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	4e-011	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	5.9
3693	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	9e-009	220578	(D00570) open reading frame (251 AA)	1.1
3694	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	1e-010	416563	INTESTINAL MEMBRANE A4 PROTEIN A4 differentiation-dependent protein [Homo sapiens]	0.021
3695	AB018374	Mus musculus GARP34 mRNA, complete cds	4e-074	3724364	(AB018374) GARP34 [Mus musculus]	2e-017
3696	AB018374	Mus musculus GARP34 mRNA, complete cds	4e-074	3724364	(AB018374) GARP34 [Mus musculus]	2e-017
3697	AB013721	Oryctolagus cuniculus mRNA for mitsugumin 23, complete cds	4e-038	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3698	U33147	Human mammaglobin mRNA, complete cds > :: gb|I65735|I65735 Sequence 1 from patent US 5668267	1.1	1946371	(U93215) regulatory protein Viviparous-1 isolog	2.5
3699	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	0.0006	2132981	probable membrane protein YPL105c - yeast	5.1
3700	U08802	HIV-1 sample 026 clone 06 from Thailand partial cds.	0.47	3880139	(Z68121) Similarity to Yeast nitrogen regulatory protein GLN3 (PIR Acc. No. S22280)	7.3
3701	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	2e-011	<NONE>	<NONE>	<NONE>
3702	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.002	<NONE>	<NONE>	<NONE>
3703	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	1e-011	<NONE>	<NONE>	<NONE>
3704	Z56740	H.sapiens CpG DNA, clone 13b5, reverse read cpg13b5.rt1c	4e-043	2465332	(U92819) unnamed HERV-H protein [Homo sapiens]	0.007
3705	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	1e-008	<NONE>	<NONE>	<NONE>
3706	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	3e-009	1293790	(U56248) Similar to polyketide synthase. [Caenorhabditis briggsae]	2.9

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3707	AF023283	Chikungunya virus S27 3'UTR	0.39	3560261	(AL031535) RNA binding protein	4.5
3708	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	2e-006	<NONE>	<NONE>	<NONE>
3709	AF030944	Brugia malayi microfilarial sheath protein SHP3a	0.12	<NONE>	<NONE>	<NONE>
3710	AE000700	Aquifex aeolicus section 32 of 109 of the complete genome	0.15	<NONE>	<NONE>	<NONE>
3711	AJ001050	Homo sapiens mRNA for thioredoxin reductase	4e-042	1843434	(D88687) KM-102-derived reductase-like factor [Homo sapiens]	3e-038
3712	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	0.002	625090	(U19464) outer arm dynein beta heavy chain [Paramecium tetraurelia] >gi|1588498|prf||2208428A dynein:SUBUNIT =heavy chain [Paramecium tetraurelia]	2.7
3713	AG001414	Homo sapiens genomic DNA, 21q region, clone: 9H11X4	0.46	<NONE>	<NONE>	<NONE>
3714	AB007930	Homo sapiens mRNA for KIAA0461 perotein, partial cds	0	3413884	(AB007930) KIAA0461 perotein [Homo sapiens]	2e-068
3715	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	9e-007	<NONE>	<NONE>	<NONE>
3716	Y09999	H.sapiens CHOP gene, intron 1	2e-007	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3717	AF023461	Homo sapiens FRA3B region sequence	0.13	2501500	ECDYSTEROID UDP-GLUCOSYLTRANSFERASE PRECURSOR >gi|1563727|gnl|PID|e267373 (Y08294) ecdysteroid UDP-glucosyltransferase [Lacanobia oleracea granulovirus]	5.6
3718	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	2e-005	2330794	(Z98601) hypothetical protein	0.004
3719	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	7e-007	1363246	TIF1 protein - mouse >gi|998815|bbs|167126	5e-007
3720	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	6e-006	1314732	(U54640) 185 kDa silk protein [Chironomus pallidivittatus]	0.17
3721	U09933	Human urokinase-type plasminogen receptor, exon 3	5e-025	3523099	(AF016271) Ksp-cadherin [Mus musculus]	7.6
3722	M30187	S.cerevisiae mitochondrion Tyr-tRNA gene.	0.13	218437	(D90352) myo-inositol transporter	7.3
3723	X79703	O.aries gene for beta-casein	0.043	141103	HYPOTHETICAL PROTEIN ORF-1137 mouse	4.5
3724	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	9e-009	2132008	hypothetical protein YOL072w - yeast	9.9
3725	L39210	Homo sapiens inosine monophosphate dehydrogenase type II gene, complete cds	2e-078	2224711	(AB002383) KIAA0385 [Homo sapiens]	2e-018

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3726	U52832	Homo sapiens Cri-du-chat region mRNA, clone CSC3	2e-005	<NONE>	<NONE>	<NONE>
3727	AF015043	Homo sapiens EH-binding protein mRNA, partial cds	e-169	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	3.4
3728	D28485	Human MSMB gene for beta-microseminoprotein (MSP), promoter region and exon1	4e-011	<NONE>	<NONE>	<NONE>
3729	M33027	Human vasoactive intestinal peptide/PHM-27 gene, exons 1-6.	0.043	<NONE>	<NONE>	<NONE>
3730	X15377	Human gene for the light and heavy chains of myeloperoxidase	2e-024	1346141	GLYCEROL KINASE (ATP:GLYCEROL 3-PHOSPHOTRANSFERASE) (GLYCEROKINASE) (GK) Mycoplasma genitalium (SGC3) >gi|3844648 (U39683) glycerol kinase (glpK) [Mycoplasma genitalium]	3e-011
3731	X57103	Human h-lys gene for lysozyme (upstream region)	0.0005	<NONE>	<NONE>	<NONE>
3732	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	3e-010	3319482	(AF077546) No definition line found [Caenorhabditis elegans]	9.8
3733	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	1e-012	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	5.5

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3734	U83857	Human Aac11 (aac11) mRNA, complete cds	2e-027	2623755	(U35846) unknown [Mus musculus]	3e-005
3735	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	1e-013	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	2.5
3736	U09367	Human zinc finger protein ZNF136	1e-065	1731412	ZINC FINGER PROTEIN 136 human >gi|487785 (U09367) zinc finger protein ZNF136	7e-060
3737	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	6e-006	2507475	PAIRED AMPHIPATHIC HELIX PROTEIN	5.8
3738	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.002	3702452	(X80031) type IV collagen alpha 3 chain	1.5
3739	AF086022	Homo sapiens full length insert cDNA clone YW23E02	3.5	<NONE>	<NONE>	<NONE>
3740	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.0002	2960225	(AL022120) PPE [Mycobacterium tuberculosis]	7.4
3741	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	2e-006	<NONE>	<NONE>	<NONE>
3742	AJ005866	Homo sapiens mRNA for putative Sqv-7-like protein, partial	e-177	4008517	(AJ005866) Sqv-7-like protein [Homo sapiens]	9e-045

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3743	AF043231	Emericella nidulans cAMP-dependent protein kinase regulatory subunit (pkaR) gene, complete cds	1.1	<NONE>	<NONE>	<NONE>
3744	AB002319	Human mRNA for KIAA0321 gene, partial cds	5e-066	2224583	(AB002319) KIAA0321 [Homo sapiens]	2e-024
3745	M33132	Human proliferating cell nucleolar protein P120 gene, exons 1-15.	8e-018	113668	!!!! ALU CLASS C WARNING ENTRY !!!!	0.077
3746	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	9e-009	2394463	(AF024498) No definition line found [Caenorhabditis elegans]	1.2
3747	Z69944	S.pombe chromosome I cosmid c1F12.	4.4	<NONE>	<NONE>	<NONE>
3748	Z81014	Human DNA sequence from cosmid U65A4, between markers DXS366 and DXS87 on chromosome X *	4e-022	896065	(U28831) protein that is immuno-reactive with anti-PTH polyclonal antibodies [Homo sapiens]	0.075
3749	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.0002	3877203	(Z70780) similar to initiation factor IF-2; cDNA EST CEMSD25F comes from this gene	4.4
3750	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	2e-007	<NONE>	<NONE>	<NONE>
3751	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	3e-008	2065210	(Y12713) Pro-Pol-dUTPase polyprotein	2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3752	M36072	Human ribosomal protein L7a (surf 3) large subunit mRNA, complete cds.	1e-054	133014	60S RIBOSOMAL PROTEIN L7A (PLA-X POLYPEPTIDE) (SURF-3) >gi|71116|pir||R5HU7A ribosomal protein L7a - human >gi|71117|pir||R5RT7A ribosomal protein L7a - rat >gi|34203 (X52138) L7a protein [Homo sapiens] >gi|35512 (X06705) PLA-X polypeptide [Homo sapiens]	0.019
3753	AB001615	Homo sapiens DNA for cGMP-binding cGMP-specific phosphodiesterase (PDE5), exon 1	6e-006	<NONE>	<NONE>	<NONE>
3754	X57103	Human h-lys gene for lysozyme (upstream region)	5e-015	113670	!!!! ALU CLASS E WARNING ENTRY !!!!	3.3
3755	L09708	Homo sapiens complement component 2 (C2) gene allele b, exons 10 through 18 and complete cds	6e-005	1143705	(X89760) Hox2a gene product [Zea mays]	9.7
3756	X73685	C.aethiops hsp70 mRNA	2e-088	1322309	(U55176) heat shock cognate 70.II [Xenopus laevis]	2e-025
3757	Z57594	H.sapiens CpG DNA, clone 186c5, reverse read cpg186c5.rt1b .	0.002	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3758	AF095927	Rattus norvegicus protein phosphatase 2C mRNA, complete cds	e-117	3777604	(AF095927) protein phosphatase 2C [Rattus norvegicus]	4e-040
3759	U30788	Rattus norvegicus Tclone4 mRNA	5e-024	135576	LARGE TEGUMENT PROTEIN (VIRION PROTEIN UL36) >gi|73851|pir||WMBEH6 UL36 protein - human herpesvirus 1 (strain 17) >gi|59536|gnl|PID|e312351 1]	1.6
3760	Z96177	H.sapiens telomeric DNA sequence, clone 10QTEL040, read 10QTELOO040.seq	3e-009	1082626	myosin heavy chain VA - human (fragment)	5.8
3761	M37463	E.gracilis chloroplast ribosomal protein genes rpl23, rpl2, rps19, rpl22, and rps3, complete cds.	0.38	2734883	(U75311) pyruvate decarboxylase 2 [Pichia stipitis]	3.4
3762	AF086241	Homo sapiens full length insert cDNA clone ZD29F04	4e-064	3702137	(AL031393) dJ733D15.1 (Zinc-finger protein) [Homo sapiens]	1e-040
3763	AF086241	Homo sapiens full length insert cDNA clone ZD29F04	4e-064	3702137	(AL031393) dJ733D15.1 (Zinc-finger protein) [Homo sapiens]	1e-040
3764	AF008227	Drosophila melanogaster odd Oz product (odz) gene, exons 3, 4, 5, 6, 7, and complete cds	3.6	2661842	(Y15732) DNA polymerase beta [Xenopus laevis]	2e-020
3765	AF039688	Homo sapiens antigen NY-CO-3 (NY-CO-3) mRNA, partial cds	0	3170176	(AF039688) antigen NY-CO-3 [Homo sapiens]	2e-073

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3766	AF037332	Homo sapiens Eph-like receptor tyrosine kinase hEphB1b (EphB1) mRNA, complete cds	0.37	1255919	(X96511) MAFB protein [Coturnix japonica]	5.6
3767	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	6e-006	<NONE>	<NONE>	<NONE>
3768	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.005	<NONE>	<NONE>	<NONE>
3769	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	3e-010	<NONE>	<NONE>	<NONE>
3770	X57103	Human h-lys gene for lysozyme (upstream region)	5e-015	113670	!!!! ALU CLASS E WARNING ENTRY !!!!	3.3
3771	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.0002	2947096	(U81032) TniQ [Pseudomonas stutzeri]	0.86
3772	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.0002	2947096	(U81032) TniQ [Pseudomonas stutzeri]	0.86
3773	M84326	Human ADP-ribosylation factor 1 mRNA, complete cds	0	283748	collagen alpha 2(I) chain homolog - sea urchin (Strongylocentrotus purpuratus) >gi|161436 purpuratus]	0.14
3774	X82575	G.gallus mRNA for Cnot	0.39	3327136	(AB014561) KIAA0661 protein [Homo sapiens]	3e-033

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3775	L43001	Bos taurus guanylyl cyclase-activating protein 2	3e-072	1730238	GUANYLATE CYCLASE ACTIVATING PROTEIN 2 (GCAP 2) (RETINAL GUANYLYL CYCLASE ACTIVATOR PROTEIN P24) >gi|2136762|pir||A 57604 guanylate cyclase-activating protein 2 - bovine >gi|1002750 cyclase-activating protein 2 [Bos taurus]	1e-030
3776	U47322	Cloning vector DNA, complete sequence.	7e-007	3335349	(AC004512) Similar to gb|U46691 putative chromatin structure regulator (SUPT6H) from Homo sapiens. ESTs gb|T42908, gb|AA586170 and gb|AA395125 come from this gene. [Arabidopsis thaliana]	9.2
3777	L09647	Rattus norvegicus hepatocyte nuclear factor 3a	2e-069	404764	(L10409) fork head related protein [Mus musculus]	3e-031
3778	U72756	Lycianthes heteroclita NADH dehydrogenase subunit protein, partial cds	0.37	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3779	M94314	Homo sapiens ribosomal protein L30 mRNA, complete cds	1e-073	3876073	(Z81505) similar to Zinc finger, C3HC4 type (RING finger); cDNA EST EMBL:D28025 comes from this gene; cDNA EST EMBL:D28024 comes from this gene; cDNA EST EMBL:D33210 comes from this gene; cDNA EST EMBL:D33441 comes from this...	1.4
3780	AF053315	Reporter vector pNFkB-Luc, complete sequence	9e-019	987050	(X65335) lacZ gene product [unidentified cloning vector]	0.3
3781	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	4e-011	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	4.5
3782	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	1e-013	1695957	(U78693) NADH dehydrogenase [Holmskioldia sanguinea]	1.9
3783	AF074990	Homo sapiens full length insert cDNA YH85A11	0.005	1881709	(U89517) polyprotein [Dengue virus type 2]	9.6
3784	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	9e-009	<NONE>	<NONE>	<NONE>
3785	AF020038	Homo sapiens NADP-dependent isocitrate dehydrogenase (IDH) mRNA, complete cds	4e-011	3647352	(Z97348) MAL3P1.11 [Plasmodium falciparum]	9.6

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3786	Z75199	S.cerevisiae chromosome XV reading frame ORF YOR291w	8e-028	3880560	(Z70271) Similarity to Yeast E1-E2 ATPase (SW:YED1_YEAST); cDNA EST EMBL:D37634 comes from this gene; cDNA EST EMBL:D34653 comes from this gene; cDNA EST EMBL:D34527 comes from this gene; cDNA EST EMBL:D32311 comes from this...	7e-048
3787	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	3e-008	<NONE>	<NONE>	<NONE>
3788	M86400	Human phospholipase A2 mRNA, complete cds. > :: gb|I34404|I34404 Sequence 8 from patent US 5597719	5e-088	<NONE>	<NONE>	<NONE>
3789	X03100	Human HLA-SB(DP) alpha gene	0.47	3941737	(AF109719) BAT2 [Mus musculus]	2.4
3790	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	5e-015	3043662	(AB011141) KIAA0569 protein [Homo sapiens]	9.6
3791	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	2e-014	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	0.29
3792	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	4e-012	345555	Ig light chain - rainbow trout (fragment)	1.1

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3793	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	5e-014	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	5.6
3794	AF064104	Homo sapiens Cdc14B1 phosphatase mRNA, complete cds	3e-030	2662463	(AF023158) tyrosine phosphatase [Homo sapiens]	1e-008
3795	U29348	Salmonella enterica strain s2978 invasion protein SpaO (spaO), SpaP (spaP) and SpaQ (spaQ) genes, complete cds	0.0005	2291118	(AF016414) No definition line found [Caenorhabditis elegans]	9.6
3796	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	6e-016	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	5.6
3797	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	3e-010	1168719	C6.1A PROTEIN	0.004
3798	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	2e-006	481236	hypothetical protein - Madagascar periwinkle roseus]	3.4
3799	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	3e-008	423157	finger protein ZNF33A - human (fragment)	4.3
3800	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	4e-012	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	5.5
3801	U61950	Caenorhabditis elegans cosmid C45E5	1.2	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3802	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	3e-008	1703028	CLATHRIN COAT ASSEMBLY PROTEIN AP47 HOMOLOG 2 (CLATHRIN COAT ASSOCIATED PROTEIN AP47 HOMOLOG 2) (GOLGI ADAPTOR AP-1 47 KD PROTEIN HOMOLOG 2) (HA1 47 KD SUBUNIT HOMOLOG 2) (CLATHRIN ASSEMBLY PROTEIN ASSEMBLY PROTEIN COMPL... >gi|2134919|pir||A 57170 clathri	9.6
3803	M31651	Homo sapiens sex hormone-binding globulin (SHBG) gene, complete cds	7e-017	<NONE>	<NONE>	<NONE>
3804	D00596	Homo sapiens gene for thymidylate synthase, exons 1, 2, 3, 4, 5, 6, 7, complete cds	6e-038	<NONE>	<NONE>	<NONE>
3805	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	3e-010	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	3.7
3806	D45906	Human mRNA for LIMK-2, complete cds	4e-096	<NONE>	<NONE>	<NONE>
3807	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	2e-006	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3808	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.004	<NONE>	<NONE>	<NONE>
3809	AF045798	Xenopus laevis gremlin mRNA, complete cds	0.36	3551167	(AB012131) Ich1 [Coprinus cinereus]	4.1
3810	D78275	Human mRNA for proteasome subunit p42, complete cds	8e-019	1709804	26S PROTEASE REGULATORY SUBUNIT S10B (P44) (CONSERVED ATPASE DOMAIN PROTEIN 44) 26S proteasome regulatory subunit [Homo sapiens]	0.001
3811	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	4e-009	<NONE>	<NONE>	<NONE>
3812	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	3e-009	<NONE>	<NONE>	<NONE>
3813	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	9e-014	3193162	(AF067618) No definition line found [Caenorhabditis elegans]	1e-027
3814	AF085858	Homo sapiens full length insert cDNA clone YN49B07	1e-017	3329465	(AF064553) NSD1 protein [Mus musculus]	4e-007
3815	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	3e-005	<NONE>	<NONE>	<NONE>
3816	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	0.0003	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3817	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	1e-006	<NONE>	<NONE>	<NONE>
3818	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	2	<NONE>	<NONE>	<NONE>
3819	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	4e-006	416673	ATP SYNTHASE A CHAIN (PROTEIN 6) 3.6.1.34) protein 6 - liverwort (Marchantia polymorpha) mitochondrion >gi|786191 (M68929) atp6 [Marchantia polymorpha]	1.3
3820	L14684	Rattus norvegicus nuclear-encoded mitochondrial elongation factor G mRNA, complete cds.	e-115	585084	ELONGATION FACTOR G, MITOCHONDRIAL PRECURSOR (MEF-G) >gi|543383|pir||S40780 translation elongation factor G, mitochondrial - rat >gi|310102	5e-038
3821	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	2e-012	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	2.2
3822	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	7e-012	1665789	(D87450) Similar to D.melanogaster parallel sister chromatids protein [Homo sapiens]	8.5
3823	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	2e-009	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3824	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	3e-015	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	2.2
3825	L48489	Homo sapiens N-acetylglucosaminyltransferase III	1e-038	728831	!!!! ALU SUBFAMILY J WARNING ENTRY	1e-008
3826	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	8e-008	<NONE>	<NONE>	<NONE>
3827	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	1e-014	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	2.9
3828	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	1e-011	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	1.4
3829	AB012162	Homo sapiens mRNA for APC 2 protein, complete cds	1e-017	3894265	(AB012162) APC 2 protein [Homo sapiens]	0.45
3830	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	6e-010	1723680	HYPOTHETICAL 14.1 KD PROTEIN IN UPF3-SMD1 INTERGENIC REGION >gi|2132599|pir||S64368 probable membrane protein YGR073c - yeast (Saccharomyces cerevisiae) >gi|1323101|gnl|PID|e243468 (Z72858) ORF YGR073c [Saccharomyces cerevisiae]	1.3

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3831	S54914	bup=5'of bmi-1 proviral insertion locus [mice, Genomic/mRNA, 2022 nt]	e-140	265569	(S54914) bup=5'of bmi-1 proviral insertion locus [mice, Peptide, 195 aa] [Mus sp.]	2e-059
3832	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	2e-009	<NONE>	<NONE>	<NONE>
3833	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	2e-012	<NONE>	<NONE>	<NONE>
3834	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	1e-015	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	2.9
3835	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	4e-007	1805270	(U81983) endothelial PAS domain protein 1 [Mus musculus]	6.6
3836	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
3837	X92814	H.sapiens mRNA for rat HREV107-like protein	1e-032	1709969	H-REV 107 PROTEIN	3e-013
3838	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	1e-011	2183251	(AF002227) putative polyprotein [border disease virus strain C413]	0.015
3839	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	1e-009	1142660	(U23502) POM1 [Plasmodium chabaudi chabaudi]	7.3
3840	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	4e-012	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	3.3
3841	U47322	Cloning vector DNA, complete sequence.	2e-058	224398	ORF [Simian virus 40]	4e-005

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3842	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	2e-012	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	2.9
3843	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	1e-011	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	3.3
3844	Y15059	Homo sapiens hng/RC3 gene, exons 2,3 & 4	0.053	<NONE>	<NONE>	<NONE>
3845	X99330	R.norvegicus mRNA for IP63 protein	2e-027	<NONE>	<NONE>	<NONE>
3846	AF100303	Caenorhabditis elegans cosmid Y7G10A	0.53	<NONE>	<NONE>	<NONE>
3847	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
3848	AF040094	Mus musculus inositol polyphosphate 5-phosphatase II (INPP5P) mRNA, complete cds	0.15	<NONE>	<NONE>	<NONE>
3849	Y15724	Homo sapiens SERCA3 gene, exons 1-7 (and joined CDS)	2e-013	<NONE>	<NONE>	<NONE>
3850	AB011144	Homo sapiens mRNA for KIAA0572 protein, partial cds	0	3043668	(AB011144) KIAA0572 protein [Homo sapiens]	1e-080
3851	AF020762	Homo sapiens clone 1400 unknown protein mRNA, partial cds	0	2738927	(AF020762) unknown protein [Homo sapiens]	2.8
3852	Z99706	Human DNA sequence from cosmid U226D1 on chromosome X. Contains STS, complete sequence [Homo sapiens]	0.0002	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3853	M73700	Human neutrophil lactoferrin mRNA, complete cds and 5' promoter region.	0.0002	<NONE>	<NONE>	<NONE>
3854	D31793	Human CD40 ligand (CD40L) gene, 5' flanking region and exon 1	0.046	<NONE>	<NONE>	<NONE>
3855	U16300	Human lysyl hydroxylase (PLOD) gene, intron 9, complete sequence.	0.0002	126363	LAMININ ALPHA-1 CHAIN PRECURSOR precursor - human	0.18
3856	U61241	Homo sapiens p47-phox pseudogene, clone P41, exon 1	0.14	<NONE>	<NONE>	<NONE>
3857	D37791	Mouse mRNA for beta-1,4-galactosyltransferase	e-105	3880102	(Z93390) similar to FYVE zinc finger; cDNA EST yk265b4.5 comes from this gene; cDNA EST yk359g9.5 comes from this gene; cDNA EST yk319c2.5 comes from this gene [Caenorhabditis elegans] zinc finger; cDNA EST yk265b4.5 comes from this gene; cDNA EST yk359g9	3e-021
3858	Z57667	H.sapiens CpG DNA, clone 18a8, reverse read cpg18a8.rt1b .	1.2	<NONE>	<NONE>	<NONE>
3859	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	2e-014	2879809	(AJ223320) trp-like protein [Loligo forbesi]	1.5

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3860	U22296	Rattus norvegicus casein kinase 1 gamma 1 isoform mRNA, complete cds	e-126	3024053	CASEIN KINASE I, GAMMA 1 ISOFORM kinase 1 gamma 1 isoform [Rattus norvegicus]	1e-061
3861	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	5e-014	113669	!!!! ALU CLASS D WARNING ENTRY !!!!	2.6
3862	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	3e-009	<NONE>	<NONE>	<NONE>
3864	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	1e-010	<NONE>	<NONE>	<NONE>
3865	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	1e-011	3182957	CGMP-INHIBITED 3',5'-CYCLIC PHOSPHODIESTERASE B (CYCLIC GMP INHIBITED PHOSPHODIESTERASE B) (CGI-PDE B) (CGIPDE1) phophodiesterase - human >gi|1145302 (U38178) cyclic nucleotide phophodiesterase [Homo sapiens] 3B [Homo sapiens]	4.4
3866	AF099004	Caenorhabditis elegans cosmid C07D2	0.2	<NONE>	<NONE>	<NONE>
3867	Z23091	H.sapiens GPV gene encoding platelet glycoprotein V precursor	5e-013	728836	!!!! ALU SUBFAMILY SP WARNING ENTRY	0.82

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3868	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	3e-007	2291255	(AF016430) weak similarity to Bacillus subtillis spore coat protein precursor (GB:L42066) and Dictyostelium discoideum calcium binding protein (NID:g426313) in proline-rich regions [Caenorhabditis elegans]	8.4
3869	U58739	Caenorhabditis elegans cosmid F28C10.	0.33	<NONE>	<NONE>	<NONE>
3870	L48473	Homo sapiens (subclone 7_e11 from P1 H16) DNA sequence.	3e-008	<NONE>	<NONE>	<NONE>
3871	U95097	Xenopus laevis mitotic phosphoprotein 43 mRNA, partial cds	0.015	<NONE>	<NONE>	<NONE>
3872	Z73360	Human DNA sequence from cosmid 92M18, BRCA2 gene region chromosome 13q12-13.	4e-020	<NONE>	<NONE>	<NONE>
3873	Z71572	O.aries DNA for immunoglobulin joining regions	1.2	1699130	(U80027) weak similarity to Arabadopsis thaliana phytochrome E (PIR:S41912) [Caenorhabditis elegans]	6.1
3874	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	6e-010	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	1.7

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3875	AB018263	Homo sapiens mRNA for KIAA0720 protein, partial cds	1.2	107240	oncogene 1 (tre-2 locus) (clone 210) - human	0.049
3876	U87998	Mus musculus cyclin G1 gene, partial cds	0.14	<NONE>	<NONE>	<NONE>
3877	AE001408	Plasmodium falciparum chromosome 2, section 45 of 73 of the complete sequence	1.8	<NONE>	<NONE>	<NONE>
3878	AF061244	Agrocybe aegerita B type DNA polymerase (Mtpol) gene, complete cds; tRNA-Asn gene, complete sequence; and unknown genes, mitochondrial genes for mitochondrial products	0.16	3153241	(AF053004) class I cytokine receptor [Homo sapiens]	5.8
3879	M73047	Homo sapiens tripeptidyl peptidase II mRNA, complete cds.	3e-028	136107	TRIPEPTIDYL-PEPTIDASE II (TPP II) tripeptidyl-peptidase II (EC 3.4.14.10) - human sapiens]	0.35
3880	AB011393	Suncus murinus mitochondrial DNA, D-loop region, partial sequence, isolate TKU-M205	0.17	107422	proline-rich protein PRB3S (cys) - human	0.4
3881	X69951	H.sapiens gene for casein kinase II alpha subunit > subunit alpha [human, Genomic, 18862 nt]	1e-008	113668	!!!! ALU CLASS C WARNING ENTRY !!!!	0.54

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3882	U54558	Human translation initiation factor eIF3 p66 subunit mRNA, complete cds	3e-018	<NONE>	<NONE>	<NONE>
3883	AB012259	Homo sapiens DNA, anonymous heat-stable fragment RP12-8	5e-012	<NONE>	<NONE>	<NONE>
3884	U44130	Xenopus laevis p58 mRNA, partial cds	0.15	3873716	(Z74026) similar to 1-aminocyclopropane-1-carboxylate synthase; cDNA EST EMBL:D34239 comes from this gene; cDNA EST EMBL:D35575 comes from this gene; cDNA EST EMBL:D64242 comes from this gene; cDNA EST EMBL:D67126 comes from... 1-aminocyclopropane-1-carbo	5.3
3885	AB007917	Homo sapiens mRNA for KIAA0448 protein, complete cds	0.006	<NONE>	<NONE>	<NONE>
3886	AJ223824	Lycopersicon esculentum cv Red River unknown sequence PCR random amplified RAPD band 9	0.045	<NONE>	<NONE>	<NONE>
3887	U47322	Cloning vector DNA, complete sequence.	3e-008	2183251	(AF002227) putative polyprotein [border disease virus strain C413]	0.67

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3888	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	4e-006	<NONE>	<NONE>	<NONE>
3889	U67564	Methanococcus jannaschii section 106 of 150 of the complete genome	1.3	2920535	(AF018081) type XVIII collagen [Homo sapiens]	0.73
3890	AE000720	Aquifex aeolicus section 52 of 109 of the complete genome	1.3	<NONE>	<NONE>	<NONE>
3891	AB011230	Zaglossus bruijni mitochondrial gene for NADH dehydrogenase subunit 1, partial cds	3.6	<NONE>	<NONE>	<NONE>
3892	Z96177	H.sapiens telomeric DNA sequence, clone 10QTEL040, read 10QTELOO040.seq	1e-042	987050	(X65335) lacZ gene product [unidentified cloning vector]	0.0001
3893	AF067646	Cloning vector pCMV-scriptEX, complete sequence	3e-029	987050	(X65335) lacZ gene product [unidentified cloning vector]	0.001
3894	Z69919	Human DNA sequence from cosmid 91K3, Huntington's Disease Region, chromosome 4p16.3 contains CpG island.	3.8	<NONE>	<NONE>	<NONE>
3895	X75757	G.gallus cycB3 mRNA.	6e-036	729112	G2/MITOTIC-SPECIFIC CYCLIN B3	4e-013
3896	L27833	Bos taurus pregnancy-associated glycoprotein-1	0.48	854348	(X87336) DNA endonuclease [Peperomia polybotrya]	7.5

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3897	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.14	3169059	(AL023704) weak similarity to B.subtilis spore outgrowth factor B [Schizosaccharomyces pombe]	5e-052
3898	X64123	H.sapiens PVR gene for poliovirus receptor (exon 8)	7e-006	2444416	(AF020484) NADH dehydrogenase-like protein [Gleditsia fera]	0.55
3899	Z81043	Caenorhabditis elegans cosmid C29F3, complete sequence [Caenorhabditis elegans]	0.44	266459	P-SELECTIN PRECURSOR (GRANULE MEMBRANE PROTEIN 140) (GMP-140) (PADGEM) (CD62P) mouse >gi|200553 (M87861) P-selectin [Mus musculus]	1.8
3900	AJ001235	Papio hamadryas ERV-9 like LTR insertion	3e-050	3126961	(AF061747) cell division protein FtsZ homolog	1.2
3901	AE001314	Chlamydia trachomatis section 41 of 87 of the complete genome	1.2	<NONE>	<NONE>	<NONE>
3902	X82895	H.sapiens mRNA for DLG2	2e-048	3659505	(AC005084) similar to mouse mCASK-A; similar to e1288039	1e-054
3903	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	2e-006	<NONE>	<NONE>	<NONE>
3904	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	9e-009	436923	(U01849) ORF1 [Trypanosoma brucei]	0.08

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3905	D88982	Clostridium botulinum DNA for C2 toxin component-I and component-II, complete cds	0.38	1082769	RNA helicase A - human	5.6
3906	D50418	Mouse mRNA for AREC3, partial cds	1e-041	2137398	homeotic protein AREC3 (clone SM) - mouse	0.044
3907	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	6e-005	<NONE>	<NONE>	<NONE>
3908	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	2e-007	2314677	(AE000648) cation-transporting ATPase, P-type (copA)	0.36
3909	U72745	Dictyostelium discoideum cysteine proteinase	0.014	<NONE>	<NONE>	<NONE>
3910	AJ011972	Homo sapiens mRNA for histone deacetylase-like protein (JM21)	3e-081	<NONE>	<NONE>	<NONE>
3911	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	3e-011	<NONE>	<NONE>	<NONE>
3912	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.002	<NONE>	<NONE>	<NONE>
3913	AC001032	Homo sapiens (subclone 2_c11 from P1 H48) DNA sequence	9e-009	130402	RETROVIRUS-RELATED POL POLYPROTEIN	3.2
3914	J04830	S.cerevisiae CBP3 protein gene, complete cds.	3.3	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3915	D78572	House mouse; Musculus domesticus mRNA for membrane glycoprotein, complete cds > :: dbj|E12950|E12950 cDNA GA3-43 encoding novel polypeptide which appear when differentiate from embryo-tumor cell P19 to nerve cell	4e-044	1545807	(D78572) membrane glycoprotein [Mus musculus]	1e-020
3916	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	1e-012	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	1.1
3917	U29923	Human AMP deaminase (AMPD3) gene, intron 1a and promoter 1b.	0.04	3256504	(AP000001) 115aa long hypothetical protein [Pyrococcus horikoshii]	0.094
3918	Z68327	Human DNA sequence from cosmid U25D11, between markers DXS366 and DXS87 on chromosome X.	5e-015	<NONE>	<NONE>	<NONE>
3919	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	1e-013	<NONE>	<NONE>	<NONE>
3920	M89955	Human 5-HT1D-type serotonin receptor gene, complete cds.	0	112819	5-HYDROXYTRYPTAMINE 1D RECEPTOR human >gi|177772 (M89955) 5-HT1D-type serotonin receptor receptor:ISOTYPE =1D-alpha [Homo	3e-053

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					sapiens]	
3921	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	2e-008	3879698	(Z78065) predicted using Genefinder	9.1
3922	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	0.002	3184285	(AC004136) hypothetical protein [Arabidopsis thaliana]	9.5
3923	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	0.005	139805	XFIN PROTEIN >gi|65234 (X06021) Xfin protein (AA 1 - 1350) [Xenopus laevis]	1.9
3924	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	4e-012	<NONE>	<NONE>	<NONE>
3925	AF013711	Homo sapiens 22 kDa actin-binding protein	1e-020	103509	I factor 2 (transposon) - fruit fly protein [Drosophila teissieri]	5.5
3926	S83526	red photopigment gene {Alu repeat region, long intron 1} [human, peripheral blood leucocytes, Genomic, 1987 nt]	7e-006	<NONE>	<NONE>	<NONE>
3927	AB011542	Homo sapiens mRNA for MEGF9, partial cds	0	3449310	(AB011542) MEGF9 [Homo sapiens]	2e-095

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3928	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	2e-006	<NONE>	<NONE>	<NONE>
3929	X67312	P.pijperi mitochondrion DNA for Vaccinia virus-like terminal loop structure	6e-006	<NONE>	<NONE>	<NONE>
3930	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	3e-010	3080474	(AL022602) cell divisin protein FtsW	1.2
3931	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	4e-006	3769486	(AF074946) DNA polymerase [hemorrhagic enteritis virus]	1.3
3932	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	3e-010	<NONE>	<NONE>	<NONE>
3933	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	3e-008	1890266	(U88585) NADH-dehydrogenase subunit 1 [Quedius mesomelinus]	4.2
3934	Z12112	pWE15A cosmid vector DNA	1e-051	987050	(X65335) lacZ gene product [unidentified cloning vector]	4e-009
3935	AF023180	Listeria monocytogenes low temperature requirement A protein (ltrA) gene, complete cds	0.005	<NONE>	<NONE>	<NONE>
3936	D10856	D. melanogaster cyclin A gene	0.37	2315521	(AF016452) similar to the beta transducin family	1e-028

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3937	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	9e-009	3687507	(AL031788) C2H2 type zinc finger protein [Schizosaccharomyces pombe]	7.3
3938	Z80361	H.sapiens HLA-DRB pseudogene, repeat region;	2e-078	<NONE>	<NONE>	<NONE>
3939	L22551	Plasmodium yoelii yoelii merozoite surface protein 1 gene, 5' end.	1.2	<NONE>	<NONE>	<NONE>
3940	X74178	B.taurus microsatellite DNA INRA153	0.005	2291118	(AF016414) No definition line found [Caenorhabditis elegans]	2.5
3941	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	9e-010	1354361	(U52008) Mrp50 [Streptococcus pyogenes]	0.48
3942	U41635	Human OS-9 precurosor mRNA, complete cds	0.12	<NONE>	<NONE>	<NONE>
3943	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	1e-011	<NONE>	<NONE>	<NONE>
3944	M37470	Human beta-N-acetylhexosaminidase (HEXB) gene, deletion junction.	5e-025	728832	!!!! ALU SUBFAMILY SB WARNING ENTRY	4.3
3945	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	6e-006	97885	salivary agglutinin receptor precursor - Streptococcus sanguis	0.84

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3946	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	3e-010	140550	HYPOTHETICAL 259 KD PROTEIN (ORF 2136) >gi|81341|pir||A05 037 hypothetical protein 2136 - liverwort (Marchantia polymorpha) chloroplast >gi|11665	2.5
3947	L13176	Papio anubis apolipoprotein C-I gene, partail mRNA.	0.0005	<NONE>	<NONE>	<NONE>
3948	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	7e-006	580702	(X74410) fixP gene product [Azorhizobium caulinodans]	2.9
3949	X92987	B.primigenius mRNA for coat protein gamma-cop	2e-036	1706000	COATOMER GAMMA SUBUNIT (GAMMA-COAT PROTEIN) (GAMMA-COP) >gi|1066165 (X92987) coat protein gamma-cop [Bos primigenius]	2e-008
3950	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	8e-008	223232	protein src [Avian sarcoma virus]	0.37
3951	AF037350	Rattus norvegicus NF-E2-related factor 2 mRNA, complete cds	1e-013	3004573	(AC004520) similar to NFE2-related transcription factors; similar to I48694 (PID:g2137676) [Homo sapiens]	8e-073
3952	AJ011972	Homo sapiens mRNA for histone deacetylase-like protein (JM21)	8e-092	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3953	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	3e-009	<NONE>	<NONE>	<NONE>
3954	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	3e-009	<NONE>	<NONE>	<NONE>
3955	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	3e-009	630444	CR5 protein - Trypanosoma brucei >gi|468424	4.3
3956	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	3e-009	630444	CR5 protein - Trypanosoma brucei >gi|468424	4.3
3957	AF086172	Homo sapiens full length insert cDNA clone ZB89E10	9e-062	1172991	60S RIBOSOMAL PROTEIN L21 sapiens] >gi|984143 (X89401) ribosomal protein L21 [Homo sapiens] >gi|1096939|prf|2113200B ribosomal protein L21	9e-024
3958	D42084	Human mRNA for KIAA0094 gene, partial cds	2e-058	1703270	PUTATIVE METHIONINE AMINOPEPTIDASE 1 (METAP 1) (PEPTIDASE M 1) (KIAA0094) product is related to S.cerevisiae methionine aminopeptidase. [Homo sapiens]	1e-016

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3959	AF034755	Homo sapiens microphthalmia-associated transcription factor (MITF) gene, promoter region and partial cds	2e-005	<NONE>	<NONE>	<NONE>
3960	Z96177	H.sapiens telomeric DNA sequence, clone 10QTEL040, read 10QTELOO040.seq	3e-011	<NONE>	<NONE>	<NONE>
3961	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	1e-012	141028	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 >gi|76351|pir||QQUTC5 NADH dehydrogenase (ubiquinone)	1.1
3962	U93237	Human menin (MEN1) gene, complete cds	0.37	134853	TRANSCRIPTION INITIATION PROTEIN SPT5 yeast (Saccharomyces cerevisiae) >gi|172680 (M62882) SPT5 protein [Saccharomyces cerevisiae] >gi|854480 (Z49810) Spt5p [Saccharomyces cerevisiae]	0.49
3963	Z93782	Caenorhabditis elegans cosmid R12G8, complete sequence [Caenorhabditis elegans]	0.008	1171084	A/G-SPECIFIC ADENINE GLYCOSYLASE	6.5
3964	U11270	Human antithrombin III gene, exon 1 and partial cds.	2e-023	728837	!!!! ALU SUBFAMILY SQ WARNING ENTRY	9e-006

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3965	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	8e-007	3650488	(AF042273) signal transducing adaptor molecule 2A [Homo sapiens]	3.6
3966	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	2e-006	<NONE>	<NONE>	<NONE>
3967	AF086207	Homo sapiens full length insert cDNA clone ZC48C05	1e-009	1077301	probable membrane protein YOL101c - yeast similarity with bee NADH-ubiquinone oxidoreductase chain 2 [Saccharomyces cerevisiae] >gi|1419955|gnl|PID|e252291	0.41
3968	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	4e-011	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	6.2
3969	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	2e-005	2274853	(AJ000502) iron regulatory protein	0.15
3970	U82165	Cercopithecus aethiops transmembrane glycoprotein CD99-cos7 mRNA, partial cds	2e-015	2735010	(U82166) CD99 type II-COS7 [Cercopithecus aethiops]	0.011
3971	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	0.0002	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3972	M87680	Human simple repeat polymorphism.	3e-040	3874946	(Z79598) cDNA EST EMBL:D34748 comes from this gene; cDNA EST yk218e6.5 comes from this gene; cDNA EST yk244e3.5 comes from this gene; cDNA EST yk248a4.5 comes from this gene; cDNA EST yk250a3.5 comes from this gene; cDNA EST...	1e-008
3973	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	3e-010	119396	ENV POLYPROTEIN (COAT POLYPROTEIN) reticuloendotheliosis virus >gi|61786 (X01455) env-protein (capsid protein) [Reticuloendotheliosis virus] >gi|209712 (K02537) envelope polyprotein [Avian reticuloendotheliosis virus A]	4.6
3974	AB011143	Homo sapiens mRNA for KIAA0571 protein, complete cds	e-151	1708199	HSC70-INTERACTING PROTEIN	4e-023
3975	AC001050	Homo sapiens (subclone 3_e9 from P1 H55) DNA sequence	1e-019	728831	!!!! ALU SUBFAMILY J WARNING ENTRY	3e-006
3976	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	3e-008	1077543	probable membrane protein YDR198c - yeast	5.9

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3977	AJ005175	Drosophila virilis mRNA for GAGA factor class B-isoform	0.056	<NONE>	<NONE>	<NONE>
3978	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	2e-014	478731	replication protein - Butyrivibrio fibrisolvens plasmid pRJF1 >gi|152515 (M94552) replication protein [Plasmid pRJF1]	1.5
3979	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	1e-006	3319480	(AF077546) No definition line found [Caenorhabditis elegans]	6.5
3980	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	9e-014	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	3
3981	AF003350	Mus musculus Npc1 gene, and npc-nih intron containing the MaLR inserted sequence	4e-007	1170261	OUTER MEMBRANE USHER PROTEIN HIFC PRECURSOR	6.4
3982	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.001	<NONE>	<NONE>	<NONE>
3983	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	1e-006	<NONE>	<NONE>	<NONE>
3984	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	4e-007	<NONE>	<NONE>	<NONE>
3985	AB007939	Homo sapiens mRNA for KIAA0470 protein, complete cds	e-163	3413902	(AB007939) KIAA0470 protein [Homo sapiens]	2e-057

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3986	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	2e-010	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	2.9
3987	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	1e-006	<NONE>	<NONE>	<NONE>
3988	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	1e-006	<NONE>	<NONE>	<NONE>
3989	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	0.008	2414527	(Z99263) hypothetical protein MLCB637.01c [Mycobacterium leprae]	1.3
3990	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.074	464237	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4	2.2
3991	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	3e-010	3876367	(Z69360) Weak similarity to Eimeria thrombospondin (PIR Acc. No. A45517); cDNA EST EMBL:M89266 comes from this gene; cDNA EST yk295b9.5 comes from this gene [Caenorhabditis elegans] Eimeria thrombospondin (PIR Acc. No. A45517); cDNA EST EMBL:M89266 comes	7.7

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3992	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.0002	400624	SODIUM- AND CHLORIDE-DEPENDENT GABA TRANSPORTER 2 >gi|348413|pir||A45078 gamma-aminobutyric acid transporter protein 2 - rat >gi|202523 (M95762) GABA transporter [Rattus norvegicus]	0.62
3993	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	6e-015	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	5.9
3994	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	5e-012	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	6.9
3995	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	3e-008	2286159	(AF007831) glycoprotein H [Human herpesvirus 7]	6.3
3996	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	2e-014	<NONE>	<NONE>	<NONE>
3997	D16888	Human HepG2 3' region cDNA, clone hmd2c03	e-104	<NONE>	<NONE>	<NONE>
3998	U00995	Rattus norvegicus TA1 mRNA, complete cds.	1e-031	3639058	(AF077866) amino acid transporter E16 [Homo sapiens]	1e-050

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
3999	AF037219	Homo sapiens PIX1 mRNA sequence	5e-013	586863	HYPOTHETICAL 9.2 KD PROTEIN IN RECR-BOFA INTERGENIC REGION >gi|1075824|pir||A 41869 bofA 5'-region hypothetical protein orf74 - Bacillus subtilis subtilis] >gi|2632289|gnl|PI D|e1181955 (Z99104) yaaL	2.7
4000	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	1e-009	<NONE>	<NONE>	<NONE>
4001	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	6e-015	<NONE>	<NONE>	<NONE>
4002	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	2e-013	549734	HYPOTHETICAL 105.7 KD PROTEIN IN TPK3-PIR1 INTERGENIC REGION >gi|481105|pir||S3 7786 hypothetical protein YKL165c - yeast (Saccharomyces cerevisiae) >gi|407483 (Z26877) unknown [Saccharomyces cerevisiae] >gi|486289 (Z28165) ORF YKL165c	3e-019

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
4003	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	2e-014	<NONE>	<NONE>	<NONE>
4004	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	9e-008	228110	T cell receptor variable region:SUBUNIT =beta:ISOTYPE=1 9 [Rattus norvegicus]	3.6
4005	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	2e-014	930045	(X15332) alpha-1 (III) collagen [Homo sapiens]	0.52
4006	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	1e-010	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	6.2
4007	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	2e-015	2960195	(Y13051) tax [Human T-cell lymphotropic virus type 2b]	0.68
4008	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	4e-007	3523099	(AF016271) Ksp-cadherin [Mus musculus]	6.6
4009	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	6e-015	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	5.7
4010	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	6e-015	<NONE>	<NONE>	<NONE>
4011	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	3e-009	2121280	(AF000270) lipoprotein [Borrelia burgdorferi]	1.5

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
4012	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	4e-012	<NONE>	<NONE>	<NONE>
4013	L20489	Zea mays NADH dehydrogenase subunit 4 (complex I) (nad4) gene, exon 4.	3.5	<NONE>	<NONE>	<NONE>
4014	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	2e-014	<NONE>	<NONE>	<NONE>
4015	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	2e-016	927407	(X89858) actin binding protein [Drosophila melanogaster]	0.02
4016	U05659	Human 17beta-hydroxysteroid dehydrogenase type 3 mRNA, complete cds	1e-092	1169300	ESTRADIOL 17 BETA-DEHYDROGENASE 3 DEHYDROGENASE) >gi|1085271|pir||S43928 17-beta-hydroxysteroid dehydrogenase - human >gi|531162 hydroxysteroid dehydrogenase:ISOTYPE=3 [Homo sapiens]	4e-029
4017	U02428	Cloning vector pDR2, complete sequence	2e-066	987050	(X65335) lacZ gene product [unidentified cloning vector]	2e-009

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
4018	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	8e-018	3979938	(AL034393) predicted using Genefinder; cDNA EST yk343c12.5 comes from this gene; cDNA EST yk402e12.5 comes from this gene; cDNA EST yk457e8.5 comes from this gene; cDNA EST yk470f2.5 comes from this gene; cDNA EST yk281e3.5 ...	7e-009
4019	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	9e-009	<NONE>	<NONE>	<NONE>
4020	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	1e-010	804806	(M13100) unknown protein [Rattus norvegicus]	5.7
4021	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	2e-014	<NONE>	<NONE>	<NONE>
4022	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	1e-011	<NONE>	<NONE>	<NONE>
4023	U49974	Human mariner2 transposable element, complete consensus sequence	e-124	1698455	(U49974) mariner transposase [Homo sapiens]	2e-028
4024	L31840	Rattus norvegicus nuclear pore complex protein NUP107 mRNA, complete cds.	e-175	1709212	NUCLEAR PORE COMPLEX PROTEIN NUP107	3e-093

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
4025	AB001632	Homo sapiens DNA for cGMP-binding cGMP-specific phosphodiesterase (PDE5), exon 18	7e-007	<NONE>	<NONE>	<NONE>
4026	X96401	H.sapiens mRNA for ROX protein	8e-070	<NONE>	<NONE>	<NONE>
4027	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.015	<NONE>	<NONE>	<NONE>
4028	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	9e-010	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	3.2
4029	AJ006064	Rattus norvegicus mRNA for coronin-like protein	e-124	3757680	(AJ006064) coronin-like protein [Rattus norvegicus]	2e-091
4030	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	1e-009	1184072	(U40766) COL-1 [Meloidogyne incognita]	0.019
4031	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	0.002	231721	T-CELL SURFACE GLYCOPROTEIN CD8 ALPHA CHAIN PRECURSOR (T-LYMPHOCYTE DIFFERENTIATION ANTIGEN T8/LEU-2) >gi|38145 (X60223) CD8 alpha chain	5.8
4032	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	1e-009	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
4033	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	0.005	<NONE>	<NONE>	<NONE>
4034	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	4e-011	1020391	(L48340) alcohol dehydrogenase [Methylobacterium extorquens]	1.4
4035	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.0002	2291282	(AF016433) similar to C. elegans olfactory receptor ODR-10 (NID:g1235900) [Caenorhabditis elegans]	4.4
4036	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	1e-010	478993	DNA-binding protein TAF-II 250K - fruit fly TATA-binding protein associated factor II 250, TBP associated factor II 250, TAFII250 {C-terminal}	5e-006
4037	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	1e-011	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	4.4
4038	X03100	Human HLA-SB(DP) alpha gene	2e-025	<NONE>	<NONE>	<NONE>
4039	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	8e-008	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
4040	J03798	Human autoantigen small nuclear ribonucleoprotein Sm-D mRNA, complete cds.	2e-048	3874988	(Z74029) Similarity to C.elegans alcohol dehydrogenase (WP:C17G10.8); cDNA EST EMBL:D66106 comes from this gene; cDNA EST EMBL:D69117 comes from this gene; cDNA EST EMBL:D69761 comes from this gene; cDNA EST EMBL:C12156 come...	5.6
4041	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	6e-006	2292986	(AJ000496) cyclic nucleotide-gated channel beta subunit [Rattus norvegicus]	0.5
4042	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	3e-010	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	2.5
4043	AF020187	Amblyomma americanum ecdsyteroid receptor	1.2	<NONE>	<NONE>	<NONE>
4044	Z68758	Human DNA sequence from cosmid cN85E10 on chromosome 22q11.2-qter	2e-035	<NONE>	<NONE>	<NONE>
4045	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	8e-008	2529632	(L78917) virion protein [Rubella virus]	4.6
4046	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	6e-005	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
4047	AB007957	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488	2e-016	728831	!!!! ALU SUBFAMILY J WARNING ENTRY	0.063
4048	M64716	Human ribosomal protein S25 mRNA, complete cds.	3e-082	2660720	(AF029678) PHF1 [Homo sapiens]	7e-013
4049	AB002437	Homo sapiens mRNA from chromosome 5q21-22, clone:LI33	6e-026	<NONE>	<NONE>	<NONE>
4050	Z74893	S.cerevisiae chromosome XV reading frame ORF YOL151w	0.13	<NONE>	<NONE>	<NONE>
4051	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	7e-006	<NONE>	<NONE>	<NONE>
4052	U43416	Human replication control protein 1 (PARC1) mRNA, complete cds.	2e-056	728831	!!!! ALU SUBFAMILY J WARNING ENTRY	0.007
4053	AF042346	Homo sapiens putative phenylalanyl-tRNA synthetase beta-subunit mRNA, complete cds	0	4104933	(AF042346) putative phenylalanyl-tRNA synthetase beta-subunit; PheHB [Homo sapiens]	e-123
4054	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
4055	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
4056	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	3e-009	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	5.6
4057	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	0.0005	2981221	(AF053091) eyelid [Drosophila melanogaster]	2.6

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
4058	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	2e-006	<NONE>	<NONE>	<NONE>
4059	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	8e-007	<NONE>	<NONE>	<NONE>
4060	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	3e-010	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	9.6
4061	U11081	Human type 1 vasoactive intestinal peptide receptor (V1RG) gene, exon 3.	0.43	<NONE>	<NONE>	<NONE>
4062	X82272	Human endogenous retrovirus env mRNA	8e-081	1196429	(M14123) pol/env ORF (bases 3878-8257) first start codon at 4172; Xxx; putative [Homo sapiens]	6e-058
4063	S61789	NF1=neurofibromatosis type 1 {deletion breakpoint, tetrameric STR} [human, neurofibrosarcoma tissue, Genomic Mutant, 698 nt]	0.0005	2494294	NEUROGENIC LOCUS NOTCH 3 PROTEIN	4.3
4064	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.0005	3264773	(AF072439) zinc-finger protein-37; ZFP-37 [Rattus norvegicus]	3.3
4065	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	3e-010	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	4.5
4066	U47322	Cloning vector DNA, complete sequence.	9e-054	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	0.6

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
4067	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	1e-009	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	3.4
4068	U31557	Ovine adenovirus IVa2 protein gene, DNA polymerase gene, terminal protein gene and 52,55 kDa protein gene, partial cds	0.0002	3002875	(AF042104) envelope glycoprotein [Human immunodeficiency virus type 1]	2.6
4069	AL023973	Human DNA sequence from clone 1033E15 on chromosome 22q13.1-13.2. Contains part of a novel gene, ESTs and a GSS, complete sequence [Homo sapiens]	7e-017	728831	!!!! ALU SUBFAMILY J WARNING ENTRY	0.061
4070	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	2e-005	<NONE>	<NONE>	<NONE>
4071	X07679	Xenopus laevis XK70A gene for type I keratin	0.39	2281044	(Z95636) laminin alpha 5 chain [Homo sapiens]	0.9
4072	X96886	H.sapiens spcDNA, clone 2-65	5e-014	<NONE>	<NONE>	<NONE>
4073	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	9e-008	<NONE>	<NONE>	<NONE>
4074	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	6e-005	1079278	activin receptor II STK3 precursor - African clawed frog >gi|260044|bbs|118656 (S49438) activin receptor, XAR1 [Xenopus, oocytes, Peptide,	1.3

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					510 aa]	
4075	AF097909	Peptostreptococcus micros fibril-like structure subunit FibA (fibA) gene, complete cds; excreted protein FibB (fibB) gene, partial cds; and unknown gene	0.046	<NONE>	<NONE>	<NONE>
4076	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	4e-010	<NONE>	<NONE>	<NONE>
4077	AL009008	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-58, complete sequence	0.45	<NONE>	<NONE>	<NONE>
4078	L34686	Serpulina hyodysenteriae flagellar protein	0.015	<NONE>	<NONE>	<NONE>
4079	AJ130718	Homo sapiens mRNA for glycoprotein-associated amino acid transporter y+LAT1	1e-022	3582136	(AB015432) LAT1 (L-type amino acid transporter 1) [Rattus norvegicus]	2e-008
4080	X51969	Cyprinus carpio growth hormone gene	1.2	<NONE>	<NONE>	<NONE>
4081	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	3e-010	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	1.2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
4082	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	4e-011	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	3.4
4083	L38961	Human putative transmembrane protein precursor (B5) mRNA, complete cds	1e-071	1174470	OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG (B5) (INTEGRAL MEMBRANE PROTEIN 1) musculus] >gi|1588285|prf||2208301A integral membrane protein [Mus musculus]	1e-008
4084	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	2e-013	267449	HYPOTHETICAL 12.5 KD PROTEIN ZK637.2 IN CHROMOSOME III >gi|102507|pir||S15787 hypothetical protein 1 (cosmid ZK637) - Caenorhabditis elegans Genefinder; cDNA EST yk217b5.3 comes from this gene; cDNA EST yk217b5.5 comes from this gene; cDNA EST yk340g12.3	7e-014
4085	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	8e-008	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	3.4
4086	X77733	T.aestivum VDAC 1 mRNA.	0.005	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
4087	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	1e-009	3123172	ZINC FINGER PROTEIN 151 (MIZ-1 PROTEIN) >gi|2230871|gnl|PID|e286602 (Y09723) Miz-1 protein [Homo sapiens]	2e-010
4088	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	1e-010	180498	(M17517) complement H factor [Homo sapiens]	5.8
4089	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	8e-007	<NONE>	<NONE>	<NONE>
4090	U24697	Chironomus samoensis nanos homolog (Cs nos) gene, complete cds.	0.13	3880999	(AL021492) Y45F10D.11 [Caenorhabditis elegans]	7e-022
4091	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	4e-012	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	5.7
4092	U81504	Homo sapiens beta-3A-adaptin subunit of the AP-3 complex mRNA, complete cds	6e-088	2199512	(U81504) beta-3A-adaptin subunit of the AP-3 complex [Homo sapiens]	0.0001
4093	AF053304	Homo sapiens mitotic checkpoint component Bub3	e-108	3378104	(AF047473) testis mitotic checkpoint BUB3 [Homo sapiens]	3e-024
4094	S70431	type-1 angiotensin II receptor {exons 1 and 2, promoter} [human, peripheral lymphocytes, Genomic, 2853 nt, segment 1 of 2]	4e-013	126295	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG	3e-005

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
4095	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	4e-013	<NONE>	<NONE>	<NONE>
4096	D10355	Human mRNA for alanine aminotransferase	3e-082	111345	alanine transaminase (EC 2.6.1.2) - rat	4e-042
4097	AF043252	Homo sapiens mitochondrial outer membrane protein (Tom40) gene, nuclear gene encoding mitochondrial protein, exons 7, 8 and 9	e-167	3941342	(AF043250) mitochondrial outer membrane protein [Homo sapiens] >gi|3941347 (AF043253) mitochondrial outer membrane protein [Homo sapiens] >gi|4105703 (AF050154) D19S1177E [Homo sapiens]	7e-013
4098	U41668	Human deoxyguanosine kinase mRNA, complete cds	e-125	2833282	DEOXYGUANOSINE KINASE PRECURSOR sapiens]	2e-009
4099	AF017416	Bacillus thuringiensis d-endotoxin gene, complete cds	0.14	<NONE>	<NONE>	<NONE>
4100	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	1e-008	<NONE>	<NONE>	<NONE>
4101	AF017416	Bacillus thuringiensis d-endotoxin gene, complete cds	0.14	<NONE>	<NONE>	<NONE>
4102	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	1e-008	<NONE>	<NONE>	<NONE>
4103	AJ003081	Homo sapiens repetitive DNA	5e-024	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
4104	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	8e-007	<NONE>	<NONE>	<NONE>
4105	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	7e-006	1572756	(U70848) C43G2.1 gene product [Caenorhabditis elegans]	4e-038
4106	U33915	Craterostigma plantagineum myb-related transcription factor (cpm10) gene, complete cds	0.14	<NONE>	<NONE>	<NONE>
4107	U46493	Cloning vector pFlp recombinase gene, complete cds	5e-033	987050	(X65335) lacZ gene product [unidentified cloning vector]	0.004
4108	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	1e-009	3417298	(AC002044) Alpha-fetoprotein enhancer binding protein (3' partial) [Homo sapiens]	0.33
4109	M16039	Dictyostelium discoideum pst-cath gene encoding pst-cathepsin, complete cds.	0.0002	<NONE>	<NONE>	<NONE>
4110	D21851	Human mRNA for KIAA0028 gene, partial cds	6e-005	<NONE>	<NONE>	<NONE>
4111	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	7e-007	1723920	HYPOTHETICAL 37.4 KD PROTEIN IN SEC27-SSM1B INTERGENIC REGION >gi|2131603|pir||S64149 hypothetical protein YGL136c - yeast (Saccharomyces cerevisiae) >gi|1246842|gnl|PI	8e-006

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					D|e210737 (X92670) G2830	
4112	X75861	H.sapiens TEGT gene	e-180	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	2.6
4113	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	8e-008	1399962	(U62317) choline kinase isolog 384D8_3 [Homo sapiens]	0.67
4114	Y07660	M.tuberculosis accBC gene	2e-059	465847	HYPOTHETICAL 66.5 KD PROTEIN F02A9.5 IN CHROMOSOME III >gi|280542|pir||S28313 hypothetical protein F02A9.5 - Caenorhabditis elegans Genefinder; similar to Propionyl-CoA carboxylase beta chain; cDNA EST EMBL:M89018 comes from this gene; cDNA EST EMBL:D2806	4e-056
4115	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.014	765086	(D30786) feline CD9 [Felis catus]	1.9

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
4116	D29011	Human mRNA for proteasome subunit X, complete cds	e-125	2136006	proteasome subunit MB1 - human (fragment) MB1=LMP7 homolog [human, JY T-cells, Peptide Partial, 215 aa] [Homo sapiens]	4e-008
4117	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	4e-012	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	6.2
4118	Z11692	H.sapiens mRNA for elongation factor 2	e-178	119172	ELONGATION FACTOR 2 (EF-2) eEF-2 - human >gi|31106 (X51466) elongation factor 2 factor 2 [Homo sapiens]	6e-054
4119	AF070530	Homo sapiens clone 24751 unknown mRNA	0	3387886	(AF070530) unknown [Homo sapiens]	4e-013
4120	D12646	Mouse kif4 mRNA for microtubule-based motor protein KIF4, complete cds	6e-057	1170659	KINESIN-LIKE PROTEIN KIF4 musculus]	2c-022
4121	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	1e-009	<NONE>	<NONE>	<NONE>
4122	X75861	H.sapiens TEGT gene	e-180	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	2.6
4123	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	4e-012	630864	LRR47 protein - fruit fly (Drosophila melanogaster) >gi|415947 (X75760) LRR47 [Drosophila melanogaster]	0.0002

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
4124	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	5e-014	3876775	(Z81077) predicted using Genefinder; Similarity to Yeast protein 8248 (TR:G587531)	1e-015
4125	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	2e-008	480516	transposase (clone 22.5) - African malaria mosquito transposon mariner (fragment) >gi|159600	2.8
4126	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	8e-008	<NONE>	<NONE>	<NONE>
4127	X65279	pWE15 cosmid vector DNA	2e-066	987050	(X65335) lacZ gene product [unidentified cloning vector]	4e-015
4128	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	4e-012	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	3.8
4129	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	3e-008	<NONE>	<NONE>	<NONE>
4130	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	3e-008	<NONE>	<NONE>	<NONE>
4131	X74871	H.sapiens gene for RNA pol II largest subunit, exons 20-22	1.1	1182038	(Z69368) unknown [Schizosaccharomyces pombe]	0.86
4132	M64983	Human fibrinogen beta chain gene, complete mRNA. > gb|I47706|I47706 Sequence 3 from patent US 5639940	0.23	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
4133	D12646	Mouse kif4 mRNA for microtubule-based motor protein KIF4, complete cds	6e-057	1170659	KINESIN-LIKE PROTEIN KIF4 musculus]	2e-022
4134	D86957	Human mRNA for KIAA0202 gene, partial cds	1.1	<NONE>	<NONE>	<NONE>
4135	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	7e-006	<NONE>	<NONE>	<NONE>
4136	M20902	Human apolipoprotein C-I (VLDL) gene, complete cds.	4e-008	<NONE>	<NONE>	<NONE>
4137	L36849	Cloning vector pZEO (isolate SV1) phleomycin/zeocin-binding protein gene, complete cds.	9e-040	987050	(X65335) lacZ gene product [unidentified cloning vector]	9e-007
4138	X80910	H.sapiens PPP1CB mRNA	0	<NONE>	<NONE>	<NONE>
4139	M77812	Rabbit myosin heavy chain mRNA, complete cds.	0.0002	2088793	(AF003150) similar to cuticular collagen [Caenorhabditis elegans]	0.23
4140	U41165	Human recombination 'hot spot' region associated with the CMT1A duplication and the HNPP deletion containing a mariner transposon-like element	0.13	<NONE>	<NONE>	<NONE>
4141	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	0.0006	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
4142	AC001502	Homo sapiens (subclone 2_c7 from P1 H43) DNA sequence	0.014	3164130	(D78600) cytochrome P450 monooxygenase	7.5
4143	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	2e-005	<NONE>	<NONE>	<NONE>
4144	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
4145	L31760	Human STS UT8178.	0.17	<NONE>	<NONE>	<NONE>
4146	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	5e-013	<NONE>	<NONE>	<NONE>
4147	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.0006	2662587	(AF036696) contains similarity to Brassica oleracea non-green plastid phosphate/triose-phosphate translocator precursor (GB:U13632) [Caenorhabditis elegans]	2e-016
4148	X56807	Human DSC2 mRNA for desmocollins type 2a and 2b	6e-037	319943	desmocollin 3b precursor - human	7e-014
4149	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	1e-012	<NONE>	<NONE>	<NONE>
4150	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	2e-005	2854155	(AF045640) contains similarity to ion channel proteins	3.4

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
4151	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	3e-010	2507153	VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS16 >gi|2133204|pir||S 62031 vacuolar protein sorting-associated protein VPS16 - yeast (Saccharomyces cerevisiae) >gi|1171414 (U44030) Vsp16p: Vacuolar sorting protein [Saccharomyces cerevisiae]	0.011
4152	D12646	Mouse kif4 mRNA for microtubule-based motor protein KIF4, complete cds	2e-035	3877579	(Z82271) Similarity to Mouse kinensin-like protein KIF4 (SW:P33174); cDNA EST EMBL:D27320 comes from this gene; cDNA EST EMBL:D27322 comes from this gene; cDNA EST EMBL:D27321 comes from this gene; cDNA EST EMBL:D35764 comes... Mouse kinensin-like protein	2e-054

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
4153	D12646	Mouse kif4 mRNA for microtubule-based motor protein KIF4, complete cds	2e-035	3877579	(Z82271) Similarity to Mouse kinensin-like protein KIF4 (SW:P33174); cDNA EST EMBL:D27320 comes from this gene; cDNA EST EMBL:D27322 comes from this gene; cDNA EST EMBL:D27321 comes from this gene; cDNA EST EMBL:D35764 comes... Mouse kinensin-like protein	2e-054
4154	D12646	Mouse kif4 mRNA for microtubule-based motor protein KIF4, complete cds	2e-035	3877579	(Z82271) Similarity to Mouse kinensin-like protein KIF4 (SW:P33174); cDNA EST EMBL:D27320 comes from this gene; cDNA EST EMBL:D27322 comes from this gene; cDNA EST EMBL:D27321 comes from this gene; cDNA EST EMBL:D35764 comes... kinensin-like protein KIF4	9e-058
4155	M30539	Human SK2 c-Ha-ras-1 oncogene-encoded protein gene, exon 1.	0.13	137334	66 KD PROTEIN >gi|77357|pir||JQ0107 hypothetical 66K protein - Ononis yellow mosaic virus	10

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
4156	L05096	Homo sapiens ribosomal protein L39 mRNA, complete cds	2e-086	1173044	60S RIBOSOMAL PROTEIN L39 norvegicus] >gi|1373419 (U57846) ribosomal protein L39 ribosomal protein L39 [Homo sapiens]	3e-007
4157	D13749	Plasmid pKA1 DNA	2e-025	987050	(X65335) lacZ gene product [unidentified cloning vector]	0.18
4158	AF007157	Homo sapiens clone 23856 unknown mRNA, partial cds	2e-057	2131036	(Z95890) PE_PGRS [Mycobacterium tuberculosis]	6.3
4159	AF031400	Poecilia orri NADH dehydrogenase subunit 2 gene, mitochondrial gene encoding mitochondrial protein, complete cds	1.2	3327168	(AB014577) KIAA0677 protein [Homo sapiens]	0.0008
4160	U58468	Human vasoactive intestinal peptide gene, 5' flanking sequence from -5172 to -1924	3e-009	<NONE>	<NONE>	<NONE>
4161	D11078	Homo sapiens RGH2 gene, retrovirus-like element	4e-032	2119507	alpha-1C-adrenergic receptor isoform 2 - human >gi|927209|gnl|PID|d1007476 (D32202) alpha 1C adrenergic receptor isoform 2 [Homo sapiens]	1.2
4162	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
4163	M31061	Human ornithine decarboxylase gene, complete cds.	2e-023	728831	!!!! ALU SUBFAMILY J WARNING ENTRY	0.002

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
4164	M19980	M.fervidus gap gene encoding glyceraldehyde-3-phosphate dehydrogenase, complete cds.	0.4	1825606	(U88169) similar to molybdoterin biosynthesis MOEB proteins [Caenorhabditis elegans]	3e-057
4165	D17036	Human HepG2 partial cDNA, clone hmd3e08m5	5e-025	<NONE>	<NONE>	<NONE>
4166	L14714	C. elegans cosmid ZC97.	0.39	3874412	(Z70034) similarity to 35.1KD hypothetical yeast protein (Swiss Prot accession number P38805); cDNA EST CEMSE65F comes from this gene; cDNA EST EMBL:T01315 comes from this gene; cDNA EST yk452e10.3 comes from this gene; cDNA... 35.1KD hypothetical yeast p	1e-033
4167	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	8e-008	<NONE>	<NONE>	<NONE>
4168	Z49867	Caenorhabditis elegans cosmid C33D3, complete sequence [Caenorhabditis elegans]	0.044	3876784	(Z81530) predicted using Genefinder	5.9
4169	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	9e-010	3549676	(AL031394) putative protein	3.1
4170	D87001	Human (lambda) DNA for immunoglobulin light chain	0.36	3133246	(AB013170) NADH dehydrogenase subunit 5	2.4

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
4171	M37191	Human ras inhibitor mRNA, partial cds.	e-122	107561	Ras inhibitor (clone JC310) - human sapiens]	3e-035
4172	AB018374	Mus musculus GARP34 mRNA, complete cds	2e-046	3724364	(AB018374) GARP34 [Mus musculus]	2e-008
4173	X62527	R.norvegicus gene for CNS-myelin proteolipid protein (exon 6)	1.2	1155068	(X94976) cell wall-plasma membrane linker protein	1.6
4174	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	8e-008	2781355	(AC003113) F24O1.11 [Arabidopsis thaliana]	0.52
4175	AF002715	Homo sapiens MAP kinase kinase kinase (MTK1) mRNA, complete cds	e-168	2352277	(AF002715) MAP kinase kinase kinase [Homo sapiens]	1e-042
4176	U07807	Human metallothionein IV (MTIV) gene, complete cds.	0.047	<NONE>	<NONE>	<NONE>
4177	D11129	Pneumonia virus of mice gene 7	0.14	<NONE>	<NONE>	<NONE>
4178	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	2e-006	<NONE>	<NONE>	<NONE>
4179	AF070557	Homo sapiens clone 24422 mRNA sequence	0	<NONE>	<NONE>	<NONE>
4180	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	0.005	<NONE>	<NONE>	<NONE>
4181	AF045765	Homo sapiens G protein-coupled receptor	9e-018	728833	!!!! ALU SUBFAMILY SB1 WARNING ENTRY	0.051
4182	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
4183	X62162	B.burgdorferi gene for pC protein	0.41	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
4184	Z81315	Human DNA sequence from fosmid F62D4 on chromosome 22q12-qter > :: emb|Z81316|HSF 62D4A Human DNA sequence from fosmid F62D4 on chromosome 22, complete sequence	1.2	<NONE>	<NONE>	<NONE>
4185	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	3e-009	<NONE>	<NONE>	<NONE>
4186	L08108	Human low-affinity Fc-receptor IIB gene, exons 4-7.	0.0006	462387	IMMEDIATE-EARLY PROTEIN IE180 herpesvirus 1 (strain Kaplan) >gi|334071 (M34651) immediate-early protein [Pseudorabies virus]	0.25
4187	AJ228330	Pinus pinaster reverse transcriptase gene of Line-retroelement (clone pPpLi1)	1.3	3108187	(AC004663) Notch 3 [Homo sapiens]	1.3
4188	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
4189	AF048991	Homo sapiens MutS homolog 5 (MSH5) gene, exons 13 through 25 and complete cds	0.002	3986756	(AF109905) NG23 [Mus musculus]	0.066
4190	Z59608	H.sapiens CpG DNA, clone 165g8, reverse read cpg165g8.rt1a .	2e-014	1055183	(U40061) Similar to sodium-dependent phosphate transporter. [Caenorhabditis elegans]	2.4

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
4191	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.0002	<NONE>	<NONE>	<NONE>
4192	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.0002	<NONE>	<NONE>	<NONE>
4193	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	2e-006	2128837	hypothetical protein MJ1401 - Methanococcus jannaschii >gi|1592049 (U67580) putative ATP dependent RNA helicase [Methanococcus jannaschii]	7.6
4194	X99691	B.taurus DNA for agouti gene	9e-009	<NONE>	<NONE>	<NONE>
4195	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	8e-008	306929	(M28696) IgG Fc receptor beta-Fc-gamma-RII [Homo sapiens]	0.64
4196	U37521	Sus scrofa E-selectin gene, complete cds	0.042	539800	calcium-activated potassium channel mSlo - mouse >gi|347144 (L16912) mSlo [Mus musculus]	3.3
4197	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	0.0002	<NONE>	<NONE>	<NONE>
4198	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	0.0002	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
4199	V01087	Hemagglutinin gene of influenza virus strain A/duck/Ukraine/1/63 > :: gb|J02109|FLAHAMU Influenza A/duck/ukraine/1/63 (h3n8), hemagglutinin (seg 4), cdna.	0.18	4038537	(AL021106) 1-evidence=predicted by match; 1-match_accession=AA392988; 1-match_description=LD12167.5prime LD Drosophila melanogaster embryo BlueScript Drosophila melanogaster cDNA clone LD12167 5prime.; 1-match_species=Drosop...	8.5
4200	X83107	H.sapiens Bmx mRNA for cytoplasmic tyrosine kinase	0.38	1147597	(U31221) viscerotropic leishmaniasis antigen [Leishmania tropica]	3.3
4201	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	2e-014	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	1.9
4202	X71642	M.musculus GEG-154 mRNA	3.5	2760302	(D89074) hypothetical protein [Vibrio cholerae O139 fs1 phage]	1.5
4203	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	2e-013	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	3.7
4204	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	9e-009	1574918	(U19728) organic anion transporter [Raja erinacea]	5.8
4205	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	4e-012	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
4206	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	4e-011	<NONE>	<NONE>	<NONE>
4207	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	2e-007	<NONE>	<NONE>	<NONE>
4208	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	4e-011	<NONE>	<NONE>	<NONE>
4209	U50523	Human BRCA2 region, mRNA sequence CG037	0	3121764	ARP2/3 COMPLEX 34 KD SUBUNIT	9e-026
4210	X80909	H.sapiens alpha NAC mRNA	8e-050	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	5.9
4211	AF039955	Homo sapiens liver CC chemokine-1 precursor	7e-006	<NONE>	<NONE>	<NONE>
4212	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	3e-010	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	4.6
4213	L35670	Homo sapiens (subclone H8 10_g5 from P1 35 H5 C8) DNA sequence.	7e-017	<NONE>	<NONE>	<NONE>
4214	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.0002	<NONE>	<NONE>	<NONE>
4215	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
4216	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
4217	L33354	Lobostemon fruticosus Buek chloroplast trnL(UAA)-trnF(GAA) intergenic spacer DNA.	0.35	1483615	(Z77856) beta-glucosidase [Thermotoga neapolitana]	9

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
4218	Z12112	pWE15A cosmid vector DNA	5e-033	987050	(X65335) lacZ gene product [unidentified cloning vector]	4e-008
4219	X65279	pWE15 cosmid vector DNA	2e-079	987050	(X65335) lacZ gene product [unidentified cloning vector]	3e-015
4220	AF052165	Homo sapiens clone 24522 mRNA sequence	e-170	2065177	(Y12790) Supt5h protein [Homo sapiens] sapiens]	1e-059
4221	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	2e-006	<NONE>	<NONE>	<NONE>
4222	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	2e-014	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	1.9
4223	AF055024	Homo sapiens clone 24763 mRNA sequence	0	<NONE>	<NONE>	<NONE>
4224	S39048	knob associated histidine-rich protein KAHRP	0.39	<NONE>	<NONE>	<NONE>
4225	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	4e-011	<NONE>	<NONE>	<NONE>
4226	U34377	Human tyrosine kinase TXK (txk) gene, exon 13.	2e-028	1709347	SERINE/THREONINE-PROTEIN KINASE NRK2 (SERINE/THREONINE KINASE 2) >gi|348245 (L20321) protein serine/threonine kinase [Homo sapiens]	8e-008

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
4227	U25748	Pan troglodytes epididymal secretory protein precursor (EPI-1) mRNA, complete cds.	0	3182993	EPIDIDYMAL SECRETORY PROTEIN E1 PRECURSOR (EPI-1) (HE1) (EPIDIDYMAL SECRETORY PROTEIN 14.6) (ESP14.6) >gi|106343|pir||S25641 hypothetical protein - human >gi|2134519|pir||I53929 epididymal secretory protein 14.6 - crab-eating macaque human >gi|37477 (X676	7e-040
4228	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
4229	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.017	<NONE>	<NONE>	<NONE>
4230	X74929	H.sapiens KRT8 mRNA for keratin 8	6e-036	<NONE>	<NONE>	<NONE>
4231	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	8e-007	<NONE>	<NONE>	<NONE>
4232	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	5e-013	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	6
4233	U41010	Caenorhabditis elegans cosmid T05A12	4.2	<NONE>	<NONE>	<NONE>
4234	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	3e-007	1363925	hypothetical protein 2 - North American opossum (fragment) >gi|897721 (Z48955) ORF-2, putative RT [Didelphis	4.7

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					virginiana]	
4235	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	0.0002	439493	(D26086) zinc-finger protein [Petunia x hybrida]	8.5
4236	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	0.0002	2501599	HYPOTHETICAL 29.1 KD PROTEIN W06E11.4 IN CHROMOSOME III >gi|669022 (U20862) W06E11.4 gene product [Caenorhabditis elegans]	0.002
4237	X94118	P.falciparum PK4 gene	1.2	<NONE>	<NONE>	<NONE>
4238	Z18944	S.cerevisiae BDF1 gene	7.30E-01	2119161	unknown - chicken (fragment) >gi|537433	0.61
4239	AF031939	Mus musculus RalBP1-associated EH domain protein Reps1 (reps1) mRNA, complete cds	e-154	2677843	(AF031939) RalBP1-associated EH domain protein Reps1	5e-016
4240	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	1e-014	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	2.9
4241	L35566	Gallus gallus homeobox protein (LH-2) mRNA, complete cds.	3e-044	1708809	HOMEOBOX PROTEIN LH-2 >gi|508712	4e-021
4242	Z83086	H.sapiens Fanconi anaemia group A gene, exon 29	3.00E-07	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
4243	U63810	Homo sapiens WD40 protein Ciao 1 mRNA, complete cds	0.00E+00	3219331	(AC004020) Unknown gene product [Homo sapiens]	1e-096
4244	U15110	Mycoplasma capricolum ptsI-crr operon phosphocarrier protein enzyme I (ptsI) and phosphocarrier protein enzyme IIA (crr) genes, complete cds, and lipopolysaccharide biosynthesis (kdtB) gene, complete cds.	1.1	<NONE>	<NONE>	<NONE>
4245	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
4246	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	4e-011	730888	OCTAPEPTIDE-REPEAT PROTEIN T2	1.4
4247	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.074	<NONE>	<NONE>	<NONE>
4248	AJ224152	Plasmodium berghei gene encoding cdc2-related kinase 2	0.54	<NONE>	<NONE>	<NONE>
4249	M24971	D.discoideum CT-rich satellite rDNA, clone pCT11.	2e-008	119110	EBNA-1 NUCLEAR PROTEIN herpesvirus 4 (strain B95-8) >gi|1334880 (V01555) BKRF1 encodes EBNA-1 protein, latent cycle gene. [Human herpesvirus 4]	2e-009
4250	Z72969	S.cerevisiae chromosome VII reading frame ORF YGR184c	1.2	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
4251	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
4252	AJ224326	Homo sapiens mRNA for putative ribulose-5-phosphate-epimerase, partial cds	0	<NONE>	<NONE>	<NONE>
4253	U45245	Homo sapiens paired-box protein PAX2 (PAX2) gene, promoter and exon 1	2.1	<NONE>	<NONE>	<NONE>
4254	AE001157	Borrelia burgdorferi (section 43 of 70) of the complete genome	0.63	<NONE>	<NONE>	<NONE>
4255	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	3e-010	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	5.8
4256	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	0.0005	2773162	(AF039595) sulfonylurea receptor 1B [Rattus norvegicus]	9.6
4257	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	5e-009	<NONE>	<NONE>	<NONE>
4258	L11130	Influenza A/gull/MD/19/77 (H2N8) hemagglutinin	0.67	<NONE>	<NONE>	<NONE>
4259	AB018270	Homo sapiens mRNA for KIAA0727 protein, partial cds	0	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	3
4260	U67494	Methanococcus jannaschii section 36 of 150 of the complete genome	0.014	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
4261	L09209	Homo sapiens amyloid protein homologue mRNA, complete cds > :: gb|I13782|I13782 Sequence 12 from patent US 5441931 > :: gb|I68752|I68752 Sequence 12 from patent US 5677146	6e-089	<NONE>	<NONE>	<NONE>
4262	M27866	Human retinoblastoma susceptibility protein gene, exon 27. > :: gb|I09392| Sequence 25 from Patent WO 8906703	e-158	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	1.7
4263	U59629	Human transcription factor LZIP-alpha mRNA, complete cds	1e-052	2828799	(U55386) unknown [Anabaena PCC7120]	0.097
4264	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	2e-006	3176395	(AB015041) PIF1 [Caenorhabditis elegans]	3e-005
4265	AF069250	Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds	2e-068	3037018	(AF041330) NADH dehydrogenase subunit 5 [Bodo saltans]	0.002
4266	M11560	Human aldolase A mRNA, complete cds.	0.00E+00	113606	FRUCTOSE-BISPHOSPHATE ALDOLASE A fructose-bisphosphate aldolase (EC 4.1.2.13) A - human sapiens]	5e-055

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
4267	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	2e-009	<NONE>	<NONE>	<NONE>
4268	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	1e-005	2688708	(AE001176) conserved hypothetical protein [Borrelia burgdorferi]	8.5
4269	L35566	Gallus gallus homeobox protein (LH-2) mRNA, complete cds.	6e-041	1708809	HOMEOBOX PROTEIN LH-2 >gi|508712	7e-019
4270	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	1.00E-11	1709997	DNA REPAIR PROTEIN RAD18 >gi|1150622 protein rad18 [Schizosaccharomyces pombe]	6e-027
4271	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	2e-009	586442	NUCLEOPORIN NUP170 (NUCLEAR PORE PROTEIN NUP170) >gi|626192|pir||S45429 probable membrane protein YBL079w - yeast (Saccharomyces cerevisiae) cerevisiae] >gi|536127 (Z35840) ORF YBL079w	0.44
4272	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	3e-013	<NONE>	<NONE>	<NONE>
4273	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
4274	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
4275	X00334	Drosophila virilis simple DNA sequence (pDv-19)	6e-010	119110	EBNA-1 NUCLEAR PROTEIN herpesvirus 4 (strain B95-8) >gi|1334880 (V01555) BKRF1 encodes EBNA-1 protein, latent cycle gene. [Human herpesvirus 4]	2e-016
4276	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	2e-007	<NONE>	<NONE>	<NONE>
4277	AF069250	Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds	2e-068	3037018	(AF041330) NADH dehydrogenase subunit 5 [Bodo saltans]	0.002
4278	Y10183	H.sapiens mRNA for MEMD protein	e-162	<NONE>	<NONE>	<NONE>
4279	D86960	Human mRNA for KIAA0205 gene, complete cds	2e-078	<NONE>	<NONE>	<NONE>
4280	X65319	Cloning vector pCAT-Enhancer	3e-081	987050	(X65335) lacZ gene product [unidentified cloning vector]	3e-015
4281	X86693	H.sapiens mRNA for hevin like protein	0.18	<NONE>	<NONE>	<NONE>
4282	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	0.0001	<NONE>	<NONE>	<NONE>
4283	M33156	A.aegypti D7 gene, exons 1-5.	1.30E+00	<NONE>	<NONE>	<NONE>
4284	X02317	Human mRNA for Cu/Zn superoxide dismutase (SOD)	0	218564	(D90358) HB-SOD [Schizosaccharomyces pombe]	7e-032

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
4285	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	2.00E-04	<NONE>	<NONE>	<NONE>
4286	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	2.00E-04	<NONE>	<NONE>	<NONE>
4287	X02317	Human mRNA for Cu/Zn superoxide dismutase (SOD)	0	134611	SUPEROXIDE DISMUTASE (CU-ZN) dismutase (aa 1-154) [Homo sapiens] >gi|338276 (K00065) superoxide dismutase [Homo sapiens] >gi|1237407 (L44139) Cu/Zn-superoxide dismutase [Homo sapiens]	2e-079
4288	X04408	Human mRNA for coupling protein G(s) alpha subunit adenylyl cyclase)	0	386748	(M14631) guanine nucleotide-binding protein alpha subunit	2e-073
4289	M28161	Rabbit MHC class II RLA-DR-alpha gene, complete cds.	2.4	<NONE>	<NONE>	<NONE>
4290	U33956	Human Down Syndrome region of chromosome 21, genomic sequence, clone A12H1-1F8.	0.37	<NONE>	<NONE>	<NONE>
4291	U90331	Mus musculus neural plakophilin related arm-repeat protein (NPRAP) mRNA, complete cds	0.15	135063	SUPPRESSOR OF SABLE PROTEIN fruit fly (Drosophila melanogaster) >gi|158517 (M57889) su(s) protein	5.2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					[Drosophila melanogaster]	
4292	AF045531	Homo sapiens germline chromosome 22, 22q11.2 region	0.005	<NONE>	<NONE>	<NONE>
4293	D86960	Human mRNA for KIAA0205 gene, complete cds	2e-078	<NONE>	<NONE>	<NONE>
4294	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	2e-005	<NONE>	<NONE>	<NONE>
4295	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	5.00E-03	<NONE>	<NONE>	<NONE>
4296	U17073	Neurospora crassa frequency (frq) mRNA, complete cds.	0.041	3152938	(AF065482) sorting nexin 2 [Homo sapiens]	0.83
4297	M93051	Pisum sativum ascorbate peroxidase (ApxI) gene, complete cds.	0.2	<NONE>	<NONE>	<NONE>
4298	U28153	Caenorhabditis elegans UNC-76 (unc-76) gene, complete cds.	0.37	<NONE>	<NONE>	<NONE>
4299	U28153	Caenorhabditis elegans UNC-76 (unc-76) gene, complete cds.	0.37	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
4300	U20240	Human C/EBP gamma mRNA, complete cds > :: gb|G28590|G28590 human STS SHGC-35371.	e-141	1705750	CCAAT/ENHANCER BINDING PROTEIN GAMMA (C/EBP GAMMA) >gi|1363931|pir||JC4243 transcription CCAAT enhancer binding protein-gamma - human >gi|727294 (U20240) C/EBP gamma [Homo sapiens]	1e-011
4301	Y16359	Calonectris diomedea random amplified polymorphic DNA, clone Cd-O8f1	4e-075	595780	(U13871) lacZ alpha peptide [Cloning vector]	0.0001
4302	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	5e-013	<NONE>	<NONE>	<NONE>
4303	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
4304	U90331	Mus musculus neural plakophilin related arm-repeat protein (NPRAP) mRNA, complete cds	0.15	135063	SUPPRESSOR OF SABLE PROTEIN fruit fly (Drosophila melanogaster) >gi|158517 (M57889) su(s) protein [Drosophila melanogaster]	5.2
4305	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
4306	D86960	Human mRNA for KIAA0205 gene, complete cds	0	1653865	(D90917) UDP-N-acetylglucosamine -N-acetylmuramyl-(pentape ptide) pyrophosphoryl - undecaprenol N-acetylglucosamine transferase [Synechocystis sp.]	4.40E+00

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
4307	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	1e-013	4105520	(AF046933) carboxysome structural polypeptide	2.4
4308	Y14723	Choanomphalus incertus mitochondrial cytochrome c oxidase subunit I gene, partial	0.36	<NONE>	<NONE>	<NONE>
4309	AB018327	Homo sapiens mRNA for KIAA0784 protein, partial cds	0	3882289	(AB018327) KIAA0784 protein [Homo sapiens]	4e-041
4310	AB007860	Homo sapiens KIAA0400 mRNA, complete cds	0	<NONE>	<NONE>	<NONE>
4311	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
4312	U96440	Drosophila melanogaster cut gene, partial sequence	0.053	119110	EBNA-1 NUCLEAR PROTEIN herpesvirus 4 (strain B95-8) >gi|1334880 (V01555) BKRF1 encodes EBNA-1 protein, latent cycle gene. [Human herpesvirus 4]	0.0004
4313	X64707	H.sapiens BBC1 mRNA	3e-090	1350662	60S RIBOSOMAL PROTEIN L13 (A52)	2e-025
4314	U67522	Methanococcus jannaschii section 64 of 150 of the complete genome	0.38	<NONE>	<NONE>	<NONE>
4315	M11560	Human aldolase A mRNA, complete cds.	0.00E+00	113606	FRUCTOSE-BISPHOSPHATE ALDOLASE A fructose-bisphosphate aldolase (EC 4.1.2.13) A - human sapiens]	5e-055

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
4316	X92098	H.sapiens mRNA for transmembrane protein rmp24	e-123	3914237	COP-COATED VESICLE MEMBRANE PROTEIN P24 PRECURSOR (P24A) (RNP24) >gi|1212965|gnl|PID|e205529	1e-017
4317	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
4318	D86960	Human mRNA for KIAA0205 gene, complete cds	0	1653865	(D90917) UDP-N-acetylglucosamine -N-acetylmuramyl-(pentape ptide) pyrophosphoryl - undecaprenol N-acetylglucosamine transferase [Synechocystis sp.]	4.40E+00
4319	M83094	Homo sapiens cytosolic selenium-dependent glutathione peroxidase gene, complete cds, and rhoh12 gene, 3' end.	0.00E+00	<NONE>	<NONE>	<NONE>
4320	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	5e-015	<NONE>	<NONE>	<NONE>
4321	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	7e-007	<NONE>	<NONE>	<NONE>
4322	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	3.3	<NONE>	<NONE>	<NONE>
4323	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	1.40E-02	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
4324	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
4325	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	3e-010	<NONE>	<NONE>	<NONE>
4326	AF088034	Homo sapiens full length insert cDNA clone ZC24F03	0	854598	(X87611) ORF YJR83.18 [Saccharomyces cerevisiae]	2e-024
4327	U47322	Cloning vector DNA, complete sequence.	6.00E-06	<NONE>	<NONE>	<NONE>
4328	U47322	Cloning vector DNA, complete sequence.	6.00E-06	<NONE>	<NONE>	<NONE>
4329	D86960	Human mRNA for KIAA0205 gene, complete cds	0.00E+00	1653865	(D90917) UDP-N-acetylglucosamine -N-acetylmuramyl-(pentape ptide) pyrophosphoryl - undecaprenol N-acetylglucosamine transferase [Synechocystis sp.]	1.4
4330	Z70316	D.melanogaster mRNA for tyramine-beta-hydroxylase	1.5	<NONE>	<NONE>	<NONE>
4331	L28010	Homo sapiens HnRNP F protein mRNA, complete cds	3e-070	1710628	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN F (HNRNP F) >gi|631210|pir||S43484 hnRNP F protein - human >gi|452048 (L28010) HnRNP F protein [Homo sapiens]	2e-005
4332	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	1.40E-01	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
4333	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	0.13	<NONE>	<NONE>	<NONE>
4334	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.004	1723286	VERY HYPOTHETICAL 11.9 KD PROTEIN C4H3.12C IN CHROMOSOME I >gi|1184025 (Z69380) unknown	3.1
4335	<NONE>	<NONE>	<NONE>	2314752	(AE000654) rare lipoprotein A (rlpA) [Helicobacter pylori]	7.3
4336	AB007963	Homo sapiens mRNA for KIAA0494 protein, complete cds	8e-078	3413938	(AB007963) KIAA0494 protein [Homo sapiens]	1.00E-11
4337	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
4338	X12597	Human mRNA for high mobility group-1 protein	3e-048	123371	HIGH MOBILITY GROUP PROTEIN HMG1 protein HMG-1 - pig >gi|164490 (M21683) non-histone protein HMG1 [Sus scrofa]	0.006
4339	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	1e-013	2853095	(AL021767) very hypothetical protein	0.043
4340	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	8e-007	<NONE>	<NONE>	<NONE>
4341	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	7e-006	3063453	(AC003981) F22O13.15 [Arabidopsis thaliana]	4.5

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
4342	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	4.00E-11	231629	BILE-SALT-ACTIVATED LIPASE PRECURSOR ESTER LIPASE) (STEROL ESTERASE) (CHOLESTEROL ESTERASE) salt-activated lipase [Homo sapiens] sapiens]	9.6
4343	L31732	Human STS UT643, 5' primer bind.	1.6	<NONE>	<NONE>	<NONE>
4344	AF037332	Homo sapiens Eph-like receptor tyrosine kinase hEphB1b (EphB1) mRNA, complete cds	0.66	<NONE>	<NONE>	<NONE>
4345	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
4346	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	2.00E-05	<NONE>	<NONE>	<NONE>
4347	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	4e-007	<NONE>	<NONE>	<NONE>
4348	Z30961	H.sapiens DNA for Mhc Alu elements	7.00E-17	728835	!!!! ALU SUBFAMILY SC WARNING ENTRY	0.5
4349	U34887	Yeast integrating vector pRS306 containing a fragment of lacZ.	7e-068	3152967	(Y14016) hypothetical protein	9
4350	D28124	Human mRNA for unknown product, complete cds	0	1825638	(U88172) similar to protein-tyrosine phosphatase	0.062
4351	AF069503	Carcharhinus plumbeus microsatellite repeat region	4.20E+00	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
4352	AF069503	Carcharhinus plumbeus microsatellite repeat region	4.20E+00	<NONE>	<NONE>	<NONE>
4353	D10848	Alkalophilic Bacillus sp. genomic DNA for lipo-penicillinase	0.033	<NONE>	<NONE>	<NONE>
4354	D28124	Human mRNA for unknown product, complete cds	0	1825638	(U88172) similar to protein-tyrosine phosphatase	0.062
4355	U19482	Mus musculus C10-like chemokine mRNA, complete cds	3.70E+00	<NONE>	<NONE>	<NONE>
4356	AF050068	Homo sapiens growth arrest specific 11	1.4	1916844	(U82987) Bcl-2 binding component 3 [Homo sapiens]	0.042
4357	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	2e-005	<NONE>	<NONE>	<NONE>
4358	AE000026	Mycoplasma pneumoniae section 26 of 63 of the complete genome	1.3	<NONE>	<NONE>	<NONE>
4359	<NONE>	<NONE>	<NONE>	2114321	(D88733) membrane glycoprotein [Equine herpesvirus 1]	8.00E-01
4360	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
4361	Y07660	M.tuberculosis accBC gene	2e-068	465847	HYPOTHETICAL 66.5 KD PROTEIN F02A9.5 IN CHROMOSOME III >gi|280542|pir||S28313 hypothetical protein F02A9.5 - Caenorhabditis elegans Genefinder; similar to Propionyl-CoA carboxylase beta chain; cDNA EST EMBL:M89018 comes from this gene; cDNA EST EMBL:D2806	4e-079
4362	U12022	Human calmodulin (CALM1) gene, exons 2,3,4,5 and 6, and complete cds	e-127	<NONE>	<NONE>	<NONE>
4363	AC001178	Homo sapiens (subclone 2_g12 from BAC H94) DNA sequence	3.00E-28	<NONE>	<NONE>	<NONE>
4364	<NONE>	<NONE>	<NONE>	4063042	(AF068065) GP900; mucin-like glycoprotein [Cryptosporidium parvum]	0.52
4365	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
4366	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	1.00E-12	<NONE>	<NONE>	<NONE>
4367	X14448	Human GLA gene for alpha-D-galactosidase A (EC 3.2.1.22)	3	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
4368	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	5.00E-04	3873753	(Z66519) similar to phytoene synthase precursor; cDNA EST yk340f7.3 comes from this gene; cDNA EST yk340f7.5 comes from this gene [Caenorhabditis elegans]	2e-008
4369	X04098	Human mRNA for cytoskeletal gamma-actin	0	<NONE>	<NONE>	<NONE>
4370	M13452	Human lamin A mRNA, 3'end.	0	125962	LAMIN A (70 KD LAMIN)	3e-057
4371	AF068863	Homo sapiens oligodendrocyte-specific protein	3.4	<NONE>	<NONE>	<NONE>
4372	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	1.40E-01	<NONE>	<NONE>	<NONE>
4373	L04636	Homo sapiens pre-mRNA splicing factor 2 p32 subunit (SF2p32) mRNA, complete cds.	0	730772	COMPLEMENT COMPONENT 1, Q SUBCOMPONENT BINDING PROTEIN PRECURSOR (GLYCOPROTEIN GC1QBP) (GC1Q-R PROTEIN) (HYALURONAN-BINDING PROTEIN 1) chain precursor - human >gi|338045 (L04636) splicing factor [Homo sapiens] >gi|472956 (X75913) gCIq-R [Homo sapiens] >gi	2e-050
4374	M59832	Human merosin mRNA, 3' end.	0.043	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
4375	<NONE>	<NONE>	<NONE>	188864	(M74027) mucin [Homo sapiens]	0.042
4376	X17206	Human mRNA for LLRep3	0	88570	ribosomal protein S2 - human (fragment) sapiens]	6e-078
4377	X17206	Human mRNA for LLRep3	0	88570	ribosomal protein S2 - human (fragment) sapiens]	6e-078
4378	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
4379	X98420	S.shibatae topR gene	1.10E+00	2746890	(AF040655) No definition line found [Caenorhabditis elegans]	9.3
4380	X98420	S.shibatae topR gene	1.10E+00	2746890	(AF040655) No definition line found [Caenorhabditis elegans]	9.3
4381	X75787	P.falciparum (FAF-2) mRNA for aspartic hemoglobinase	4	<NONE>	<NONE>	<NONE>
4382	AF044209	Homo sapiens nuclear receptor co-repressor N-CoR mRNA, complete cds	0	3510603	(AF044209) nuclear receptor co-repressor N-CoR [Homo sapiens]	4e-029
4383	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
4384	X64707	H.sapiens BBC1 mRNA	e-110	1350662	60S RIBOSOMAL PROTEIN L13 (A52)	0.003
4385	Z70316	D.melanogaster mRNA for tyramine-beta-hydroxylase	1.5	<NONE>	<NONE>	<NONE>
4386	AF000371	Vitis vinifera UDP glucose:flavonoid 3-o-glucosyltransferase mRNA, partial cds	0.19	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
4387	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	3e-013	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	1.8
4388	AE000688	Aquifex aeolicus section 20 of 109 of the complete genome	3.8	<NONE>	<NONE>	<NONE>
4389	L05612	Dictyostelium purpureum DNA sequence, repeat region.	2.8	<NONE>	<NONE>	<NONE>
4390	U33761	Human cyclin A/CDK2-associated p45 (Skp2) mRNA, complete cds	2e-079	2134952	cyclin A/CDK2-associated p45 - human sapiens]	1e-025
4391	U48288	Rattus norvegicus A-kinase anchoring protein AKAP 220 mRNA, complete cds	0.48	<NONE>	<NONE>	<NONE>
4392	AB007963	Homo sapiens mRNA for KIAA0494 protein, complete cds	0.00E+00	3413938	(AB007963) KIAA0494 protein [Homo sapiens]	6e-071
4393	<NONE>	<NONE>	<NONE>	119110	EBNA-1 NUCLEAR PROTEIN herpesvirus 4 (strain B95-8) >gi|1334880 (V01555) BKRF1 encodes EBNA-1 protein, latent cycle gene. [Human herpesvirus 4]	6e-027
4394	U52784	Ansonia muelleri CMNH H1476 16S rRNA gene, mitochondrial gene encoding mitochondrial rRNA, partial sequence	0.014	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
4395	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
4396	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
4397	U38376	Rattus norvegicus cytosolic phospholipase A2 mRNA, complete cds	1.1	<NONE>	<NONE>	<NONE>
4398	U78770	Mus musculus spasmolytic polypeptide (mSP) gene, complete cds	0.028	<NONE>	<NONE>	<NONE>
4399	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.12	<NONE>	<NONE>	<NONE>
4400	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	2e-014	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	5.8
4401	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	0.0003	<NONE>	<NONE>	<NONE>
4402	X70288	H.sapiens gene for thioredoxin, exons 4 and 5	3e-030	<NONE>	<NONE>	<NONE>
4403	X76683	Plasmid vector pHM2 betalactamase gene	7e-080	987050	(X65335) lacZ gene product [unidentified cloning vector]	3e-015
4404	X69295	H.sapiens MSX2 mRNA for transcription factor	0.43	<NONE>	<NONE>	<NONE>
4405	U20371	Mus musculus homeobox protein (Hoxa11) gene, complete cds.	0.6	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
4406	D49842	Rabbit mRNA for CD86, complete cds	1.10E+00	135554	TETRACYCLINE RESISTANCE PROTEIN Bacillus cereus plasmid pBC16 >gi|72838|pir||YTSOG tetracycline resistance protein - Streptococcus agalactiae plasmid pMV158 >gi|80428|pir||JQ1211 tetracycline resistance protein - Bacillus sp. plasmid pTB19 >gi|151696 (M63	1.4
4407	AB007194	Oryza sativa mRNA for fructose-1,6-bisphosphatase (plastidic isoform), complete cds	3.5	<NONE>	<NONE>	<NONE>
4408	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	1e-007	<NONE>	<NONE>	<NONE>
4409	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
4410	U28924	Pisum sativum cytosolic glutamine synthetase	0.008	3769486	(AF074946) DNA polymerase [hemorrhagic enteritis virus]	1.3
4411	D30783	Homo sapiens mRNA for epiregulin, complete cds	0	1723438	HYPOTHETICAL 52.3 KD PROTEIN C56F8.06C IN CHROMOSOME I PRECURSOR >gi|1204228 (Z69728) unknown [Schizosaccharomyces pombe]	0.13
4412	AJ012449	Homo sapiens mRNA for NS1-binding protein	0	3851214	(AJ012449) NS1-binding protein [Homo sapiens]	4e-088

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
4413	X62357	H.sapiens Alu repeat (clones 2-48)	1e-006	<NONE>	<NONE>	<NONE>
4414	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	6.00E-05	<NONE>	<NONE>	<NONE>
4415	Z15015	D.pulex mitochondrion genes for NADH dehydrogenase subunit 2, cytochrome C oxidase subunit I, tRNA-Val, tRNA-Ile, tRNA-Gln, tRNA-fMet, tRNA-Trp, tRNA-Cys, tRNA-Tyr, small subunit rRNA, large subunit rRNA	2.2	1076802	extensin-like protein - maize >gi|600118	8e-027
4416	D87942	Homo sapiens mRNA for alpha(1,2)fucosyl transferase, complete cds	2e-027	728838	!!!! ALU SUBFAMILY SX WARNING ENTRY	7.5
4417	D86977	Human mRNA for KIAA0224 gene, complete cds	0	3024898	PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE KIAA0224 (HA4657) putative ATP-dependent RNA helicase K03H1.2 of C.elegans(S41025) [Homo sapiens] >gi|3123906 (AF038391) pre-mRNA splicing factor [Homo sapiens]	2e-053

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
4418	L28010	Homo sapiens HnRNP F protein mRNA, complete cds	0	1710628	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN F (HNRNP F) >gi|631210|pir||S43484 hnRNP F protein - human >gi|452048 (L28010) HnRNP F protein [Homo sapiens]	5e-045
4419	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	3e-009	<NONE>	<NONE>	<NONE>
4420	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	3e-009	<NONE>	<NONE>	<NONE>
4421	X14313	Arabidopsis CRB gene for 12S seed storage protein > gene, exons 1-4.	0.24	<NONE>	<NONE>	<NONE>
4422	X14313	Arabidopsis CRB gene for 12S seed storage protein > gene, exons 1-4.	0.24	<NONE>	<NONE>	<NONE>
4423	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	3e-009	<NONE>	<NONE>	<NONE>
4424	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	3.00E-08	1125753	(U42833) coded for by C. elegans cDNA CEESN37F; Similar to ammonium transport protein. [Caenorhabditis elegans]	1e-019
4425	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	2.00E-05	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
4426	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	3e-009	1125753	(U42833) coded for by C. elegans cDNA CEESN37F; Similar to ammonium transport protein. [Caenorhabditis elegans]	2e-008
4427	AF053649	Homo sapiens cellular apoptosis susceptibility protein (CSE1) gene, exons 15 and 16	3e-008	<NONE>	<NONE>	<NONE>
4428	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	1e-007	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	8.8
4429	X94253	S.scrofa mRNA for heterogeneous nuclear ribonucleoprotein	6e-023	<NONE>	<NONE>	<NONE>
4430	AF005039	Homo sapiens secretory carrier membrane protein	0	2232243	(AF005039) secretory carrier membrane protein [Homo sapiens]	8e-008
4431	AF037332	Homo sapiens Eph-like receptor tyrosine kinase hEphB1b (EphB1) mRNA, complete cds	0.12	3861156	(AJ235272) unknown [Rickettsia prowazekii]	0.37
4432	D28124	Human mRNA for unknown product, complete cds	7e-067	<NONE>	<NONE>	<NONE>
4433	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	3e-013	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
4434	M93426	Human protein tyrosine phosphatase zeta-polypeptide (PTPRZ) mRNA, complete cds. > :: gb|G20044|G20044 sWSS1987 Eric D. Green Homo sapiens STS genomic, sequence tagged site [Homo sapiens]	0	400199	PROTEIN-TYROSINE PHOSPHATASE ZETA PRECURSOR (R-PTP-ZETA) >gi|476869|pir||A46151 protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type zeta - human >gi|190744 (M93426) protein tyrosine phosphatase zeta-polypeptide [Homo sapiens]	4e-051
4435	U54562	Human translation initiation factor eIF3 p48 subunit (Int-6) mRNA, complete cds	0	2498490	VIRAL INTEGRATION SITE PROTEIN INT-6 >gi|1854579 (L35556) Int-6 [Mus musculus] sapiens] >gi|2351382 (U54562) eIF3-p48 [Homo sapiens] sapiens]	e-110
4436	U54562	Human translation initiation factor eIF3 p48 subunit (Int-6) mRNA, complete cds	0	2498490	VIRAL INTEGRATION SITE PROTEIN INT-6 >gi|1854579 (L35556) Int-6 [Mus musculus] sapiens] >gi|2351382 (U54562) eIF3-p48 [Homo sapiens] sapiens]	e-110
4437	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.12	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
4438	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	3e-009	<NONE>	<NONE>	<NONE>
4439	X03558	Human mRNA for elongation factor 1 alpha subunit	0	1169475	ELONGATION FACTOR 1-ALPHA 1	4e-083
4440	J03607	Human 40-kDa keratin intermediate filament precursor gene.	0	1070608	keratin 19, type I, cytoskeletal - human sapiens]	4e-058
4441	<NONE>	<NONE>	<NONE>	4063042	(AF068065) GP900; mucin-like glycoprotein [Cryptosporidium parvum]	0.011
4442	<NONE>	<NONE>	<NONE>	4063042	(AF068065) GP900; mucin-like glycoprotein [Cryptosporidium parvum]	0.011
4443	Y13401	Homo sapiens CD3 delta gene, enhancer sequence	8e-008	<NONE>	<NONE>	<NONE>
4444	X04409	Human mRNA for coupling protein G(s) alpha-subunit (alpha-S1) (stimulatory regulatory component Gs of adenylyl cyclase)	0	71879	GTP-binding regulatory protein Gs alpha chain G-s-alpha-4 [Homo sapiens]	7e-092
4445	AF038958	Homo sapiens synaptic glycoprotein SC2 spliced variant mRNA, complete cds	1e-072	3329386	(AF038958) synaptic glycoprotein SC2 spliced variant	6e-019
4446	D17244	Human HepG2 3' region MboI cDNA, clone hmd4h04m3	1e-075	2500256	50S RIBOSOMAL PROTEIN L13 protein L13 [Streptomyces coelicolor]	0.043

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
4447	<NONE>	<NONE>	<NONE>	4063042	(AF068065) GP900; mucin-like glycoprotein [Cryptosporidium parvum]	0.005
4448	M24597	Beet curly top virus (clone pBCT028) DNA, complete genome.	4.1	<NONE>	<NONE>	<NONE>
4449	U59706	Gallus gallus alternatively spliced AMPA glutamate receptor, isoform GluR2 flop, (GluR2) mRNA, partial cds.	0.014	3283975	(AF072521) poly-(ADPribosyl)-transferase homolog PARP	0.02
4450	AJ010014	Homo sapiens mRNA for M96A protein	0	3342452	(AF072814) PHD finger DNA binding protein isoform 1	2e-029
4451	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
4452	X06960	Aspergillus nidulans mitochondrial DNA for cytochrome oxidase subunit 3, tRNA-Tyr	0.23	<NONE>	<NONE>	<NONE>
4453	L01089	Human profilaggrin (FLG) gene exons 2-3, 5'end.	1.3	<NONE>	<NONE>	<NONE>
4454	X65319	Cloning vector pCAT-Enhancer	1e-071	987050	(X65335) lacZ gene product [unidentified cloning vector]	1e-014
4455	X87212	H.sapiens mRNA for cathepsin C	0	1582221	prepro-cathepsin C [Homo sapiens]	6e-046
4456	X53123	Cloning vector pAST 19a for C. elegans	5	<NONE>	<NONE>	<NONE>
4457	D15057	Human mRNA for DAD-1, complete cds	0	2944452	(AF051310) defender against death 1 [Mus musculus]	1e-015

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
4458	X83860	H.sapiens mRNA for prostaglandin E receptor (EP3c)	1.2	2137044	unknown protein - rabbit (fragment) cuniculus]	7e-014
4459	M95058	Rattus rattus steroid 5-alpha-reductase 2 mRNA, complete cds.	0.42	<NONE>	<NONE>	<NONE>
4460	AF044588	Homo sapiens protein regulating cytokinesis 1	2e-043	2865521	(AF044588) protein regulating cytokinesis 1; PRC1 [Homo sapiens]	4e-015
4461	X54282	Human chromosome 11 DNA, approx. 20 kb 3' of beta-globin gene, nuclear scaffold associated region	0.014	1911867	cadherin 3 [Caenorhabditis elegans, Peptide, 3337 aa]	9.8
4462	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	3e-010	3875640	(Z92781) F09C3.3 [Caenorhabditis elegans]	9.6
4463	M73791	Human novel gene mRNA, complete cds.	0	1172810	60S RIBOSOMAL PROTEIN L10 (QM PROTEIN HOMOLOG) >gi|543339|pir||JC 2013 ribosomal protein L10, cytosolic - mouse >gi|2143959|pir||JC4911 ribosomal protein L10 - rat >gi|407466 (X75312) QM protein [Mus musculus] >gi|410742 (M93980) 24.6 kda protein [Mus musc	7e-085
4464	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
4465	Z27116	S.cerevisiae HBS1, MRP-L20 and PRP-16 genes	0.058	<NONE>	<NONE>	<NONE>
4466	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
4467	M96575	Drosophila melanogaster collagen type IV gene, complete cds.	3.60E+00	<NONE>	<NONE>	<NONE>
4468	D50010	Human DNA for alpha-platelet-derived growth factor receptor, exon 15	1e-006	<NONE>	<NONE>	<NONE>
4469	X70649	Homo sapiens DDX1 gene, complete CDS	0	539572	DEAD box protein RB - human	3e-036
4470	AJ223377	Puumala virus S-segment RNA	1.4	<NONE>	<NONE>	<NONE>
4471	Y14599	Staphylococcus xylosus lacR, lacP, lacH genes and 2 ORF's	1.4	3659505	(AC005084) similar to mouse mCASK-A; similar to e1288039	0.63
4472	X13336	Spinach plastid genes rps3, rps19, rpl14, rpl16 and rpl22 for ribosomal proteins S3, S19, L14, L16 and L22	0.15	1330375	(U58758) similar to rat GAP-associated protein p190	0.27
4473	AF056022	Homo sapiens p60 katanin mRNA, complete cds	0	3283072	(AF056022) p60 katanin [Homo sapiens]	7e-029
4474	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.0002	<NONE>	<NONE>	<NONE>
4475	M86849	Human connexin 26 (GJB2) mRNA.	0	127542	ALDOSE 1-EPIMERASE PRECURSOR calcoaceticus]	5.2
4476	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
4477	X95455	G.gallus mRNA for RING zinc finger	9e-031	1321818	(X95455) RING zinc finger protein protein [Gallus	9e-038

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					gallus]	
4478	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	0.13	<NONE>	<NONE>	<NONE>
4479	J03607	Human 40-kDa keratin intermediate filament precursor gene.	0	1070608	keratin 19, type I, cytoskeletal - human sapiens]	9e-068
4480	M90104	Human splicing factor SC35 mRNA, complete cds.	e-120	3929382	SPLICING FACTOR, ARGININE/SERINE-RICH 10 (PUTATIVE MYELIN REGULATORY FACTOR 1) (MRF-1) >gi|555924 (U14648) putative myelin regulatory factor 1; MRF-1 [Mus musculus]	1.1
4481	AF020762	Homo sapiens clone 1400 unknown protein mRNA, partial cds	6e-067	<NONE>	<NONE>	<NONE>
4482	AE001386	Plasmodium falciparum chromosome 2, section 23 of 73 of the complete sequence	0.72	<NONE>	<NONE>	<NONE>
4483	AF054868	Pseudomonas aeruginosa autoinducer synthetase chloramphenicol-sensitive protein (rarD), and hypothetical protein (yafL) gene...	0.005	1709793	SALIVARY PROLINE-RICH PROTEIN PO sapiens]	0.13
4484	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
4485	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
4486	AE001406	Plasmodium falciparum chromosome 2, section 43 of 73 of the complete sequence	0.001	<NONE>	<NONE>	<NONE>
4487	AE001417	Plasmodium falciparum chromosome 2, section 54 of 73 of the complete sequence	2.1	<NONE>	<NONE>	<NONE>
4488	X90446	Canine herpesvirus DNA for ORF 1 (HSV1 UL44, EHV1 ORF 15 homolog) ORF2 (EHV1 ORF 16 homolog)	4.4	<NONE>	<NONE>	<NONE>
4489	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.17	4008355	(Z68297) Similarity to Yeast TAT-binding homolog 7 (SW:TBP7_YEAST); cDNA EST EMBL:D37124 comes from this gene; cDNA EST EMBL:D35150 comes from this gene; cDNA EST EMBL:D35400 comes from this gene; cDNA EST EMBL:D34900 comes ... >gi|4008373|gnl|PID|e135984	3e-007
4490	D78130	Homo sapiens mRNA for squalene epoxidase, complete cds	0	2443316	(D78130) squalene epoxidase [Homo sapiens]	5e-008
4491	L18931	Buchnera aphidicola Arginyl tRNA synthetase	0.16	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		promoter region.				
4492	X17206	Human mRNA for LLRep3	e-112	1350976	40S RIBOSOMAL PROTEIN S2 >gi|939718	2e-005
4493	D28473	Human T-lymphocyte mRNA for isoleucyl-tRNA synthetase, complete cds	e-157	440799	(U04953) isoleucyl-tRNA synthetase [Homo sapiens]	3e-005
4494	L13624	Cercopithecus aethiops C4 complement	3.6	<NONE>	<NONE>	<NONE>
4495	M13011	Rat c-ras-H-1 gene, complete cds.	0.25	<NONE>	<NONE>	<NONE>
4496	Y10252	L.japonicus panC gene	0.38	627071	histidine-rich protein - Plasmodium lophurae	4.4
4497	X76683	Plasmid vector pHM2 betalactamase gene	1e-093	987050	(X65335) lacZ gene product [unidentified cloning vector]	3e-015
4498	M24486	Human prolyl 4-hydroxylase alpha subunit mRNA, complete cds, clone PA-11.	0	129365	PROLYL 4-HYDROXYLASE ALPHA SUBUNIT 1.14.11.2) alpha chain - chicken	2e-057
4499	D80004	Human mRNA for KIAA0182 gene, partial cds	2e-068	<NONE>	<NONE>	<NONE>
4500	U22233	Human methylthioadenosine phosphorylase (MTAP) mRNA, complete cds.	0	<NONE>	<NONE>	<NONE>
4501	D63875	Human mRNA for KIAA0155 gene, complete cds > :: gb|G28541|G28541 human STS SHGC-31621.	0	961442	(D63875) KIAA0155 gene product is related to C.elegans B0464.2 protein. [Homo sapiens]	2e-019

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
4502	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
4503	X85018	H.sapiens mRNA for UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase (T1)	e-110	1709559	POLYPEPTIDE N-ACETYLGALACTOSAMINYLTRANSFERASE (PROTEIN-UDP ACETYLGALACTOSAMINYLTRANSFERASE) N-ACETYLGALACTOSAMINYLTRANSFERASE) (GALNAC-T1) polypeptide N-acetylgalactosaminyltransferase [Rattus norvegicus]	2e-018
4504	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
4505	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
4506	AF067782	Papio hamadryas BC200 alpha scRNA gene, complete sequence	0.48	<NONE>	<NONE>	<NONE>
4507	AF073298	Homo sapiens 4F5rel mRNA, complete cds	e-166	3641536	(AF073297) 4F5rel [Mus musculus] >gi|3641538 (AF073298) 4F5rel [Homo sapiens]	3e-013
4508	M12922	Yeast (S.cerevisiae) chromosome III L terminal region DNA.	2e-010	188864	(M74027) mucin [Homo sapiens]	6e-023
4509	X69524	M.squamata cabc1 mRNA for chlorophyll a/b/c binding protein precursor	1.3	<NONE>	<NONE>	<NONE>
4510	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	1.2	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
4512	U12404	Human Csa-19 mRNA, complete cds.	0	1709973	60S RIBOSOMAL PROTEIN L10A (CSA-19)	4e-056
4513	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	8e-014	<NONE>	<NONE>	<NONE>
4514	<NONE>	<NONE>	<NONE>	121627	GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN 1 PRECURSOR >gi|82244|pir||A26 099 glycine-rich cell wall structural protein - garden petunia >gi|20553 hybrida] >gi|225181|prf||12 10313A Gly rich structural protein [Petunia sp.]	2e-030
4515	D87255	Hepatitis G virus RNA for polyprotein, complete cds	0.19	930045	(X15332) alpha-1 (III) collagen [Homo sapiens]	0.002
4516	U31820	Gallus gallus Mel-1a melatonin receptor mRNA, complete cds.	3.3	1718187	ENVELOPE GLYCOPROTEIN GP340 glycoprotein 350/220 - human herpesvirus 4 >gi|59164 virus] >gi|306293 (L07923) glycoprotein 340	0.096
4517	X68107	M.sativa msCHSII mRNA for chalcone synthase	3.4	<NONE>	<NONE>	<NONE>
4518	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
4519	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	6e-006	1065484	(U40415) similar to S. cerevisiae LAG1 (SP:P38703)	0.001

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
4520	D87671	Rat mRNA for TIP120, complete cds	1e-043	1799570	(D87671) TIP120 [Rattus norvegicus]	0.01
4521	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
4522	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
4523	X16869	Human mRNA for elongation factor 1-alpha (clone CEF4)	4e-022	1085204	translation elongation factor eEF-1 alpha chain - zebra fish >gi|408805 (L23807) elongation factor 1-alpha [Danio rerio] >gi|454915 (X77689) translational elongation factor-1 alpha [Danio rerio] >gi|1009241 rerio] >gi|1091578|prf||2021264A elongation fact	5.1
4524	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	3e-010	<NONE>	<NONE>	<NONE>
4525	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	2e-007	<NONE>	<NONE>	<NONE>
4526	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
4527	AF069250	Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds	7e-080	3037018	(AF041330) NADH dehydrogenase subunit 5 [Bodo saltans]	0.0001
4528	AF069250	Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds	7e-080	3037018	(AF041330) NADH dehydrogenase subunit 5 [Bodo saltans]	0.0001

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
4529	U66532	Human beta4-integrin (ITGB4) gene, exons 7,8,9,10,11 and 12	0.51	119110	EBNA-1 NUCLEAR PROTEIN herpesvirus 4 (strain B95-8) >gi|1334880 (V01555) BKRF1 encodes EBNA-1 protein, latent cycle gene. [Human herpesvirus 4]	1e-023
4530	X65319	Cloning vector pCAT-Enhancer	1e-074	987050	(X65335) lacZ gene product [unidentified cloning vector]	8e-011
4531	AJ010841	Homo sapiens mRNA for putative thioredoxin-like protein	8e-028	3646128	(AJ010841) thioredoxin-like protein	0.062
4532	D14034	Human gene for Zn-alpha2-glycoprotein, complete cds	0.005	<NONE>	<NONE>	<NONE>
4533	M12670	Human fibroblast collagenase inhibitor mRNA, complete cds.	6e-098	1351250	METALLOPROTEINASE INHIBITOR 1 PRECURSOR (TIMP-1) >gi|1363927|pir||JC4303 matrix metalloproteinase-1 tissue inhibitor - baboon >gi|561546 hamadryas cynocephalus]	7e-008
4534	M17196	A.californica (marine gastropod mollusc) neuropeptide gene (ganglion R14), exon 1, 5' end.	0.019	2135765	mucin 2 precursor, intestinal - human	0.003
4535	AJ001454	Homo sapiens mRNA for testican-3	1.4	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
4536	X75757	G.gallus cycB3 mRNA.	9e-040	729112	G2/MITOTIC-SPECIFIC CYCLIN B3	9e-019
4537	Z27116	S.cerevisiae HBS1, MRP-L20 and PRP-16 genes	0.058	<NONE>	<NONE>	<NONE>
4538	AF083322	Homo sapiens centriole associated protein CEP110 mRNA, complete cds	9e-051	1079393	chromokinesin - chicken >gi|603761 (U18309) chromokinesin [Gallus gallus]	0.012
4539	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
4540	M26325	Human cytokeratin 18 mRNA, 3' end.	0	125083	KERATIN, TYPE I CYTOSKELETAL 18 keratin 18, type I, cytoskeletal - human >gi|34037	2e-093
4541	U37066	Human endogenous retrovirus strain XA38 pol polyprotein (pol) gene, partial cds	1.3	252486	P-selectin, CD62 [mice, Peptide, 768 aa] musculus]	1.8
4542	Z30543	Turkey herpesvirus (HVT-delUs-Beta1 PKI3) gene for protein kinase	2e-027	<NONE>	<NONE>	<NONE>
4543	M90077	Wheat translation elongation factor 1 alpha-subunit (TEF1) mRNA, complete cds.	0.14	<NONE>	<NONE>	<NONE>
4544	AJ001235	Papio hamadryas ERV-9 like LTR insertion	2e-044	<NONE>	<NONE>	<NONE>
4545	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
4546	AF100654	Caenorhabditis elegans cosmid C24E9	0.41	<NONE>	<NONE>	<NONE>
4547	L28821	Homo sapiens alpha mannosidase II isozyme mRNA, complete cds.	0	1679607	(X97650) myosin-I [Mus musculus]	4.5

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
4548	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	4e-013	<NONE>	<NONE>	<NONE>
4549	L20140	Zea mays pollen specific pectate lyase homologue gene, complete cds.	0.92	<NONE>	<NONE>	<NONE>
4550	U33955	Human Down Syndrome region of chromosome 21, genomic sequence, clone A12H1-1F2.	4.4	<NONE>	<NONE>	<NONE>
4551	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	0.0005	<NONE>	<NONE>	<NONE>
4552	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	0.042	<NONE>	<NONE>	<NONE>
4553	X12660	Human chromosome 14 Ig JH (switch mu) DNA showing scattered homology to bcl2 gene exon 2 3'UTR	1e-006	2117245	(Z95586) hypothetical protein Rv1592c	2.1
4554	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.002	284314	modulator recognition factor 1 - human factor I [Homo sapiens]	7.1
4555	AF070523	Homo sapiens JWA protein mRNA, complete cds	0	3322740	(AE001222) conserved hypothetical protein [Treponema pallidum]	5.9
4556	Z11900	H.sapiens OTF3 gene	0.13	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
4557	M24972	D.discoideum CT-rich satellite rDNA, clone pCT8.	4e-007	2605798	(AF027735) minor ampullate silk protein MiSp1 [Nephila clavipes]	5.30E-01
4558	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	8e-007	<NONE>	<NONE>	<NONE>
4559	D32056	Human gene for 2-oxoglutarate dehydrogenase, exon 1 sequence	0.06	<NONE>	<NONE>	<NONE>
4560	AF034085	Caenorhabditis elegans UNC-45 (unc-45) gene, complete cds	0.025	1652167	(D90903) hypothetical protein	4.8
4561	AF091242	Homo sapiens ATP sulfurylase/APS kinase 2 mRNA, complete cds	0.0003	<NONE>	<NONE>	<NONE>
4562	M31520	Human ribosomal protein S24 mRNA.	1e-031	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	5.7
4563	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
4564	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	0.0005	<NONE>	<NONE>	<NONE>
4565	AB015432	Rattus norvegicus mRNA for LAT1 (L-type amino acid transporter 1), complete cds	4e-022	1665759	(D87432) Similar to Schistosoma mansoni amino acid permease (L25068). [Homo sapiens]	5e-024
4566	AE001397	Plasmodium falciparum chromosome 2, section 34 of 73 of the complete sequence	0.0005	3875266	(Z77655) predicted using Genefinder; similar to 7tm receptor [Caenorhabditis elegans]	5.90E+00

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
4567	AE001397	Plasmodium falciparum chromosome 2, section 34 of 73 of the complete sequence	0.0005	3875266	(Z77655) predicted using Genefinder; similar to 7tm receptor [Caenorhabditis elegans]	5.90E+00
4568	Y15155	Homo sapiens PHKB gene, exon 8, and repetitive elements	4e-033	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	5.7
4569	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	2.00E-03	2622750	(AE000921) DNA topoisomerase I [Methanobacterium thermoautotrophicum]	2.6
4570	AE000688	Aquifex aeolicus section 20 of 109 of the complete genome	4.5	<NONE>	<NONE>	<NONE>
4571	Z95123	Caenorhabditis elegans cosmid VZK822l, complete sequence [Caenorhabditis elegans]	0.4	<NONE>	<NONE>	<NONE>
4572	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	3.00E-08	<NONE>	<NONE>	<NONE>
4573	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	4e-012	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	3.3
4574	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	7e-006	<NONE>	<NONE>	<NONE>
4575	U18671	Human Stat2 gene, complete cds.	2e-023	728831	!!!! ALU SUBFAMILY J WARNING ENTRY	0.002

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
4576	Z83241	Caenorhabditis elegans cosmid T25C8, complete sequence [Caenorhabditis elegans]	1.1	1176988	IOLD PROTEIN protein [Bacillus subtilis] >gi|2636519|gnl|PID|e1184698 catabolism [Bacillus subtilis]	5.3
4577	L04690	Cricetulus griseus cholesterol 7-alpha-hydroxylase gene, complete cds. > :: gb|I26617|I26617 Sequence 35 from patent US 5558999 > :: gb|AR008072|AR008072 Sequence 35 from patent US 5753431	3.2	212906	(L02621) intestinal zipper protein [Gallus gallus]	4.1
4578	Z54191	A.pleuropneumoniae tfbB gene encoding transferrin receptor.	0.54	2102696	(U72761) karyopherin beta 3 [Homo sapiens]	8.6
4579	X17025	Human homolog of yeast IPP isomerase > :: gb|G27043|G27043 human STS SHGC-31614.	2e-035	<NONE>	<NONE>	<NONE>
4580	L32977	Homo sapiens (clone f17252) ubiquinol cytochrome c reductase Rieske iron-sulphur protein (UQCRFS1) gene, exon 2	0.00E+00	1351361	UBIQUINOL-CYTOCHROME C REDUCTASE IRON-SULFUR SUBUNIT PRECURSOR (RIESKE IRON-SULFUR PROTEIN) (RISP) >gi|488299 (L32977) Rieske Fe-S protein	1e-070
4581	M26708	Human prothymosin alpha mRNA (ProT-alpha), complete cds.	0	190369	(J04798) open reading frame A; putative [Homo sapiens]	6e-018

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
4582	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	2e-014	2314130	(AE000607) H. pylori predicted coding region HP0985	3.3
4583	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	4e-011	1236083	(U49507) Lisch7 [Mus musculus]	4.3
4584	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	2e-014	348196	(L19917) immunoglobulin heavy-chain subgroup VIII V-D-J region [Homo sapiens]	9.7
4585	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
4586	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
4587	X52601	H.sapiens hTOP1 gene for topoisomerase, 5'end	4.6	<NONE>	<NONE>	<NONE>
4588	AF038604	Caenorhabditis elegans cosmid B0546	0.17	<NONE>	<NONE>	<NONE>
4589	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
4590	U23441	Tetrahymena thermophila B internal deletion sequence.	0.0005	1469281	(U08801) envelope glycoprotein [Human immunodeficiency virus type 1]	1.1
4591	AC005276	Homo sapiens clone fragment UWGC:gap3 from 7q31.3, complete sequence [Homo sapiens]	0.009	<NONE>	<NONE>	<NONE>
4592	D84117	Homo sapiens DNA for prostacyclin synthase, exon 3	0.48	<NONE>	<NONE>	<NONE>
4593	U28153	Caenorhabditis elegans UNC-76 (unc-76) gene, complete cds.	1.30E-01	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
4594	U67274	Human metastasis suppressor (KAI1) gene, exon 1, and complete cds	1e-008	<NONE>	<NONE>	<NONE>
4595	AF009621	Onchocerca volvulus cytosolic Cu/Zn superoxide dismutase (OvSOD1) and extracellular Cu/Zn superoxide dismutase (OvSOD2) genes, complete cds	4	<NONE>	<NONE>	<NONE>
4596	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
4597	<NONE>	<NONE>	<NONE>	2078483	(U43200) antifreeze glycopeptide AFGP polyprotein precursor [Boreogadus saida]	0.78
4598	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
4599	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
4600	AL021806	Homo sapiens DNA sequence from PAC 779B17 on chromosome 22q13.1. Contains exon trap, complete sequence	4e-029	728836	!!!! ALU SUBFAMILY SP WARNING ENTRY	0.002
4601	AL022222	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-118, complete sequence	4.9	<NONE>	<NONE>	<NONE>
4602	Z73149	N.tabacum DNA (recombination breakpoint between T-DNA and plant DNA)	1.6	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
4603	AF082835	Mus spretus E6-AP ubiquitin-protein ligase	4	<NONE>	<NONE>	<NONE>
4604	AF050123	Homo sapiens hypoxia-inducible factor 1 alpha subunit (HIF1A) gene, exon 10	3e-009	728838	!!!! ALU SUBFAMILY SX WARNING ENTRY	6.7
4605	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	7e-006	<NONE>	<NONE>	<NONE>
4606	AF001355	Pseudomonas syringae pv. syringae DNA binding protein HpkR (hpkR), histidine protein kinase HpkY (hpkY), phosphate acceptor regulatory protein CheY-2 (cheY-2), ankyrin AnkF (ankF), and catalase isozyme catalytic subuni...	2.1	3041736	TRANSCRIPTION FACTOR SOX-11	8.9
4607	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	8.00E-08	3123155	HYPOTHETICAL 49.0 KD TRP-ASP REPEATS CONTAINING PROTEIN F55F8.5 IN CHROMOSOME I family [Caenorhabditis elegans]	2e-027
4608	<NONE>	<NONE>	<NONE>	1170978	MYOCYTE NUCLEAR FACTOR (MNF) musculus]	0.18
4609	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	4e-009	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	8.9

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
4610	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	2e-007	<NONE>	<NONE>	<NONE>
4611	X75861	H.sapiens TEGT gene	e-177	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	2.8
4612	U19867	Cloning vector pSPL3, exon splicing vector, complete sequence, HIV envelope protein gp160 and beta-lactamase, complete cds.	5e-055	987050	(X65335) lacZ gene product [unidentified cloning vector]	3e-011
4613	U73332	Human non-coding genomic sequence upstream from unique L0 sequence in the alpha-globin gene cluster	8e-008	<NONE>	<NONE>	<NONE>
4614	<NONE>	<NONE>	<NONE>	193952	(J03770) homeobox protein [Mus musculus]	6
4615	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	6e-006	586875	HYPOTHETICAL 29.2 KD PROTEIN IN METS-KSGA INTERGENIC REGION >gi|2127033|pir||S 66068 hypothetical protein - Bacillus subtilis subtilis] >gi|2632306|gnl|PI D|e1181972 (Z99104) similar to hypothetical proteins [Bacillus subtilis]	5e-019
4616	K00384	Yeast (S.cerevisiae) mitochondrial var1 gene, 5'	0.001	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		flank.				
4617	J04628	Rattus norvegicus 3-hydroxyiso-butyrate mRNA, 3' end.	e-154	416873	3-HYDROXYISOBUTYRATE DEHYDROGENASE PRECURSOR (HIBADH) >gi|111295|pir||A32867 3-hydroxyisobutyrate dehydrogenase (EC 1.1.1.31) precursor - rat (fragment) >gi|556389 (J04628) 3-hydroxyisobutyrate dehydrogenase [Rattus norvegicus]	1e-049
4618	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	0.38	<NONE>	<NONE>	<NONE>
4619	U10361	Saccharomyces cerevisiae Snf8p (SNF8) gene, complete cds.	2.7	<NONE>	<NONE>	<NONE>
4620	D42044	Human mRNA for KIAA0090 gene, partial cds	e-151	577301	(D42044) The ha3523 gene product is related to S.cerevisiae gene product located in chromosome III. [Homo sapiens]	4e-052
4621	U10361	Saccharomyces cerevisiae Snf8p (SNF8) gene, complete cds.	2.7	<NONE>	<NONE>	<NONE>
4622	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
4623	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	3.00E-10	<NONE>	<NONE>	<NONE>
4624	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	3.00E-10	<NONE>	<NONE>	<NONE>
4625	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
4626	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
4627	X06747	Human hnRNP core protein A1	7e-049	87650	heterogeneous ribonuclear particle protein A1.beta - human >gi|36102 (X06747) protein A1-alpha (AA 1-320) [Homo sapiens]	6e-005
4628	X03559	Human mRNA for F1-ATPase beta subunit (F-1 beta) > :: dbj|D00022|HUMF1B Homo sapiens mRNA for F1 beta subunit, complete cds	e-100	114549	ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR >gi|106207|pir||A33370 H+-transporting ATP synthase (EC 3.6.1.34) beta chain precursor, mitochondrial - human >gi|179281 (M27132) ATP synthase beta subunit precursor [Homo sapiens]	2e-024
4629	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
4630	K00915	paramecium species 1,168 mt dna dimer: replication init. region.	7.00E-05	<NONE>	<NONE>	<NONE>
4631	K00915	paramecium species 1,168 mt dna dimer: replication init. region.	7.00E-05	<NONE>	<NONE>	<NONE>
4632	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
4633	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
4634	Z28261	S.cerevisiae chromosome XI reading frame ORF YKR036c	0.042	417748	PROTEIN TRANSPORT PROTEIN SEC13	0.0002
4635	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	2e-005	<NONE>	<NONE>	<NONE>
4636	AF088034	Homo sapiens full length insert cDNA clone ZC24F03	0	854598	(X87611) ORF YJR83.18 [Saccharomyces cerevisiae]	2e-024
4637	M83094	Homo sapiens cytosolic selenium-dependent glutathione peroxidase gene, complete cds, and rhoh12 gene, 3' end.	3.00E-08	<NONE>	<NONE>	<NONE>
4638	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	2e-006	1176711	HYPOTHETICAL 21.6 KD PROTEIN F37A4.2 IN CHROMOSOME III >gi|1078851|pir||S 44639 F37A4.2 protein - Caenorhabditis elegans >gi|458960	2e-017
4639	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	2e-006	1176711	HYPOTHETICAL 21.6 KD PROTEIN F37A4.2 IN CHROMOSOME III >gi|1078851|pir||S 44639 F37A4.2 protein - Caenorhabditis elegans >gi|458960	2e-017

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
4640	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	2e-006	<NONE>	<NONE>	<NONE>
4641	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	2e-006	<NONE>	<NONE>	<NONE>
4642	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	2e-005	4056582	(AF039530) RepA [Egyptian sugarcane streak virus]	3.4
4643	U96174	Onchocerca volvulus OvB8 mRNA, partial cds	3.2	<NONE>	<NONE>	<NONE>
4644	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
4645	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	6e-005	3236220	(U62541) immunoreactive 14 kDa protein BA14k [Brucella abortus]	4.5
4646	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	6e-005	3236220	(U62541) immunoreactive 14 kDa protein BA14k [Brucella abortus]	4.5
4647	AL010224	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-04, complete sequence	0.003	2492906	ANNEXIN VII (SYNEXIN) frog >gi|790544 (U16365) annexin VII [Xenopus laevis]	1.4
4648	L39413	Atractylodes japonica chloroplast NADH dehydrogenase (ndhF) gene, complete cds	0.003	<NONE>	<NONE>	<NONE>
4649	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete	4e-013	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		cds				
4650	U79403	Meleagris gallopavo microsatellite repeat sequence	0.46	2498691	OUTER DENSE FIBER PROTEIN bovine >gi|1165006 (X69514) outer dense fiber protein protein [Bos taurus]	1.4
4651	U27780	Stealth virus 1 clone C16138 T3.1	2	<NONE>	<NONE>	<NONE>
4652	U27780	Stealth virus 1 clone C16138 T3.1	2	<NONE>	<NONE>	<NONE>
4653	U78817	Saccharomyces cerevisiae killer virus M1, complete genome	0.026	<NONE>	<NONE>	<NONE>
4654	U78817	Saccharomyces cerevisiae killer virus M1, complete genome	0.026	<NONE>	<NONE>	<NONE>
4655	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
4656	X07036	Human mRNA stimulatory GTP-binding protein alpha subunit	3e-071	232142	GUANINE NUCLEOTIDE-BINDING PROTEIN G(S), ALPHA SUBUNIT (ADENYLATE CYCLASE-STIMULATING G ALPHA PROTEIN) >gi|71886|pir||RGPGA2 GTP-binding regulatory protein Gs alpha-2 chain (adenylate cyclase-stimulating) - pig >gi|1958 (X63893) alpha-stimulatory subunit	8e-027

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
4657	L05586	Kinetoplast Trypanosoma brucei (IsTaR 1 serodeme) putative NADH dehydrogenase subunit (nd9) mRNA, complete cds.	0.0001	4063042	(AF068065) GP900; mucin-like glycoprotein [Cryptosporidium parvum]	0.19
4658	AF044763	Cecropis ariel microsatellite HrU6 allele 1 repeat region	3e-006	<NONE>	<NONE>	<NONE>
4659	X82630	A.longa plastid rps12, orf126 and orf288 genes	0.22	<NONE>	<NONE>	<NONE>
4660	U68098	Human poly(A)-binding protein (PABP) gene, exons 6 and 7	0.023	<NONE>	<NONE>	<NONE>
4661	U68098	Human poly(A)-binding protein (PABP) gene, exons 6 and 7	0.023	<NONE>	<NONE>	<NONE>
4662	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	1e-011	1022683	(U23146) SSeCKS [Rattus norvegicus]	1.4
4663	M15353	Homo sapiens cap-binding protein mRNA, complete cds	0	<NONE>	<NONE>	<NONE>
4664	Z57610	H.sapiens CpG DNA, clone 187a10, reverse read cpg187a10.rt1a .	3e-048	417134	HEPATOCYTE NUCLEAR FACTOR 3-BETA norvegicus]	2.00E-10
4665	L11707	Hevea brasiliensis Mn-superoxide dismutase (SODMn) gene, complete cds.	2.6	<NONE>	<NONE>	<NONE>
4666	D42073	Human mRNA for reticulocalbin, complete cds	3e-019	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	6.4

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
4667	L12350	Human thrombospondin 2 (THBS2) mRNA, complete cds.	0	<NONE>	<NONE>	<NONE>
4668	L11707	Hevea brasiliensis Mn-superoxide dismutase (SODMn) gene, complete cds.	2.6	<NONE>	<NONE>	<NONE>
4669	AC000043	Homo sapiens Chromosome 22q13 Cosmid Clone p74a8, complete sequence [Homo sapiens]	2e-016	134589	TRANSCRIPTION REGULATORY PROTEIN SNF2 SWI2) (REGULATORY PROTEIN GAM1) (TRANSCRIPTION FACTOR TYE3) >gi|101629|pir||S15047 SNF2 protein - yeast protein [Saccharomyces cerevisiae] >gi|172632 (M61703) SNF2protein [Saccharomyces cerevisiae] cerevisiae] >gi|127	1.5
4670	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	6e-006	69700	interleukin-1 beta precursor - bovine	0.6
4671	U44975	Homo sapiens DNA-binding protein CPBP (CPBP) mRNA, partial cds	2e-045	1848233	(U44975) DNA-binding protein CPBP [Homo sapiens]	0.009

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
4672	AF038406	Homo sapiens NADH dehydrogenase-ubiquinone Fe-S protein 8 23 kDa subunit (NDUFS8) gene, nuclear gene encoding mitochondrial protein, complete cds	0	2326168	(U32107) type VII collagen [Mus musculus]	1.5
4673	X67951	H.sapiens mRNA for proliferation-associated gene	0	548453	THIOREDOXIN PEROXIDASE 2 CELL ENHANCING FACTOR A) (NKEF-A) >gi|423025|pir||A46711 proliferation associated gene (pag) protein - human gene product [Homo sapiens]	2e-083
4674	AC001013	Homo sapiens (subclone 2_d1 from P1 H43) DNA sequence	2e-017	2072961	(U93568) putative p150 [Homo sapiens]	0.0001
4675	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	4e-012	1589837	(U68729) cuticle preprocollagen [Meloidogyne incognita]	0.035
4676	M15353	Homo sapiens cap-binding protein mRNA, complete cds	0	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
4677	M37583	Human histone (H2A.Z) mRNA, complete cds.	0	121994	HISTONE H2A.Z >gi|89608|pir||S03642 histone H2A.Z - bovine >gi|92380|pir||S03644 histone H2A.Z - rat >gi|106267|pir||A35881 histone H2A.Z - human sapiens] >gi|57808 (X52316) histone H2A.Z (AA 1-127) taurus] >gi|184060 (M37583) histone (H2A.Z) [Homo sapien	1e-055
4678	M15353	Homo sapiens cap-binding protein mRNA, complete cds	0	<NONE>	<NONE>	<NONE>
4679	Z57610	H.sapiens CpG DNA, clone 187a10, reverse read cpg187a10.rt1a.	4e-094	404764	(L10409) fork head related protein [Mus musculus]	4e-024
4680	Z57610	H.sapiens CpG DNA, clone 187a10, reverse read cpg187a10.rt1a.	4e-094	404764	(L10409) fork head related protein [Mus musculus]	4e-024
4681	Z57610	H.sapiens CpG DNA, clone 187a10, reverse read cpg187a10.rt1a.	4e-094	404764	(L10409) fork head related protein [Mus musculus]	4e-024
4682	L11707	Hevea brasiliensis Mn-superoxide dismutase (SODMn) gene, complete cds.	2.6	<NONE>	<NONE>	<NONE>
4683	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
4684	<NONE>	<NONE>	<NONE>	2114323	(D88734) membrane glycoprotein [Equine herpesvirus 1]	0.052

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
4685	AJ224875	Homo sapiens mRNA for putative glucosyltransferase, partial cds	0	2996578	(AJ224875) glucosyltransferase [Homo sapiens]	e-118
4686	AB019534	Homo sapiens gene for cathepsin L2, complete cds	2e-045	<NONE>	<NONE>	<NONE>
4687	J03799	Human colin carcinoma laminin-binding protein mRNA, complete cds.	e-166	34272	(X15005) pot. lamimin-binding protein (AA 1 - 300) [Homo sapiens]	5e-032
4688	<NONE>	<NONE>	<NONE>	2114323	(D88734) membrane glycoprotein [Equine herpesvirus 1]	0.052
4689	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	9e-009	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	9.8
4690	D44598	Saccharomyces cerevisiae chromosome VI phage 4121	1e-009	3947877	(AL034382) putative mitosis and maintenance of ploidy protein [Schizosaccharomyces pombe]	6e-061
4691	AF053520	Homo sapiens allele 12 fragile site locus	0.61	<NONE>	<NONE>	<NONE>
4692	D16195	Mouse gene for acrogranin precursor, complete cds	0.059	<NONE>	<NONE>	<NONE>
4693	U90904	Human clone 23773 mRNA sequence	0	3130153	(AB008857) calcium2+ sensing receptor	1.5
4694	L22398	Homo sapiens DNA sequence, repeat region.	7e-017	987050	(X65335) lacZ gene product [unidentified cloning vector]	0.1
4695	L22398	Homo sapiens DNA sequence, repeat region.	7e-017	987050	(X65335) lacZ gene product [unidentified cloning vector]	0.1

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
4696	J03746	Human glutathione S-transferase mRNA, complete cds.	e-170	121740	GLUTATHIONE S-TRANSFERASE, MICROSOMAL >gi|87562|pir||B28083 glutathione transferase glutathione S-transferase [Homo sapiens] >gi|1195483 sapiens] >gi|1621433 (U71213) microsomal glutathione s-transferase [Homo sapiens]	2e-038
4697	AF082283	Homo sapiens CARD-containing apoptotic signaling protein (BCL10) mRNA, complete cds	5e-046	4049460	(AJ006288) bcl-10 [Homo sapiens] signaling protein [Homo sapiens]	0.005
4698	D64142	Human mRNA for histone H1x, complete cds	1e-039	<NONE>	<NONE>	<NONE>
4699	AB001899	Homo sapiens PACE4 gene, exon 2	4e-012	3860844	(AJ235271) NADH DEHYDROGENASE I CHAIN L	3.5
4700	X16869	Human mRNA for elongation factor 1-alpha (clone CEF4)	0	1169475	ELONGATION FACTOR 1-ALPHA 1	6e-061
4701	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	6.00E-05	<NONE>	<NONE>	<NONE>
4702	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	4e-013	2501465	PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE FAM (UBIQUITIN THIOLESTERAS	0.0003

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					E FAM)	
4703	D44598	Saccharomyces cerevisiae chromosome VI phage 4121	1e-009	3947877	(AL034382) putative mitosis and maintenance of ploidy protein [Schizosaccharomyces pombe]	6e-061
4704	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	6e-006	<NONE>	<NONE>	<NONE>
4705	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	1e-012	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	6.4
4706	AB001899	Homo sapiens PACE4 gene, exon 2	4e-012	3860844	(AJ235271) NADH DEHYDROGENASE I CHAIN L	3.4
4707	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
4708	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	1e-008	<NONE>	<NONE>	<NONE>
4709	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	1e-009	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	6.40E+00
4710	L39064	Homo sapiens interleukin 9 receptor precursor (IL9R) gene, complete cds	1e-006	4063042	(AF068065) GP900; mucin-like glycoprotein	1e-006
4711	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	0.0002	331908	(K02714) envelope polyprotein [Friend murine leukemia virus]	8

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
4712	AF065249	Entodinium caudatum 14-3-3 protein mRNA, partial cds	1	<NONE>	<NONE>	<NONE>
4713	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	2e-013	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	7.9
4714	<NONE>	<NONE>	<NONE>	186396	(M94131) mucin [Homo sapiens]	2.5
4715	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	8e-009	<NONE>	<NONE>	<NONE>
4716	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
4717	Z56314	H.sapiens CpG DNA, clone 10h10, reverse read cpg10h10.rt1a .	4e-012	2444024	(U77782) N-methyl-D-aspartate receptor 2C subunit precursor [Homo sapiens]	9.8
4718	D55696	Human mRNA for cysteine protease, complete cds	e-113	2842759	LEGUMAIN PRECURSOR (ASPARAGINYL ENDOPEPTIDASE) >gi|1743266|gnl|PID|e286211 (Y09862) legumain [Homo sapiens]	1e-006
4719	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	9e-008	<NONE>	<NONE>	<NONE>
4720	D63480	Human mRNA for KIAA0146 gene, partial cds	0	1469874	(D63480) The KIAA0146 gene product is novel. [Homo sapiens]	2e-079
4721	AB001579	Rice dwarf virus genomic RNA, segment 2, complete sequence	1.3	<NONE>	<NONE>	<NONE>
4722	<NONE>	<NONE>	<NONE>	3873550	(AL033534) serine-rich protein	2.7

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
4723	AL010156	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-87, complete sequence	0.77	<NONE>	<NONE>	<NONE>
4724	AF059198	Homo sapiens protein kinase/endoribonulcease	2	119110	EBNA-1 NUCLEAR PROTEIN herpesvirus 4 (strain B95-8) >gi|1334880 (V01555) BKRF1 encodes EBNA-1 protein, latent cycle gene. [Human herpesvirus 4]	8e-007
4725	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
4727	D38616	Human mRNA for phosphorylase kinase alpha subunit, complete cds	3.5	3522948	(AC004411) hypothetical protein [Arabidopsis thaliana]	0.18
4728	D38616	Human mRNA for phosphorylase kinase alpha subunit, complete cds	3.5	3522948	(AC004411) hypothetical protein [Arabidopsis thaliana]	0.18
4729	Z11808	T.glis interphotoreceptor retinoid binding protein gene, exon 1	1.6	<NONE>	<NONE>	<NONE>
4730	AF065988	Homo sapiens keratocan gene, complete cds	1.4	<NONE>	<NONE>	<NONE>
4731	X60026	M.domesticus small nuclear 4.5 S RNA gene	0.0003	2853301	(AF007194) mucin [Homo sapiens]	5.5
4732	M13793	Mouse 56 kdal protein mRNA from an interferon activated gene, exon 1, 5' end.	0.3	136814	HYPOTHETICAL PROTEIN UL11 RL11 FAMILY [Human cytomegalovirus]	2.3

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
4733	D55696	Human mRNA for cysteine protease, complete cds	e-113	2842759	LEGUMAIN PRECURSOR (ASPARAGINYL ENDOPEPTIDASE) >gi|1743266|gnl|PID|e286211 (Y09862) legumain [Homo sapiens]	1e-006
4734	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
4735	<NONE>	<NONE>	<NONE>	322647	glycine-rich protein GRP22 - rape >gi|17821	3e-021
4736	<NONE>	<NONE>	<NONE>	188864	(M74027) mucin [Homo sapiens]	0.002
4737	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	2e-005	<NONE>	<NONE>	<NONE>
4738	AB018270	Homo sapiens mRNA for KIAA0727 protein, partial cds	0	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	1.8
4739	AB018270	Homo sapiens mRNA for KIAA0727 protein, partial cds	0	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	1.8
4740	AE001382	Plasmodium falciparum chromosome 2, section 19 of 73 of the complete sequence	0.25	<NONE>	<NONE>	<NONE>
4741	AE001382	Plasmodium falciparum chromosome 2, section 19 of 73 of the complete sequence	0.25	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
4742	X55038	Mouse mCENP-B gene for centromere autoantigen B	0.001	3879362	(Z81113) similar to DnaJ, prokaryotic heat shock protein, Zinc finger, C2H2 type; cDNA EST yk290e12.5 comes from this gene; cDNA EST yk290e12.3 comes from this gene; cDNA EST yk447h4.5 comes from this gene; cDNA EST yk474e4....	7e-007
4743	AF054024	Rattus norvegicus polymorphic marker D9UIA2 sequence	0.62	<NONE>	<NONE>	<NONE>
4744	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	0.0005	<NONE>	<NONE>	<NONE>
4745	Z11808	T.glis interphotoreceptor retinoid binding protein gene, exon 1	1.6	<NONE>	<NONE>	<NONE>
4746	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
4747	AF047470	Homo sapiens malate dehydrogenase precursor complete cds	1e-019	2995307	(AL022268) putative aminotransferase	0.12
4748	AF029890	Homo sapiens hepatitis B virus X interacting protein (XIP) mRNA, complete cds	e-161	2745883	(AF029890) hepatitis B virus X interacting protein [Homo sapiens]	2e-044

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
4750	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	8e-008	1723019	HYPOTHETICAL 29.6 KD PROTEIN CY251.12C >gi|1405764|gnl|PID|e249453 (Z74410) hypothetical protein Rv0093c [Mycobacterium tuberculosis]	2.5
4751	M37583	Human histone (H2A.Z) mRNA, complete cds.	0	121994	HISTONE H2A.Z >gi|89608|pir||S03642 histone H2A.Z - bovine >gi|92380|pir||S03644 histone H2A.Z - rat >gi|106267|pir||A35881 histone H2A.Z - human sapiens] >gi|57808 (X52316) histone H2A.Z (AA 1-127) taurus] >gi|184060 (M37583) histone (H2A.Z) [Homo sapien	1e-055
4752	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	5e-014	<NONE>	<NONE>	<NONE>
4753	X65279	pWE15 cosmid vector DNA	7e-079	987050	(X65335) lacZ gene product [unidentified cloning vector]	1e-013
4754	D38549	Human mRNA for KIAA0068 gene, partial cds	e-169	<NONE>	<NONE>	<NONE>
4755	L27835	Pangasianodon gigas growth hormone (GH) mRNA, complete cds.	1.5	538251	(D00322) polyprotein [Tomato black ring virus]	5.8

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
4756	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	0.0002	1477565	(U50078) p619 [Homo sapiens]	8.9
4757	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	0.0002	1477565	(U50078) p619 [Homo sapiens]	8.9
4758	U47414	Human cyclin G2 mRNA, complete cds	e-116	<NONE>	<NONE>	<NONE>
4759	AB014560	Homo sapiens mRNA for KIAA0660 protein, complete cds	e-173	<NONE>	<NONE>	<NONE>
4760	L35664	Homo sapiens (subclone H8 8_f5 from P1 35 H5 C8) DNA sequence.	1e-030	2072966	(U93570) p40 [Homo sapiens]	0.001
4761	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	4e-013	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	3.1
4762	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	4e-013	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	3.1
4763	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	1e-012	<NONE>	<NONE>	<NONE>
4764	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	1e-012	<NONE>	<NONE>	<NONE>
4765	M59317	Mouse low affinity IgE receptor (FceRII) gene sequence.	1e-006	2135765	mucin 2 precursor, intestinal - human	0.0003

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P.VALUE	ACCESSION	DESCRIPTION	P VALUE
4766	D14034	Human gene for Zn-alpha2-glycoprotein, complete cds	3e-008	119379	RETROVIRUS-RELATED ENV POLYPROTEIN	6e-007
4767	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
4768	M61185	Bovine glutamic acid-rich protein mRNA, complete cds.	0.01	2781362	(AC003113) F24O1.18 [Arabidopsis thaliana]	1.1
4769	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
4770	Z62012	H.sapiens CpG DNA, clone 61g4, reverse read cpg61g4.rt1a	0.076	1582765	YFW1 gene [Saccharomyces cerevisiae]	2.9
4771	M29065	Human hnRNP A2 protein mRNA.	0	4049652	(AF063866) ORF MSV017 hypothetical protein [Melanoplus sanguinipes entomopoxvirus]	5.9
4772	D12525	Homo sapiens cytochrome P450IA1 gene, 3'flanking region	6e-016	728837	!!!! ALU SUBFAMILY SQ WARNING ENTRY	9.6
4773	M16660	Human 90-kDa heat-shock protein gene, cDNA, complete cds.	e-109	2119731	HSP90 - mouse (fragment) protein {C-terminal} [mice, heart, Peptide Partial, 194 aa] [Mus sp.]	1e-023
4774	AF043105	Homo sapiens glutathione S-transferase mu 3	9e-020	728831	!!!! ALU SUBFAMILY J WARNING ENTRY	0.63
4775	U43374	Human normal keratinocyte mRNA.	0	120179	FINQ PROTEIN >gi|73172|pir||BV ECFQ finQ protein - Escherichia coli plasmid R820a	9
4776	U00684	Human unknown mRNA.	2e-014	2224667	(AB002361) KIAA0363 [Homo sapiens]	6.6

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
4777	M22299	Human T-plastin polypeptide mRNA, complete cds, clone p4. > :: gb|I08151| Sequence 1 from Patent EP 0345726	4e-008	<NONE>	<NONE>	<NONE>
4778	M95623	Homo sapiens hydroxymethylbilane synthase gene, complete cds.	3e-018	3002527	(AF010144) neuronal thread protein AD7c-NTP [Homo sapiens]	0.52
4779	X52329	pBluescript II KS(-) vector DNA, phagemid excised from lambda ZAPII	0	2117615	catalase - Campylobacter jejuni	2e-009
4780	X52329	pBluescript II KS(-) vector DNA, phagemid excised from lambda ZAPII	0	2117615	catalase - Campylobacter jejuni	2e-009
4781	AF061034	Homo sapiens FIP2 alternatively translated mRNA, complete cds	0	3127084	(AF061034) FIP2 [Homo sapiens]	9e-089
4782	Z64776	H.sapiens CpG DNA, clone 167d8, forward read cpg167d8.ft1b .	0.0002	1777782	(U52513) ISG family member [Homo sapiens]	1.8
4783	D31786	Acyrthosiphon kondoi endosymbiont DNA, S10 and spc ribosomal protein gene operons, complete and partial cds	1.1	2134310	cell division control protein CDC37 homolog splice form 1 - chicken	4e-005
4784	L05491	Homo sapiens T-plastin gene, last exon (16).	0	2506254	T-PLASTIN	3e-018
4785	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	8e-007	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
4786	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	7e-006	3877438	(Z72510) similar to G-protein coupled receptor [Caenorhabditis elegans]	2
4787	L38250	Mycoplasma penetrans p35 lipoprotein and p33 lipoprotein genes, complete cds	0.041	<NONE>	<NONE>	<NONE>
4788	J03537	Human ribosomal protein S6 mRNA, complete cds.	e-138	133978	40S RIBOSOMAL PROTEIN S6 protein S6 - rat >gi|70933|pir||R3 MS6 ribosomal protein S6 - mouse >gi|319910|pir||R3 HU6 ribosomal protein S6 - human >gi|36148 (X67309) ribosomal protein S6 [Homo sapiens] >gi|54010 (Y00348) ribosomal protein S6 [Mus musculus] >g	3e-033
4789	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	1e-011	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	2.6
4790	AF041210	Homo sapiens midline 1 fetal kidney isoform 3	0.41	<NONE>	<NONE>	<NONE>
4791	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	3e-010	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	3.2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
4792	S60885	LYAR=cell growth regulating nucleolar protein	2e-026	2498524	CELL GROWTH REGULATING NUCLEOLAR PROTEIN >gi|423488|pir||A40683 cell growth regulating nucleolar protein LYAR - mouse >gi|300372|bbs|131782	0.43
4793	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
4794	U28687	Human zinc finger containing protein ZNF157	3e-027	1731444	ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2) >gi|1020145 (M27878) DNA binding protein	3e-008
4795	AF086438	Homo sapiens full length insert cDNA clone ZD80G11	0.0002	<NONE>	<NONE>	<NONE>
4796	L28997	Homo sapiens ARL1 mRNA, complete cds	3e-006	<NONE>	<NONE>	<NONE>
4797	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	3e-008	1280126	(U55375) K03E6.4 [Caenorhabditis elegans]	2e-012
4798	AE001415	Plasmodium falciparum chromosome 2, section 52 of 73 of the complete sequence	0.015	<NONE>	<NONE>	<NONE>
4799	D21853	Human mRNA for KIAA0111 gene, complete cds	0	729821	EUKARYOTIC INITIATION FACTOR 4A-LIKE NUK-34 (HA0659) >gi|631472|pir||S45142 translation initiation factor eIF-4A2 homolog - human >gi|496902	2e-010

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
4800	M76425	H.sapiens intron 2 Alu repetitive element.	0.014	<NONE>	<NONE>	<NONE>
4801	X87212	H.sapiens mRNA for cathepsin C	0	1582221	prepro-cathepsin C [Homo sapiens]	1e-052
4802	D80005	Human mRNA for KIAA0183 gene, partial cds	e-114	1136426	(D80005) KIAA0183 [Homo sapiens]	7e-025
4803	AF026029	Homo sapiens poly(A) binding protein II (PABP2) gene, complete cds	2e-055	<NONE>	<NONE>	<NONE>
4804	Z68322	Human DNA sequence from cosmid L79F5, Huntington's Disease Region, chromosome 4p16.3	2e-016	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	5.6
4805	M63180	Human threonyl-tRNA synthetase mRNA, complete cds	0	135177	THREONYL-TRNA SYNTHETASE, CYTOPLASMIC (THREONINE--TRNA LIGASE) (THRRS) 6.1.1.3) - human >gi|1464742 (M63180) threonyl-tRNA synthetase [Homo sapiens]	5e-070
4806	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	3.7	<NONE>	<NONE>	<NONE>
4807	D16431	Human mRNA for hepatoma-derived growth factor, complete cds	3e-010	<NONE>	<NONE>	<NONE>
4808	AF086168	Homo sapiens full length insert cDNA clone ZB82D09	e-148	1465826	(U64856) weak similarity to TPR domains [Caenorhabditis elegans]	2e-014

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
4809	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	4e-012	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	4.4
4810	M34651	Pseudorabies virus with upstream and downsteam sequences.	0.4	417134	HEPATOCYTE NUCLEAR FACTOR 3-BETA norvegicus]	0.047
4811	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	3e-010	1353390	(U34998) Rad9 [Coprinus cinereus]	3e-010
4812	M94314	Homo sapiens ribosomal protein L30 mRNA, complete cds	1e-064	<NONE>	<NONE>	<NONE>
4813	X95276	P.falciparum complete gene map of plastid-like DNA (IR-B)	0.001	<NONE>	<NONE>	<NONE>
4814	X12716	Human Retrovirus mRNA for LTR (clone cH6)	5e-024	<NONE>	<NONE>	<NONE>
4815	J03537	Human ribosomal protein S6 mRNA, complete cds.	e-138	133978	40S RIBOSOMAL PROTEIN S6 protein S6 - rat >gi|70933|pir||R3 MS6 ribosomal protein S6 - mouse >gi|319910|pir||R3 HU6 ribosomal protein S6 - human >gi|36148 (X67309) ribosomal protein S6 [Homo sapiens] >gi|54010 (Y00348) ribosomal protein S6 [Mus musculus] >g	3e-033
4816	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
4817	U61945	Caenorhabditis elegans cosmid C49C8.	1.8	<NONE>	<NONE>	<NONE>
4818	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
4819	M20020	Human ribosomal protein S6 mRNA, complete cds.	7e-072	225901	ribosomal protein S6 [Rattus norvegicus]	2e-015
4820	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.058	<NONE>	<NONE>	<NONE>
4821	AL023973	Human DNA sequence from clone 1033E15 on chromosome 22q13.1-13.2. Contains part of a novel gene, ESTs and a GSS, complete sequence [Homo sapiens]	3e-009	2352260	(AF000949) keratin [Canis familiaris]	0.037
4822	M37430	Pea Chloroplast 4.5S, 5S, 16S and 23S mRNA.	4.7	4093193	(AF106583) unknown [Caenorhabditis elegans]	4.8
4823	M63488	Human replication protein A 70kDa subunit mRNA complete cds.	0	1350579	REPLICATION PROTEIN A 70 KD DNA-BINDING SUBUNIT (RP-A) (RF-A) (REPLICATION FACTOR-A PROTEIN 1) (SINGLE-STRANDED DNA-BINDING PROTEIN) subunit [Homo sapiens]	8e-079
4824	X83791	C.tentans BR1 gene	1.2	<NONE>	<NONE>	<NONE>
4825	U67576	Methanococcus jannaschii section 118 of 150 of the complete genome	4	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
4826	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	1e-009	<NONE>	<NONE>	<NONE>
4827	X65319	Cloning vector pCAT-Enhancer	2e-077	987050	(X65335) lacZ gene product [unidentified cloning vector]	2e-011
4828	X03558	Human mRNA for elongation factor 1 alpha subunit	0	1169475	ELONGATION FACTOR 1-ALPHA 1	e-109
4829	X76538	H.sapiens Mpv17 mRNA	6.00E-98	730059	MPV17 PROTEIN >gi|631208|pir||S45343 glomerulosclerosis protein Mpv17 - human	3e-010
4830	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
4831	<NONE>	<NONE>	<NONE>	2078483	(U43200) antifreeze glycopeptide AFGP polyprotein precursor [Boreogadus saida]	0.014
4832	X83617	H.sapiens mRNA for RanBP1	3.4	3924670	(AC004990) supported by Genscan and several ESTs: C83049	3e-040
4833	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	1e-011	3024677	ISOLEUCYL-TRNA SYNTHETASE isoleucyl-tRNA synthetase (ileS) [Helicobacter pylori]	0.005
4834	J02763	Human calcyclin gene, complete cds.	1e-043	<NONE>	<NONE>	<NONE>
4835	L10910	Homo sapiens splicing factor (CC1.3) mRNA, complete cds.	0.00E+00	<NONE>	<NONE>	<NONE>
4836	X53586	Human mRNA for integrin alpha 6	2e-099	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	5

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
4837	Z57594	H.sapiens CpG DNA, clone 186c5, reverse read cpg186c5.rt1b .	1.4	<NONE>	<NONE>	<NONE>
4838	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
4839	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	7e-007	<NONE>	<NONE>	<NONE>
4840	Y00371	Human hsc70 gene for 71 kd heat shock cognate protein > :: gb|AR013986|AR013986 Sequence 15 from patent US 5773245	e-145	987050	(X65335) lacZ gene product [unidentified cloning vector]	7e-011
4841	AF074991	Homo sapiens full length insert cDNA YH88A03	0.0005	<NONE>	<NONE>	<NONE>
4842	AF055030	Homo sapiens clone 24538 mRNA sequence	2e-049	2842711	ZINC-FINGER PROTEIN UBI-D4 sapiens]	2e-016
4843	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	2e-005	1353531	(U38906) ORF14 [Bacteriophage r1t]	7.1
4844	Z57588	H.sapiens CpG DNA, clone 186b7, reverse read cpg186b7.rt1b .	0.41	<NONE>	<NONE>	<NONE>
4845	X65319	Cloning vector pCAT-Enhancer	9e-051	987050	(X65335) lacZ gene product [unidentified cloning vector]	0.37
4846	X78411	B.pasteurii ureA, ureB and ureC genes.	3.1	<NONE>	<NONE>	<NONE>
4847	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	3e-009	2224697	(AB002376) KIAA0378 [Homo sapiens]	5e-008

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
4848	U78729	Homo sapiens mad protein homolog Smad2 gene, exon 6	4.7	<NONE>	<NONE>	<NONE>
4849	D55696	Human mRNA for cysteine protease, complete cds	0	2842759	LEGUMAIN PRECURSOR (ASPARAGINYL ENDOPEPTIDASE) >gi|1743266|gnl|PID|e286211 (Y09862) legumain [Homo sapiens]	3e-030
4850	U95097	Xenopus laevis mitotic phosphoprotein 43 mRNA, partial cds	0.43	3005603	(AF053141) progesterone receptor [Equus caballus]	2.2
4851	U46118	Rattus norvegicus cytochrome P450 3A9 mRNA, complete cds	0.38	<NONE>	<NONE>	<NONE>
4852	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	2e-006	2495726	HYPOTHETICAL PROTEIN KIAA0254 sapiens]	1e-005
4853	L10911	Homo sapiens splicing factor (CC1.4) mRNA, complete cds.	e-117	<NONE>	<NONE>	<NONE>
4854	D00132	Acremonium chrysogenum ARS DNA fragment	1.7	130998	SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONE CP7) [CONTAINS: BASIC PEPTIDE P-F] glycoprotein precursor PRB2 - human (fragment) precursor [Homo sapiens]	0.45
4855	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	4e-011	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	5.9

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
4856	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
4857	AC002186	Homo sapiens (subclone 1_f12 from P1 H115) DNA sequence	1e-041	2072966	(U93570) p40 [Homo sapiens]	4e-013
4858	AF053520	Homo sapiens allele 12 fragile site locus	0.61	<NONE>	<NONE>	<NONE>
4859	X65319	Cloning vector pCAT-Enhancer	2e-077	987050	(X65335) lacZ gene product [unidentified cloning vector]	2e-011
4860	AJ005866	Homo sapiens mRNA for putative Sqv-7-like protein, partial	e-179	4008517	(AJ005866) Sqv-7-like protein [Homo sapiens]	3e-049
4861	AF052165	Homo sapiens clone 24522 mRNA sequence	4e-072	2065177	(Y12790) Supt5h protein [Homo sapiens] sapiens]	1e-021
4862	M90058	Human serglycin gene, exons 1,2, and 3.	0.005	<NONE>	<NONE>	<NONE>
4863	U17662	Human neurofibromatosis 1 (NF1) gene, exons 4c and 5 and partial cds	1.3	<NONE>	<NONE>	<NONE>
4864	U64453	Human ELK1 pseudogene (ELK2) and immunoglobulin heavy chain gamma pseudogene (IGHGP)	3e-018	<NONE>	<NONE>	<NONE>
4865	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	2e-005	<NONE>	<NONE>	<NONE>
4866	X16826	Drosophila melanogaster DNA for 60C beta tubulin gene making beta 3 tubulin isoform	2.2	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
4867	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	4e-009	<NONE>	<NONE>	<NONE>
4868	X65319	Cloning vector pCAT-Enhancer	8e-081	987050	(X65335) lacZ gene product [unidentified cloning vector]	3e-015
4869	AL031322	S.pombe chromosome II cosmid c17D1	0.38	<NONE>	<NONE>	<NONE>
4870	M11560	Human aldolase A mRNA, complete cds.	0	553861	(J05517) aldolase A [Mus musculus]	2e-066
4871	U28831	Human protein immuno-reactive with anti-PTH polyclonal antibodies mRNA, partial cds. > :: gb|I40055|I40055 Sequence 1 from patent US 5618695	e-106	896065	(U28831) protein that is immuno-reactive with anti-PTH polyclonal antibodies [Homo sapiens]	1e-014
4872	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	2e-005	<NONE>	<NONE>	<NONE>
4873	<NONE>	<NONE>	<NONE>	107112	mucin, tracheal (AMN-22) - human (fragment)	4e-009
4874	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	1e-011	<NONE>	<NONE>	<NONE>
4875	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	1e-011	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
4876	D85752	Enterococcus faecalis plasmid pPD1 bacA, bacB, bacC, bacD, bacE, bacF, bacG, bacH and bacI genes, complete cds	0.042	1123087	(U42436) C49H3.3 gene product [Caenorhabditis elegans]	0.001
4877	AC001443	Homo sapiens (subclone 2_f10 from BAC 2913	1e-033	2072961	(U93568) putative p150 [Homo sapiens]	3e-007
4878	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	4e-012	<NONE>	<NONE>	<NONE>
4879	S81433	heme oxygenase-2 {5' region, alternative splicing}	4.2	<NONE>	<NONE>	<NONE>
4880	M34312	S.cerevisiae telomeric sequence DNA, clone YLP108CA-4-ii.	5e-010	188864	(M74027) mucin [Homo sapiens]	2e-007
4881	AF075079	Homo sapiens full length insert cDNA YQ80A08	1.00E-12	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	4.6
4882	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.015	3176689	(AC003671) Contains similarity to ubiquitin carboxyl-terminal hydrolase 14 gb|Z35927 from S. cerevisiae. [Arabidopsis thaliana]	4.5
4883	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.12	<NONE>	<NONE>	<NONE>
4884	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	7e-007	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
4885	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	7e-007	<NONE>	<NONE>	<NONE>
4886	U74586	Rattus norvegicus double-stranded RNA specific adenosine deaminase (RED2) mRNA, complete cds	3.5	2828280	(AL021687) putative protein [Arabidopsis thaliana] >gi|2832633|gnl|PID|e1249651 (AL021711) putative protein [Arabidopsis thaliana]	4e-008
4887	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	5e-014	2497599	LAMININ BETA-2 CHAIN PRECURSOR	5.4
4888	D78572	House mouse; Musculus domesticus mRNA for membrane glycoprotein, complete cds > :: dbj|E12950|E12950 cDNA GA3-43 encoding novel polypeptide which appear when differentiate from embryo-tumor cell P19 to nerve cell	7e-017	1545807	(D78572) membrane glycoprotein [Mus musculus]	1.2
4889	L07273	Rattus norvegicus carboxypeptidase E (CPE) gene, exon 1.	3.2	<NONE>	<NONE>	<NONE>
4890	Z46629	Homo sapiens SOX9 mRNA. > :: gb|G28593|G28593 human STS SHGC-35378.	e-132	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
4891	M30802	Human aromatase cytochrome P-450 gene, exon 8.	3.3	<NONE>	<NONE>	<NONE>
4892	M28699	Homo sapiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds.	5e-088	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	5.2
4893	M89955	Human 5-HT1D-type serotonin receptor gene, complete cds.	0	2494923	5-HYDROXYTRYPTAMINE 1D RECEPTOR 1D [Cavia porcellus]	3e-008
4894	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.0002	<NONE>	<NONE>	<NONE>
4895	AF004230	Homo sapiens monocyte/macrophage Ig-related receptor MIR-7 (MIR cl-7) mRNA, complete cds	2e-012	<NONE>	<NONE>	<NONE>
4896	D50463	Mouse SDR1 mRNA, complete cds	0	1806276	(X99337) glycoprotein 55 [Rattus norvegicus]	e-103
4897	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
4898	AB014597	Homo sapiens mRNA for KIAA0697 protein, partial cds	2e-067	3327208	(AB014597) KIAA0697 protein [Homo sapiens]	9e-051
4899	AF047598	Homo sapiens origin recognition complex subunit 4 (ORC4L) mRNA, complete cds	e-110	2736149	(AF022108) putative replication initiator origin recognition complex subunit Orc4Lp [Homo sapiens] subunit 4; Orc4p [Homo sapiens]	7e-005

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
4900	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	7e-007	<NONE>	<NONE>	<NONE>
4901	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	7e-007	<NONE>	<NONE>	<NONE>
4902	U22325	Mus musculus faciogenital dysplasis (Fgd1) mRNA, complete cds.	1.20E+00	<NONE>	<NONE>	<NONE>
4903	U22325	Mus musculus faciogenital dysplasis (Fgd1) mRNA, complete cds.	1.20E+00	<NONE>	<NONE>	<NONE>
4904	U22325	Mus musculus faciogenital dysplasis (Fgd1) mRNA, complete cds.	1.20E+00	<NONE>	<NONE>	<NONE>
4905	U26162	Human myosin regulatory light chain mRNA, complete cds.	0	228542	myosin:SUBUNIT =regulatory light chain	3e-068
4906	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
4907	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	1e-011	3822225	(AF079183) RING-H2 finger protein RHG1a [Arabidopsis thaliana]	4e-006
4908	X65319	Cloning vector pCAT-Enhancer	1e-075	987050	(X65335) lacZ gene product [unidentified cloning vector]	8e-019
4909	AJ010475	Arabidopsis thaliana mRNA for DEAD box RNA helicase, RH28	0.62	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
4910	U48364	Mus musculus muscle-specific transcriptional activator alpha-NAC gp220 (Naca) mRNA, complete cds	0.2	<NONE>	<NONE>	<NONE>
4911	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
4912	J03750	Mouse single stranded DNA binding protein p9 mRNA, complete cds.	e-135	1709514	ACTIVATED RNA POLYMERASE II TRANSCRIPTIONAL COACTIVATOR P15 (PC4) (P14) cofactor p15 - human >gi|531395 (U12979) PC4 [Homo sapiens] >gi|619161 (X79805) PC4, p15 [Homo sapiens]	1e-020
4913	U70263	Border disease virus strain BD31, complete genome	3.2	<NONE>	<NONE>	<NONE>
4914	AB012086	Canine herpesvirus gene for immediate-early protein, complete cds	0.37	<NONE>	<NONE>	<NONE>
4915	X05908	Human mRNA for lipocortin	e-162	113944	ANNEXIN I (LIPOCORTIN I) (CALPACTIN II) (CHROMOBINDIN 9) (P35) (PHOSPHOLIPASE A2 INHIBITORY PROTEIN) >gi|71756|pir||LUHU annexin I - human >gi|34388	9e-041
4916	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
4917	U90911	Human clone 23652 mRNA sequence	0.13	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
4918	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	8e-007	<NONE>	<NONE>	<NONE>
4919	X57830	H.sapiens serotonin 5-HT2 receptor mRNA > :: gb|G28536|G28536 human STS SHGC-31576.	4e-011	<NONE>	<NONE>	<NONE>
4920	U67559	Methanococcus jannaschii section 101 of 150 of the complete genome	3.5	<NONE>	<NONE>	<NONE>
4921	M20020	Human ribosomal protein S6 mRNA, complete cds.	0	133978	40S RIBOSOMAL PROTEIN S6 protein S6 - rat >gi|70933|pir||R3 MS6 ribosomal protein S6 - mouse >gi|319910|pir||R3 HU6 ribosomal protein S6 - human >gi|36148 (X67309) ribosomal protein S6 [Homo sapiens] >gi|54010 (Y00348) ribosomal protein S6 [Mus musculus] >g	2e-072
4922	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	6e-006	<NONE>	<NONE>	<NONE>
4923	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	6e-006	<NONE>	<NONE>	<NONE>
4924	X76683	Plasmid vector pHM2 betalactamase gene	e-160	987050	(X65335) lacZ gene product [unidentified cloning vector]	3e-015

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
4925	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
4926	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	0.002	<NONE>	<NONE>	<NONE>
4927	D50369	Homo sapiens mRNA for low molecular mass ubiquinone-binding protein, complete cds	e-152	3024781	UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX UBIQUINONE-BINDING PROTEIN QP-C PROTEIN) (COMPLEX III SUBUNIT VII) >gi|2605590 (D50369) low molecular mass ubiquinone-binding protein [Homo sapiens]	6e-023
4928	M63391	Human desmin gene, complete cds.	4e-013	<NONE>	<NONE>	<NONE>
4929	D38417	Mouse mRNA for arylhydrocarbon receptor, complete cds	e-110	<NONE>	<NONE>	<NONE>
4930	U38253	Rattus norvegicus initiation factor eIF-2B gamma subunit (eIF-2B gamma) mRNA, complete cds	e-175	2494312	TRANSLATION INITIATION FACTOR EIF-2B GAMMA SUBUNIT (EIF-2B GDP-GTP EXCHANGE FACTOR) subunit [Rattus norvegicus]	4e-040
4931	D38417	Mouse mRNA for arylhydrocarbon receptor, complete cds	e-110	<NONE>	<NONE>	<NONE>
4932	U50767	Mus musculus alpha 1 type I collagen gene, partial cds and 3' flanking region.	1.2	<NONE>	<NONE>	<NONE>
4933	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
4934	U86137	Mus musculus telomerase protein-1 mRNA, complete cds	1.70E-01	3327208	(AB014597) KIAA0697 protein [Homo sapiens]	9e-006
4935	S57980	Crp1=cystatin-related protein-1 [rats, Genomic, 7673 nt]	0.041	<NONE>	<NONE>	<NONE>
4936	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
4937	AB012047	Arabidopsis thaliana gene for sulfate transporter, complete cds, clone:AST56	0.14	3915658	ATP-DEPENDENT RNA HELICASE A helicase II [Homo sapiens]	6.1
4938	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	2e-007	<NONE>	<NONE>	<NONE>
4939	AB018374	Mus musculus GARP34 mRNA, complete cds	3e-037	<NONE>	<NONE>	<NONE>
4940	AF001498	Campylobacter jejuni polysaccharide biosynthesis protein homolog gene, partial cds, galactosyl transferase homolog, UDP-galactose phosphate transferase homolog, acetyl transferase homolog and aminotransferase homolog gen...	3e-005	<NONE>	<NONE>	<NONE>
4941	J04617	Human elongation factor EF-1-alpha gene, complete cds. > :: dbj|E02629|E02629 DNA of human polypeptide chain elongation factor-	3e-090	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		1 alpha				
4942	Z54349	H.sapiens MN/CA9 GENE	2e-007	<NONE>	<NONE>	<NONE>
4943	AF077374	Homo sapiens small proline-rich protein (SPRR3) gene, exons 1, 2, and 3 and complete cds	1.3	<NONE>	<NONE>	<NONE>
4944	X59828	Human chromosome 22 flanking hypervariable simple repeat DNA (clone HZREP42)	0.0003	<NONE>	<NONE>	<NONE>
4945	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	1.00E-09	124180	TRANSCRIPTIONAL REGULATOR IE63 human herpesvirus 1 (strain 17) herpesvirus 1] >gi|221713 (D00374) immediate early transcriptional modulating protein IE63 (gene UL54) herpesvirus 1]	5.8
4946	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	1.00E-09	124180	TRANSCRIPTIONAL REGULATOR IE63 human herpesvirus 1 (strain 17) herpesvirus 1] >gi|221713 (D00374) immediate early transcriptional	5.8

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					modulating protein IE63 (gene UL54) herpesvirus 1]	
4947	X76683	Plasmid vector pHM2 betalactamase gene	8e-092	987050	(X65335) lacZ gene product [unidentified cloning vector]	3e-015
4948	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
4949	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	2.00E-04	<NONE>	<NONE>	<NONE>
4950	X16972	Drosophila melanogaster cecropin gene cluster	1.20E-01	1362688	morphogen Xhh precursor - African clawed frog >gi|790938 (L39213) morphogen [Xenopus laevis]	1.9
4951	U12022	Human calmodulin (CALM1) gene, exons 2,3,4,5 and 6, and complete cds	0	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	5.9
4952	X56536	Rabbit mRNA for pH regulatory protein (Na+/H+ exchanger), partial	2.3	119110	EBNA-1 NUCLEAR PROTEIN herpesvirus 4 (strain B95-8) >gi|1334880 (V01555) BKRF1 encodes EBNA-1 protein, latent cycle gene. [Human herpesvirus 4]	4e-018

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
4953	AF037438	Homo sapiens short chain L-3-hydroxyacyl-CoA dehydrogenase (SCHAD) gene, complete cds	2e-006	<NONE>	<NONE>	<NONE>
4954	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	4e-012	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	3.4
4955	AB000467	Homo sapiens mRNA, partial cds, clone:RES4-25	2e-012	<NONE>	<NONE>	<NONE>
4956	U31525	Human glycogenin mRNA, complete cds	0	1707996	GLYCOGENIN >gi|2135280|pir||JC4695 glycogenin glucosyltransferase (EC 2.4.1.186) - human	5e-042
4957	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
4958	AF003836	Mesocricetus auratus isopentenyl diphosphate:dimethylallyl diphosphate isomerase mRNA, complete cds	1.30E+00	<NONE>	<NONE>	<NONE>
4959	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
4960	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
4961	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	4.90E-02	<NONE>	<NONE>	<NONE>
4962	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	4.90E-02	<NONE>	<NONE>	<NONE>
4963	L32537	Homo sapiens (clone XP6G6B) mRNA, partial EST.	5.00E-03	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
4964	L32537	Homo sapiens (clone XP6G6B) mRNA, partial EST.	5.00E-03	<NONE>	<NONE>	<NONE>
4965	X63787	T.thermophila gene for snRNA U3-2	0.41	<NONE>	<NONE>	<NONE>
4966	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
4967	U27341	Bos taurus endothelin converting enzyme-2 Sequence 1 from patent US 5736376	7e-015	<NONE>	<NONE>	<NONE>
4968	U35114	Human apolipoprotein E (APOE) gene, hepatic control region HCR-2	9e-005	<NONE>	<NONE>	<NONE>
4969	M86374	Rat tropoelastin gene, intron 25 (partial).	0.13	<NONE>	<NONE>	<NONE>
4970	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	2e-007	<NONE>	<NONE>	<NONE>
4971	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	2e-007	<NONE>	<NONE>	<NONE>
4972	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	2e-007	<NONE>	<NONE>	<NONE>
4973	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	7.00E-07	<NONE>	<NONE>	<NONE>
4974	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	7.00E-07	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
4975	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	7.00E-07	<NONE>	<NONE>	<NONE>
4976	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.005	2995290	(AL022268) putative transmembrane transport protein [Streptomyces coelicolor]	1.50E-02
4977	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.005	2995290	(AL022268) putative transmembrane transport protein [Streptomyces coelicolor]	1.50E-02
4978	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.005	2995290	(AL022268) putative transmembrane transport protein [Streptomyces coelicolor]	1.50E-02
4979	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	2.00E-05	2983512	(AE000718) putative protein [Aquifex aeolicus]	2.2
4980	X56536	Rabbit mRNA for pH regulatory protein (Na+/H+ exchanger), partial	2.3	119110	EBNA-1 NUCLEAR PROTEIN herpesvirus 4 (strain B95-8) >gi|1334880 (V01555) BKRF1 encodes EBNA-1 protein, latent cycle gene. [Human herpesvirus 4]	4e-018
4981	Z11508	A.thaliana rpl15 gene for plastid ribosomal protein CL15	5.00E-03	3283910	(AF070638) unknown [Homo sapiens]	2.5
4982	X95834	H.sapiens DNA sequence surrounding NotI site, clone NRLA143D	7e-070	1588365	signal peptidase:SUBUNIT=12kD [Homo sapiens]	1e-043,

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
4983	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	2e-007	4008081	(AF106835) putative DnaJ [Methylovorus sp. strain SS1]	3e-010
4984	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
4985	U43626	Human chromosome 15q11-q13 putative DNA replication origin in the g-aminobutyric acid receptor b3 and a5 gene cluster	2e-018	2197085	(AF003535) ORF2-like protein [Homo sapiens]	0.0002
4986	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
4987	D21272	Rice mRNA for ADP-glucose pyrophosphorylase	1.1	1708084	EXOGLUCANASE B PRECURSOR 1,4-beta-cellobiosidase (EC 3.2.1.91) precursor - Cellulomonas fimi >gi|790698 (L38827) beta-1,4-cellobiohydrolase [Cellulomonas fimi]	5.8
4988	U59706	Gallus gallus alternatively spliced AMPA glutamate receptor, isoform GluR2 flop, (GluR2) mRNA, partial cds.	0.015	<NONE>	<NONE>	<NONE>
4989	AF086033	Homo sapiens full length insert cDNA clone YW26E09	e-174	<NONE>	<NONE>	<NONE>
4990	L31840	Rattus norvegicus nuclear pore complex protein NUP107 mRNA, complete cds.	e-179	1709212	NUCLEAR PORE COMPLEX PROTEIN NUP107	2e-083

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
4991	AF052144	Homo sapiens clone 24573 and 24786 mRNA sequences	e-170	1174415	SPIDROIN 2 (DRAGLINE SILK FIBROIN 2) >gi|345426|pir||A44112 spidroin 2, dragline silk fibroin - orb spider (Nephila clavipes) (fragment) clavipes]	4.8
4992	M22406	Human intestinal mucin mRNA, partial cds, clone SMUC 42.	0.085	188864	(M74027) mucin [Homo sapiens]	1e-009
4993	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
4994	U24697	Chironomus samoensis nanos homolog (Cs nos) gene, complete cds.	0.13	3880999	(AL021492) Y45F10D.11 [Caenorhabditis elegans]	7e-022
4995	M64716	Human ribosomal protein S25 mRNA, complete cds.	4e-074	2943738	(AB011550) Drosophila Policomblike-related gene containing PHD fingers. [Mus musculus]	4e-011
4996	X54326	H.sapiens mRNA for glutaminyl-tRNA synthetase	0	135104	MULTIFUNCTIONAL AMINOACYL-TRNA SYNTHETASE (CONTAINS: GLUTAMYL-TRNA SYNTHETASE glutamyl-prolyl-tRNA synthetase - human >gi|31958	1e-088
4997	Z12112	pWE15A cosmid vector DNA	2e-028	987050	(X65335) lacZ gene product [unidentified cloning vector]	2e-007
4998	Z62939	H.sapiens CpG DNA, clone 75f1, forward read cpg75f1.ft1b .	3e-010	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
4999	<NONE>	<NONE>	<NONE>	2134574	mucin - rhesus macaque (fragment) >gi|437055	5e-005
5000	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	9e-009	<NONE>	<NONE>	<NONE>
5001	Z93950	H.sapiens DNA; chromosome Y repeat regions	0.15	<NONE>	<NONE>	<NONE>
5002	X64037	H.sapiens mRNA for RNA polymerase II associated protein RAP74	5e-056	<NONE>	<NONE>	<NONE>
5003	M37583	Human histone (H2A.Z) mRNA, complete cds.	e-132	121994	HISTONE H2A.Z >gi|89608|pir||S03642 histone H2A.Z - bovine >gi|92380|pir||S03644 histone H2A.Z - rat >gi|106267|pir||A35881 histone H2A.Z - human sapiens] >gi|57808 (X52316) histone H2A.Z (AA 1-127) taurus] >gi|184060 (M37583) histone (H2A.Z) [Homo sapien	2e-044
5004	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	4e-011	<NONE>	<NONE>	<NONE>
5005	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	4e-011	<NONE>	<NONE>	<NONE>
5006	M94764	Glycine max cv. Dare nodulin 26 gene fragment.	0.043	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
5007	Z34287	B.subtilis (SO113) genomic DNA (5425bp)	1.2	<NONE>	<NONE>	<NONE>
5008	X76683	Plasmid vector pHM2 betalactamase gene	6e-078	987050	(X65335) lacZ gene product [unidentified cloning vector]	2e-014
5009	D17577	Mouse mRNA for kinesin-like protein (Kif1b), complete cds	e-109	2497524	KINESIN-LIKE PROTEIN KIF1B mouse >gi|407339|gnl|PID|d1005029 (D17577) Kif1b [Mus musculus]	9e-041
5010	X91192	H.sapiens PLC beta 3 gene (exon 1) and SOM172 gene (exon 1)	1e-096	3294231	(AJ223970) mono-methyl transferase	3
5011	D88271	Human (lambda) DNA for immunogloblin light chain	1e-021	<NONE>	<NONE>	<NONE>
5012	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
5013	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
5014	AF052133	Homo sapiens clone 23970 mRNA sequence	0	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	5.9
5015	M21731	Human lipocortin-V mRNA, complete cds.	e-169	999934	Annexin V (Lipocortin V, Endonexin Ii, Placental Anticoagulant Protein) Mutant With Glu 17 Replaced By Gly, Glu 78 Replaced By Gln (E17g,E78q) Complexed With Calcium	4e-005

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
5016	M21731	Human lipocortin-V mRNA, complete cds.	e-169	999934	Annexin V (Lipocortin V, Endonexin Ii, Placental Anticoagulant Protein) Mutant With Glu 17 Replaced By Gly, Glu 78 Replaced By Gln (E17g,E78q) Complexed With Calcium	4e-005
5017	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
5018	L44118	Homo sapiens proximal CMT1A-REP repeat	0.0005	<NONE>	<NONE>	<NONE>
5019	Y16849	Bacillus sp. D3 xynA and abfA genes and ORF1	2e-015	<NONE>	<NONE>	<NONE>
5020	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	2e-006	465975	PUTATIVE ATP-DEPENDENT RNA HELICASE T26G10.1 IN CHROMOSOME III >gi|482102|pir||S40731 ATP-dependent RNA helicase homolog T26G10.1 - Caenorhabditis elegans >gi|3880293|gnl|PID|e1349766 1397-1495 which introduced stop codon at 3' splice; 5' splice looks v.	9e-005
5021	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	2e-006	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
5022	U02455	Cloning vector rpDR2, complete sequence.	0.35	2132302	hypothetical protein YPR144c - yeast similarity near C-terminus to RNA Polymerase beta subunit (Swiss Prot. accession number P11213) and CCAAT-binding transcription factor (PIR accession number A36368) [Saccharomyces cerevisiae]	1e-031
5023	X97999	H.sapiens mRNA for transcription factor IID, subunit TAFII55	0	3024690	TRANSCRIPTION INITIATION FACTOR TFIID 55 KD SUBUNIT (TAFII-55) (TAFII55) factor IID [Homo sapiens]	4e-083
5024	X71642	M.musculus GEG-154 mRNA	3e-092	<NONE>	<NONE>	<NONE>
5025	X71642	M.musculus GEG-154 mRNA	3e-092	<NONE>	<NONE>	<NONE>
5026	AB018270	Homo sapiens mRNA for KIAA0727 protein, partial cds	4e-061	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	7.6
5027	D90086	Human pyruvate dehydrogenase (EC 1.2.4.1) beta subunit gene, exons 1-10	4e-011	2143936	probable regulatory protein 322 - rat	7.7
5028	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.002	<NONE>	<NONE>	<NONE>
5029	X65319	Cloning vector pCAT-Enhancer	2e-081	987050	(X65335) lacZ gene product [unidentified cloning vector]	3e-015
5030	<NONE>	<NONE>	<NONE>	188864	(M74027) mucin [Homo sapiens]	0.001

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
5031	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	0.0002	3258141	(AP000007) 138aa long hypothetical protein [Pyrococcus horikoshii]	9.6
5032	X98001	H.sapiens mRNA for geranylgeranyl transferase II	e-129	2506788	GERANYLGERANYL TRANSFERASE TYPE II BETA SUBUNIT (RAB GERANYLGERANYLTRANSFERASE BETA SUBUNIT) (RAB GERANYL-GERANYLTRANSFERASE BETA SUBUNIT) transferase II [Homo sapiens]	3e-026
5033	U72789	Human cosmid U197H5, complete sequence [Homo sapiens]	5e-023	<NONE>	<NONE>	<NONE>
5034	U72789	Human cosmid U197H5, complete sequence [Homo sapiens]	5e-023	<NONE>	<NONE>	<NONE>
5035	U19239	Choristoneura fumiferana entomopoxvirus spheroidin gene, complete cds, G4R gene, partial cds, and nucleoside triphosphate phosphohydrolase (NPH I) gene, partial cds	3.8	<NONE>	<NONE>	<NONE>
5036	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	8e-009	2690166	(AE000788) B. burgdorferi predicted coding region BBK23	4

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
5037	U66871	Human enhancer of rudimentary homolog mRNA, complete cds	0	2498336	ENHANCER OF RUDIMENTARY HOMOLOG homologous to DROER protein [Homo sapiens] >gi|1519519 sapiens]	6e-057
5038	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
5039	X99728	H.sapiens NDUFV3 gene, exon 3	3e-092	2829450	NADH-UBIQUINONE OXIDOREDUCTASE 9 KD SUBUNIT PRECURSOR (COMPLEX I-9KD) (CI-9KD)	1e-015
5040	X78730	M. musculus DNA for the flanking seqeunces of the hypothalamic GRH first exons	2	<NONE>	<NONE>	<NONE>
5041	X84373	H.sapiens mRNA for nuclear factor RIP140 > :: gb|G28540|G28540 human STS SHGC-31616.	e-155	<NONE>	<NONE>	<NONE>
5042	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
5043	X82272	Human endogenous retrovirus env mRNA	8e-081	1196429	(M14123) pol/env ORF (bases 3878-8257) first start codon at 4172; Xxx; putative [Homo sapiens]	6e-058
5044	AF029982	Mus musculus sarco(endo)plasmic reticulum calcium ATPase (SERCA2) gene, promoter region, exons 1-3, and partial cds	0.003	3873550	(AL033534) serine-rich protein	0.018
5045	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
5046	Y12781	Homo sapiens mRNA for transducin (beta) like 1 protein	1e-084	3021409	(Y12781) transducin (beta) like 1 protein [Homo sapiens]	2e-064

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
5047	S63912	D10S102=FBRNP [human, fetal brain, mRNA, 3043 nt]	4e-084	<NONE>	<NONE>	<NONE>
5048	X91192	H.sapiens PLC beta 3 gene (exon 1) and SOM172 gene (exon 1)	1e-096	3294231	(AJ223970) mono-methyl transferase	3
5049	X03558	Human mRNA for elongation factor 1 alpha subunit	0	1169475	ELONGATION FACTOR 1-ALPHA 1	e-108
5050	L31783	Mus musculus uridine kinase mRNA, partial cds	3e-029	1718058	URIDINE KINASE (URIDINE MONOPHOSPHO KINASE) >gi|471981 (L31783) uridine kinase	4e-011
5051	X75652	A.longa plastid genes for tRNAs, ribosomal protein, rRNA and elongation factor	1.3	<NONE>	<NONE>	<NONE>
5052	Z93123	M.acuminata mRNA; clone pBAN UD75	1.1	<NONE>	<NONE>	<NONE>
5053	D16901	Human HepG2 3' region cDNA, clone hmd2h05	1.5	<NONE>	<NONE>	<NONE>
5054	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	1e-011	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	5.7

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
5055	AF043252	Homo sapiens mitochondrial outer membrane protein (Tom40) gene, nuclear gene encoding mitochondrial protein, exons 7, 8 and 9	e-106	3941342	(AF043250) mitochondrial outer membrane protein [Homo sapiens] >gi|3941347 (AF043253) mitochondrial outer membrane protein [Homo sapiens] >gi|4105703 (AF050154) D19S1177E [Homo sapiens]	6e-007
5056	X66494	R.norvegicus CHOT1 mRNA	1e-012	1545807	(D78572) membrane glycoprotein [Mus musculus]	3e-007
5057	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
5058	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	2e-007	3513368	(AB017202) entactin-2 [Mus musculus]	3e-005
5059	U77107	Fundulus lineolatus cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, partial cds	0.37	3947877	(AL034382) putative mitosis and maintenance of ploidy protein [Schizosaccharomyces pombe]	7e-026
5060	X52317	Human mRNA for histone H2A.Z	5e-014	<NONE>	<NONE>	<NONE>
5061	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	3e-008	<NONE>	<NONE>	<NONE>
5062	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	1.2	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
5063	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.0002	<NONE>	<NONE>	<NONE>
5064	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	1e-011	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	1.5
5065	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.0002	<NONE>	<NONE>	<NONE>
5066	X15943	Huamn calcitonin/alpha-CGRP gene	1e-012	1575563	(U66464) hematopoietic progenitor kinase [Homo sapiens]	5.6
5067	AF001175	Homo sapiens ribonuclease P protein subunit p14 (Rpp14) mRNA, complete cds	0	4100563	(AF001175) ribonuclease P protein subunit p14 [Homo sapiens]	2e-032
5068	L29260	Arabidopsis thaliana 1-amino-1-cyclopropanecarboxylate synthase (ACS5) gene, complete cds.	0.41	<NONE>	<NONE>	<NONE>
5069	X57268	Mouse DNA for t-haplotype-specific elements (located in H-2 complex, ETn related)	1.2	<NONE>	<NONE>	<NONE>
5070	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	1e-010	2072296	(U95098) mitotic phosphoprotein 44 [Xenopus laevis]	5.5
5071	Y11896	M.musculus mRNA for Brx gene, partial	3e-018	2196874	(Y11896) BRX protein [Mus musculus]	3e-011

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
5072	Y00711	Human mRNA for lactate dehydrogenase B (LDH-B)	0	126041	L-LACTATE DEHYDROGENASE H CHAIN dehydrogenase B (AA 1 - 334) [Homo sapiens] >gi|1200083	e-102
5073	AF065482	Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds	0	3152938	(AF065482) sorting nexin 2 [Homo sapiens]	3e-072
5074	M86374	Rat tropoelastin gene, intron 25 (partial).	0.13	<NONE>	<NONE>	<NONE>
5075	D50418	Mouse mRNA for AREC3, partial cds	6e-047	2495271	SKELETAL MUSCLE-SPECIFIC ARE BINDING PROTEIN AREC3 (HOMEOBOX PROTEIN SIX4) M18) - mouse >gi|1255626|gnl|PID|d1009550 (D50416) AREC3	2e-006
5076	D17448	Microcystis aeruginosa plasmid pMA2 DNA, complete genome sequence	0.13	<NONE>	<NONE>	<NONE>
5077	M29548	Human elongation factor 1-alpha (EF1A) mRNA, partial cds.	e-166	1169475	ELONGATION FACTOR 1-ALPHA 1	6e-010
5078	AF081496	Homo sapiens kinetochore protein BUB3 (BUB3) mRNA, complete cds	6e-044	2921873	(AF047472) spleen mitotic checkpoint BUB3 [Homo sapiens] protein BUB3 [Homo sapiens]	3e-006
5079	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	7e-007	<NONE>	<NONE>	<NONE>
5080	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
5081	M14123	Human endogenous retrovirus HERV-K10.	2e-065	1196429	(M14123) pol/env ORF (bases 3878-8257) first start codon at 4172; Xxx; putative [Homo sapiens]	6e-037
5082	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
5083	D30655	Homo sapiens mRNA for eukaryotic initiation factor 4AII, complete cds	0	673433	(X56953) protein synthesis initiation factor 4A [Mus musculus]	2e-092
5084	X16869	Human mRNA for elongation factor 1-alpha (clone CEF4)	5e-045	3122072	ELONGATION FACTOR 1-ALPHA 1 chicken >gi|488468 (L00677) elongation factor 1 alpha	1e-009
5085	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
5086	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
5087	U78310	Homo sapiens pescadillo mRNA, complete cds	e-122	2194203	(U78310) pescadillo [Homo sapiens]	9e-009
5088	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
5089	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	2e-005	<NONE>	<NONE>	<NONE>
5090	U09368	Human zinc finger protein ZNF140	0	1731416	ZINC FINGER PROTEIN 140 human >gi|487787 (U09368) zinc finger protein ZNF140	2e-062
5091	M98509	Human NFB genomic fragment.	1e-010	<NONE>	<NONE>	<NONE>
5092	AB002322	Human mRNA for KIAA0324 gene, partial cds	e-130	2996650	(AC004493) KIAA0324 [Homo sapiens]	9e-018
5093	AJ007670	Homo sapiens mRNA for LGMD2B protein	2e-014	403460	(L24521) transformation-related protein [Homo sapiens]	3.8

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
5094	X16869	Human mRNA for elongation factor 1-alpha (clone CEF4)	0	181967	(M29548) elongation factor 1-alpha [Homo sapiens]	2e-036
5095	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	7e-007	<NONE>	<NONE>	<NONE>
5096	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.0005	<NONE>	<NONE>	<NONE>
5097	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	2e-006	<NONE>	<NONE>	<NONE>
5098	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	2e-006	<NONE>	<NONE>	<NONE>
5099	U45421	Borrelia burgdorferi 2.9-1 locus, ORF 5-8, ORF-A-D, REP+, REP-, and lipoprotein (LP) genes, complete cds	0.014	3510605	(AF044267) gyrase subunit B [Chlamydia trachomatis]	3.4
5100	L54057	Homo sapiens CLP mRNA, partial cds.	0	<NONE>	<NONE>	<NONE>
5101	D14660	Human mRNA for KIAA0104 gene, complete cds	0	1350786	PUTATIVE 60S RIBOSOMAL PROTEIN sapiens] >gi|3947438 (AC005034) ribosomal protein-like	e-111

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
5102	X78627	H.sapiens mRNA for translin.	0	1082873	translin - human >gi|607130 (X78627) translin [Homo sapiens] >gi|1586346|prf||2203413A recombination hotspot-binding protein [Homo sapiens]	5e-068
5103	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.0001	<NONE>	<NONE>	<NONE>
5104	M12585	Mouse alpha-1 antitrypsin gene, segment 1.	2e-006	3873550	(AL033534) serine-rich protein	1.7
5105	X52967	Human mRNA for ribosomal protein L7	0	423072	ribosomal protein L7 - human	7e-061
5106	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	7e-007	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
5107	X78722	M.musculus GLUT2 gene for glucose transporter	0.34	1685115	(U68754) putative transcription factor [Dictyostelium discoideum]	3.8
5108	AF002677	Dictyostelium discoideum DEAD-box RNA helicase	0.28	3293508	(AF069188) NADH dehydrogenase 1 [Ephedrus laevicollis]	0.81
5109	AB018263	Homo sapiens mRNA for KIAA0720 protein, partial cds	0.87	107240	oncogene 1 (tre-2 locus) (clone 210) - human	0.19
5110	AF017115	Homo sapiens cytochrome c oxidase subunit IV precursor (COX4) gene, nuclear gene encoding mitochondrial protein, complete cds	0.77	<NONE>	<NONE>	<NONE>
5111	AE001383	Plasmodium falciparum chromosome 2, section 20 of 73 of the complete sequence	0.15	2315754	(AF016681) No definition line found [Caenorhabditis elegans]	9.6
5112	D49577	Pig mRNA for rearranged T-cell receptor delta-chain/Vdelta1.14-Ddeltas-Jdelta1, partial cds	0.91	<NONE>	<NONE>	<NONE>
5113	U63810	Homo sapiens WD40 protein Ciao 1 mRNA, complete cds	0.0	3219331	(AC004020) Unknown gene product [Homo sapiens]	3e-92
5114	AF085858	Homo sapiens full length insert cDNA clone YN49B07	e-172	3329465	(AF064553) NSD1 protein [Mus musculus]	8e-54
5115	X01682	Mouse gene for cytochrome P3-450	0.026	1381394	(U40989) tat interactive protein [Homo sapiens]	4.0

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
5116	AE001432	Plasmodium falciparum chromosome 2, section 69 of 73 of the complete sequence	1.5	3873713	(Z74026) cDNA EST yk452h4.3 comes from this gene; cDNA EST yk452h4.5 comes from this gene	9e-11
5117	U31973	Human phosphodiesterase A' subunit (PDE6C) mRNA, complete cds. > :: gb|G28549|G28549 human STS SHGC-31657.	2.3	136976	PROTEIN UL87 >gi|76594|pir||S09851 hypothetical protein UL87 - human cytomegalovirus cytomegalovirus]	8.1
5118	X02212	Chicken alpha-cardiac actin gene	2.6	<NONE>	<NONE>	<NONE>
5119	AE000838	Methanobacterium thermoautotrophicum from bases 494834 to 505698 (section 44 of 148) of the complete genome	0.89	765086	(D30786) feline CD9 [Felis catus]	1.4
5120	U89744	Rattus norvegicus putative cell surface antigen mRNA, complete cds	0.68	728850	GLUCOAMYLASE S1/S2 PRECURSOR (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE) >gi|626156|pir||S48478 glucan 1,4-alpha-glucosidase (EC 3.2.1.3) - yeast sta1, len: 1367, CAI: 0.3, AMYH_YEAST P08640 GLUCOAMYLASE S1 (EC 3.2.1.3) [Saccharomyc	9e-06

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
5121	J04974	Human alpha-2 type XI collagen mRNA (COL11A2).	1.2	114887	BREAKPOINT CLUSTER REGION PROTEIN protein, splice form 1 - human >gi|29421 (X02596) bcr gene product [Homo sapiens]	9.4
5122	AL021806	Homo sapiens DNA sequence from PAC 779B17 on chromosome 22q13.1. Contains exon trap, complete sequence	0.046	2827756	EPHRIN TYPE-A RECEPTOR 1 PRECURSOR	1.9
5123	X68826	P.sativum mRNA for fructose 1,6 biphosphatase	0.95	1314248	(U24681) NADH:cytochrome c reductase [synthetic construct]	2e-05
5124	M14431	Bacteriophage phi-29 gene-16 gene, complete cds.	0.035	<NONE>	<NONE>	<NONE>
5125	U17033	Human 180 kDa transmembrane PLA2 receptor mRNA, complete cds.	0.36	722372	(U23139) similar to beta transducin proteins containing TRP-ASP domains [Caenorhabditis elegans]	3e-08
5126	Z50202	P.vulgaris arc5-1 gene	0.007	1151256	(U43319) transmembrane receptor [Mus musculus]	0.13
5127	AF013711	Homo sapiens 22 kDa actin-binding protein	2e-10	<NONE>	<NONE>	<NONE>
5128	AF086324	Homo sapiens full length insert cDNA clone ZD53E07	5e-09	3318653	(U83192) post-synaptic density protein 95 [Homo sapiens]	0.001
5129	D90117	T. thermophila mRNA for citrate synthase (EC 4.1.3.7)	0.63	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
5130	D45105	Metschnikowia reukaufii 26S rRNA, partial sequence	0.78	<NONE>	<NONE>	<NONE>
5131	D85088	Ectoplana limuli DNA for 18s ribosomal RNA	0.41	267408	PROBABLE DNA PACKAGING PROTEIN packaging protein [Human herpesvirus 4]	7.2
5132	X89886	P.patens mRNA for 5-aminolevulinate dehydratase	0.41	3875246	(Z81490) similar to WD domain, G-beta repeats (2 domains); cDNA EST EMBL:T00482 comes from this gene; cDNA EST EMBL:T00923 comes from this gene; cDNA EST yk449d4.3 comes from this gene; cDNA EST yk449d4.5 comes from this gen...	2e-22
5133	AB014564	Homo sapiens mRNA for KIAA0664 protein, partial cds	0.0	2981221	(AF053091) eyelid [Drosophila melanogaster]	0.076
5134	AE001403	Plasmodium falciparum chromosome 2, section 40 of 73 of the complete sequence	0.003	2495297	HYPOTHETICAL 26.3 KD HOMEOBOX PROTEIN C02F12.5 IN CHROMOSOME X >gi|1109893 (U41545) strong similarity to homeobox proteins; similar to inhibitor domain of tissue factor pathway inhibitor	3.7

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
5135	U92574	Fugu rubripes homeobox protein HOXB-1 (FrHOXB-1) gene, complete cds	0.54	<NONE>	<NONE>	<NONE>
5136	U31118	Xenopus laevis cytoplasmic myosin II regulatory light chain mRNA, complete cds	0.26	3879530	(Z49130) cDNA EST yk486b9.3 comes from this gene; cDNA EST yk486b9.5 comes from this gene	8e-07
5137	L49035	Gorilla gorilla ABC-transporter (TAP2) mRNA, complete cds	0.21	4007066	(AJ131571) X protein [Hepatitis B virus]	1.3
5138	AF068628	Mus musculus DNA cytosine-5 methyltransferase 3B3 (Dnmt3b) mRNA, alternatively spliced, complete cds	4e-04	<NONE>	<NONE>	<NONE>
5139	M64982	Human fibrinogen alpha chain gene, complete mRNAs.	0.062	<NONE>	<NONE>	<NONE>
5140	M19262	Rat clathrin light chain (LCB3) mRNA, complete cds.	0.25	2088802	(AF003151) D1007.4 gene product [Caenorhabditis elegans]	0.012
5141	X94947	L.esculentum mRNA for homeobox protein	3.7	2315770	(AF016683) K09F6.1 gene product [Caenorhabditis elegans]	0.096
5142	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
5143	M33782	Human TFEB protein mRNA, partial cds.	0.36	<NONE>	<NONE>	<NONE>
5144	AB011098	Homo sapiens mRNA for KIAA0526 protein, complete cds	2e-07	2501115	TBX2 PROTEIN (T-BOX PROTEIN 2)	0.90

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
5145	AF039029	Homo sapiens snurportin1 mRNA, complete cds	0.0	3834390	(AF039029) snurportin1 [Homo sapiens]	e-108
5146	U22970	Human interferon-inducible peptide (6-16) gene, complete cds	0.21	<NONE>	<NONE>	<NONE>
5147	D63880	Human mRNA for KIAA0159 gene, complete cds	2e-64	<NONE>	<NONE>	<NONE>
5148	AB011174	Homo sapiens mRNA for KIAA0602 protein, partial cds	e-164	3043728	(AB011174) KIAA0602 protein [Homo sapiens]	2e-53
5149	AF053551	Homo sapiens metaxin 2 (MTX2) mRNA, nuclear gene encoding mitochondrial protein, complete cds	0.0	3283049	(AF053551) metaxin 2 [Homo sapiens]	1e-76
5150	Y13382	Arabidopsis thaliana ferrochelatase-I gene and promoter sequence	0.012	<NONE>	<NONE>	<NONE>
5151	AF044854	Colias eurytheme large subunit ribosomal RNA gene, partial sequence; tRNA-Val gene, complete sequence; and small subunit ribosomal RNA gene, partial sequence, mitochondrial genes for mitochondrial RNAs	1.3	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
5152	AF005059	Toxoplasma gondii p97 mRNA, complete cds	0.90	2570049	(Y08701) Pinin [Mus musculus]	1.3
5153	D84307	Human mRNA for phosphoethanolamine cytidylyltransferase, complete cds	0.013	<NONE>	<NONE>	<NONE>
5154	D38050	Aspen prxA3a gene for peroxidase, complete cds	0.018	1723942	HYPOTHETICAL 20.8 KD PROTEIN IN COX4-GTS1 INTERGENIC REGION >gi|2131614|pir||S61134 hypothetical protein YGL183c - yeast (Saccharomyces cerevisiae) >gi|1143564|gnl|PID|e199057 (X91489) putative HMG box [Saccharomyces cerevisiae]	0.39
5155	AL010208	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-103, complete sequence	0.13	1850115	(Z86089) fadD2 [Mycobacterium tuberculosis]	1.5
5156	U07807	Human metallothionein IV (MTIV) gene, complete cds.	0.004	<NONE>	<NONE>	<NONE>
5157	AF048991	Homo sapiens MutS homolog 5 (MSH5) gene, exons 13 through 25 and complete cds	0.001	3986756	(AF109905) NG23 [Mus musculus]	0.007

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
5158	U39079	Schizosaccharomyces pombe ARS binding protein 1	0.50	<NONE>	<NONE>	<NONE>
5159	X01706	Mouse intracisternal A-particle (IAP) gene 62 long terminal repeat (LTR)	0.41	2224713	(AB002384) KIAA0386 [Homo sapiens]	8e-04
5160	AF030558	Rattus norvegicus phosphatidylinositol 5-phosphate 4-kinase gamma mRNA, complete cds	8e-13	<NONE>	<NONE>	<NONE>
5161	L06453	Strongylocentrotus purpuratus (clone C) high mobility group 1 protein (HMG1 homologue) gene, complete cds.	0.33	3914031	BETA-GALACTOSIDE SPECIFIC LECTIN I A CHAIN (MLA) (ML-I A) (RRNA N-GLYCOSIDASE)	0.087
5162	Z68320	Caenorhabditis elegans cosmid W07A12, complete sequence [Caenorhabditis elegans]	0.28	2500558	PUTATIVE RIBONUCLEASE III (RNASE III) >gi|3876420|gnl|PID|e1346063 (Z81070) similar to ribonuclease [Caenorhabditis elegans]	2e-25
5163	U40397	Mus musculus serum amyloid A-4 protein (Saa4) gene, complete cds	5e-04	<NONE>	<NONE>	<NONE>
5164	X00367	Chlamydomonas chloroplast DNA region with ARS element 03 (ARS = autonomously replicating sequence)	0.046	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
5165	U43838	Glycine max choline kinase GmCK1p mRNA, complete cds	1.2	132918	50S RIBOSOMAL PROTEIN L35, CHLOROPLAST PRECURSOR (CL35) >gi|81486|pir||A36107 ribosomal protein L35 precursor, chloroplast - spinach oleracea]	2.4
5166	U67590	Methanococcus jannaschii section 132 of 150 of the complete genome	0.097	<NONE>	<NONE>	<NONE>
5167	AB006787	Mus musculus mRNA for apoptosis signal-regulating kinase 1, complete cds	0.39	1263187	(U24215) HOMODA hydrolase [Pseudomonas putida] putida]	0.83
5168	U43567	Trypanosoma cruzi kinetoplast maxicircle DNA, clone TRCKPMAX	0.054	<NONE>	<NONE>	<NONE>
5169	U04706	Bos taurus 50 kDa protein (adp50) mRNA, complete cds.	0.0	2498104	ADRENAL MEDULLA 50 KD PROTEIN	8e-83
5170	L14684	Rattus norvegicus nuclear-encoded mitochondrial elongation factor G mRNA, complete cds.	e-137	585084	ELONGATION FACTOR G, MITOCHONDRIAL PRECURSOR (MEF-G) >gi|543383|pir||S40780 translation elongation factor G, mitochondrial - rat >gi|310102	3e-59
5171	U01120	Human glucose-6-phosphatase mRNA, complete cds. >	2e-04	544361	GLUCOSE-6-PHOSPHATASE (G6PASE) 3.1.3.9) - human >gi|452444 (U01120) glucose-6-phosphatase [Homo sapiens]	4e-12

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
5172	D87671	Rat mRNA for TIP120, complete cds	e-144	1799570	(D87671) TIP120 [Rattus norvegicus]	3e-69
5173	U22296	Rattus norvegicus casein kinase 1 gamma 1 isoform mRNA, complete cds	e-120	3024053	CASEIN KINASE I, GAMMA 1 ISOFORM kinase 1 gamma 1 isoform [Rattus norvegicus]	8e-54
5174	Y07648	A.thaliana nit2 gene, nit1 gene and nit3 gene	0.007	2429486	(AF025464) No definition line found [Caenorhabditis elegans]	9.5
5175	AB013721	Oryctolagus cuniculus mRNA for mitsugumin 23, complete cds	3e-91	3628745	(AB013721) mitsugumin 23 [Oryctolagus cuniculus]	0.006
5176	M74069	Saccharomyces cerevisiae endochitinase (CTS1-1) gene, complete cds.	2.5	<NONE>	<NONE>	<NONE>
5177	Z61469	H.sapiens CpG DNA, clone 52h1, forward read cpg52h1.ft1a .	1e-77	1184072	(U40766) COL-1 [Meloidogyne incognita]	0.002
5178	AF015043	Homo sapiens EH-binding protein mRNA, partial cds	0.0	2492914	APOLIPOPROTEIN C-IV PRECURSOR cluster E-C1-C2 linked gene [Mus musculus]	3.0
5179	X74560	H.sapiens (clone pS2) sequence	3e-04	3687469	(AL031798) putative diphthine synthase	3e-23
5180	X94768	H.sapiens RP3 gene (XLRP gene 3)	1e-05	<NONE>	<NONE>	<NONE>
5181	X80937	M.musculus mRNA for RIP1 protein	0.48	107750	synapsin Ib - human	3e-04
5182	M12759	Human Ig J chain gene, exons 3 and 4.	0.036	<NONE>	<NONE>	<NONE>

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
5183	M30773	Human calcineurin B mRNA, complete cds	0.002	3878494	(Z79602) predicted using Genefinder; Similarity to Yeast hypothetical protein YAE2 gene; cDNA EST EMBL:M88949 comes from this gene	3e-06
5184	U08831	Human immunodeficiency virus type 1, sample 019 from Thailand (E2TH019W.01di 1sCD), envelope glycoprotein c2v3 region (env) gene, partial cds.	0.015	<NONE>	<NONE>	<NONE>
5185	Z98303	Human DNA sequence from BAC 140H19 on chromosome Xq24-25. Contains STS	0.005	<NONE>	<NONE>	<NONE>
5186	AE000952	Archaeoglobus fulgidus section 155 of 172 of the complete genome	2e-07	3257245	(AP000003) 571aa long hypothetical oxaloacetate decarboxylase alpha chain [Pyrococcus horikoshii]	5e-08
5187	L48476	Homo sapiens (subclone 3_e10 from P1 H21) DNA sequence.	2e-04	3877439	(Z72510) similarity to yeast UTR3 protein (Swiss Prot accession number P21374); cDNA EST EMBL:D72822 comes from this gene; cDNA EST EMBL:D75763 comes from this gene; cDNA EST yk274e3.3 comes from this gene; cDNA EST	0.19

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					yk274e3....	
5188	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	3e-09	<NONE>	<NONE>	<NONE>
5189	AF055022	Homo sapiens clone 24684 mRNA sequence	e-102	2708743	(AC003952) putative Tal-1-like reverse transcriptase	4.0
5190	AJ009761	Homo sapiens mRNA for putative dimethyladenosine transferase, partial	e-121	4050050	(AF102147) putative dimethyladenosine transferase [Homo sapiens]	8e-48
5191	Y08238	H.pylori clpB gene	0.27	1572756	(U70848) C43G2.1 gene product [Caenorhabditis elegans]	1e-21
5192	<NONE>	<NONE>	<NONE>	2828280	(AL021687) putative protein [Arabidopsis thaliana] >gi|2832633|gnl|PID|e1249651 (AL021711) putative protein [Arabidopsis thaliana]	9e-36
5193	J00747	Rat insulin-I (ins-1) gene.	6e-05	4154522	(AE001441) putative [Helicobacter pylori]	3.2
5194	U64454	Human 3' of immunoglobulin heavy chain locus	0.83	281204	gene LF3 protein - human herpesvirus 4 virus]	0.069

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
5195	AB002383	Human mRNA for KIAA0385 gene, complete cds	8e-13	2498318	DXS6673E PROTEIN retardation candidate gene [Homo sapiens]	2e-24
5196	M81840	Human NRL gene product mRNA, complete cds.	0.029	3875740	(Z81497) similar to mannosyl-oligosaccharide alpha-1, 2-mannosidase; cDNA EST EMBL:D67155 comes from this gene; cDNA EST EMBL:D64219 comes from this gene; cDNA EST yk260e12.3 comes from this gene; cDNA EST yk260e12.5 comes f...	6e-18
5197	U12523	Rattus norvegicus ultraviolet B radiation-activated UV98 mRNA, partial sequence.	1e-10	3219914	HYPOTHETICAL 16.8 KD PROTEIN C30D10.04 IN CHROMOSOME II >gi|2276353|gnl|PID|e330328 pombe]	2e-11
5198	AB017026	Mus musculus mRNA for oxysterol-binding protein, complete cds	0.0	3551523	(AB017026) oxysterol-binding protein	e-120
5199	U83981	Homo sapiens apoptosis associated protein (GADD34) mRNA, complete cds	e-119	3258618	(U83981) apoptosis associated protein [Homo sapiens]	7e-26

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
5200	U37580	Streptomyces coelicolor phosphotyrosine protein phosphatase (ptpA) gene, putative cystathionine gamma-lyase (cysA) gene, and LysR-like protein gene, complete cds	0.048	2459916	(AF005859) anon2D7 [Drosophila melanogaster]	0.18
5201	D00723	Human mRNA for hydrogen carrier protein, a component of an enzyme complex, glycine synthase (EC 2.1.2.10)	3e-19	<NONE>	<NONE>	<NONE>
5202	X89366	A.thaliana DNA for 40 kDa protein gene	0.025	1209669	(U38810) CAGR1 [Homo sapiens] >gi|3098420 (AF040945) homeotic regulator homolog MAB21 [Mus musculus]	0.008
5203	AF067158	HIV-1 isolate 301905 from India, complete genome	2.4	<NONE>	<NONE>	<NONE>
5204	U09954	Human ribosomal protein L9 gene, 5' region and complete cds.	5e-37	<NONE>	<NONE>	<NONE>
5205	AF029984	Lycopersicon esculentum COP1 homolog (COP1) mRNA, complete cds	7e-37	4090943	(AF029984) COP1 homolog [Lycopersicon esculentum]	2e-49
5206	U43076	Mus musculus cdc37 homolog mRNA, complete cds	2e-17	2655422	(AF035530) CDC37 [Gallus gallus]	2e-22

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
5207	U07745	Lycopersicon esculentum biotin-containing subunit of methylcrotonyl-CoA carboxylase mRNA, partial cds.	4e-32	533707	(U12536) 3-methylcrotonyl-CoA carboxylase precursor	4e-49
5208	X74465	Human papillomavirus type 10 genomic DNA	1.3	3879121	(Z70310) predicted using Genefinder; Similarity to Mouse ankyrin (PIR Acc. No. S37771); cDNA EST EMBL:T01923 comes from this gene; cDNA EST EMBL:D32335 comes from this gene; cDNA EST EMBL:D32723 comes from this gene; cDNA ES... Genefinder; Similarity to M	2e-56
5209	X99261	A.evecta gene encoding blue-light photoreceptor, intron	0.14	2257939	(AF005665) properdin [Homo sapiens]	7.6
5210	M35296	Human tyrosine kinase arg gene mRNA.	1.1	1125781	(U42841) short region of weak similarity to chicken limb deformity protein (PIR:S24286) [Caenorhabditis elegans]	0.61
5211	Z57610	H.sapiens CpG DNA, clone 187a10, reverse read cpg187a10.rt1a .	e-102	404764	(L10409) fork head related protein [Mus musculus]	1e-16

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
5212	X85753	Homo sapiens mRNA for CDK8 protein kinase > :: emb|A61243|A61243 Sequence 1 from Patent WO9709432	6e-59	1171821	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 >gi|559499|gnl|PID|e1192548 (X54253) ND5 protein	9.5
5213	U27341	Bos taurus endothelin converting enzyme-2 Sequence 1 from patent US 5736376	7e-61	2136744	endothelin converting enzyme-2 - bovine	3e-29
5214	U63648	Mus musculus p160 myb-binding protein (P160) mRNA, complete cds	4e-58	2645205	(U63648) p160 myb-binding protein [Mus musculus]	2e-34
5215	AF035940	Homo sapiens MAGOH mRNA, complete cds	e-140	2306969	(AF007860) xl-Mago [Xenopus laevis]	3e-76
5216	X80045	O.aries mRNA for acetyl-CoA carboxylase	2e-54	542750	acetyl-CoA carboxylase (EC 6.4.1.2) - human sapiens] >gi|740964|prf||2006242A Ac-CoA carboxylase	8e-10
5217	Z46372	R.norvegicus RNA for DNA topoisomerase II.	e-134	3876360	(Z68315) Similarity to Human MAP kinase phosphatase-1 (SW:PTN7_HUMAN) [Caenorhabditis elegans]	3e-12
5218	AF035940	Homo sapiens MAGOH mRNA, complete cds	e-143	2330011	(AF007862) mm-Mago [Mus musculus] >gi|2909828 (AF035939) similar to mago nashi [Mus musculus] >gi|2909830	7e-81

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
5219	Z72521	Human DNA sequence from cosmid N29F4 on chromosome 22q11.2-qter contains STS	6e-04	<NONE>	<NONE>	<NONE>
5220	S74340	{clone E572, estrogen induced gene} [rats, Sprague-Dawley, hypothalamus, mRNA Partial, 130 nt]	4e-29	<NONE>	<NONE>	<NONE>
5221	AL008711	Human DNA sequence from PAC 390N22 on chromosome Xp22.2	0.33	1184707	(U40868) folylpolyglutamate synthetase [Homo sapiens]	7.9
5222	AE000012	Mycoplasma pneumoniae section 12 of 63 of the complete genome	0.15	<NONE>	<NONE>	<NONE>
5223	D78333	Human mRNA for testis-specific TCP20, complete cds	e-113	2501141	T-COMPLEX PROTEIN 1, ZETA-LIKE SUBUNIT (TCP-1-ZETA-LIKE) (CCT-ZETA-LIKE) TCP20 [Homo sapiens]	2e-42
5224	AF042333	Oryza sativa 24-methylene lophenol C24(1)methyltransferase mRNA, complete cds	0.003	3883124	(AF082300) arabinogalactan-protein [Arabidopsis thaliana]	0.006
5225	U15426	Human anonymous mRNA sequence with CCA repeat region.	4e-06	1123105	(U42438) similar to S. cerevisiae longevity-assurance protein 1 (SP:P38703) [Caenorhabditis elegans]	0.34

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
5226	AF052497	Homo sapiens clone B18 unknown mRNA	0.003	1144514	(U34781) Antho-LWamidII preprohormone [Anthopleura elegantissima] >gi|1586846|prf||2204411A prepro-hormone	4.3
5227	D86590	Zinnia elegans mRNA for cinnamyl alcohol dehydrogenase, partial cds	0.13	<NONE>	<NONE>	<NONE>
5228	AF081144	Rattus norvegicus CL1AA mRNA, complete cds	5e-14	1718004	TEGUMENT PROTEIN UL49 HOMOLOG herpesvirus 1] >gi|995634 (Z54206) UL49 [Bovine herpesvirus 1] >gi|2653299|gnl|PID|e1187295 (AJ004801) virion protein (tegument) [Bovine herpesvirus type 1.1]	1.4
5229	M63016	Human X chromosome enhancer-like sequence.	6e-04	<NONE>	<NONE>	<NONE>
5230	L24755	Mus musculus bone morphogenetic protein (Bmp-1) mRNA, complete cds.	1.2	<NONE>	<NONE>	<NONE>
5231	<NONE>	<NONE>	<NONE>	2828280	(AL021687) putative protein [Arabidopsis thaliana] >gi|2832633|gnl|PID|e1249651 (AL021711) putative protein [Arabidopsis thaliana]	9e-36

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
5232	U27341	Bos taurus endothelin converting enzyme-2 Sequence 1 from patent US 5736376	1e-22	2136744	endothelin converting enzyme-2 - bovine	2e-09
5233	M81840	Human NRL gene product mRNA, complete cds.	0.030	3875740	(Z81497) similar to mannosyl-oligosaccharide alpha-1, 2-mannosidase; cDNA EST EMBL:D67155 comes from this gene; cDNA EST EMBL:D64219 comes from this gene; cDNA EST yk260e12.3 comes from this gene; cDNA EST yk260e12.5 comes f...	6e-18
5234	AJ000097	Homo sapiens mRNA for EYA1B gene	2.7	3395586	(AL031179) similarity to phosphomannomutases [Schizosaccharomyces pombe]	6e-38
5235	U30788	Rattus norvegicus Tclone4 mRNA	1e-68	3523162	(AF076292) TGF-beta/activin signal transducer FAST-1p	1.4
5236	U88964	Human HEM45 mRNA, complete cds	0.0	2062680	(U88964) HEM45 [Homo sapiens]	7e-77
5237	AF061016	Homo sapiens UDP-glucose dehydrogenase (UGDH) mRNA, complete cds	0.0	3127127	(AF061016) UDP-glucose dehydrogenase [Homo sapiens] dehydrogenase [Homo sapiens]	5e-90
5238	D43921	Mouse AZ1 mRNA for pre-acrosome localization protein, complete cds	3e-15	2137118	acrosomal protein AZ1 - mouse localization protein [Mus musculus]	0.007

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
5239	AF056022	Homo sapiens p60 katanin mRNA, complete cds	0.0	3283072	(AF056022) p60 katanin [Homo sapiens]	2e-60
5240	U77949	Human Cdc6-related protein (HsCDC6) mRNA, complete cds	1e-83	<NONE>	<NONE>	<NONE>
5241	AJ005016	Homo sapiens mRNA for putative ABC transporter, partial	0.0	3005931	(AJ005016) ABC transporter [Homo sapiens]	3e-70
5242	X56756	Sheep mRNA for tumor necrosis factor alpha	4.5	<NONE>	<NONE>	<NONE>
5243	AF020833	Homo sapiens eukaryotic translation initiation factor 3 subunit (p42) mRNA, complete cds	0.0	2460200	(AF020833) eukaryotic translation initiation factor 3 subunit [Homo sapiens]	e-158
5244	X69878	H.sapiens Flt4 mRNA for transmembrane tyrosine kinase	4e-43	<NONE>	<NONE>	<NONE>
5245	M27826	Human endogenous retroviral protease mRNA, complete cds.	1e-66	<NONE>	<NONE>	<NONE>
5246	U20285	Human Gps1 (GPS1) mRNA, complete cds	2e-54	644879	(U20285) Gps1 [Homo sapiens]	8e-20
5247	AF049528	Homo sapiens huntingtin-interacting protein HYPA/FBP11 (HYPA) mRNA, partial cds	5e-75	3341990	(AF049528) huntingtin-interacting protein HYPA/FBP11	2e-20

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
5248	U87277	Human splicing factor SRp30c gene, exon 1	0.14	267449	HYPOTHETICAL 12.5 KD PROTEIN ZK637.2 IN CHROMOSOME III >gi|102507|pir||S15787 hypothetical protein 1 (cosmid ZK637) – Caenorhabditis elegans Genefinder; cDNA EST yk217b5.3 comes from this gene; cDNA EST yk217b5.5 comes from this gene; cDNA EST yk340g12.3	1e-08
5249	D16919	Human HepG2 3' region cDNA, clone hmd3e06	e-164	3152559	(AC002986) Similarity to A. thaliana gene product F21M12.20, gb|AC000132. EST gb|Z25651 comes from this gene. [Arabidopsis thaliana]	2e-52
5250	AJ006064	Rattus norvegicus mRNA for coronin-like protein	e-142	3757680	(AJ006064) coronin-like protein [Rattus norvegicus]	5e-73
5251	AB011000	Mus musculus mRNA for choline/ethanolamine kinase, complete cds	1e-18	2780752	(AB006607) choline/ethanolamine kinase	0.001

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
5252	X80169	M.musculus mRNA for 200 kD protein	0.0	1717793	PROTEIN TSG24 (MEIOTIC CHECK POINT REGULATOR) >gi|1083553|pir||A 55117 tsg24 protein - mouse	e-150

Table 3 Polynucleotides encoding gene products of a protein family or having a known functional domain(s).

SEQ ID NO:	Validation Sequence	Biological Activity (Profile)	Start	Stop	Score	Direction
3920	393.E10.sp6:148957	7tm_1	531	710	9520	for
2667	172.F10.sp6:133946	7tm_2	45	724	8708	rev
2758	177.C6.sp6:134733	7tm_2	41	697	9828	rev
2933	184.C7.sp6:135556	7tm_2	3	834	8987	for
3129	121.E12.sp6:131940	7tm_2	245	1324	9550	rev
3365	172.A7.sp6:133883	7tm_2	94	761	8743	rev
3418	123.F9.sp6:132333	7tm_2	203	585	8785	rev
3419	123.F9.sp6:132333	7tm_2	203	585	8785	rev
3597	394.G2.sp6:149165	7tm_2	73	793	9209	for
3648	370.C5.sp6:141726	7tm_2	76	770	9269	for
3686	370.B1.sp6:141710	7tm_2	89	662	8791	for
3695	368.A12.sp6:141322	7tm_2	121	719	9015	rev
3696	368.A12.sp6:141322	7tm_2	121	719	9015	rev
4172	219.C10.sp6:139007	7tm_2	46	774	11394	rev
4216	368.D11.sp6:141357	7tm_2	66	775	9384	rev
4228	368.A11.sp6:141321	7tm_2	7	1079	9097	for
4441	99.F7.sp6:131296	7tm_2	534	1265	10956	rev
4442	99.F7.sp6:131296	7tm_2	534	1265	10956	rev
4482	100.D2.sp6:131459	7tm_2	122	1404	9296	rev
4495	395.B12.sp6:149307	7tm_2	79	1432	10427	rev
4525	90.B4.sp6:130874	7tm_2	4	691	9435	for
4616	100.D5.sp6:131462	7tm_2	655	1349	9255	for
4653	100.D7.sp6:131464	7tm_2	357	1346	11461	rev
4654	100.D7.sp6:131464	7tm_2	357	1346	11461	rev
4658	100.H6.sp6:131511	7tm_2	119	1035	10001	rev
4659	100.G6.sp6:131499	7tm_2	363	1188	9901	rev
4660	100.F6.sp6:131487	7tm_2	50	1127	8799	for
4661	100.F6.sp6:131487	7tm_2	50	1127	8799	for
4710	367.H9.sp6:141210	7tm_2	143	1266	11883	rev
4755	370.F4.sp6:141761	7tm_2	78	704	8942	for
4856	367.H11.sp6:141212	7tm_2	176	1227	9975	rev
4885	123.E10.sp6:132322	7tm_2	210	691	9071	rev
4900	123.E10.sp6:132322	7tm_2	210	691	9071	rev
4901	123.E10.sp6:132322	7tm_2	210	691	9071	rev
2656	176.H11.sp6:134606	ANK	207	290	4450	for
2555	180.C9.sp6:135947	asp	156	670	6710	for
3632	368.H11.sp6:141405	asp	136	1226	6880	rev
4205	368.B5.sp6:141327	asp	309	806	6073	for
4251	369.D6.sp6:141546	asp	434	1332	6263	rev
4253	396.F9.sp6:149544	asp	97	1106	5999	rev
4261	216.G10.sp6:139247	asp	74	703	6188	rev
4365	122.H12.sp6:132168	asp	152	1040	6183	rev
4498	80.H6.sp6:130297	asp	61	418	5944	rev
4664	172.E5.sp6:133929	asp	219	976	6434	for
4718	185.D9.sp6:135762	asp	31	872	5944	rev
4733	185.D9.sp6:135762	asp	31	872	5944	rev
4746	176.B10.sp6:134533	asp	253	1446	6079	rev

SEQ ID NO:	Validation Sequence	Biological Activity (Profile)	Start	Stop	Score	Direction
4822	177.F3.sp6:134766	asp	0	894	6336	rev
4854	184.F11.sp6:135596	asp	61	737	6416	rev
4856	367.H11.sp6:141212	asp	81	1187	6182	rev
4929	180.E6.sp6:135968	asp	81	706	6150	for
4931	180.E6.sp6:135968	asp	81	706	6150	for
2723	180.F2.sp6:135976	ATPases	135	627	11664	for
2842	217.H11.sp6:139452	ATPases	2	701	5972	for
3019	216.B1.sp6:139178	ATPases	170	616	6150	for
3046	121.B8.sp6:131900	ATPases	13	635	5867	rev
3190	80.D2.sp6:130245	ATPases	13	386	6068	for
3290	176.C6.sp6:134541	ATPases	85	579	5883	for
3670	369.C10.sp6:141538	ATPases	329	730	6206	for
3998	394.H8.sp6:149183	ATPases	21	571	5954	rev
4119	218.F11.sp6:138852	ATPases	313	816	6057	for
4159	219.A7.sp6:138980	ATPases	88	662	6145	for
4223	368.F9.sp6:141379	ATPases	178	648	5937	for
4384	181.G11.sp6:135354	ATPases	362	769	5900	rev
4473	369.B4.sp6:141520	ATPases	4	412	14130	for
4540	218.C8.sp6:138813	ATPases	12	576	5782	rev
4560	404.G6.sp6:162933	ATPases	86	605	6001	rev
4689	367.H8.sp6:141209	ATPases	17	476	5905	rev
4785	184.E5.sp6:135578	ATPases	184	632	5943	for
4792	184.C6.sp6:135555	ATPases	333	813	5773	for
4847	184.B11.sp6:135548	ATPases	14	498	6140	for
5041	377.C1.sp6:141918	ATPases	4	655	5933	for
3404	176.F10.sp6:134581	Bcl-2	69	356	16419	for
4036	367.F5.sp6:141182	bromodomain	40	210	8810	for
4489	369.D3.sp6:141543	bromodomain	63	230	10270	for
3408	172.E1.sp6:133925	BZIP	146	298	4066	for
3951	393.G5.sp6:148976	BZIP	116	304	5931	for
4850	172.E9.sp6:133933	BZIP	91	260	4366	for
3618	370.B12.sp6:141721	cyclin	118	324	8980	for
3895	395.G6.sp6:149361	cyclin	11	281	6930	for
4536	395.G8.sp6:149363	cyclin	12	279	5950	for
4455	99.F5.sp6:131294	Cys-protease	72	348	18479	for
4684	180.D1.sp6:135951	Cys-protease	38	992	10103	rev
4688	180.D1.sp6:135951	Cys-protease	38	992	10103	rev
4801	177.E4.sp6:134755	Cys-protease	48	326	19999	for
4659	100.G6.sp6:131499	DAG_PE_bind	605	702	6290	rev
4821	377.C8.sp6:141925	Dead_box_helic	172	828	7867	rev
5083	216.A1.sp6:139166	Dead_box_helic	44	589	26532	for
2734	177.G4.sp6:134779	EFhand	79	153	3780	for
2893	185.A1.sp6:135718	EFhand	287	358	2580	rev
3775	377.A5.sp6:141898	EFhand	477	563	3010	for
4056	367.B7.sp6:141136	EFhand	225	272	2500	rev
4152	218.B10.sp6:138803	EFhand	40	114	2640	rev
4153	218.B10.sp6:138803	EFhand	40	114	2640	rev
4154	218.C10.sp6:138815	EFhand	39	113	2640	rev
4905	393.H12.sp6:148995	EFhand	145	231	4640	for
4943	219.A9.sp6:138982	EFhand	685	750	2550	rev

SEQ ID NO:	Validation Sequence	Biological Activity (Profile)	Start	Stop	Score	Direction
2849	218.B5.sp6:138798	Ets_Nterm	340	531	10400	for
2728	180.A2.sp6:135916	FNtypeII	291	423	6400	rev
3018	216.C1.sp6:139190	FNtypeII	501	634	6460	for
4496	218.G1.sp6:138854	FNtypeII	20	141	6180	rev
4914	393.H8.sp6:148991	FNtypeII	448	576	6110	for
2504	181.C3.sp6:135298	G-alpha	66	715	8084	rev
3290	176.C6.sp6:134541	G-alpha	62	690	9062	for
4288	121.B4.sp6:131896	G-alpha	46	447	21415	for
4444	217.D12.sp6:139405	G-alpha	15	702	40404	for
4562	404.B7.sp6:162874	G-alpha	120	682	8424	for
2503	180.A11.sp6:135925	helicase_C	165	479	4494	for
4469	369.C4.sp6:141532	helicase_C	559	756	3732	rev
5020	185.D12.sp6:135765	helicase_C	381	534	5000	for
4241	396.H8.sp6:149567	homeobox	80	230	5170	for
2550	180.E5.sp6:135967	mkk	342	612	5791	for
3407	172.F1.sp6:133937	mkk	94	669	5688	rev
3451	123.A2.sp6:132266	mkk	26	378	7889	for
3600	394.B3.sp6:149106	mkk	32	782	9544	for
3646	370.H4.sp6:141785	mkk	18	307	9394	for
3680	369.G11.sp6:141587	mkk	182	725	5375	for
4175	219.H10.sp6:139067	mkk	280	723	15454	for
4205	368.B5.sp6:141327	mkk	249	725	5502	for
4278	181.C9.sp6:135304	mkk	168	880	5551	rev
4322	121.F6.sp6:131946	mkk	111	730	5399	for
4777	177.E2.sp6:134753	mkk	288	636	5720	rev
4482	100.D2.sp6:131459	PDEase	849	1195	5945	for
2578	181.H11.sp6:135366	protkinase	116	710	5531	for
2712	177.G7.sp6:134782	protkinase	6	511	5445	for
2835	218.C1.sp6:138806	protkinase	127	747	5492	for
2843	218.E1.sp6:138830	protkinase	64	726	5592	rev
2971	217.F4.sp6:139421	protkinase	83	702	5818	rev
3009	217.A4.sp6:139361	protkinase	57	682	5395	rev
3084	121.E2.sp6:131930	protkinase	69	658	5593	rev
3226	100.D8.sp6:131465	protkinase	174	620	5453	for
3274	100.C3.sp6:131448	protkinase	228	736	5616	for
3356	172.B5.sp6:133893	protkinase	148	715	5381	for
3377	172.B6.sp6:133894	protkinase	119	775	5616	for
3451	123.A2.sp6:132266	protkinase	24	384	9797	for
3600	394.B3.sp6:149106	protkinase	357	780	11395	for
3635	377.G11.sp6:141976	protkinase	117	739	5992	for
3646	370.H4.sp6:141785	protkinase	24	275	8338	for
3665	370.F2.sp6:141759	protkinase	33	800	5658	for
3669	369.B10.sp6:141526	protkinase	1	482	5504	rev
3700	369.D2.sp6:141542	protkinase	28	661	5428	for
3710	369.G6.sp6:141582	protkinase	71	631	5751	for
3791	396.C11.sp6:149510	protkinase	27	709	5793	rev
3905	393.H7.sp6:148990	protkinase	88	680	5470	rev
3919	393.D10.sp6:148945	protkinase	72	594	5617	for
4044	367.G4.sp6:141193	protkinase	30	699	5439	for
4072	368.B2.sp6:141324	protkinase	44	800	5556	for

SEQ ID NO:	Validation Sequence	Biological Activity (Profile)	Start	Stop	Score	Direction
4117	218.D11.sp6:138828	protkinase	38	781	6423	for
4175	219.H10.sp6:139067	protkinase	277	717	15720	for
4373	216.E5.sp6:139218	protkinase	115	710	5537	for
4569	100.C10.sp6:131455	protkinase	56	783	5556	rev
4755	370.F4.sp6:141761	protkinase	39	803	5635	for
4760	370.F3.sp6:141760	protkinase	188	775	5771	for
4807	184.H3.sp6:135612	protkinase	23	699	5515	for
5059	180.B5.sp6:135931	protkinase	182	671	5718	rev
5102	393.F4.sp6:148963	protkinase	28	650	5345	for
3671	369.D10.sp6:141550	ras	12	332	9802	for
3936	393.A3.sp6:148902	Thioredox	0	263	5887	rev
3927	393.F11.sp6:148970	TNFR_c6	151	261	6445	for
2956	184.E10.sp6:135583	transmembrane4	19	483	8339	rev
2981	217.E6.sp6:139411	transmembrane4	83	728	8417	for
3836	396.C9.sp6:149508	transmembrane4	300	924	9444	rev
4038	367.A6.sp6:141123	transmembrane4	32	495	8407	rev
4364	123.A1.sp6:132265	transmembrane4	1289	1548	8114	rev
4406	122.C1.sp6:132097	transmembrane4	6	535	8122	for
4431	122.E4.sp6:132124	transmembrane4	10	530	8829	for
4441	99.F7.sp6:131296	transmembrane4	613	1253	9443	rev
4442	99.F7.sp6:131296	transmembrane4	613	1253	9443	rev
4653	100.D7.sp6:131464	transmembrane4	335	1207	8255	rev
4654	100.D7.sp6:131464	transmembrane4	335	1207	8255	rev
4710	367.H9.sp6:141210	transmembrane4	398	1130	8352	rev
4944	180.H7.sp6:136005	transmembrane4	356	983	8356	rev
3381	176.D9.sp6:134556	trypsin	164	764	9670	rev
4684	180.D1.sp6:135951	trypsin	371	1229	10479	rev
4688	180.D1.sp6:135951	trypsin	371	1229	10479	rev
2754	177.H6.sp6:134793	WD_domain	345	437	6510	for
3046	121.B8.sp6:131900	WD_domain	98	193	6400	for
3227	100.B10.sp6:131443	WD_domain	544	642	6590	for
4243	121.A8.sp6:131888	WD_domain	93	188	6400	for
5046	185.F10.sp6:135787	WD_domain	382	480	5880	for
3129	121.E12.sp6:131940	Wnt_dev_sign	101	821	12160	rev
3173	99.G6.sp6:131307	Wnt_dev_sign	49	880	12334	rev
3390	176.C9.sp6:134544	Wnt_dev_sign	249	854	11038	rev
3391	176.C9.sp6:134544	Wnt_dev_sign	249	854	11038	rev
3656	370.G6.sp6:141775	Wnt_dev_sign	211	785	11490	rev
3836	396.C9.sp6:149508	Wnt_dev_sign	282	1017	12318	rev
4253	396.F9.sp6:149544	Wnt_dev_sign	482	1298	11217	rev
4330	122.A2.sp6:132074	Wnt_dev_sign	94	933	12383	rev
4359	123.B2.sp6:132278	Wnt_dev_sign	538	1435	11785	for
4364	123.A1.sp6:132265	Wnt_dev_sign	760	1544	12660	rev
4375	122.G10.sp6:132154	Wnt_dev_sign	29	884	11603	rev
4385	122.A2.sp6:132074	Wnt_dev_sign	94	933	12383	rev
4409	121.F12.sp6:131952	Wnt_dev_sign	9	734	11167	rev
4441	99.F7.sp6:131296	Wnt_dev_sign	560	1399	13749	rev
4442	99.F7.sp6:131296	Wnt_dev_sign	560	1399	13749	rev
4535	395.F10.sp6:149353	Wnt_dev_sign	100	907	11535	rev
4586	123.A4.sp6:132268	Wnt_dev_sign	80	1122	11249	rev

SEQ ID NO:	Validation Sequence	Biological Activity (Profile)	Start	Stop	Score	Direction
4605	404.D5.sp6:162896	Wnt_dev_sign	31	816	11304	rev
4653	100.D7.sp6:131464	Wnt_dev_sign	467	1314	11882	rev
4654	100.D7.sp6:131464	Wnt_dev_sign	467	1314	11882	rev
4665	177.B11.sp6:134726	Wnt_dev_sign	137	1266	12708	rev
4668	177.B11.sp6:134726	Wnt_dev_sign	137	1266	12708	rev
4682	177.B11.sp6:134726	Wnt_dev_sign	137	1266	12708	rev
4710	367.H9.sp6:141210	Wnt_dev_sign	692	1481	12886	rev
4718	185.D9.sp6:135762	Wnt_dev_sign	129	890	11145	rev
4724	377.D2.sp6:141931	Wnt_dev_sign	400	1227	11044	rev
4733	185.D9.sp6:135762	Wnt_dev_sign	129	890	11145	rev
4856	367.H11.sp6:141212	Wnt_dev_sign	295	1669	13366	rev
4866	377.D4.sp6:141933	Wnt_dev_sign	549	1380	14522	rev
4925	219.B12.sp6:138997	Wnt_dev_sign	312	1214	13188	rev
4959	219.B12.sp6:138997	Wnt_dev_sign	312	1214	13188	rev
3409	172.D1.sp6:133913	Y_phosphatase	476	804	6932	for
3418	123.F9.sp6:132333	Y_phosphatase	28	439	6096	rev
3419	123.F9.sp6:132333	Y_phosphatase	28	439	6096	rev
3657	370.H6.sp6:141787	Y_phosphatase	148	554	6481	for
3804	404.B10.sp6:162877	Y_phosphatase	104	466	6446	rev
3806	404.D10.sp6:162901	Y_phosphatase	9	614	6516	for
3974	395.F2.sp6:149345	Y_phosphatase	164	645	6093	rev
4238	121.E9.sp6:131937	Y_phosphatase	240	777	6147	rev
4263	216.F10.sp6:139235	Y_phosphatase	21	504	6342	for
4343	122.E9.sp6:132129	Y_phosphatase	381	807	6036	rev
4363	123.B1.sp6:132277	Y_phosphatase	61	510	6229	rev
4434	219.F4.sp6:139037	Y_phosphatase	2	261	10353	for
4473	369.B4.sp6:141520	Y_phosphatase	231	768	6110	rev
4629	404.E11.sp6:162914	Y_phosphatase	580	920	6005	rev
5094	217.A3.sp6:139360	Y_phosphatase	263	622	6222	rev
2738	177.A6.sp6:134709	Zincfing_C2H2	65	127	4380	for
2760	177.A6.sp6:134709	Zincfing_C2H2	65	127	4380	for
2832	218.B2.sp6:138795	Zincfing_C2H2	94	156	4940	for
3736	377.H8.sp6:141985	Zincfing_C2H2	495	557	4850	for
3762	377.G2.sp6:141967	Zincfing_C2H2	52	114	4380	for
3763	377.G2.sp6:141967	Zincfing_C2H2	52	114	4380	for
4794	377.G4.sp6:141969	Zincfing_C2H2	247	308	3930	for
5090	185.C4.sp6:135745	Zincfing_C2H2	238	300	4540	for
3774	377.E4.sp6:141945	Zincfing_C3HC4	128	244	9335	for
4477	181.E3.sp6:135322	Zincfing_C3HC4	321	445	8221	for

Table 19. Polynucleotides Specifically Expressed in Colon

SEQ ID NO:	Sequence Name	cluster	lib 1 clones	lib 2 clones	lib 15 clones	lib 16 clones	lib 17 clones	lib 18 clones	lib 19 clones	lib 20 clones
3	RTA00000197AF.e.24.1	39250	2	0	0	0	0	0	0	0
7	RTA00000197AR.e.12.1	22095	3	0	0	0	0	0	0	0
16	RTA00000196AF.e.16.1	39252	2	0	0	0	0	0	0	0
18	RTA00000196AF.c.17.1	39602	2	0	0	0	0	0	0	0
21	RTA00000131A.g.19.2	36535	2	0	0	0	0	0	0	0
22	RTA00000187AR.o.10.2	8984	4	3	0	0	0	2	0	0
23	RTA00000198R.b.08.1	22636	3	0	0	0	0	0	0	0
26	RTA00000200R.g.09.1	22785	3	0	0	0	0	0	0	0
29	RTA00000200AF.b.19.1	22847	3	0	0	0	0	0	0	0
31	RTA00000200F.m.15.1	22601	3	0	0	0	1	0	0	0
37	RTA00000181AF.n.15.2	86128	1	0	0	0	0	0	0	0
38	RTA00000196R.k.07.1	22443	2	0	0	0	0	0	0	1
40	RTA00000200AR.e.02.1	36059	2	0	0	0	1	1	1	0
48	RTA00000177AR.a.23.5	6995	4	2	0	0	0	0	0	0
49	RTA00000198R.o.05.1	26702	2	0	0	0	0	0	0	0
50	RTA00000201R.a.02.1	35362	2	0	0	0	0	0	0	0
61	RTA00000197AF.h.11.1	22264	3	0	0	0	0	0	0	0
66	RTA00000199F.c.09.2	16824	3	1	0	0	0	0	0	0
75	RTA00000180AR.h.19.2	84182	1	0	0	0	0	0	0	0
78	RTA00000199R.f.09.1	22907	3	0	0	0	0	0	0	0
79	RTA00000199AF.p.4.1	10282	3	3	0	0	0	0	0	0
85	RTA00000200R.o.03.1	22807	3	0	0	0	0	0	0	0
86	RTA00000189AF.l.22.1	33333	1	1	0	0	0	0	0	0
87	RTA00000195AF.d.20.1	37574	2	0	0	0	0	0	0	0
92	RTA00000198AF.j.18.1	22759	3	0	0	0	0	0	0	0
95	RTA00000180AF.g.3.1	9024	5	2	0	0	0	0	0	0
102	RTA00000199R.j.08.1	37844	2	0	0	0	0	0	0	0
103	RTA00000199F.e.10.1	22906	3	0	0	0	0	0	1	0
105	RTA00000179AF.g.12.3	36390	2	0	0	0	0	0	0	0
108	RTA00000183AR.h.23.2	18957	3	0	0	0	0	0	0	0
109	RTA00000197AF.d.12.1	39546	2	0	0	0	0	0	0	0
116	RTA00000181AR.k.24.3	7005	8	2	0	0	0	0	0	0
119	RTA00000181AR.k.24.2	7005	8	2	0	0	0	0	0	0
124	RTA00000199AR.m.06.1	19122	3	0	0	0	0	0	0	0
129	RTA00000134A.d.10.1	18957	3	0	0	0	0	0	0	0
137	RTA00000181AF.m.4.3	13238	4	1	0	0	0	0	0	0
141	RTA00000196AF.c.6.1	23148	3	0	0	0	0	0	0	0
142	RTA00000198AF.k.19.1	75879	1	0	0	0	0	0	0	0

SEQ ID NO:	Sequence Name	cluster	lib 1 clones	lib 2 clones	lib 15 clones	lib 16 clones	lib 17 clones	lib 18 clones	lib 19 clones	lib 20 clones
143	RTA00000199R.h.09.1	76020	1	0	0	0	0	0	0	0
144	RTA00000198AF.o.18.1	13018	4	0	0	0	1	0	0	0
148	RTA00000199F.h.17.2	36254	2	0	0	0	0	0	0	0
149	RTA00000181AR.h.06.3	87226	1	0	0	0	0	0	0	0
166	RTA00000198AF.f.21.1	22676	3	0	0	0	0	0	0	0
173	RTA00000200AR.b.07.1	17125	4	0	0	0	0	0	0	0
178	RTA00000200F.o.03.1	22807	3	0	0	0	0	0	0	0
180	RTA00000199AF.j.12.1	22461	3	0	0	0	0	0	0	0
185	RTA00000195AF.d.4.1	22766	3	0	0	0	0	0	0	0
194	RTA00000200R.k.01.1	40049	2	0	0	0	0	0	0	0
195	RTA00000198AF.c.10.1	77149	1	0	0	0	0	0	0	0
198	RTA00000197AR.e.07.1	86969	1	0	0	0	0	0	0	0
199	RTA00000199R.c.09.1	16824	3	1	0	0	0	0	0	0
206	RTA00000181AF.o.04.2	22205	3	0	0	0	0	0	0	0
207	RTA00000199AF.l.19.1	22460	3	0	0	0	0	0	0	0
208	RTA00000198AF.h.22.1	22366	2	1	0	0	0	0	0	0
211	RTA00000199AF.m.15.1	10101	3	0	0	0	0	0	0	0
212	RTA00000197AF.j.9.1	13236	4	1	0	0	0	0	0	0
230	RTA00000185AR.b.18.1	12171	3	2	0	0	0	0	0	0
235	RTA00000201AF.a.02.1	35362	2	0	0	0	0	0	0	0
236	RTA00000183AR.h.23.1	18957	3	0	0	0	0	0	0	0
238	RTA00000187AR.k.12.1	78415	1	0	0	0	0	0	0	0
242	RTA00000198AF.m.17.1	77992	1	0	0	0	0	0	0	0
243	RTA00000181AF.m.15.3	12081	4	0	0	0	0	0	0	0
248	RTA00000198R.c.14.1	39814	2	0	0	0	0	0	0	0
249	RTA00000200R.o.03.2	22807	3	0	0	0	0	0	0	0
251	RTA00000192AF.n.13.1	8210	2	6	0	0	0	0	0	0
256	RTA00000184AR.e.15.1	16347	4	0	0	0	0	0	0	0
260	RTA00000198R.m.17.1	77992	1	0	0	0	0	0	0	0
270	RTA00000178R.l.08.1	39648	2	0	0	0	0	0	0	0
278	RTA00000198AF.p.16.1	71877	1	0	0	0	0	0	0	0
280	RTA00000193AF.b.18.1	7542	8	0	0	2	1	0	1	0
284	RTA00000199F.d.10.2	22049	3	0	0	0	0	0	0	0
287	RTA00000200AF.b.07.1	17125	4	0	0	0	0	0	0	0
288	RTA00000181AR.i.06.3	19119	3	0	0	0	0	0	0	0
289	RTA00000196F.k.07.1	22443	2	0	0	0	0	0	0	1
294	RTA00000198AF.k.23.1	8995	2	5	0	0	0	0	0	0
296	RTA00000196AF.f.20.1	22774	3	0	0	0	0	0	0	0
300	RTA00000195AF.c.12.1	37582	2	0	0	0	0	0	0	0

SEQ ID NO:	Sequence Name	cluster	lib 1 clones	lib 2 clones	lib 15 clones	lib 16 clones	lib 17 clones	lib 18 clones	lib 19 clones	lib 20 clones
302	RTA00000186AF.d.1.2	40044	2	0	0	1	0	0	0	0
307	RTA00000200F.n.05.2	18989	3	0	0	0	0	0	0	0
308	RTA00000178AF.j.20.1	15066	4	0	0	0	0	0	0	0
310	RTA00000188AF.m.08.1	22155	3	0	0	0	0	0	0	0
315	RTA00000199R.d.23.1	37477	2	0	0	0	0	0	0	0
319	RTA00000200F.n.05.1	18989	3	0	0	0	0	0	0	0
320	RTA00000196AF.m.13.1	16290	4	0	0	0	0	0	0	0
325	RTA00000182AF.d.18.4	37435	2	0	0	0	0	0	0	0
328	RTA00000200AF.g.09.1	22785	3	0	0	0	0	0	0	0
330	RTA00000177AR.m.17.4	14391	3	1	0	0	0	0	0	0
331	RTA00000197AR.c.20.1	16282	4	0	0	0	0	0	0	0
337	RTA00000177AR.m.17.3	14391	3	1	0	0	0	0	0	0
342	RTA00000196AF.d.10.1	22256	3	0	0	0	0	0	0	0
343	RTA00000201F.a.18.1	16837	2	2	0	0	0	0	0	0
344	RTA00000198AF.o.02.1	68756	1	0	0	0	0	0	0	0
345	RTA00000187AF.h.21.1	39171	2	0	0	0	0	0	0	0
347	RTA00000199F.b.03.2	38340	2	0	0	0	0	0	0	0
358	RTA00000198AF.g.7.1	13386	3	2	0	0	0	0	0	0
362	RTA00000197AR.c.24.1	82498	1	0	0	0	0	0	0	0
371	RTA00000197F.e.7.1	86969	1	0	0	0	0	0	0	0
378	RTA00000181AF.k.24.3	7005	8	2	0	0	0	0	0	0
382	RTA00000200AF.j.6.1	22902	3	0	0	0	0	0	0	0
384	RTA00000196AF.h.17.1	39215	2	0	0	0	0	0	0	0
392	RTA00000185AF.b.11.2	9024	5	2	0	0	0	0	0	0
397	RTA00000198AF.b.22.1	38956	2	0	0	0	0	0	0	0
399	RTA00000186AF.m.15.2	40122	2	0	0	0	0	0	0	0
406	RTA00000199F.f.09.2	22907	3	0	0	0	0	0	0	0
408	RTA00000183AR.l.15.1	39383	2	0	0	0	0	0	0	0
413	RTA00000200F.a.12.1	16751	4	0	0	0	0	0	0	0
416	RTA00000199F.a.5.1	22134	3	0	0	0	0	0	0	0
418	RTA00000187AR.k.01.1	78356	1	0	0	0	0	0	0	0
424	RTA00000187AR.j.24.1	78356	1	0	0	0	0	0	0	0
426	RTA00000199AF.o.19.1	36927	2	0	0	0	0	0	0	0
429	RTA00000196F.i.19.1	39498	2	0	0	0	0	0	0	0
430	RTA00000198R.k.23.1	8995	2	5	0	0	0	0	0	0
432	RTA00000198AF.o.05.1	26702	2	0	0	0	0	0	0	0
433	RTA00000198R.j.18.1	22759	3	0	0	0	0	0	0	0
435	RTA00000182AR.c.22.1	16283	3	0	0	0	0	0	0	0
438	RTA00000180AR.g.03.4	9024	5	2	0	0	0	0	0	0

SEQ ID NO:	Sequence Name	cluster	lib 1 clones	lib 2 clones	lib 15 clones	lib 16 clones	lib 17 clones	lib 18 clones	lib 19 clones	lib 20 clones
451	RTA00000200AF.b.20.1	40403	2	0	0	0	0	0	0	0
455	RTA00000198AF.d.12.1	21142	2	1	0	0	0	0	0	0
456	RTA00000200AF.b.12.1	22053	3	0	0	0	0	0	0	0
457	RTA00000191AR.l.7.2	14391	3	1	0	0	0	0	0	0
461	RTA00000190AF.e.13.1	38961	2	0	0	0	0	0	0	0
462	RTA00000196AF.n.17.1	12477	4	1	0	0	0	0	0	0
467	RTA00000195AF.b.19.1	77678	1	0	0	0	0	0	0	0
475	RTA00000187AR.m.3.3	17055	4	0	0	0	0	0	0	0
476	RTA00000200R.g.15.1	22898	3	0	0	0	0	0	0	0
482	RTA00000187AF.j.7.1	78091	1	0	0	0	0	0	0	0
485	RTA00000196AF.c.14.1	23105	3	0	0	0	0	0	0	0
486	RTA00000190AR.p.22.2	16368	4	0	0	0	0	0	0	0
492	RTA00000198AF.b.8.1	22636	3	0	0	0	0	0	0	0
493	RTA00000177AF.m.17.1	14391	3	1	0	0	0	0	0	0
494	RTA00000200AF.k.1.1	40049	2	0	0	0	0	0	0	0
498	RTA00000190AF.h.12.1	12977	5	0	0	0	0	0	0	0
499	RTA00000199F.b.22.2	17018	4	0	0	0	0	0	0	0
508	RTA00000187AF.i.14.2	19406	2	1	0	0	0	0	0	0
511	RTA00000196AF.g.10.1	12498	3	1	1	0	0	0	0	0
517	RTA00000184AF.e.14.1	16347	4	0	0	0	0	0	0	0
522	RTA00000178AR.h.17.2	23824	2	1	0	0	0	0	0	0
531	RTA00000195F.a.3.1	27179	2	0	0	0	0	0	0	0
544	RTA00000196F.j.13.1	23170	3	0	0	0	0	0	0	0
547	RTA00000196AF.g.8.1	39665	2	0	0	0	0	0	0	0
549	RTA00000198AF.c.16.1	26801	2	0	0	0	0	0	0	0
553	RTA00000201F.b.22.1	35728	2	0	0	0	0	0	0	1
559	RTA00000197AF.p.20.1	22795	3	0	0	0	0	0	0	0
563	RTA00000192AR.o.16.2	9061	5	2	0	0	0	0	0	0
565	RTA00000191AF.c.10.1	40422	2	0	0	0	0	0	0	0
568	RTA00000196AF.p.01.2	87143	1	0	0	0	0	0	0	0
578	RTA00000180AF.g.17.1	16653	3	1	0	0	0	0	0	0
583	RTA00000190AR.h.12.2	12977	5	0	0	0	0	0	0	0
585	RTA00000198AF.n.18.1	16715	3	1	0	0	0	0	0	0
586	RTA00000199R.o.11.1	23172	3	0	0	0	0	0	0	0
588	RTA00000191AF.b.4.1	14936	3	0	0	0	0	0	0	0
589	RTA00000192AF.l.1.1	16392	3	0	0	0	0	0	0	0
593	RTA00000196R.c.14.2	23105	3	0	0	0	0	0	0	0
595	RTA00000195R.a.06.1	35265	2	0	1	0	0	0	0	0
602	RTA00000195AF.b.21.1	39055	2	0	0	0	0	0	0	0

SEQ ID NO:	Sequence Name	cluster	lib 1 clones	lib 2 clones	lib 15 clones	lib 16 clones	lib 17 clones	lib 18 clones	lib 19 clones	lib 20 clones
612	RTA00000197AR.e.22.1	78758	1	0	0	0	0	0	0	0
615	RTA00000197R.p.20.1	22795	3	0	0	0	0	0	0	0
618	RTA00000192AF.a.14.1	6874	6	3	0	0	1	0	0	0
623	RTA00000198R.b.24.1	19047	3	0	0	0	0	0	0	0
627	RTA00000199F.h.15.2	22269	3	0	0	0	0	0	0	0
628	RTA00000198AF.g.16.1	6602	1	1	0	0	0	0	0	0
634	RTA00000192AF.j.6.1	11494	4	0	0	0	0	0	0	0
635	RTA00000181AF.p.7.3	38773	2	0	0	0	0	0	0	0
637	RTA00000200AF.g.15.1	22898	3	0	0	0	0	0	0	0
643	RTA00000184AF.c.9.1	16245	4	0	0	0	0	0	0	0
645	RTA00000177AF.k.9.1	16245	4	0	0	0	0	0	0	0
649	RTA00000190AR.l.19.2	88204	1	0	0	0	0	0	0	0
662	RTA00000201R.a.15.1	57347	1	0	0	0	0	0	0	0
664	RTA00000195R.a.23.1	86432	1	0	0	0	0	0	0	0
670	RTA00000186AF.p.17.3	38383	2	0	0	0	0	0	0	0
674	RTA00000197AR.e.24.1	39250	2	0	0	0	0	0	0	0
683	RTA00000187AR.j.01.1	79028	1	0	0	0	0	0	0	0
686	RTA00000201F.f.07.1	51116	1	0	0	0	0	0	0	0
694	RTA00000201R.c.19.1	22357	2	1	0	0	0	0	0	0
702	RTA00000177AR.b.8.5	17062	3	0	0	0	0	0	0	0
712	RTA00000201F.b.21.1	9071	3	4	0	0	0	0	0	0
717	RTA00000200F.o.10.2	36432	2	0	0	0	0	0	0	0
718	RTA00000196F.l.14.2	23144	3	0	0	0	0	0	0	0
725	RTA00000197AF.b.1.1	12134	1	1	0	0	0	0	0	0
733	RTA00000200AF.d.20.1	26600	2	0	0	0	0	0	0	0
743	RTA00000178AF.k.9.1	16342	3	0	0	0	0	0	0	0
748	RTA00000198AF.b.24.1	19047	3	0	0	0	0	0	0	0
757	RTA00000406F.d.16.1	15040	2	2	0	0	0	0	0	0
760	RTA00000408F.o.12.2	78578	1	0	0	0	0	0	0	0
761	RTA00000119A.j.15.1	79623	1	0	0	0	0	0	0	0
762	RTA00000413F.d.12.1	66467	1	0	0	0	0	0	0	0
763	RTA00000423F.i.12.1	9118	4	3	0	0	0	0	0	0
766	RTA00000411F.k.05.1	64777	1	0	0	0	0	0	0	0
769	RTA00000419F.b.09.1	78128	1	0	0	0	0	0	0	0
772	RTA00000411F.m.15.1	78014	1	0	0	0	0	0	0	0
774	RTA00000123A.k.23.1	80313	1	0	0	0	0	0	0	0
777	RTA00000130A.m.15.1	81630	1	0	0	0	0	0	0	0
778	RTA00000411F.k.20.1	64973	1	0	0	0	0	0	0	0
780	RTA00000418F.k.05.1	73021	1	0	0	0	0	0	0	0

SEQ ID NO:	Sequence Name	cluster	lib 1 clones	lib 2 clones	lib 15 clones	lib 16 clones	lib 17 clones	lib 18 clones	lib 19 clones	lib 20 clones
781	RTA00000423F.h.18.1	37972	2	0	0	0	0	0	0	0
783	RTA00000422F.p.06.2	39282	2	0	0	0	0	0	0	0
784	RTA00000404F.n.16.2	39095	2	0	0	0	0	0	0	0
785	RTA00000411F.m.24.1	77568	1	0	0	0	0	0	0	0
786	RTA00000134A.j.10.1	81383	1	0	0	0	0	0	0	0
787	RTA00000409F.j.02.1	76417	1	0	0	0	0	0	0	0
788	RTA00000403F.j.15.1	23840	2	1	0	0	0	0	0	0
789	RTA00000411F.n.11.1	77276	1	0	0	0	0	0	0	0
790	RTA00000339F.i.13.1	5970	6	4	0	0	0	0	0	0
792	RTA00000406F.o.15.1	37482	2	0	0	0	0	0	0	0
793	RTA00000412F.g.04.2	64457	1	0	0	0	0	0	0	0
795	RTA00000352R.l.06.1	40343	2	0	0	0	0	0	0	0
796	RTA00000419F.b.12.1	63148	1	0	0	0	0	0	0	0
797	RTA00000423F.k.17.2	37512	2	0	0	0	0	0	0	0
799	RTA00000418F.k.14.1	76133	1	0	0	0	0	1	0	0
800	RTA00000409F.l.12.1	26755	1	0	0	0	0	0	0	0
801	RTA00000404F.c.20.1	39088	2	0	0	0	0	0	1	0
802	RTA00000423F.g.09.1	38958	2	0	0	0	0	0	0	0
804	RTA00000406F.d.12.1	38575	2	0	0	0	0	0	0	0
805	RTA00000411F.f.02.1	63386	1	0	0	0	0	0	0	0
806	RTA00000129A.n.21.1	79381	1	0	0	0	0	0	0	0
807	RTA00000409F.m.12.1	73490	1	0	0	0	0	0	0	0
808	RTA00000410F.c.04.1	74099	1	0	0	0	0	0	0	0
810	RTA00000406F.m.09.1	26891	2	0	0	0	0	0	0	0
811	RTA00000411F.b.06.1	77884	1	0	0	0	0	0	0	0
812	RTA00000409F.l.21.1	73143	1	0	0	0	0	0	0	0
818	RTA00000404F.l.20.2	38638	2	0	0	0	0	0	0	0
819	RTA00000413F.d.18.1	65305	1	0	0	0	0	0	0	0
820	RTA00000404F.p.04.2	39069	2	0	0	0	0	0	0	0
821	RTA00000405F.g.19.2	37150	2	0	0	0	0	0	0	0
822	RTA00000409F.a.22.1	75200	1	0	0	0	0	0	0	0
824	RTA00000405F.o.18.1	11016	4	2	0	0	0	0	0	0
829	RTA00000408F.e.22.2	26930	1	0	0	0	0	0	0	0
831	RTA00000413F.d.16.1	63331	1	0	0	0	0	0	0	0
834	RTA00000419F.g.08.1	66700	1	0	0	0	0	0	0	0
835	RTA00000122A.g.16.1	81366	1	0	0	0	0	0	0	0
836	RTA00000419F.c.16.1	65254	1	0	0	0	0	0	0	0
837	RTA00000411F.b.03.1	23634	1	2	0	0	0	0	0	0
842	RTA00000403F.l.20.1	18267	1	0	0	0	0	0	0	0

SEQ ID NO:	Sequence Name	cluster	lib 1 clones	lib 2 clones	lib 15 clones	lib 16 clones	lib 17 clones	lib 18 clones	lib 19 clones	lib 20 clones
845	RTA00000411F.a.02.1	78537	1	0	0	0	0	0	0	0
847	RTA00000412F.l.04.1	66372	1	0	0	0	0	0	0	0
849	RTA00000406F.a.23.1	38712	2	0	0	0	0	0	0	0
851	RTA00000120A.n.19.3	80004	1	0	0	0	0	0	0	0
852	RTA00000403F.e.01.1	38965	2	0	0	0	0	0	0	0
853	RTA00000411F.l.03.1	62702	1	0	0	0	0	0	0	0
856	RTA00000121A.m.2.1	81064	1	0	0	0	0	0	0	0
858	RTA00000418F.j.12.1	73316	1	0	0	0	0	0	0	0
862	RTA00000125A.g.16.1	21497	2	1	0	0	0	0	0	0
863	RTA00000418F.o.18.1	78676	1	0	0	0	0	0	0	0
865	RTA00000408F.k.14.1	73856	1	0	0	0	0	0	0	0
871	RTA00000403F.o.15.1	39140	2	0	0	0	0	0	0	0
872	RTA00000341F.m.13.1	26502	1	0	0	0	0	0	0	0
873	RTA00000408F.h.03.1	78382	1	0	0	0	0	0	0	0
874	RTA00000423F.k.05.1	37472	2	0	0	0	0	0	0	0
876	RTA00000418F.p.19.1	78544	1	0	0	0	0	0	0	0
877	RTA00000420F.f.06.1	64812	1	0	0	0	0	0	0	0
878	RTA00000122A.j.18.1	81317	1	0	0	0	0	0	0	0
879	RTA00000420F.d.05.1	64432	1	0	0	0	0	0	0	0
880	RTA00000403F.m.18.1	39185	2	0	0	0	0	0	0	0
882	RTA00000411F.j.05.1	40709	1	1	0	0	0	0	0	0
883	RTA00000403F.a.04.1	23529	2	1	0	0	0	0	0	0
885	RTA00000406F.f.12.1	21895	2	1	0	0	0	0	0	0
886	RTA00000418F.g.22.1	74837	1	0	0	0	0	0	0	0
888	RTA00000404F.l.20.1	38638	2	0	0	0	0	0	0	0
889	RTA00000408F.i.08.2	75811	1	0	0	0	0	0	0	0
890	RTA00000122A.d.5.1	81155	1	0	0	0	0	0	0	0
894	RTA00000419F.b.19.1	65534	1	0	0	0	0	0	0	0
896	RTA00000418F.k.19.1	74932	1	0	0	0	0	0	0	0
900	RTA00000419F.g.12.1	66171	1	0	0	0	0	0	0	0
901	RTA00000404F.n.11.2	38001	2	0	0	0	0	0	0	0
904	RTA00000419F.o.24.1	65092	1	0	0	0	0	0	0	0
905	RTA00000419F.k.19.1	75447	1	0	0	0	0	0	0	0
907	RTA00000127A.i.20.1	81418	1	0	0	0	0	0	0	0
908	RTA00000422F.g.22.1	22561	3	0	0	0	0	0	0	0
910	RTA00000413F.h.13.1	65190	1	0	0	0	0	0	0	0
913	RTA00000348R.j.16.1	7005	8	2	0	0	0	0	0	0
916	RTA00000418F.n.22.1	79062	1	0	0	0	0	0	0	0
917	RTA00000406F.l.08.1	39016	2	0	0	0	0	0	0	0

SEQ ID NO:	Sequence Name	cluster	lib 1 clones	lib 2 clones	lib 15 clones	lib 16 clones	lib 17 clones	lib 18 clones	lib 19 clones	lib 20 clones
920	RTA00000409F.j.07.1	75190	1	0	0	0	0	0	0	0
923	RTA00000411F.e.22.1	63638	1	0	0	0	0	0	0	0
924	RTA00000347F.a.17.1	16723	3	1	0	0	0	0	0	0
926	RTA00000404F.n.20.1	26865	2	0	0	0	0	0	0	0
929	RTA00000404F.b.02.1	38984	2	0	0	0	0	0	0	0
931	RTA00000403F.b.10.1	73268	1	0	0	0	0	0	0	0
932	RTA00000406F.i.12.1	39080	2	0	0	0	0	0	0	0
933	RTA00000406F.h.08.1	16228	2	2	0	0	0	0	0	0
934	RTA00000418F.i.19.1	79180	1	0	0	0	0	0	0	0
936	RTA00000412F.h.21.1	64348	1	0	0	0	0	0	0	0
938	RTA00000120A.g.18.1	81255	1	0	0	0	0	0	0	0
940	RTA00000423F.j.05.1	37958	2	0	0	0	0	0	0	0
941	RTA00000132A.k.6.1	81284	1	0	0	0	0	0	0	0
943	RTA00000406F.p.04.1	37458	2	0	0	0	0	0	0	0
944	RTA00000347F.a.13.1	22446	3	0	0	0	0	0	0	0
945	RTA00000419F.p.23.1	64748	1	0	0	0	0	0	0	0
946	RTA00000419F.d.17.1	64353	1	0	0	0	0	0	0	0
949	RTA00000124A.k.5.1	80252	1	0	0	0	0	0	0	0
950	RTA00000404F.h.22.1	18735	2	1	0	0	0	0	1	0
952	RTA00000410F.o.05.1	75262	1	0	0	0	0	0	0	0
953	RTA00000339R.l.14.1	19119	3	0	0	0	0	0	0	0
954	RTA00000403F.m.13.2	39077	2	0	0	0	0	0	0	0
957	RTA00000419F.g.22.1	64515	1	0	0	0	0	0	0	0
958	RTA00000404F.g.21.1	37947	2	0	0	0	0	0	0	0
960	RTA00000138A.n.4.1	21920	2	1	0	0	0	0	0	0
961	RTA00000410F.b.15.1	77100	1	0	0	0	0	0	0	0
963	RTA00000419F.j.23.1	74470	1	0	0	0	0	0	0	0
964	RTA00000411F.j.02.1	65310	1	0	0	0	0	0	0	0
965	RTA00000419F.p.24.1	63477	1	0	0	0	0	0	0	0
966	RTA00000404F.a.19.1	38624	2	0	0	0	0	0	0	0
973	RTA00000346F.e.13.1	74653	1	0	0	0	0	0	0	0
974	RTA00000419F.c.18.1	41394	1	1	0	0	0	0	0	0
978	RTA00000404F.e.22.1	11344	3	3	0	0	0	0	0	0
981	RTA00000125A.k.10.1	81644	1	0	0	0	0	0	0	0
982	RTA00000347F.c.06.1	18846	2	1	0	0	0	0	0	0
983	RTA00000411F.k.19.1	64200	1	0	0	0	0	0	0	0
984	RTA00000345F.i.09.1	27250	2	0	0	0	0	0	0	0
985	RTA00000423F.k.01.1	40426	2	0	0	0	0	0	0	0
986	RTA00000408F.d.06.1	78997	1	0	0	0	0	0	0	0

SEQ ID NO:	Sequence Name	cluster	lib 1 clones	lib 2 clones	lib 15 clones	lib 16 clones	lib 17 clones	lib 18 clones	lib 19 clones	lib 20 clones
987	RTA00000128A.b.20.1	79761	1	0	0	0	0	0	0	0
989	RTA00000195AF.d.4.1	22766	3	0	0	0	0	0	0	0
991	RTA00000403F.h.12.1	15205	2	1	0	0	0	0	0	0
992	RTA00000119A.j.22.1	80336	1	0	0	0	0	0	0	0
995	RTA00000126A.n.7.2	79557	1	0	0	1	0	0	0	0
997	RTA00000404F.j.08.1	39066	2	0	0	0	0	0	0	0
998	RTA00000410F.c.14.1	77809	1	0	0	0	0	0	0	0
999	RTA00000120A.g.23.1	81189	1	0	0	0	0	0	0	0
1000	RTA00000195AF.d.20.1	37574	2	0	0	0	0	0	0	0
1002	RTA00000412F.j.17.1	64071	1	0	0	0	0	0	0	0
1004	RTA00000119A.j.10.1	79646	1	0	0	0	0	0	0	0
1010	RTA00000419F.o.16.1	62867	1	0	0	0	0	0	0	0
1012	RTA00000411F.c.17.1	77664	1	0	0	0	0	0	0	0
1013	RTA00000406F.k.15.1	38549	2	0	0	0	0	0	0	0
1014	RTA00000406F.a.02.1	37744	2	0	0	0	0	0	0	0
1016	RTA00000341F.b.06.1	17008	4	0	0	0	0	0	0	0
1017	RTA00000409F.n.14.1	78190	1	0	0	0	0	0	0	0
1019	RTA00000345F.j.08.1	16731	3	1	0	0	0	0	0	0
1021	RTA00000419F.g.15.1	32519	1	1	0	0	0	0	0	0
1022	RTA00000423F.a.19.1	21396	1	2	0	0	0	0	0	0
1024	RTA00000422F.e.08.1	39020	2	0	0	0	0	0	0	0
1025	RTA00000411F.d.15.1	74890	1	0	0	0	0	0	0	0
1027	RTA00000411F.l.15.1	66704	1	0	0	0	0	0	0	0
1029	RTA00000405F.e.08.1	37916	2	0	0	0	1	0	0	0
1030	RTA00000353R.j.24.1	23089	3	0	0	0	0	0	0	0
1032	RTA00000418F.o.06.1	75930	1	0	0	0	0	0	0	0
1033	RTA00000404F.c.10.1	23534	2	1	0	0	0	0	0	0
1034	RTA00000418F.i.21.1	78728	1	0	0	0	0	0	0	0
1036	RTA00000411F.l.13.1	43114	1	1	0	0	0	0	0	0
1037	RTA00000407F.a.24.1	37560	2	0	0	0	0	0	0	0
1038	RTA00000346F.n.06.1	12439	4	0	0	0	0	0	0	0
1039	RTA00000412F.l.21.1	65183	1	0	0	0	0	0	0	0
1040	RTA00000413F.i.02.1	65857	1	0	0	0	0	0	0	0
1041	RTA00000404F.i.19.1	38698	2	0	0	0	0	0	0	0
1043	RTA00000403F.a.11.1	73109	1	0	0	0	0	0	0	0
1045	RTA00000411F.k.16.1	64759	1	0	0	0	0	0	1	0
1046	RTA00000405F.c.01.1	19236	2	0	0	0	0	0	0	0
1047	RTA00000423F.i.18.1	14996	4	0	0	0	0	0	0	0
1050	RTA00000406F.a.07.1	26607	2	0	0	0	0	0	0	0

SEQ ID NO:	Sequence Name	cluster	lib 1 clones	lib 2 clones	lib 15 clones	lib 16 clones	lib 17 clones	lib 18 clones	lib 19 clones	lib 20 clones
1051	RTA00000347F.d.06.1	39122	2	0	0	0	0	0	0	0
1052	RTA00000419F.b.18.1	67034	1	0	0	0	0	0	0	0
1053	RTA00000406F.h.07.1	38003	2	0	0	0	0	0	0	0
1054	RTA00000405F.l.15.1	19575	2	1	0	0	0	0	0	0
1055	RTA00000406F.g.17.1	37979	2	0	0	0	0	0	0	0
1058	RTA00000130A.h.22.1	80933	1	0	0	0	0	0	0	0
1061	RTA00000404F.d.13.1	39036	2	0	0	0	0	0	0	0
1064	RTA00000340F.n.01.1	39081	2	0	0	0	0	0	0	0
1065	RTA00000419F.d.06.1	65496	1	0	0	0	0	0	0	0
1066	RTA00000419F.n.09.1	66070	1	0	0	0	0	0	0	0
1067	RTA00000399F.i.08.1	38927	2	0	0	0	0	0	0	0
1069	RTA00000423F.g.13.1	38028	2	0	0	0	0	0	0	0
1072	RTA00000195AF.b.21.1	39055	2	0	0	0	0	0	0	0
1073	RTA00000403F.h.05.1	39096	2	0	0	0	0	0	0	0
1075	RTA00000422F.p.07.2	39024	2	0	0	1	0	0	0	0
1078	RTA00000421F.n.19.1	16409	3	1	0	0	0	0	0	0
1080	RTA00000345F.k.21.1	40204	2	0	0	0	0	0	0	0
1082	RTA00000405F.a.11.1	39124	2	0	0	0	0	0	0	0
1084	RTA00000413F.e.16.1	63836	1	0	0	0	0	0	0	0
1086	RTA00000404F.o.18.2	39110	2	0	0	0	0	0	0	0
1087	RTA00000409F.i.24.1	76967	1	0	0	0	0	0	0	0
1091	RTA00000340F.n.13.1	17055	4	0	0	0	0	0	0	0
1092	RTA00000340F.p.04.1	78533	1	0	0	0	0	0	0	0
1093	RTA00000411F.c.05.1	73368	1	0	0	0	0	0	0	0
1097	RTA00000404F.i.02.1	39015	2	0	0	0	0	0	0	0
1099	RTA00000403F.m.15.2	26901	2	0	0	0	0	0	0	0
1100	RTA00000412F.h.23.2	65118	1	0	0	0	0	0	0	0
1101	RTA00000418F.j.08.1	73382	1	0	0	0	0	0	0	0
1102	RTA00000125A.n.4.1	81984	1	0	0	0	0	0	0	0
1103	RTA00000412F.l.19.1	65825	1	0	0	0	0	0	0	0
1105	RTA00000129A.p.3.1	32644	1	1	0	0	0	0	0	0
1106	RTA00000340F.p.20.1	17008	4	0	0	0	0	0	0	0
1107	RTA00000411F.a.10.1	73073	1	0	0	0	0	0	0	0
1108	RTA00000409F.n.17.1	76725	1	0	0	0	0	0	0	0
1109	RTA00000404F.c.03.2	39198	2	0	0	0	0	0	0	0
1110	RTA00000420F.a.19.1	34192	1	1	0	0	0	0	0	0
1114	RTA00000420F.d.12.1	64095	1	0	0	0	0	0	0	0
1115	RTA00000409F.j.19.1	73792	1	0	0	0	0	0	0	0
1116	RTA00000422F.d.16.1	39133	2	0	0	0	0	0	0	0

SEQ ID NO:	Sequence Name	cluster	lib 1 clones	lib 2 clones	lib 15 clones	lib 16 clones	lib 17 clones	lib 18 clones	lib 19 clones	lib 20 clones
1117	RTA00000418F.m.16.1	74986	1	0	0	0	0	0	0	0
1118	RTA00000405F.c.11.1	39068	2	0	0	0	0	0	0	0
1119	RTA00000404F.k.22.1	39084	2	0	0	0	0	0	0	0
1120	RTA00000418F.k.07.1	75067	1	0	0	0	0	0	0	0
1121	RTA00000403F.c.10.1	75261	1	0	0	0	0	0	0	0
1124	RTA00000410F.m.05.1	74964	1	0	0	0	0	0	0	0
1125	RTA00000405F.i.20.1	38532	2	0	0	0	0	0	0	0
1127	RTA00000408F.p.24.1	74286	1	0	0	0	0	0	0	0
1128	RTA00000418F.k.18.1	75385	1	0	0	0	0	0	0	0
1129	RTA00000422F.m.04.1	38702	2	0	0	0	0	0	0	0
1133	RTA00000403F.a.07.1	73559	1	0	0	0	0	0	0	0
1135	RTA00000403F.b.19.1	22327	2	1	0	0	0	0	0	0
1136	RTA00000418F.m.23.1	77195	1	0	0	0	0	0	0	0
1138	RTA00000404F.i.18.1	21912	2	1	0	0	0	0	0	0
1139	RTA00000422F.i.14.1	39300	2	0	0	0	0	0	0	0
1140	RTA00000418F.m.14.1	75711	1	0	0	1	0	0	0	0
1141	RTA00000406F.o.12.1	37459	2	0	0	0	0	0	0	0
1143	RTA00000411F.a.07.1	74547	1	0	0	0	0	0	0	0
1144	RTA00000411F.c.02.1	72852	1	0	0	0	0	0	0	0
1146	RTA00000130A.h.16.1	80761	1	0	0	0	0	0	0	0
1147	RTA00000410F.p.23.1	73948	1	0	0	0	0	0	0	0
1148	RTA00000418F.m.24.1	77114	1	0	0	0	0	0	0	0
1150	RTA00000408F.j.19.2	73752	1	0	0	0	0	0	0	0
1152	RTA00000118A.d.17.1	81921	1	0	0	0	0	0	0	0
1153	RTA00000407F.b.04.1	63221	1	0	0	0	0	0	0	0
1154	RTA00000411F.e.07.1	65008	1	0	0	0	0	0	0	0
1156	RTA00000132A.c.11.1	87278	1	0	0	0	0	0	0	0
1157	RTA00000420F.e.16.1	63639	1	0	0	0	0	0	0	0
1159	RTA00000404F.b.11.1	39079	2	0	0	0	0	0	0	0
1160	RTA00000418F.k.17.1	75390	1	0	0	0	0	0	0	0
1161	RTA00000129A.k.12.1	79322	1	0	0	0	0	0	0	0
1162	RTA00000340R.m.07.1	78415	1	0	0	0	0	0	0	0
1163	RTA00000405F.d.14.1	35209	2	0	0	0	0	0	1	0
1164	RTA00000406F.f.11.1	38601	2	0	0	0	0	0	0	0
1165	RTA00000120A.h.5.1	80344	1	0	0	0	0	0	0	0
1167	RTA00000411F.g.06.1	66065	1	0	0	0	0	0	0	0
1168	RTA00000408F.d.16.1	76318	1	0	0	0	0	0	0	0
1171	RTA00000404F.c.19.1	39026	2	0	0	0	0	0	0	1
1173	RTA00000410F.a.01.1	73354	1	0	0	0	0	0	0	0

SEQ ID NO:	Sequence Name	cluster	lib 1 clones	lib 2 clones	lib 15 clones	lib 16 clones	lib 17 clones	lib 18 clones	lib 19 clones	lib 20 clones
1174	RTA00000408F.h.08.1	74575	1	0	0	0	0	0	0	0
1175	RTA00000422F.b.16.1	17045	4	0	0	0	0	0	0	0
1176	RTA00000419F.f.10.1	66193	1	0	0	0	0	0	0	0
1177	RTA00000418F.l.04.1	74140	1	0	0	0	0	0	0	0
1178	RTA00000410F.a.16.1	73548	1	0	0	0	0	0	0	0
1179	RTA00000138A.e.13.1	79608	1	0	0	0	0	0	0	0
1180	RTA00000130A.b.5.1	79579	1	0	0	0	0	0	0	0
1181	RTA00000408F.j.15.2	74759	1	0	0	0	0	0	0	0
1182	RTA00000410F.m.20.1	74285	1	0	0	0	0	0	0	0
1185	RTA00000419F.e.04.1	62963	1	0	0	0	0	0	0	0
1187	RTA00000418F.g.05.1	73075	1	0	0	0	0	0	0	0
1188	RTA00000419F.n.02.1	65963	1	0	0	0	0	0	0	0
1191	RTA00000119A.m.15.1	80989	1	0	0	0	0	0	0	0
1194	RTA00000413F.g.23.1	40700	1	1	0	0	0	0	0	0
1195	RTA00000403F.a.18.1	75726	1	0	0	0	0	0	0	0
1196	RTA00000404F.m.20.2	39144	2	0	0	0	0	0	0	0
1199	RTA00000419F.h.04.1	65034	1	0	0	0	0	0	0	0
1200	RTA00000408F.d.12.1	75782	1	0	0	0	0	0	0	0
1201	RTA00000133A.m.19.2	80167	1	0	0	0	0	0	0	0
1206	RTA00000126A.o.22.1	81752	1	0	0	0	0	0	0	0
1207	RTA00000419F.n.13.1	66026	1	0	0	0	0	0	0	0
1208	RTA00000130A.h.13.1	80790	1	0	0	0	0	0	0	0
1212	RTA00000411F.m.19.1	74924	1	0	0	0	0	0	0	0
1214	RTA00000419F.k.06.1	78493	1	0	0	0	0	0	0	0
1216	RTA00000412F.d.16.1	26829	1	0	0	0	0	0	0	0
1217	RTA00000119A.j.23.1	79835	1	0	0	0	0	0	0	0
1219	RTA00000195AF.c.12.1	37582	2	0	0	0	0	0	0	0
1223	RTA00000423F.c.19.1	40472	2	0	0	0	0	0	0	0
1224	RTA00000405F.g.24.1	39076	2	0	0	0	0	0	0	0
1226	RTA00000419F.c.11.1	65504	1	0	0	0	0	0	0	0
1227	RTA00000135A.f.14.2	79969	1	0	0	0	0	0	0	0
1228	RTA00000403F.a.05.1	18808	1	1	0	0	0	0	0	0
1229	RTA00000405F.e.17.1	38662	2	0	0	0	0	0	0	0
1230	RTA00000411F.d.05.1	75812	1	0	0	0	0	0	0	0
1232	RTA00000418F.d.03.1	76824	1	0	0	0	0	0	0	0
1233	RTA00000418F.h.08.1	76401	1	0	0	0	0	0	0	0
1234	RTA00000418F.m.10.1	79110	1	0	0	0	0	0	0	0
1235	RTA00000411F.i.15.1	31612	1	1	0	0	0	0	0	0
1236	RTA00000413F.i.23.1	63073	1	0	0	0	0	0	0	0

SEQ ID NO:	Sequence Name	cluster	lib 1 clones	lib 2 clones	lib 15 clones	lib 16 clones	lib 17 clones	lib 18 clones	lib 19 clones	lib 20 clones
1237	RTA00000411F.e.24.1	64781	1	0	0	0	0	0	0	0
1238	RTA00000406F.g.22.1	38590	2	0	0	0	0	0	0	0
1239	RTA00000126A.n.13.2	79735	1	0	0	0	0	0	0	0
1240	RTA00000419F.a.02.1	77993	1	0	0	0	0	0	0	0
1241	RTA00000346F.l.13.1	7542	8	0	0	2	1	0	1	0
1245	RTA00000120A.d.15.1	80533	1	0	0	0	0	0	0	0
1246	RTA00000418F.f.21.1	75157	1	0	0	0	0	0	0	0
1248	RTA00000129A.d.1.2	80058	1	0	0	0	0	0	0	0
1251	RTA00000419F.m.20.1	76720	1	0	0	0	0	0	0	0
1253	RTA00000406F.e.15.1	39074	2	0	0	0	0	0	0	0
1255	RTA00000411F.c.10.1	73117	1	0	0	0	0	0	0	0
1259	RTA00000413F.d.05.1	64788	1	0	0	0	0	0	0	0
1260	RTA00000121A.o.3.1	81437	1	0	0	0	0	0	0	0
1262	RTA00000420F.e.02.1	40259	2	0	0	0	0	0	0	0
1268	RTA00000126A.k.7.2	79866	1	0	0	0	0	0	0	0
1270	RTA00000419F.l.03.1	79060	1	0	0	0	0	0	0	0
1272	RTA00000118A.a.2.1	38067	2	0	0	0	0	0	0	0
1273	RTA00000410F.m.18.1	76365	1	0	0	0	0	0	0	0
1275	RTA00000406F.c.20.1	38578	2	0	0	0	0	0	0	0
1276	RTA00000413F.b.14.1	66591	1	0	0	0	0	0	0	0
1277	RTA00000406F.c.18.1	14368	2	0	0	0	0	0	0	0
1278	RTA00000418F.j.09.1	76352	1	0	0	0	0	0	0	0
1279	RTA00000419F.f.23.1	65002	1	0	0	0	0	0	0	0
1281	RTA00000411F.a.05.1	76699	1	0	0	0	0	0	0	0
1282	RTA00000419F.m.21.1	77947	1	0	0	0	0	0	0	0
1283	RTA00000405F.n.16.1	21503	2	1	1	0	0	0	0	0
1284	RTA00000422F.o.19.2	13084	3	2	0	0	0	0	0	0
1285	RTA00000408F.n.02.2	76993	1	0	0	0	0	0	0	0
1290	RTA00000119A.g.7.1	83580	1	0	0	0	0	0	0	0
1291	RTA00000411F.i.02.1	66975	1	0	0	0	0	0	0	0
1292	RTA00000408F.l.09.1	75487	1	0	0	0	0	0	0	0
1293	RTA00000423F.g.04.1	23012	2	1	0	0	0	0	0	0
1295	RTA00000418F.i.18.1	78024	1	0	0	0	0	0	0	0
1296	RTA00000411F.h.15.1	65160	1	0	0	0	0	0	0	0
1297	RTA00000410F.i.19.1	78988	1	0	0	0	0	0	0	0
1298	RTA00000419F.k.24.1	75596	1	0	0	0	0	0	0	0
1301	RTA00000409F.i.09.1	75279	1	0	0	0	0	0	0	0
1302	RTA00000419F.h.02.1	63985	1	0	0	0	0	0	0	0
1303	RTA00000413F.b.12.1	64932	1	0	0	0	0	0	0	0

SEQ ID NO:	Sequence Name	cluster	lib 1 clones	lib 2 clones	lib 15 clones	lib 16 clones	lib 17 clones	lib 18 clones	lib 19 clones	lib 20 clones
1304	RTA00000121A.h.18.1	16376	4	0	0	0	0	0	0	0
1305	RTA00000411F.n.20.1	75816	1	0	0	0	0	0	0	0
1307	RTA00000411F.n.12.1	73308	1	0	0	0	0	0	0	0
1308	RTA00000408F.j.12.2	18226	1	0	0	0	0	0	0	0
1309	RTA00000409F.i.03.1	75968	1	0	0	0	0	0	0	0
1312	RTA00000409F.j.05.1	74128	1	0	0	0	0	0	0	0
1313	RTA00000419F.m.04.1	74367	1	0	0	0	0	0	0	0
1314	RTA00000418F.k.03.1	78901	1	0	0	0	0	0	0	0
1315	RTA00000419F.d.16.1	64357	1	0	0	0	0	0	0	0
1316	RTA00000420F.e.10.1	65899	1	0	0	0	0	0	0	0
1319	RTA00000418F.k.08.1	18259	1	0	0	0	0	0	0	0
1322	RTA00000410F.c.02.1	75055	1	0	0	0	0	0	0	0
1324	RTA00000403F.h.18.1	39241	2	0	0	0	0	0	0	0
1325	RTA00000405F.n.13.1	23810	2	1	0	0	0	0	0	0
1326	RTA00000355R.e.14.1	16837	2	2	0	0	0	0	0	0
1327	RTA00000422F.l.03.1	39147	2	0	0	0	0	0	0	0
1329	RTA00000403F.o.14.1	38971	2	0	0	0	0	0	0	0
1333	RTA00000127A.f.11.1	81463	1	0	0	0	0	0	0	0
1335	RTA00000403F.o.07.1	39037	2	0	0	0	0	0	0	0
1336	RTA00000403F.d.19.1	39243	2	0	0	0	0	0	0	0
1338	RTA00000406F.i.17.1	37902	2	0	0	0	0	0	0	0
1339	RTA00000418F.d.22.1	75324	1	0	0	0	0	0	0	0
1340	RTA00000340R.o.12.1	53732	1	0	0	0	0	0	0	0
1341	RTA00000125A.g.24.1	80397	1	0	0	0	0	0	0	0
1342	RTA00000130A.o.21.1	80218	1	0	0	0	0	0	0	0
1343	RTA00000420F.a.23.1	42158	1	1	0	0	0	0	0	0
1344	RTA00000411F.m.18.1	75629	1	0	0	0	0	0	0	0
1345	RTA00000407F.b.22.1	37487	2	0	0	0	0	0	0	0
1346	RTA00000409F.a.16.1	73990	1	0	0	0	0	0	0	0
1348	RTA00000341F.k.12.1	62985	1	0	0	0	0	0	0	0
1349	RTA00000129A.c.18.2	37216	2	0	0	0	0	0	0	0
1350	RTA00000410F.d.10.1	77561	1	0	0	0	0	0	0	0
1351	RTA00000351R.i.03.1	6874	6	3	0	0	1	0	0	0
1352	RTA00000135A.l.1.2	39426	2	0	0	0	0	0	0	0
1353	RTA00000420F.b.18.1	66136	1	0	0	0	0	0	0	0
1356	RTA00000403F.o.13.1	39049	2	0	0	0	0	0	0	0
1357	RTA00000411F.f.06.1	64186	1	0	0	0	0	0	0	0
1359	RTA00000351R.c.13.1	11476	6	0	0	0	0	0	0	0
1362	RTA00000420F.d.16.1	64485	1	0	0	0	0	0	0	0

SEQ ID NO:	Sequence Name	cluster	lib 1 clones	lib 2 clones	lib 15 clones	lib 16 clones	lib 17 clones	lib 18 clones	lib 19 clones	lib 20 clones
1363	RTA00000404F.i.12.1	39001	2	0	0	0	0	0	0	0
1364	RTA00000404F.o.10.2	16785	2	2	0	0	0	0	0	0
1365	RTA00000419F.d.07.1	21421	1	2	0	0	0	0	0	0
1366	RTA00000404F.p.02.2	39097	2	0	1	0	0	0	0	0
1367	RTA00000125A.k.14.1	79457	1	0	0	0	0	0	0	0
1368	RTA00000122A.j.22.1	81151	1	0	0	0	0	0	0	0
1369	RTA00000406F.i.13.1	37904	2	0	0	0	0	0	0	0
1370	RTA00000135A.b.23.1	35241	2	0	0	0	0	0	0	0
1373	RTA00000423F.l.04.1	14320	2	0	0	0	0	0	0	0
1374	RTA00000420F.b.04.1	63820	1	0	0	0	0	0	0	0
1376	RTA00000408F.i.18.2	74410	1	0	0	0	0	0	0	0
1378	RTA00000341F.j.05.1	36177	2	0	0	0	0	0	0	0
1379	RTA00000420F.a.16.1	63345	1	0	0	0	0	0	0	0
1381	RTA00000410F.j.01.1	73399	1	0	0	0	0	0	0	0
1382	RTA00000408F.p.21.1	77930	1	0	0	0	0	0	0	0
1383	RTA00000412F.d.19.1	75743	1	0	0	0	0	0	0	0
1384	RTA00000352R.c.04.1	71976	1	0	0	0	0	0	0	0
1385	RTA00000413F.f.19.1	65189	1	0	0	0	0	0	0	0
1386	RTA00000411F.e.03.1	73648	1	0	0	0	0	0	0	0
1389	RTA00000418F.c.04.1	41587	1	1	0	0	0	0	0	0
1390	RTA00000418F.o.17.1	79069	1	0	0	0	0	0	0	0
1391	RTA00000418F.e.21.1	74773	1	0	0	0	0	0	0	0
1392	RTA00000419F.d.14.1	64945	1	0	0	0	0	0	0	0
1396	RTA00000410F.j.20.1	73601	1	0	0	0	0	0	0	0
1399	RTA00000119A.j.9.1	82060	1	0	0	0	0	0	0	0
1403	RTA00000340F.i.13.1	79299	1	0	0	0	0	0	0	0
1404	RTA00000412F.g.03.1	64740	1	0	0	0	0	0	0	0
1405	RTA00000122A.g.17.1	32655	1	1	0	0	0	0	0	0
1407	RTA00000419F.n.12.1	66086	1	0	0	0	0	0	0	0
1410	RTA00000351R.p.14.1	13166	2	3	0	0	0	0	0	0
1411	RTA00000403F.e.08.1	19126	3	0	0	0	0	0	0	0
1412	RTA00000124A.k.20.1	80913	1	0	0	0	0	0	0	0
1413	RTA00000121A.n.2.1	33585	1	1	0	0	0	0	0	0
1414	RTA00000422F.m.24.1	39159	2	0	1	0	1	1	2	2
1415	RTA00000408F.e.24.2	75002	1	0	0	0	0	0	0	0
1418	RTA00000403F.b.12.1	78775	1	0	0	0	0	0	0	0
1419	RTA00000404F.a.09.1	38985	2	0	0	0	0	0	0	0
1421	RTA00000403F.o.19.1	78615	1	0	0	0	0	0	0	0
1424	RTA00000410F.b.10.1	74504	1	0	0	0	0	0	0	0

SEQ ID NO:	Sequence Name	cluster	lib 1 clones	lib 2 clones	lib 15 clones	lib 16 clones	lib 17 clones	lib 18 clones	lib 19 clones	lib 20 clones
1426	RTA00000413F.h.12.1	66929	1	0	0	0	0	0	0	0
1427	RTA00000406F.k.14.1	38651	2	0	0	0	0	0	0	0
1429	RTA00000411F.f.17.1	65661	1	0	0	0	0	0	0	0
1430	RTA00000411F.k.10.1	64506	1	0	0	0	0	0	0	0
1431	RTA00000411F.g.21.1	64500	1	0	0	0	0	0	0	0
1432	RTA00000119A.h.24.1	82266	1	0	0	0	0	0	0	0
1434	RTA00000408F.m.22.2	72949	1	0	0	0	0	0	0	0
1437	RTA00000410F.i.17.1	78147	1	0	0	0	0	0	0	0
1440	RTA00000129A.a.13.2	79780	1	0	0	0	0	0	0	0
1441	RTA00000129A.k.21.1	82067	1	0	0	0	0	0	0	0
1442	RTA00000350R.g.10.1	9026	7	0	0	1	0	0	0	0
1443	RTA00000413F.d.23.1	66030	1	0	0	0	0	0	0	0
1447	RTA00000411F.d.10.1	76445	1	0	0	0	0	0	0	0
1448	RTA00000404F.b.19.1	39281	2	0	0	0	0	0	0	0
1449	RTA00000418F.c.07.1	73245	1	0	0	0	0	0	0	0
1450	RTA00000418F.j.15.1	74855	1	0	0	0	0	1	0	0
1453	RTA00000413F.b.16.1	65126	1	0	0	0	0	0	0	0
1455	RTA00000350R.m.14.1	39171	2	0	0	0	0	0	0	0
1456	RTA00000418F.l.11.1	77158	1	0	0	0	0	0	0	0
1457	RTA00000130A.d.5.1	82051	1	0	0	0	0	0	0	0
1458	RTA00000339F.n.05.1	39648	2	0	0	0	0	0	0	0
1460	RTA00000407F.a.23.1	23489	2	1	0	0	0	0	0	0
1462	RTA00000403F.h.11.1	39219	2	0	0	0	0	0	0	0
1463	RTA00000406F.j.13.1	38688	2	0	0	0	0	0	0	0
1464	RTA00000352R.p.09.1	16915	4	0	0	0	0	0	0	0
1465	RTA00000413F.g.24.1	65481	1	0	0	0	0	0	0	0
1469	RTA00000420F.a.08.1	19473	1	2	0	0	0	0	0	0
1472	RTA00000404F.i.22.1	39082	2	0	0	0	0	0	0	0
1473	RTA00000124A.k.23.1	81350	1	0	0	0	0	0	0	0
1474	RTA00000404F.e.11.1	38991	2	0	0	0	0	0	0	0
1475	RTA00000129A.d.2.4	80119	1	0	0	0	0	0	0	0
1478	RTA00000419F.o.15.1	32487	1	1	0	0	0	0	0	0
1479	RTA00000119A.m.17.1	79536	1	0	0	0	0	0	0	0
1480	RTA00000410F.b.07.1	78916	1	0	0	0	0	0	0	0
1481	RTA00000420F.b.19.1	36873	2	0	0	0	0	0	0	0
1483	RTA00000411F.b.21.1	10051	1	0	0	0	0	0	0	0
1485	RTA00000356R.c.16.1	16915	4	0	0	0	0	0	0	0
1487	RTA00000412F.h.11.1	63175	1	0	0	0	0	0	0	0
1490	RTA00000420F.a.11.1	66460	1	0	0	0	0	0	0	0

SEQ ID NO:	Sequence Name	cluster	lib 1 clones	lib 2 clones	lib 15 clones	lib 16 clones	lib 17 clones	lib 18 clones	lib 19 clones	lib 20 clones
1491	RTA00000120A.c.7.1	80985	1	0	0	1	0	0	0	0
1492	RTA00000404F.e.15.1	39101	2	0	0	0	0	0	0	0
1493	RTA00000422F.n.20.1	38676	2	0	0	0	0	0	1	0
1494	RTA00000423F.h.20.1	38639	2	0	0	0	0	0	0	0
1497	RTA00000410F.b.18.1	76701	1	0	0	0	0	0	0	0
1499	RTA00000423F.g.15.1	35173	2	0	0	0	0	0	0	0
1500	RTA00000413F.b.04.1	66427	1	0	0	0	0	0	0	0
1503	RTA00000346F.f.11.1	38528	2	0	0	0	0	0	0	0
1506	RTA00000422F.i.02.1	76436	1	0	0	0	0	0	0	0
1507	RTA00000410F.a.08.1	73324	1	0	0	0	0	0	0	0
1509	RTA00000419F.e.02.1	65010	1	0	0	0	0	0	0	0
1511	RTA00000403F.g.13.1	38718	2	0	0	0	0	0	0	0
1513	RTA00000407F.a.01.1	12501	3	1	0	0	0	0	0	0
1516	RTA00000411F.f.14.1	62984	1	0	0	0	0	0	0	0
1517	RTA00000411F.c.04.1	76858	1	0	0	0	0	0	0	0
1518	RTA00000135A.m.18.1	19255	2	0	0	0	0	0	0	0
1519	RTA00000413F.c.17.1	36831	2	0	0	0	0	0	0	0
1521	RTA00000404F.j.01.1	26859	2	0	0	0	0	0	0	0
1522	RTA00000138A.p.10.1	81625	1	0	0	0	0	0	0	0
1526	RTA00000423F.h.07.1	37933	2	0	0	0	0	0	0	0
1527	RTA00000413F.e.04.1	64176	1	0	0	0	0	0	0	0
1528	RTA00000406F.h.03.1	38585	2	0	0	0	0	0	0	0
1529	RTA00000403F.e.24.1	16432	2	2	0	0	0	0	0	0
1531	RTA00000403F.i.11.1	23535	2	1	0	0	0	0	0	0
1532	RTA00000419F.g.02.1	62839	1	0	0	0	0	0	0	0
1533	RTA00000347F.e.05.1	39814	2	0	0	0	0	0	0	0
1534	RTA00000408F.l.16.1	73468	1	0	0	0	0	0	0	0
1536	RTA00000423F.f.09.1	64823	1	0	0	0	0	0	0	0
1537	RTA00000419F.k.03.1	40822	1	1	0	0	0	0	0	0
1538	RTA00000406F.b.02.1	38744	2	0	0	0	0	0	0	0
1539	RTA00000418F.o.14.1	33524	1	1	0	0	0	0	0	0
1541	RTA00000404F.b.09.1	39166	2	0	0	0	0	0	0	0
1547	RTA00000406F.k.11.1	38715	2	0	0	0	0	0	0	0
1549	RTA00000406F.c.06.1	37924	2	0	0	0	0	0	0	0
1550	RTA00000418F.n.07.1	76316	1	0	0	0	0	0	0	0
1551	RTA00000419F.n.15.1	63484	1	0	0	0	0	0	0	0
1552	RTA00000408F.n.06.2	76642	1	0	0	0	0	0	0	0
1553	RTA00000420F.c.04.1	65007	1	0	0	0	0	0	0	0
1554	RTA00000411F.j.15.1	66871	1	0	0	0	0	0	0	0

SEQ ID NO:	Sequence Name	cluster	lib 1 clones	lib 2 clones	lib 15 clones	lib 16 clones	lib 17 clones	lib 18 clones	lib 19 clones	lib 20 clones
1556	RTA00000128A.m.23.1	81441	1	0	0	0	0	0	0	0
1557	RTA00000406F.g.03.1	38690	2	0	0	0	0	0	0	0
1558	RTA00000405F.h.05.2	75706	1	0	0	0	0	0	0	0
1559	RTA00000129A.n.24.1	81409	1	0	0	0	0	0	0	0
1562	RTA00000418F.n.11.1	78977	1	0	0	0	0	0	0	0
1565	RTA00000120A.h.9.1	80736	1	0	0	0	0	0	0	0
1566	RTA00000413F.a.12.1	63403	1	0	0	0	0	0	0	0
1567	RTA00000412F.o.05.1	63575	1	0	0	0	0	0	0	0
1571	RTA00000354R.n.04.1	22049	3	0	0	0	0	0	0	0
1573	RTA00000406F.h.05.1	38542	2	0	0	0	0	0	0	0
1574	RTA00000410F.b.24.1	75104	1	0	0	0	0	0	0	0
1575	RTA00000423F.d.11.1	38950	2	0	0	0	0	0	0	0
1578	RTA00000119A.k.1.1	81282	1	0	0	0	0	0	0	0
1579	RTA00000420F.f.07.1	66312	1	0	0	0	0	0	0	0
1580	RTA00000404F.k.22.2	39084	2	0	0	0	0	0	0	0
1581	RTA00000422F.e.07.1	38964	2	0	0	0	0	0	0	0
1582	RTA00000410F.f.12.1	73883	1	0	0	0	0	0	0	0
1584	RTA00000411F.m.11.1	73196	1	0	0	0	0	0	0	0
1587	RTA00000403F.o.10.2	38964	2	0	0	0	0	0	0	0
1590	RTA00000413F.c.10.1	65600	1	0	0	0	0	0	0	0
1591	RTA00000411F.b.17.1	72893	1	0	0	0	0	0	0	0
1593	RTA00000408F.k.19.1	77593	1	0	0	0	0	0	0	0
1596	RTA00000119A.i.8.1	82593	1	0	0	0	0	0	0	0
1598	RTA00000418F.g.03.1	78737	1	0	0	0	0	0	0	0
1599	RTA00000411F.a.09.1	78629	1	0	0	0	0	0	0	0
1601	RTA00000419F.j.11.1	73183	1	0	0	0	0	0	0	0
1603	RTA00000404F.n.18.2	37169	2	0	0	0	0	0	0	0
1604	RTA00000122A.n.16.1	80553	1	0	0	0	0	0	0	0
1605	RTA00000420F.c.07.1	65555	1	0	0	0	0	0	0	0
1608	RTA00000408F.j.13.2	42275	1	1	0	0	0	0	0	0
1610	RTA00000423F.a.01.1	39103	2	0	0	0	0	0	0	0
1613	RTA00000341F.e.20.1	67422	1	0	0	0	0	0	0	0
1614	RTA00000419F.m.22.1	75600	1	0	0	0	0	0	0	0
1615	RTA00000419F.m.23.1	64263	1	0	0	0	0	0	0	0
1616	RTA00000419F.b.06.1	76728	1	0	0	0	0	0	0	0
1618	RTA00000406F.p.08.1	37573	2	0	0	0	0	0	0	2
1619	RTA00000129A.n.17.1	79811	1	0	0	0	0	0	0	0
1621	RTA00000407F.b.08.1	37513	2	0	0	0	0	0	0	0
1623	RTA00000406F.i.08.1	37946	2	0	0	0	0	0	0	0

SEQ ID NO:	Sequence Name	cluster	lib 1 clones	lib 2 clones	lib 15 clones	lib 16 clones	lib 17 clones	lib 18 clones	lib 19 clones	lib 20 clones
1624	RTA00000403F.h.07.1	26856	2	0	0	0	0	0	0	0
1625	RTA00000418F.n.24.1	73153	1	0	0	0	0	0	0	0
1627	RTA00000409F.l.20.1	74394	1	0	0	0	0	0	0	0
1628	RTA00000418F.l.06.1	73317	1	0	0	0	0	0	0	0
1629	RTA00000346F.o.22.1	7381	2	6	0	0	0	0	0	0
1630	RTA00000129A.k.22.1	79639	1	0	0	0	0	0	0	0
1632	RTA00000418F.m.22.1	74567	1	0	0	0	0	0	0	0
1633	RTA00000413F.c.12.1	65334	1	0	0	0	0	0	0	0
1635	RTA00000418F.g.20.1	74626	1	0	0	0	0	0	0	0
1636	RTA00000413F.d.15.1	64943	1	0	0	0	0	0	0	0
1639	RTA00000412F.c.10.1	76372	1	0	0	0	0	0	0	0
1640	RTA00000122A.j.17.1	62736	1	0	0	0	0	0	0	0
1645	RTA00000418F.j.19.1	78399	1	0	0	0	0	0	0	0
1646	RTA00000137A.p.12.1	80614	1	0	0	0	0	0	0	0
1648	RTA00000418F.p.10.1	75323	1	0	0	0	0	0	0	0
1649	RTA00000408F.k.12.1	77246	1	0	0	0	0	0	0	0
1650	RTA00000137A.j.11.4	79752	1	0	0	0	0	0	0	0
1652	RTA00000419F.n.24.1	65995	1	0	0	0	0	0	0	0
1653	RTA00000418F.l.03.1	79058	1	0	0	0	0	0	0	0
1655	RTA00000419F.m.13.1	79052	1	0	0	0	0	0	0	0
1656	RTA00000418F.j.14.1	32623	1	1	0	0	0	0	0	0
1657	RTA00000403F.a.10.1	73952	1	0	0	0	0	0	0	0
1658	RTA00000420F.a.21.1	66241	1	0	0	0	0	0	0	0
1659	RTA00000127A.e.6.1	5885	4	2	0	0	0	0	0	0
1660	RTA00000405F.g.21.2	38966	2	0	0	0	0	0	0	0
1661	RTA00000405F.g.21.1	38966	2	0	0	0	0	0	0	0
1662	RTA00000419F.m.06.1	75749	1	0	0	0	0	0	0	0
1663	RTA00000423F.g.03.1	38007	2	0	0	0	0	0	0	0
1665	RTA00000418F.f.03.1	78911	1	0	0	0	0	0	0	0
1668	RTA00000120A.c.20.1	43235	1	1	0	0	0	1	0	0
1669	RTA00000138A.m.15.1	41603	1	1	0	0	0	0	0	0
1670	RTA00000408F.f.14.2	73024	1	0	0	0	0	0	0	0
1671	RTA00000418F.p.20.1	78023	1	0	0	0	0	0	0	0
1672	RTA00000423F.e.21.1	66961	1	0	0	0	0	0	0	0
1673	RTA00000419F.j.22.1	73525	1	0	0	0	0	0	0	0
1674	RTA00000410F.d.18.1	75458	1	0	0	0	0	0	0	0
1675	RTA00000403F.b.24.1	78838	1	0	0	0	0	0	0	0
1677	RTA00000410F.e.09.1	76093	1	0	0	0	0	0	0	0
1680	RTA00000353R.h.10.1	39498	2	0	0	0	0	0	0	0

SEQ ID NO:	Sequence Name	cluster	lib 1 clones	lib 2 clones	lib 15 clones	lib 16 clones	lib 17 clones	lib 18 clones	lib 19 clones	lib 20 clones
1682	RTA00000411F.d.21.1	74794	1	0	0	0	0	0	0	0
1683	RTA00000340F.m.04.1	19406	2	1	0	0	0	0	0	0
1684	RTA00000411F.n.09.1	78962	1	0	0	0	0	0	0	0
1685	RTA00000127A.h.22.2	13155	2	3	0	0	0	0	0	0
1686	RTA00000420F.e.09.1	66325	1	0	0	0	0	0	0	0
1687	RTA00000405F.p.03.1	11346	3	3	0	0	0	0	0	0
1688	RTA00000419F.a.18.1	78484	1	0	0	0	0	0	0	0
1691	RTA00000121A.n.23.1	26981	2	0	0	0	0	0	0	0
1692	RTA00000121A.n.15.1	40849	1	1	0	0	0	0	0	0
1693	RTA00000403F.i.23.1	11364	4	2	0	0	0	0	0	0
1694	RTA00000405F.a.03.1	39065	2	0	0	0	0	0	0	0
1696	RTA00000419F.p.08.1	65560	1	0	0	0	0	0	0	0
1697	RTA00000126A.n.6.2	79917	1	0	0	0	0	0	0	0
1698	RTA00000413F.c.03.1	64527	1	0	0	1	0	0	0	0
1699	RTA00000422F.k.24.1	39118	2	0	0	0	0	0	0	0
1700	RTA00000412F.c.17.1	75620	1	0	0	0	0	0	0	0
1702	RTA00000347F.g.08.1	23121	3	0	0	0	0	0	0	0
1703	RTA00000419F.o.06.1	64643	1	0	0	0	0	0	0	0
1704	RTA00000340R.j.07.1	38954	2	0	0	0	0	0	0	0
1705	RTA00000423F.j.02.1	38617	2	0	0	0	0	0	0	0
1706	RTA00000419F.c.04.1	63749	1	0	0	0	0	0	0	0
1707	RTA00000411F.a.01.1	74524	1	0	0	0	0	0	0	0
1708	RTA00000406F.f.05.1	22961	2	1	0	0	0	0	1	0
1709	RTA00000410F.n.05.1	77830	1	0	0	0	0	0	0	0
1710	RTA00000404F.e.06.1	39315	2	0	0	0	0	0	0	0
1712	RTA00000411F.c.03.1	79280	1	0	0	0	0	0	0	0
1718	RTA00000405F.l.07.1	38636	2	0	0	0	0	0	0	0
1720	RTA00000411F.n.06.1	73886	1	0	0	0	0	0	0	0
1721	RTA00000422F.k.15.1	19253	2	0	0	0	0	0	0	0
1722	RTA00000406F.h.16.1	38618	2	0	0	0	0	0	0	0
1723	RTA00000419F.f.24.1	18717	1	1	0	0	0	0	0	0
1724	RTA00000411F.d.18.1	76063	1	0	0	0	0	0	0	0
1727	RTA00000408F.d.15.1	78467	1	0	0	0	0	0	0	0
1728	RTA00000339F.b.22.1	6867	7	3	0	0	0	0	0	0
1730	RTA00000411F.n.02.1	78049	1	0	0	0	0	0	0	0
1731	RTA00000419F.b.17.1	63261	1	0	0	0	0	0	0	0
1733	RTA00000130A.e.20.1	79502	1	0	0	0	0	0	0	0
1735	RTA00000411F.i.13.1	66138	1	0	0	0	0	0	0	0
1736	RTA00000420F.e.20.1	64762	1	0	0	0	0	0	0	0

SEQ ID NO:	Sequence Name	cluster	lib 1 clones	lib 2 clones	lib 15 clones	lib 16 clones	lib 17 clones	lib 18 clones	lib 19 clones	lib 20 clones
1737	RTA00000126A.p.23.2	80915	1	0	0	0	0	0	0	0
1739	RTA00000406F.g.08.1	37963	2	0	0	0	0	0	0	0
1740	RTA00000409F.a.08.1	74978	1	0	0	0	0	0	0	0
1741	RTA00000406F.d.24.1	37997	2	0	0	0	0	0	0	0
1744	RTA00000418F.i.12.1	78971	1	0	0	0	0	0	0	0
1745	RTA00000121A.h.19.1	80334	1	0	0	0	0	0	0	0
1746	RTA00000419F.b.10.1	78566	1	0	0	0	0	0	0	0
1747	RTA00000406F.m.10.1	38004	2	0	0	0	0	0	0	0
1748	RTA00000406F.o.05.1	37894	2	0	0	0	0	0	0	0
1749	RTA00000408F.b.04.2	39933	2	0	0	0	0	0	0	0
1750	RTA00000411F.k.04.1	65407	1	0	0	0	0	0	0	0
1752	RTA00000134A.l.9.1	81814	1	0	0	0	0	0	0	0
1754	RTA00000418F.k.04.1	75864	1	0	0	0	0	0	0	0
1757	RTA00000419F.p.18.1	63002	1	0	0	0	0	0	0	0
1759	RTA00000419F.a.24.1	79290	1	0	0	0	0	0	0	0
1761	RTA00000129A.e.14.1	80053	1	0	0	0	0	0	0	0
1762	RTA00000404F.a.01.1	19251	2	0	0	0	0	0	0	0
1765	RTA00000408F.n.16.2	73720	1	0	0	0	0	0	0	0
1769	RTA00000412F.l.14.1	62792	1	0	0	0	0	0	0	0
1770	RTA00000129A.b.6.2	39111	2	0	0	0	0	0	0	0
1771	RTA00000406F.n.12.1	37517	2	0	0	0	0	0	0	0
1772	RTA00000418F.e.03.1	73442	1	0	0	0	0	0	0	0
1774	RTA00000403F.g.03.1	23537	2	1	0	0	0	0	0	0
1775	RTA00000412F.p.06.1	65485	1	0	0	0	0	0	0	0
1776	RTA00000419F.b.21.1	65366	1	0	0	0	0	0	0	0
1779	RTA00000351R.j.16.1	64773	1	0	0	0	0	0	0	0
1781	RTA00000419F.f.18.1	64047	1	0	0	0	0	0	0	0
1782	RTA00000423F.i.16.1	38604	2	0	0	0	0	0	0	0
1784	RTA00000411F.f.04.1	64526	1	0	0	0	0	0	0	0
1785	RTA00000125A.c.17.1	80619	1	0	0	0	0	0	0	0
1786	RTA00000404F.g.08.1	38980	2	0	0	0	0	0	0	0
1787	RTA00000423F.c.13.1	39059	2	0	0	0	0	0	0	0
1790	RTA00000404F.k.15.1	18225	2	0	0	0	0	0	0	0
1792	RTA00000339F.l.12.1	7711	4	1	0	0	0	0	0	0
1793	RTA00000406F.b.01.1	39006	2	0	0	0	0	0	0	0
1794	RTA00000407F.c.08.1	37549	2	0	0	0	0	0	0	0
1796	RTA00000403F.b.05.1	74300	1	0	0	0	0	0	0	0
1800	RTA00000408F.j.05.2	73878	1	0	0	0	0	0	0	0
1802	RTA00000419F.c.14.1	65727	1	0	0	0	0	0	0	0

SEQ ID NO:	Sequence Name	cluster	lib 1 clones	lib 2 clones	lib 15 clones	lib 16 clones	lib 17 clones	lib 18 clones	lib 19 clones	lib 20 clones
1806	RTA00000346F.h.24.1	4379	9	2	0	0	0	0	0	0
1807	RTA00000420F.b.02.1	64013	1	0	0	0	0	0	0	0
1808	RTA00000413F.b.24.1	65117	1	0	0	0	0	0	0	0
1809	RTA00000412F.d.08.1	75328	1	0	0	0	0	0	0	0
1811	RTA00000419F.m.18.1	76014	1	0	0	0	0	0	0	0
1812	RTA00000419F.l.24.1	74628	1	0	0	0	0	0	0	0
1813	RTA00000408F.c.06.1	78619	1	0	0	0	0	0	0	0
1814	RTA00000405F.h.21.2	39072	2	0	0	0	0	0	0	0
1816	RTA00000405F.g.05.2	38987	2	0	0	0	0	0	0	0
1817	RTA00000411F.f.20.1	63501	1	0	0	0	0	0	0	0
1819	RTA00000420F.d.19.1	43146	1	1	0	0	0	0	0	0
1820	RTA00000195R.a.06.1	35265	2	0	1	0	0	0	0	0
1821	RTA00000123A.f.2.1	80379	1	0	0	0	0	0	0	0
1822	RTA00000411F.j.11.1	66154	1	0	0	0	0	0	0	0
1827	RTA00000419F.j.03.1	77578	1	0	0	0	0	0	0	0
1829	RTA00000423F.h.11.1	38977	2	0	0	0	0	0	0	0
1830	RTA00000413F.b.17.1	21704	1	2	0	0	0	0	0	0
1833	RTA00000423F.f.03.1	63852	1	0	0	0	0	0	0	0
1834	RTA00000419F.e.10.1	63225	1	0	0	0	0	0	0	0
1836	RTA00000403F.d.02.1	39224	2	0	0	0	0	0	0	0
1838	RTA00000418F.j.20.1	77101	1	0	0	0	0	0	0	0
1846	RTA00000356R.h.05.1	35052	2	0	1	0	0	0	0	0
1848	RTA00000340F.i.15.1	26815	1	0	0	0	0	0	0	0
1850	RTA00000345F.c.12.1	23824	2	1	0	0	0	0	0	0
1852	RTA00000412F.o.03.1	65039	1	0	0	0	0	0	0	0
1853	RTA00000409F.d.16.1	76090	1	0	0	0	0	0	0	0
1856	RTA00000408F.j.17.2	78935	1	0	0	0	0	0	0	0
1857	RTA00000126A.j.15.2	40425	2	0	0	0	0	0	0	0
1861	RTA00000410F.b.17.1	77458	1	0	0	0	0	0	0	0
1862	RTA00000419F.l.22.1	78444	1	0	0	0	0	0	0	0
1864	RTA00000422F.f.22.1	38703	2	0	0	0	0	0	0	0
1867	RTA00000418F.c.05.1	76475	1	0	0	0	0	0	0	0
1868	RTA00000418F.p.21.1	78068	1	0	0	0	0	0	0	0
1870	RTA00000340F.i.08.1	12005	2	1	0	0	0	0	0	0
1871	RTA00000410F.o.04.1	79018	1	0	0	0	0	0	0	0
1872	RTA00000411F.l.16.1	16122	1	3	0	0	0	0	0	0
1873	RTA00000411F.j.03.1	66263	1	0	0	0	0	0	0	0
1874	RTA00000126A.k.24.1	39428	2	0	0	0	0	0	0	0
1876	RTA00000120A.m.10.3	81376	1	0	0	0	0	0	0	0

SEQ ID NO:	Sequence Name	cluster	lib 1 clones	lib 2 clones	lib 15 clones	lib 16 clones	lib 17 clones	lib 18 clones	lib 19 clones	lib 20 clones
1877	RTA00000419F.f.16.1	64679	1	0	0	0	0	0	0	0
1878	RTA00000408F.c.23.1	42261	1	1	0	0	0	0	0	0
1881	RTA00000136A.h.6.1	81620	1	0	0	0	0	0	0	0
1886	RTA00000418F.e.20.1	73741	1	0	0	0	0	0	0	0
1888	RTA00000405F.l.03.1	38580	2	0	0	0	0	0	0	0
1889	RTA00000418F.m.02.1	74550	1	0	0	0	0	0	0	0
1891	RTA00000406F.c.05.1	22077	3	0	1	0	0	0	0	0
1893	RTA00000411F.k.21.1	65349	1	0	0	0	0	0	0	0
1897	RTA00000418F.i.06.1	75151	1	0	0	0	0	0	0	0
1898	RTA00000423F.a.03.1	26796	2	0	0	0	0	0	0	0
1900	RTA00000423F.k.21.2	37499	2	0	0	0	0	0	0	0
1902	RTA00000404F.c.18.1	38982	2	0	0	0	0	0	0	0
1905	RTA00000411F.g.24.1	65233	1	0	0	0	0	0	0	0
1907	RTA00000405F.m.07.1	37733	2	0	0	0	0	0	0	0
1908	RTA00000411F.j.07.1	66963	1	0	0	0	0	0	0	0
1910	RTA00000353R.h.04.1	17123	4	0	0	0	0	0	0	0
1911	RTA00000408F.f.10.2	75309	1	0	0	0	0	0	0	0
1913	RTA00000405F.o.03.1	37575	2	0	0	0	0	0	0	0
1914	RTA00000413F.b.18.1	39873	2	0	0	0	0	0	0	0
1920	RTA00000408F.c.08.1	73473	1	0	0	0	0	0	0	0
1922	RTA00000410F.c.06.1	77784	1	0	0	0	1	0	0	0
1924	RTA00000405F.b.08.1	39182	2	0	0	0	0	0	0	0
1925	RTA00000409F.l.24.1	73174	1	0	0	0	0	0	0	0
1926	RTA00000406F.j.06.1	38952	2	0	0	0	0	0	0	0
1927	RTA00000423F.h.03.1	37903	2	0	0	0	0	0	0	0
1929	RTA00000121A.k.22.1	79523	1	0	0	0	0	0	0	0
1931	RTA00000411F.m.06.1	24195	2	1	0	0	0	0	0	0
1932	RTA00000126A.b.9.1	81279	1	0	0	0	0	0	0	0
1935	RTA00000404F.l.05.1	38671	2	0	0	0	0	0	0	0
1941	RTA00000419F.p.10.1	41448	1	1	0	0	0	0	0	0
1942	RTA00000120A.c.19.1	81016	1	0	0	0	0	0	0	0
1948	RTA00000411F.k.14.1	63987	1	0	0	0	0	0	0	0
1949	RTA00000420F.e.05.1	63908	1	0	0	0	0	0	0	0
1952	RTA00000128A.j.10.1	80085	1	0	0	0	0	0	0	0
1953	RTA00000412F.f.10.2	65405	1	0	0	0	0	0	0	0
1955	RTA00000422F.k.17.1	38955	2	0	0	0	0	0	0	0
1957	RTA00000347F.h.10.1	22779	3	0	0	0	0	0	0	0
1959	RTA00000419F.l.02.1	75736	1	0	0	0	0	0	0	0
1961	RTA00000418F.b.20.1	73560	1	0	0	0	0	0	0	0

SEQ ID NO:	Sequence Name	cluster	lib 1 clones	lib 2 clones	lib 15 clones	lib 16 clones	lib 17 clones	lib 18 clones	lib 19 clones	lib 20 clones
1964	RTA00000408F.n.05.2	77883	1	0	0	0	0	0	0	0
1965	RTA00000419F.o.09.1	66396	1	0	0	0	0	0	0	0
1970	RTA00000422F.o.08.2	26832	2	0	0	0	0	0	0	0
1973	RTA00000418F.m.18.1	76479	1	0	0	0	0	0	0	0
1974	RTA00000347F.e.20.1	39911	2	0	0	0	0	0	0	0
1975	RTA00000419F.e.23.1	65772	1	0	0	0	0	0	0	0
1982	RTA00000411F.g.05.1	64664	1	0	0	0	0	0	0	0
1983	RTA00000404F.h.10.1	37148	2	0	0	0	0	0	0	0
1984	RTA00000422F.n.14.1	26787	2	0	0	0	0	0	0	0
1986	RTA00000120A.m.13.3	80608	1	0	0	0	0	0	0	0
1987	RTA00000412F.i.03.1	65617	1	0	0	0	0	0	0	0
1988	RTA00000418F.l.02.1	39316	2	0	0	0	0	0	0	0
1990	RTA00000411F.j.04.1	66219	1	0	0	0	0	0	0	0
1995	RTA00000404F.a.18.1	36267	2	0	0	0	0	0	0	0
1996	RTA00000408F.l.14.1	12001	2	3	0	0	0	0	0	0
1997	RTA00000405F.d.10.1	39000	2	0	0	0	0	0	0	0
1999	RTA00000418F.h.23.1	75153	1	0	0	0	0	0	0	0
2001	RTA00000418F.j.11.1	73853	1	0	0	0	0	0	0	0
2002	RTA00000408F.o.13.1	74895	1	0	0	0	0	0	0	0
2003	RTA00000419F.o.07.1	14059	1	0	0	0	0	0	0	0
2004	RTA00000419F.n.17.1	63186	1	0	0	0	0	0	0	0
2005	RTA00000403F.f.15.1	22768	3	0	0	0	0	0	0	0
2006	RTA00000408F.d.03.1	22768	3	0	0	0	0	0	0	0
2008	RTA00000346F.f.02.1	62757	1	0	0	0	0	0	0	0
2010	RTA00000413F.i.21.1	64066	1	0	0	0	0	0	0	0
2012	RTA00000419F.h.21.1	64828	1	0	0	0	0	0	0	0
2021	RTA00000121A.a.2.1	81843	1	0	0	0	0	0	0	0
2022	RTA00000527F.g.13.1	36035	2	0	0	0	0	0	0	0
2025	RTA00000426F.h.11.1	75479	1	0	0	0	0	0	0	0
2030	RTA00000522F.b.22.1	75181	1	0	0	0	0	0	0	0
2033	RTA00000522F.a.23.1	38613	2	0	0	0	0	0	0	0
2035	RTA00000523F.b.02.1	65163	1	0	0	0	0	0	0	0
2036	RTA00000425F.j.14.1	73397	1	0	0	0	0	0	0	0
2039	RTA00000522F.e.16.1	75283	1	0	0	0	0	0	0	0
2042	RTA00000523F.h.17.1	65586	1	0	0	0	0	0	0	0
2044	RTA00000522F.p.07.1	76888	1	0	0	0	0	0	0	0
2045	RTA00000522F.n.08.1	76343	1	0	0	0	0	0	0	0
2046	RTA00000425F.c.06.1	78041	1	0	0	0	0	0	0	0
2047	RTA00000427F.b.23.1	64297	1	0	0	0	0	0	0	0

SEQ ID NO:	Sequence Name	cluster	lib 1 clones	lib 2 clones	lib 15 clones	lib 16 clones	lib 17 clones	lib 18 clones	lib 19 clones	lib 20 clones
2048	RTA00000527F.p.02.1	36844	2	0	0	0	0	0	0	0
2049	RTA00000427F.d.08.1	63967	1	0	0	0	0	0	0	0
2051	RTA00000426F.m.07.1	63504	1	0	0	0	0	0	0	0
2052	RTA00000427F.c.10.1	65478	1	0	0	0	0	0	0	0
2055	RTA00000424F.m.15.1	73759	1	0	0	0	0	0	0	0
2056	RTA00000426F.f.11.1	63102	1	0	0	0	0	0	0	0
2058	RTA00000426F.f.20.1	65134	1	0	0	0	0	0	0	0
2063	RTA00000527F.i.19.2	38089	2	0	0	0	0	0	0	0
2068	RTA00000523F.e.18.1	62898	1	0	0	0	0	0	0	0
2069	RTA00000527F.k.21.1	36051	2	0	0	0	0	0	0	0
2072	RTA00000522F.n.02.1	74959	1	0	0	0	0	0	0	0
2075	RTA00000425F.f.19.1	32635	1	1	0	0	0	0	0	0
2076	RTA00000528F.e.23.1	19242	3	0	0	0	0	0	0	0
2077	RTA00000522F.n.16.1	26769	1	0	0	0	0	0	0	0
2078	RTA00000427F.c.20.1	26527	1	0	0	0	0	0	0	0
2079	RTA00000527F.k.06.1	12469	3	1	0	0	0	0	0	0
2081	RTA00000523F.i.06.1	66341	1	0	0	0	0	0	0	0
2082	RTA00000427F.f.21.1	36853	2	0	0	0	0	0	0	0
2083	RTA00000427F.j.19.1	41395	1	1	0	0	0	0	0	0
2084	RTA00000522F.b.01.1	75691	1	0	0	0	0	0	0	0
2085	RTA00000424F.i.24.1	79101	1	0	0	0	0	0	0	0
2086	RTA00000523F.c.01.1	65710	1	0	0	0	0	0	0	0
2087	RTA00000427F.b.15.1	66891	1	0	0	0	0	0	0	0
2090	RTA00000522F.j.15.2	76535	1	0	0	0	0	0	0	0
2093	RTA00000426F.f.19.1	66701	1	0	1	0	0	0	0	0
2096	RTA00000523F.i.22.1	64688	1	0	0	0	0	0	0	0
2098	RTA00000425F.i.17.1	43213	1	1	0	0	0	0	0	0
2101	RTA00000425F.p.12.1	73219	1	0	0	0	0	0	0	0
2102	RTA00000427F.j.07.1	64819	1	0	0	0	0	0	0	0
2104	RTA00000527F.i.05.2	37481	2	0	0	0	0	0	0	0
2107	RTA00000523F.k.01.1	41437	1	1	0	0	0	0	0	0
2108	RTA00000425F.j.11.1	76667	1	0	0	0	0	0	0	0
2109	RTA00000424F.b.22.4	72971	1	0	0	0	0	0	0	0
2111	RTA00000525F.a.03.1	36786	2	0	0	0	0	0	0	0
2112	RTA00000527F.i.21.2	37490	2	0	0	0	0	0	0	0
2113	RTA00000424F.a.24.4	73951	1	0	0	0	0	0	0	0
2114	RTA00000522F.k.14.1	74280	1	0	0	0	0	0	0	0
2115	RTA00000522F.n.05.1	73260	1	0	0	0	0	0	0	0
2116	RTA00000523F.c.18.1	66179	1	0	0	0	0	0	0	0

SEQ ID NO:	Sequence Name	cluster	lib 1 clones	lib 2 clones	lib 15 clones	lib 16 clones	lib 17 clones	lib 18 clones	lib 19 clones	lib 20 clones
2117	RTA00000523F.b.13.1	66330	1	0	0	0	0	0	0	0
2119	RTA00000527F.p.16.1	23798	2	1	0	0	0	0	0	0
2120	RTA00000425F.c.20.1	73581	1	0	0	0	0	0	0	0
2121	RTA00000424F.i.21.1	73482	1	0	0	0	0	0	0	0
2122	RTA00000523F.j.19.1	65910	1	0	0	0	0	0	0	0
2124	RTA00000424F.b.22.1	72971	1	0	0	0	0	0	0	0
2125	RTA00000527F.b.18.1	37469	2	0	0	0	0	0	0	0
2129	RTA00000525F.e.16.1	36837	2	0	0	0	0	0	0	0
2131	RTA00000522F.d.08.1	74284	1	0	0	0	0	0	0	0
2134	RTA00000527F.g.07.1	37488	2	0	0	0	0	0	0	0
2136	RTA00000525F.b.05.1	21116	2	1	0	0	0	0	0	0
2137	RTA00000425F.n.05.1	73965	1	0	0	0	0	0	0	0
2138	RTA00000523F.d.18.1	64072	1	0	0	0	0	0	0	0
2139	RTA00000525F.a.02.1	37454	2	0	0	0	0	0	0	0
2141	RTA00000426F.h.09.1	78797	1	0	0	0	0	0	0	0
2144	RTA00000427F.g.05.1	63138	1	0	0	0	0	0	0	0
2145	RTA00000424F.m.12.1	77675	1	0	0	0	0	0	0	0
2151	RTA00000427F.h.12.1	36894	2	0	0	0	0	0	0	0
2152	RTA00000523F.c.15.1	36935	2	0	0	0	0	0	0	0
2153	RTA00000427F.k.17.1	64965	1	0	0	0	0	0	0	0
2155	RTA00000424F.c.14.3	76614	1	0	0	0	0	0	0	0
2156	RTA00000522F.k.10.2	77619	1	0	0	0	0	0	0	0
2157	RTA00000424F.m.22.1	72943	1	0	0	0	0	0	0	0
2158	RTA00000527F.h.17.1	37799	2	0	0	0	0	0	0	0
2159	RTA00000527F.c.22.1	37496	2	0	0	0	0	0	0	0
2160	RTA00000425F.k.22.1	78123	1	0	0	0	0	0	0	0
2161	RTA00000424F.m.14.1	77491	1	0	0	0	0	0	0	0
2162	RTA00000522F.k.19.1	32625	1	1	0	0	0	0	0	0
2163	RTA00000523F.i.18.1	64463	1	0	0	0	0	0	0	0
2164	RTA00000425F.j.22.1	73882	1	0	0	0	0	0	0	0
2165	RTA00000527F.g.23.1	37538	2	0	0	0	0	0	0	0
2166	RTA00000426F.m.24.1	63943	1	0	0	0	0	0	0	0
2168	RTA00000425F.d.21.1	78920	1	0	0	0	0	0	0	0
2170	RTA00000424F.d.04.3	76505	1	0	0	0	0	0	0	0
2171	RTA00000424F.d.04.1	76505	1	0	0	0	0	0	0	0
2172	RTA00000427F.c.12.1	66995	1	0	0	0	0	0	0	0
2174	RTA00000527F.l.13.1	36904	2	0	0	0	0	0	0	0
2175	RTA00000522F.h.13.1	40823	1	1	0	0	0	0	0	0
2176	RTA00000424F.l.19.1	75454	1	0	0	0	0	0	0	0

SEQ ID NO:	Sequence Name	cluster	lib 1 clones	lib 2 clones	lib 15 clones	lib 16 clones	lib 17 clones	lib 18 clones	lib 19 clones	lib 20 clones
2179	RTA00000427F.a.06.1	66550	1	0	0	0	0	0	0	0
2180	RTA00000525F.c.19.1	38159	2	0	0	0	0	0	0	0
2181	RTA00000523F.f.06.1	62871	1	0	0	0	0	0	0	0
2182	RTA00000424F.h.10.1	72925	1	0	0	0	0	0	0	0
2183	RTA00000522F.a.12.1	33515	1	1	0	0	0	0	0	0
2184	RTA00000522F.h.01.1	75010	1	0	0	0	0	0	0	0
2186	RTA00000425F.e.21.1	77203	1	0	0	0	0	0	0	0
2187	RTA00000523F.f.07.1	62799	1	0	0	0	0	0	0	0
2189	RTA00000424F.j.12.1	73827	1	0	0	0	0	0	0	0
2191	RTA00000523F.d.12.1	64888	1	0	0	0	0	0	0	0
2192	RTA00000523F.e.10.1	62878	1	0	0	0	0	0	0	0
2193	RTA00000425F.f.11.1	79275	1	0	0	0	0	0	0	0
2194	RTA00000426F.m.18.1	62974	1	0	0	0	0	0	0	0
2197	RTA00000522F.g.15.1	76536	1	0	0	0	0	0	0	0
2198	RTA00000522F.n.12.1	74117	1	0	0	0	0	0	0	0
2200	RTA00000424F.d.10.3	73110	1	0	0	0	0	0	0	0
2204	RTA00000527F.c.04.1	23090	3	0	0	0	0	0	0	0
2206	RTA00000527F.h.21.1	37630	2	0	0	0	0	0	0	0
2207	RTA00000425F.c.07.1	76042	1	0	0	0	0	0	0	0
2209	RTA00000525F.c.15.1	7692	2	0	0	0	0	0	0	0
2210	RTA00000424F.d.22.3	76189	1	0	0	0	0	0	0	0
2211	RTA00000523F.h.12.1	65745	1	0	0	0	0	0	0	0
2212	RTA00000522F.g.22.1	77504	1	0	0	0	0	0	0	0
2215	RTA00000522F.j.12.2	74341	1	0	0	0	0	0	0	0
2216	RTA00000523F.i.08.1	65099	1	0	0	0	0	0	0	0
2218	RTA00000425F.j.20.1	26760	1	0	0	0	0	0	0	0
2220	RTA00000427F.f.24.1	64572	1	0	0	0	0	0	0	0
2221	RTA00000527F.a.13.1	37740	2	0	0	0	0	0	0	0
2225	RTA00000424F.a.09.4	77833	1	0	0	0	0	0	0	0
2227	RTA00000525F.f.07.1	37500	2	0	0	0	0	0	0	0
2228	RTA00000424F.j.07.1	79211	1	0	0	0	0	0	0	0
2229	RTA00000424F.m.10.1	34251	1	1	0	0	0	0	0	0
2231	RTA00000522F.g.06.1	78221	1	0	0	0	0	0	0	0
2232	RTA00000424F.h.03.1	74447	1	0	0	0	0	0	0	0
2233	RTA00000424F.n.06.1	74737	1	0	0	0	0	0	0	0
2234	RTA00000427F.c.22.1	63990	1	0	0	0	0	0	0	0
2235	RTA00000424F.k.12.1	77666	1	0	0	0	0	0	0	0
2236	RTA00000425F.f.02.1	76982	1	0	0	0	0	0	0	0
2237	RTA00000427F.h.11.1	26494	1	0	0	0	0	0	0	0

SEQ ID NO:	Sequence Name	cluster	lib 1 clones	lib 2 clones	lib 15 clones	lib 16 clones	lib 17 clones	lib 18 clones	lib 19 clones	lib 20 clones
2238	RTA00000425F.j.16.1	75631	1	0	0	0	0	0	0	0
2240	RTA00000427F.f.17.1	63803	1	0	0	0	0	0	0	0
2241	RTA00000522F.o.18.1	76366	1	0	0	0	0	0	0	0
2242	RTA00000427F.j.22.1	66367	1	0	0	0	0	0	0	0
2243	RTA00000426F.p.10.1	65845	1	0	0	0	0	0	0	0
2244	RTA00000522F.m.02.1	76834	1	0	0	0	0	0	0	0
2247	RTA00000425F.e.15.1	75921	1	0	0	0	0	0	0	0
2250	RTA00000424F.n.13.1	74942	1	0	0	0	0	0	0	0
2251	RTA00000424F.g.14.1	74879	1	0	0	0	0	0	0	0
2252	RTA00000426F.e.17.1	64089	1	0	0	0	0	0	0	0
2256	RTA00000427F.g.19.1	64611	1	0	0	0	0	0	0	0
2258	RTA00000522F.c.01.1	74938	1	0	0	0	0	0	0	0
2259	RTA00000522F.g.17.1	76486	1	0	0	0	0	0	0	0
2260	RTA00000523F.j.17.1	63610	1	0	0	0	0	0	0	0
2261	RTA00000522F.n.14.1	73410	1	0	0	0	0	0	1	0
2263	RTA00000523F.e.20.1	65164	1	0	0	0	0	0	0	0
2264	RTA00000424F.c.15.3	73533	1	0	0	0	0	0	0	0
2265	RTA00000426F.p.09.1	66665	1	0	0	0	0	0	0	0
2266	RTA00000522F.p.09.1	75204	1	0	0	0	0	0	0	0
2267	RTA00000426F.m.21.1	64915	1	0	0	0	0	0	0	0
2268	RTA00000425F.j.21.1	77373	1	0	0	0	0	0	0	0
2270	RTA00000523F.h.21.1	41440	1	1	0	0	0	0	0	0
2271	RTA00000427F.h.24.1	65193	1	0	0	0	0	0	0	0
2272	RTA00000425F.f.24.1	40841	1	1	0	0	0	0	0	0
2273	RTA00000425F.m.03.1	76045	1	0	0	0	0	0	0	0
2274	RTA00000426F.m.08.1	63781	1	0	0	0	0	0	0	0
2275	RTA00000523F.d.24.1	64799	1	0	0	0	0	0	0	0
2276	RTA00000523F.c.14.1	66015	1	0	0	0	0	0	0	0
2277	RTA00000523F.b.20.1	66492	1	0	0	0	0	0	0	0
2278	RTA00000522F.h.07.1	75149	1	0	0	0	0	0	0	0
2279	RTA00000527F.g.10.1	37820	2	0	0	0	0	0	0	0
2282	RTA00000427F.i.22.1	63199	1	0	0	0	0	0	0	0
2284	RTA00000527F.n.07.1	15939	2	2	0	0	0	0	0	0
2285	RTA00000425F.e.09.1	75550	1	0	0	0	0	0	0	0
2286	RTA00000427F.h.02.1	63652	1	0	0	0	0	0	0	0
2287	RTA00000426F.f.16.1	65613	1	0	0	0	0	0	0	0
2288	RTA00000425F.i.21.1	75305	1	0	0	0	0	0	0	0
2289	RTA00000427F.k.19.1	62851	1	0	0	0	0	0	0	0
2291	RTA00000426F.g.16.1	41446	1	1	0	0	0	0	0	0

SEQ ID NO:	Sequence Name	cluster	lib 1 clones	lib 2 clones	lib 15 clones	lib 16 clones	lib 17 clones	lib 18 clones	lib 19 clones	lib 20 clones
2292	RTA00000527F.l.05.1	13016	4	0	0	1	1	0	0	0
2293	RTA00000426F.m.02.1	66237	1	0	0	0	0	0	0	0
2296	RTA00000522F.l.22.1	75801	1	0	0	0	0	0	0	0
2297	RTA00000427F.h.19.1	63047	1	0	0	0	0	0	0	0
2299	RTA00000522F.g.21.1	77310	1	0	0	0	0	0	0	0
2301	RTA00000522F.g.20.1	77688	1	0	0	0	0	0	0	0
2304	RTA00000425F.k.20.1	74048	1	0	0	0	0	0	0	0
2306	RTA00000522F.b.07.1	78634	1	0	0	0	0	0	0	0
2307	RTA00000426F.g.19.1	63672	1	0	0	0	0	0	0	0
2308	RTA00000525F.d.19.1	36860	2	0	0	0	0	0	0	0
2310	RTA00000427F.d.10.1	40685	1	1	0	0	0	0	0	0
2313	RTA00000424F.a.05.4	77976	1	0	0	0	0	0	0	0
2315	RTA00000424F.a.05.1	77976	1	0	0	0	0	0	0	0
2316	RTA00000522F.l.15.1	74691	1	0	0	0	0	0	0	0
2317	RTA00000425F.e.02.1	76143	1	0	0	0	0	0	0	0
2318	RTA00000525F.c.11.1	37895	2	0	0	0	0	0	0	0
2320	RTA00000522F.c.14.1	75449	1	0	0	0	0	0	0	0
2321	RTA00000424F.m.08.1	19402	1	2	0	0	0	0	0	0
2322	RTA00000527F.f.18.1	37577	2	0	0	0	0	0	0	0
2324	RTA00000522F.a.06.1	73662	1	0	0	0	0	0	0	0
2327	RTA00000522F.d.23.1	73868	1	0	0	0	0	0	0	0
2330	RTA00000523F.j.10.1	63384	1	0	0	0	0	0	0	0
2331	RTA00000527F.p.08.1	36013	2	0	0	0	0	0	0	0
2333	RTA00000426F.f.17.1	66334	1	0	0	0	0	0	0	0
2334	RTA00000523F.j.21.1	36925	2	0	0	0	0	0	0	0
2339	RTA00000523F.a.01.1	74923	1	0	0	0	0	0	0	0
2341	RTA00000427F.j.06.1	63676	1	0	0	0	0	0	0	0
2342	RTA00000424F.m.04.1	79017	1	0	0	0	0	0	0	0
2343	RTA00000523F.i.17.1	65779	1	0	0	0	0	0	0	0
2346	RTA00000525F.c.18.1	24208	2	1	0	0	0	0	0	0
2347	RTA00000527F.e.09.1	37521	2	0	0	0	0	0	0	0
2348	RTA00000424F.j.08.1	73972	1	0	0	0	0	0	0	0
2350	RTA00000527F.c.09.1	64859	1	0	0	0	0	0	0	0
2353	RTA00000523F.c.03.1	36913	2	0	0	0	0	0	0	0
2354	RTA00000427F.k.21.1	62880	1	0	0	0	0	0	0	0
2356	RTA00000427F.d.09.1	66486	1	0	0	0	0	0	0	0
2357	RTA00000426F.n.17.1	66572	1	0	0	0	0	0	0	0
2360	RTA00000426F.m.03.1	66480	1	0	0	0	0	0	0	0
2361	RTA00000424F.h.06.1	77552	1	0	0	0	0	0	0	0

SEQ ID NO:	Sequence Name	cluster	lib 1 clones	lib 2 clones	lib 15 clones	lib 16 clones	lib 17 clones	lib 18 clones	lib 19 clones	lib 20 clones
2362	RTA00000425F.d.06.1	77660	1	0	0	0	0	0	0	0
2363	RTA00000427F.e.12.1	62813	1	0	0	0	0	0	0	0
2366	RTA00000426F.n.23.1	18176	1	0	0	0	0	0	0	0
2367	RTA00000522F.m.19.1	41544	1	1	0	0	0	0	0	0
2368	RTA00000522F.a.05.1	32611	1	1	0	0	0	0	0	0
2369	RTA00000427F.i.09.1	65916	1	0	0	0	0	0	0	0
2370	RTA00000424F.j.09.1	74387	1	0	0	0	0	0	0	0
2371	RTA00000424F.n.11.1	73874	1	0	0	0	0	0	0	0
2373	RTA00000527F.e.13.1	37588	2	0	0	0	0	0	0	0
2375	RTA00000425F.j.19.1	77925	1	0	0	0	0	0	0	0
2376	RTA00000522F.g.12.1	78783	1	0	0	0	0	0	0	0
2377	RTA00000523F.a.07.1	75804	1	0	0	0	0	0	0	0
2378	RTA00000425F.e.19.1	73409	1	0	0	0	0	0	0	0
2379	RTA00000425F.n.19.1	78324	1	0	0	0	0	0	0	0
2384	RTA00000427F.k.07.1	63742	1	0	0	0	0	0	0	0
2387	RTA00000522F.a.17.1	79032	1	0	0	0	0	0	0	0
2388	RTA00000527F.l.19.1	36856	2	0	0	0	0	0	0	0
2389	RTA00000424F.i.11.1	41569	1	1	0	0	0	0	0	0
2391	RTA00000424F.d.19.3	73180	1	0	0	0	0	0	0	0
2392	RTA00000522F.j.09.2	78522	1	0	0	0	0	0	0	0
2393	RTA00000424F.m.24.1	77045	1	0	0	0	0	0	0	0
2394	RTA00000522F.j.19.2	76224	1	0	0	0	0	0	0	0
2398	RTA00000527F.j.12.2	37503	2	0	0	0	0	0	0	0
2399	RTA00000522F.g.11.1	75432	1	0	0	0	0	0	0	0
2400	RTA00000522F.k.02.2	77622	1	0	0	0	0	0	0	0
2401	RTA00000427F.e.13.1	66080	1	0	0	0	0	0	0	0
2402	RTA00000426F.f.18.1	63271	1	0	0	0	0	0	0	0
2403	RTA00000427F.a.12.1	63377	1	0	0	0	0	0	0	0
2404	RTA00000424F.b.23.4	77322	1	0	0	0	0	0	0	0
2408	RTA00000427F.f.02.1	36822	2	0	0	0	0	0	0	0
2410	RTA00000424F.i.15.1	78043	1	0	0	0	0	0	0	0
2412	RTA00000522F.m.03.1	79194	1	0	0	0	0	0	0	0
2413	RTA00000522F.a.20.1	74070	1	0	0	0	0	0	0	0
2414	RTA00000424F.b.15.4	74958	1	0	0	0	0	0	0	0
2415	RTA00000527F.g.14.1	37532	2	0	0	0	0	0	0	0
2416	RTA00000522F.d.06.1	74809	1	0	0	0	0	0	0	0
2418	RTA00000427F.e.10.1	64599	1	0	0	0	0	0	0	0
2419	RTA00000527F.c.16.1	22908	3	0	0	0	0	0	0	0
2421	RTA00000523F.f.17.1	63984	1	0	0	0	0	0	0	0

SEQ ID NO:	Sequence Name	cluster	lib 1 clones	lib 2 clones	lib 15 clones	lib 16 clones	lib 17 clones	lib 18 clones	lib 19 clones	lib 20 clones
2423	RTA00000527F.p.24.1	36832	2	0	0	0	0	0	0	0
2424	RTA00000425F.n.17.1	78304	1	0	0	0	0	0	0	0
2426	RTA00000425F.e.07.1	75992	1	0	0	0	0	0	0	0
2428	RTA00000523F.h.08.1	62893	1	0	0	0	0	0	0	0
2429	RTA00000522F.o.10.1	78798	1	0	0	0	0	0	0	0
2430	RTA00000425F.l.10.1	26893	1	0	0	0	0	0	0	0
2431	RTA00000427F.f.16.1	64122	1	0	0	0	0	0	0	0
2434	RTA00000425F.i.10.1	78736	1	0	0	0	0	0	0	0
2435	RTA00000426F.m.12.1	63740	1	0	0	0	0	0	0	0
2436	RTA00000527F.g.12.1	37746	2	0	0	0	0	0	0	0
2439	RTA00000425F.i.18.1	42255	1	1	0	0	0	0	0	0
2441	RTA00000424F.j.13.1	74485	1	0	0	0	0	0	0	0
2445	RTA00000424F.k.10.1	73232	1	0	0	0	0	0	0	0
2446	RTA00000522F.i.07.2	78377	1	0	0	0	0	0	0	0
2448	RTA00000522F.b.08.1	26915	1	0	0	0	0	0	0	0
2449	RTA00000522F.l.08.1	78781	1	0	0	0	0	0	0	0
2450	RTA00000525F.a.14.1	37566	2	0	0	0	0	0	0	0
2451	RTA00000424F.g.08.1	74928	1	0	0	0	0	0	0	0
2452	RTA00000425F.l.09.1	75251	1	0	0	0	0	0	0	0
2453	RTA00000522F.o.20.1	74853	1	0	0	0	0	0	0	0
2454	RTA00000527F.j.04.2	11809	3	1	0	0	0	0	0	0
2456	RTA00000523F.c.13.1	40668	1	1	0	0	0	0	0	0
2457	RTA00000427F.i.21.1	65540	1	0	0	0	0	0	0	0
2459	RTA00000522F.h.02.1	74947	1	0	0	0	0	0	0	0
2460	RTA00000522F.g.10.1	74294	1	0	0	0	0	0	0	0
2464	RTA00000425F.k.16.1	75282	1	0	0	0	0	0	0	0
2465	RTA00000525F.b.09.1	23472	2	1	0	0	0	0	0	0
2466	RTA00000522F.j.08.2	76613	1	0	0	0	0	0	0	0
2468	RTA00000523F.f.19.1	34169	1	1	0	0	0	0	0	0
2469	RTA00000425F.j.18.1	75561	1	0	0	0	0	1	0	0
2470	RTA00000426F.m.04.1	36865	2	0	0	0	0	0	0	0
2471	RTA00000527F.g.21.1	36028	2	0	0	0	0	0	0	0
2473	RTA00000525F.a.22.1	36848	2	0	0	0	0	0	0	0
2474	RTA00000522F.p.22.1	73322	1	0	0	0	0	0	0	0
2475	RTA00000424F.d.12.2	74342	1	0	0	0	0	0	0	0
2476	RTA00000424F.g.24.1	79156	1	0	0	0	0	0	0	0
2477	RTA00000427F.a.10.1	65370	1	0	0	0	0	0	0	0
2478	RTA00000426F.h.20.1	23187	3	0	0	0	0	0	0	0
2479	RTA00000424F.d.12.3	74342	1	0	0	0	0	0	0	0

SEQ ID NO:	Sequence Name	cluster	lib 1 clones	lib 2 clones	lib 15 clones	lib 16 clones	lib 17 clones	lib 18 clones	lib 19 clones	lib 20 clones
2480	RTA00000425F.c.03.1	74643	1	0	0	0	0	0	0	0
2481	RTA00000523F.f.16.1	26522	1	0	0	0	0	0	0	0
2482	RTA00000427F.f.15.1	66734	1	0	0	0	0	0	0	0
2485	RTA00000522F.p.18.1	76376	1	0	0	0	0	0	0	0
2493	RTA00000522F.g.18.1	73226	1	0	0	0	0	0	0	0
2495	RTA00000522F.h.05.1	73358	1	0	0	0	0	0	0	0
2497	RTA00000425F.n.16.1	18265	1	0	0	0	0	0	0	0
2498	RTA00000527F.l.21.1	36439	2	0	0	0	0	0	0	0
2501	RTA00000424F.d.17.3	73958	1	0	0	0	0	0	0	0
2502	RTA00000523F.j.02.1	62853	1	0	0	0	0	0	0	0

Table 21. Clones Deposited on January 22, 1999

cDNA Library Ref No.	cDNA ES17	cDNA ES18	cDNA ES19
ATCC Accession No.	ATCC No.	ATCC No.	ATCC No.
Clone Names in Library	M00001368A:D07	M00001594A:D06	M00003906A:F04
	M00003917A:D02	M00001613D:H10	M00003908A:F12
	M00001673A:A04	M00001596D:E10	M00003914A:G09
	M00003868B:G11	M00001592C:G04	M00003915C:H04
	M00003917C:D03	M00001599D:A09	M00003905D:B08
	M00003791C:E09	M00001619B:A09	M00003908C:G09
	M00003870A:C05	M00001593B:E11	M00003914B:A11
	M00003922A:D02	M00001605A:E06	M00003916C:C05
	M00003861C:H02	M00001608A:D03	M00003959A:A03
	M00003931B:A11	M00001616C:A02	M00003905D:C08
	M00001679D:B05	M00001617A:D06	M00003908D:D12
	M00001679C:D05	M00001595C:E01	M00003901B:H04
	M00001687A:G01	M00001616C:A11	M00004031A:E01
	M00003945A:E09	M00001608C:E11	M00004029C:C12
	M00003908A:H09	M00001610C:E06	M00003911A:F10
	M00001649B:G12	M00001612B:D11	M00003914C:F09
	M00003813D:H12	M00001618B:E05	M00003963D:B05
	M00004087C:D03	M00001621C:C10	M00003986C:E09
	M00004269B:C08	M00001647A:H08	M00004031A:F07
	M00004348A:A02	M00001631D:B10	M00003907C:C02
	M00001679C:D01	M00001608D:E09	M00003911B:F08
	M00001490A:E11	M00001641B:C10	M00003914C:H05
	M00001387A:E10	M00001641D:E02	M00003918C:C12
	M00001397B:G03	M00001630D:H10	M00003914C:C02
	M00001441D:E04	M00001585C:D10	M00003914A:E04
	M00001352C:G09	M00001560A:H10	M00003903B:D03
	M00001370D:A12	M00001573B:C06	M00003905A:F09
	M00001387B:A06	M00001660C:D11	M00003867C:E11
	M00001397C:A10	M00001641C:C05	M00003870B:B08
	M00001536D:G02	M00001578B:B05	M00003879D:A08
	M00003895C:A10	M00001587C:C10	M00003891D:B10
	M00001464B:B03	M00001590B:C07	M00003901C:A08
	M00004370A:G05	M00001554A:E04	M00003903C:C04
	M00001490B:H11	M00001570C:G06	M00003905A:F10
	M00001530B:D10	M00001576A:B09	M00003906C:D06
	M00001579C:E09	M00001582A:H01	M00003907D:A12
	M00001587A:H03	M00001582B:E12	M00003905C:G11
	M00001457C:H12	M00001615B:F07	M00003914D:D10
	M00001535C:E01	M00001571C:A04	M00003972A:G09
	M00001561D:C05	M00001573D:D10	M00003975D:C06
	M00001589A:C01	M00001576A:F11	M00003905C:B02
	M00001664D:G07	M00001579C:G05	M00003907D:F11
	M00001565A:H09	M00001582D:A02	M00003914A:G06
	M00001381C:B08	M00001589B:E07	M00003914D:E03
	M00001395C:F11	M00001575B:B02	M00003972C:F08
	M00001429D:F11	M00001578C:G06	M00003976C:D06
	M00001449A:F01	M00001591A:B08	M00003907C:C04
	M00001391C:H02	M00001607A:F11	M00003905B:C06
	M00001429D:H12	M00001579C:E06	M00004088C:A12
	M00001450A:G11	M00001661C:F11	M00004103C:D04
	M00001344B:F12	M00001650B:C10	M00004107A:D01

cDNA Library Ref No. ATCC Accession No.	cDNA ES17 ATCC No.	cDNA ES18 ATCC No.	cDNA ES19 ATCC No.
	M00001391D:C06	M00001654C:E04	M00004110A:E04
	M00003971A:A06	M00001656B:A08	M00004062A:H06
	M00001346A:E04	M00001662C:B02	M00004075D:C10
	M00001455C:G07	M00001656B:D05	M00004081D:H09
	M00001402D:F02	M00001661C:F10	M00004089A:B08
	M00001438D:C06	M00001663A:C11	M00004103D:F10
	M00001349B:G05	M00001669A:C10	M00004107B:B04
	M00001389C:A08	M00001651B:B12	M00004032C:B02
	M00001439B:A10	M00001653B:E06	M00004078C:F04
	M00001455B:A09	M00001659C:F02	M00004038B:H10
	M00001441B:D11	M00001661B:F03	M00004089A:E02
	M00001453A:B01	M00001663C:F10	M00004096B:F05
	M00001456D:E08	M00001669A:G12	M00004104C:H12
	M00001399A:C03	M00001674D:C10	M00004110D:A10
	M00004496C:H03	M00001651B:E06	M00004036D:F02
	M00004135D:G02	M00001651C:C05	M00004088C:E04
	M00004692A:E07	M00001657C:C07	M00004104D:A04
	M00004374D:E10	M00001662A:C12	M00004107D:E12
	M00004405D:C04	M00001663D:C06	M00004115D:D08
	M00004312B:H07	M00001590B:C05	M00003846A:D03
	M00003976C:A10	M00001483C:G06	M00004072C:F08
	M00004043A:D02	M00001653A:G07	M00004039B:G08
	M00004081C:H06	M00001625B:C10	M00003986D:D02
	M00004050D:A06	M00001626C:D12	M00003914A:B07
	M00001361B:C07	M00001634D:D02	M00003914D:B02
	M00004341B:G03	M00001641C:C06	M00003971B:B07
	M00001342B:E01	M00001642D:F02	M00003978C:A03
	M00004064D:A11	M00001647B:E04	M00003983B:C08
	M00004087A:G08	M00001632B:E05	M00004033D:D07
	M00004344B:H04	M00001639A:C11	M00004072D:H12
	M00004497A:H03	M00001642D:G10	M00004077B:H11
	M00001338C:E10	M00001624A:G11	M00004080A:F01
	M00001366D:E12	M00001626C:G08	M00004092C:B03
	M00001390D:E03	M00001672D:D04	M00004037B:C04
	M00001413B:H09	M00001639A:H06	M00004073C:D04
	M00004271B:B06	M00001662C:A04	M00004081A:A08
	M00004151D:E03	M00001641B:B01	M00004085B:B05
	M00001660B:C04	M00001673C:A02	M00004090C:C07
	M00003802D:B11	M00001650A:A12	M00004086D:B09
	M00001579C:E08	M00001659D:D03	M00004088D:B03
	M00001557D:C08	M00001661B:B05	M00004090C:C10
	M00003779B:E12	M00001671D:E10	M00004102C:D09
	M00001638A:D10	M00001652D:A06	M00004105C:E09
	M00003794A:B03	M00001654C:D05	M00004035A:G10
	M00001616C:F07	M00001656A:B07	M00003906A:H07
	M00001679A:F01	M00001647B:C09	M00004083B:G03
	M00001604C:E09	M00001635A:C06	M00001675B:E02
	M00001653B:E09	M00001482D:A04	M00003793C:D09
	M00001585A:F07	M00001485C:B10	M00003762B:H09
	M00003811D:A12	M00001457D:A07	M00001694C:F12
	M00001653C:F12	M00001461A:E05	M00001678D:C11
	M00001679D:F06	M00001477A:G07	M00001677D:B07

cDNA Library Ref No. ATCC Accession No.	cDNA ES17 ATCC No.	cDNA ES18 ATCC No.	cDNA ES19 ATCC No.
	M00003751D:B02	M00001479D:H03	M00001677B:A02
	M00003801A:B10	M00001482C:D02	M00001675B:H03
	M00003844C:A08	M00001484D:G05	M00003808D:D04
	M00001636C:C01	M00001459B:D03	M00003752B:C02
	M00001669C:B01	M00001464B:C11	M00003819D:B11
	M00003755A:A09	M00001511A:A05	M00001677D:B02
	M00003798D:H08	M00001477B:C02	M00001694C:G04
	M00001444C:D05	M00001471A:D04	M00003789C:F06
	M00004040B:F10	M00001485C:H10	M00001678C:C06
	M00001355A:C12	M00001485D:E05	M00001675B:D02
	M00001401A:H07	M00001487C:G03	M00003750C:H05
	M00001393B:B09	M00001514A:B04	M00001694A:B12
	M00001409D:F11	M00001530C:G10	M00001677B:H06
	M00001387B:H07	M00001534A:G06	M00001675C:G01
	M00001394C:C11	M00001539A:C12	M00001675B:C01
	M00001344A:H07	M00001547A:F11	M00003857B:F07
	M00001490C:D07	M00001550D:A04	M00003812B:D07
	M00001352C:F06	M00001460A:F07	M00001694B:B08
	M00001476D:G03	M00001472C:A01	M00001677B:E06
	M00001399C:D09	M00001481B:A07	M00004037A:E04
	M00001347C:G08	M00001456D:F05	M00003870A:H01
	M00001453D:G12	M00001456D:G11	M00003842C:D11
	M00001382A:F04	M00001477D:F10	M00003828B:F09
	M00001392D:H04	M00001481A:G06	M00003856C:H09
	M00001429C:G12	M00001464A:B03	M00003851A:C10
	M00001454A:C11	M00001469A:G11	M00003841C:E04
	M00001517B:G08	M00001478B:D07	M00003837C:G08
	M00001535A:D02	M00001473A:C11	M00003828B:E07
	M00001352A:E12	M00001457A:G03	M00003772C:B12
	M00001381B:F06	M00001669B:G02	M00001677D:F03
	M00004117A:D11	M00001479D:G06	M00001678B:B12
	M00004217C:D03	M00001473D:B11	M00001678D:G03
	M00004270A:F11	M00001475A:A12	M00001675C:F01
	M00003996A:A06	M00001460A:G07	M00003809A:H04
	M00004056B:D09	M00001464A:D03	M00003771D:G05
	M00004142A:B12	M00001473D:G01	M00001678A:F05
	M00001396D:B03	M00001476D:C05	M00001677B:B06
	M00001370D:E12	M00001484A:A10	M00003794A:E12
	M00001390C:C11	M00001457C:F02	M00003771B:E05
	M00003989A:H11	M00001459B:A12	M00001678A:A11
	M00001426A:A09	M00001464A:E07	M00003805B:C04
	M00004498D:D05	M00001467A:B03	M00001680B:E10
	M00001391B:G12	M00001514A:B08	M00001679B:H07
	M00001391D:D10	M00001464A:B07	M00003904D:B12
	M00001376B:A02	M00001579A:C03	M00003856C:B08
	M00001405B:D07	M00001517A:G08	M00003858D:G06
	M00001368A:A03	M00001530B:G09	M00003870B:F04
	M00001392D:B11	M00001538A:F12	M00003871C:B05
	M00003900D:B10	M00001540C:B03	M00003875A:C04
	M00001494B:C01	M00001547A:F06	M00003901B:A09
	M00001352C:A05	M00001550A:F07	M00003901C:D03
	M00001408B:G06	M00001567B:G11	M00003904C:B06

cDNA Library Ref No. ATCC Accession No.	cDNA ES17 ATCC No.	cDNA ES18 ATCC No.	cDNA ES19 ATCC No.
	M00004252C:E03	M00001572A:A10	M00003901C:F09
	M00003901C:A03	M00001575B:G01	M00003904D:B10
	M00004071D:A10	M00001487D:C11	M00003850D:H11
	M00001377B:H01	M00001577B:A03	M00003902B:D06
	M00003939A:A02	M00001539D:E10	M00003879A:C01
	M00004250D:D10	M00001587A:F05	M00003877D:G05
	M00004290A:B03	M00001560A:F03	M00003881D:C12
	M00003911D:B04	M00001569B:G11	M00003903A:H09
	M00004128B:G01	M00001573A:A06	M00003905A:A06
	M00004142A:D08	M00001575D:A10	M00003875D:D09
	M00003977A:E04	M00001583A:D01	M00003879B:A06
	M00004236C:D10	M00001587A:F08	M00003823D:G05
	M00004388B:A08	M00001590B:B02	M00003763A:C01
	M00004409B:A11	M00001553A:E07	M00003903B:C02
	M00003965A:B11	M00001560A:H06	M00003905A:E07
	M00003988A:E10	M00001589C:A11	M00003867A:D12
	M00004138A:H09	M00001538A:C08	M00003857C:C09
	M00003933C:D06	M00001531A:H03	M00003829C:D10
	M00004193C:G11	M00001548A:G01	M00003839D:E02
	M00004039C:C01	M00001531A:H07	M00003841C:F03
	M00003924B:D04	M00001542A:E04	M00003903D:C06
	M00004375C:D01	M00001487A:F10	M00003852D:E08
		M00001503C:G05	M00003845D:A09
		M00001511A:G08	M00003824A:G10
		M00001539A:H12	M00003841C:F06
		M00001542A:F06	M00003848A:C09
		M00001549A:F01	M00003857C:F11
		M00001514A:A12	M00003816C:C01
		M00001516A:D05	M00003843A:E08
		M00001546C:C07	M00003850A:F06
		M00001549A:H11	M00003813B:A11
		M00001538A:D03	M00003855C:F10
		M00001544A:C09	M00003850D:B05
		M00001546B:F12	M00003841D:F06
		M00001550A:D09	M00003858B:G05
		M00001487B:F02	M00003854D:A12
		M00001513A:G07	M00003857C:G01
		M00001530A:F12	M00003816C:E09
		M00001538A:D12	M00003813A:G04
		M00001587A:G06	M00003850D:A05
		M00001551A:D04	
		M00001485B:C03	

Table 22. Clones Deposited on January 22, 1999

cDNA Ref No.; ATCC Accession No. Clone Names in Library	cDNA Ref ES20 ATCC No.	cDNA Ref No. ES27 ATCC No.	cDNA Ref ES28 ATCC No.
	M00004891D:A07	M00001623B:G07	M00001550D:H02
	M00004118B:C11	M00001619D:G05	M00001549C:D02
	M00004105A:B10	M00001616C:C09	M00001549A:A09
	M00004099A:F11	M00001615C:F03	M00001548A:B11
	M00004037C:D07	M00001614D:D09	M00001546C:G10
	M00004033D:C05	M00001608B:A03	M00001544C:C06
	M00003983D:A09	M00001607D:F07	M00003820B:C05
	M00004029B:H08	M00001623D:C10	M00001543A:H12
	M00004927A:A02	M00001599B:E09	M00001540C:B10
	M00003983C:F10	M00001632C:C09	M00001552B:G05
	M00003980B:C06	M00001605C:D12	M00001543C:F01
	M00004033D:B07	M00001625D:C07	M00001552D:G08
	M00004034C:E08	M00001629B:E06	M00001554B:B07
	M00005100B:H07	M00001594A:B12	M00001555A:B01
	M00005136A:D10	M00001632C:A02	M00001557A:F01
	M00005173D:H02	M00001567C:H12	M00001558A:E11
	M00004891D:C11	M00001635C:A03	M00001561C:E11
	M00004101A:F07	M00001636C:H09	M00001571D:B11
	M00003982B:B06	M00001638A:E07	M00001563B:D11
	M00004108C:E01	M00001639A:F10	M00001569C:B06
	M00005136D:B07	M00001656C:G08	M00001539B:H06
	M00004118D:A11	M00001632A:F12	M00001571B:E03
	M00005102C:C01	M00001557A:D02	M00001561D:C11
	M00005177C:A01	M00001529B:C04	M00001487C:D06
	M00004927C:H11	M00001534B:C12	M00001454B:D08
	M00005174D:B02	M00001535D:C01	M00003772D:E10
	M00004027A:D06	M00001536D:A12	M00001573C:D03
	M00005217A:G10	M00001540B:C09	M00001454D:E05
	M00003984A:B06	M00001540D:D02	M00001455D:F09
	M00003851C:D07	M00001541C:B07	M00001457C:C11
	M00003959C:G06	M00001546B:B02	M00001459B:C09
	M00005100B:G11	M00001575B:C09	M00001460A:E01
	M00005213C:G01	M00001554B:C07	M00001460C:H02
	M00003982B:H07	M00001578D:C04	M00001456A:H02
	M00004029C:B03	M00001557C:H07	M00001477B:F04
	M00004033D:G06	M00001558B:D08	M00003845D:B04
	M00004091B:H09	M00001560D:A03	M00001488A:E01
	M00003959D:A04	M00001561C:F06	M00001492D:A11
	M00004030D:B06	M00001564D:C09	M00001496C:G10
	M00004034C:C06	M00003748B:F02	M00001499A:A05
	M00004030C:D12	M00001570D:A03	M00001500A:B02
	M00003982C:H10	M00001660C:B12	M00001500D:E10
	M00003971C:F09	M00001577B:H02	M00001513D:A03
	M00004031B:A06	M00001548A:A08	M00001528A:C11
	M00003966B:D02	M00003868B:D12	M00001528C:H04
	M00004028B:G08	M00001718D:F07	M00001531B:E09
	M00004031C:H10	M00003829C:A11	M00001463A:F06
	M00004076D:B09	M00003832B:E01	M00003755A:B03

cDNA Ref No.; ATCC Accession No.	cDNA Ref ES20 ATCC No.	cDNA Ref No. ES27 ATCC No.	cDNA Ref ES28 ATCC No.
	M00004092D:B11	M00003842B:D09	M00001653B:G07
	M00003981C:F05	M00003845A:H12	M00001654D:G11
	M00004031D:F05	M00003847B:G03	M00001656B:A07
	M00004097B:D03	M00003847C:E09	M00001664B:D06
	M00003986D:G07	M00003853D:G08	M00001664C:H10
	M00004033B:C02	M00003828A:E04	M00001680B:C01
	M00004037B:A04	M00003867C:H09	M00001681A:F03
	M00004092C:B12	M00003822A:F02	M00001684B:G03
	M00005140D:G09	M00003868C:H10	M00001771A:A07
	M00004897D:G05	M00003871A:A05	M00003774C:D02
	M00004960B:D12	M00003879C:G10	M00003754D:D02
	M00005134C:G04	M00003880C:F10	M00001640B:F03
	M00005139A:F01	M00003881D:D06	M00003763B:H01
	M00005176A:C12	M00003884D:G07	M00003812C:A05
	M00005178A:A07	M00003887A:A06	M00003803C:D09
	M00005212A:A02	M00003889A:D10	M00003801B:B10
	M00005229D:H07	M00003889D:B09	M00003798D:E03
	M00004115C:H04	M00003858D:F12	M00003773B:G01
	M00004687A:C03	M00003774B:B08	M00003771A:G10
	M00004900C:E11	M00001680D:D02	M00001452A:E07
	M00004695B:E04	M00001528A:F09	M00004029B:F11
	M00005134D:A06	M00003748A:B07	M00003751B:A05
	M00004103B:B07	M00001655A:F06	M00001609B:A11
	M00005177A:B06	M00003750A:D01	M00001573D:F10
	M00005178A:A08	M00003761D:E02	M00001579C:B11
	M00004104D:B05	M00003763D:E10	M00001579C:H10
	M00004117B:G01	M00003768A:E02	M00001579D:G07
	M00004900D:B10	M00003829B:G03	M00001583B:E10
	M00005134D:H03	M00003772A:D07	M00001586D:E02
	M00005173C:A02	M00001661B:C08	M00001587D:A10
	M00005177A:H09	M00003778A:D08	M00001589A:D12
	M00005178B:H01	M00003799A:D09	M00001590C:H08
	M00005216C:B09	M00003800A:C09	M00001651B:A11
	M00003826B:E11	M00003804A:H04	M00001597A:E12
	M00001596A:G06	M00003806D:G05	M00001649C:B10
	M00005100B:D02	M00003808C:B05	M00001614A:E06
	M00005137A:E01	M00003811A:E03	M00001615C:D02
	M00004119A:A06	M00003815D:H09	M00001621D:D03
	M00004891D:E07	M00003818B:G12	M00001623D:G03
	M00004958B:D01	M00003769B:D03	M00001624A:F09
	M00005102C:F09	M00001390A:A09	M00001624C:A06
	M00005136D:C01	M00001432A:E06	M00001630B:A11
	M00005174D:H02	M00001381A:D02	M00001634B:C10
	M00005177C:B04	M00001383A:G04	M00001639D:B07
	M00005218B:D09	M00001384C:E03	M00001573D:F04
	M00004102C:F03	M00001384C:F12	M00001595B:A09
	M00004114B:D09	M00001384D:H07	M00004156B:A12
	M00004119D:A07	M00001385B:F10	M00004319D:G09
	M00004895C:G05	M00001385C:H11	M00004096A:G02
	M00004235A:A12	M00001386A:C02	M00004101C:G08

cDNA Ref No.; ATCC Accession No.	cDNA Ref ES20 ATCC No.	cDNA Ref No. ES27 ATCC No.	cDNA Ref ES28 ATCC No.
	M00005134B:E01	M00001372C:F07	M00004102A:H02
	M00004115C:G03	M00001389D:G11	M00004108A:A09
	M00005175B:H04	M00001371D:G01	M00004111D:D11
	M00005214B:D11	M00001392C:D10	M00004115D:C08
	M00004102D:B05	M00001392D:H06	M00004118D:E08
	M00004115A:B12	M00001397B:B09	M00004121C:F06
	M00004119D:H06	M00001398A:G03	M00004131B:H09
	M00004897D:F03	M00001400A:F06	M00004141D:A09
	M00004960B:A09	M00001410B:G05	M00004090A:F09
	M00005134C:E11	M00001413A:F02	M00004146A:C08
	M00005138B:D12	M00001415B:E09	M00004078B:A11
	M00005176A:A05	M00001425A:C11	M00004176B:E08
	M00005214C:A09	M00001386A:D11	M00004188C:A09
	M00004102C:D01	M00001354C:B06	M00004233C:H09
	M00004960B:A08	M00001339D:G02	M00004241D:F11
	M00001476D:A09	M00001660A:C12	M00004246C:A09
	M00001572A:B06	M00001528A:A01	M00004247C:C12
	M00005217D:F12	M00001343D:C04	M00004248B:E08
	M00005233A:G08	M00001347B:E01	M00004257C:H06
	M00005236B:F10	M00001348A:D04	M00004260D:C12
	M00005259B:C01	M00001349C:C05	M00004295B:D02
	M00005254D:B08	M00001350A:D06	M00004040D:F01
	M00005259C:B05	M00001352D:C05	M00004142D:E10
	M00001575A:D06	M00001380C:E05	M00003853D:D03
	M00005259D:H08	M00001354B:B10	M00003860D:H07
	M00003813C:D08	M00001380C:F02	M00003878C:E04
	M00001530D:E06	M00001354C:C10	M00003879A:G05
	M00004891B:B12	M00001355B:G11	M00003880B:C08
	M00001596B:C11	M00001356D:F06	M00003881A:D09
	M00004300C:H09	M00001360D:E11	M00003881C:G09
	M00001486D:D12	M00001361C:H11	M00003901B:A05
	M00001585D:F03	M00001362C:A10	M00003904D:D10
	M00001596B:D09	M00001363C:H02	M00003905C:G10
	M00001570D:E06	M00001366D:G02	M00003906B:F12
	M00001582C:E01	M00001369A:H12	M00003909A:H04
	M00001586C:E06	M00001352D:D02	M00004091B:D11
	M00001593B:D10	M00001485D:B10	M00003963A:E03
	M00001595C:H11	M00001457B:E03	M00004353C:H07
	M00001596B:H05	M00001457C:C12	M00003919A:A10
	M00001576A:C11	M00001458C:E01	M00003938A:B04
	M00001596C:F09	M00001462B:A10	M00003939C:F04
	M00001567A:H05	M00001464D:F06	M00003946D:C11
	M00001585D:D11	M00001467D:H05	M00003979A:F03
	M00004688A:A02	M00001468B:H06	M00003985C:F01
	M00004927A:E06	M00001505C:H01	M00003997B:G07
	M00005229D:H09	M00001470A:H01	M00003860D:A01
	M00004117B:A12	M00001457A:B07	M00004035A:A04
	M00004187D:G09	M00001479B:A01	M00004042D:H02
	M00005173B:F01	M00001469D:D02	M00004073B:B01
	M00005218A:G05	M00001487A:A05	M00003946A:H10

cDNA Ref No.; ATCC Accession No.	cDNA Ref ES20 ATCC No.	cDNA Ref No. ES27 ATCC No.	cDNA Ref ES28 ATCC No.
	M00004118A:H08	M00001352C:H02	M00001423D:A09
	M00005134A:D11	M00001488D:C10	M00004314B:G07
	M00005176C:C09	M00001490C:C12	M00001405D:D11
	M00005230D:F06	M00001493B:D09	M00001408A:H04
	M00005234D:B04	M00001504D:D11	M00001408D:D04
	M00005101C:E09	M00001376B:C06	M00001411D:F05
	M00004206A:E02	M00001506B:D09	M00001412A:E04
	M00001570C:A05	M00001511B:C06	M00001413A:F03
	M00005231A:H04	M00001476B:F10	M00001417B:C04
	M00005235A:A03	M00001450D:D04	M00001417D:A04
	M00004118B:B04	M00001433A:G07	M00001418B:F07
	M00005136D:D06	M00001470C:B10	M00001419D:C10
	M00005231C:B01	M00001437D:C04	M00001402B:F12
	M00004153B:B03	M00001447C:C01	M00001423A:G05
	M00004897C:D06	M00001448B:F06	M00001401C:H03
	M00005136D:G06	M00001449D:A06	M00001423D:D12
	M00005212B:A02	M00001433B:H11	M00001424B:H04
	M00005232A:C10	M00001451D:C10	M00001428B:A09
	M00004692A:H10	M00001452A:C07	M00001430A:A02
	M00005101C:B09	M00001453C:A11	M00001432D:F05
	M00004144A:F04	M00001456B:C09	M00001438B:B09
	M00003852B:D11	M00001454B:G03	M00001445B:E04
	M00001660D:E05	M00001454B:G07	M00001445C:A08
	M00003808A:F09	M00001454C:C08	M00001446C:D09
	M00001656A:D10	M00001454C:F02	M00001448A:G09
	M00001671A:H06	M00001454D:D06	M00001449C:H12
	M00003809C:H07	M00001456B:F10	M00001422C:F12
	M00003853C:C06	M00001455D:A09	M00001352C:H10
	M00003860A:A08	M00001455D:A11	M00004375A:H01
	M00003822B:D08	M00001448D:F09	M00004380B:A05
	M00003845A:E12		M00004444B:D11
	M00003854C:C02		M00001338B:E02
	M00003860B:G09		M00001341A:F12
	M00003822B:G01		M00001344A:G07
	M00001670A:C11		M00001345A:G11
	M00003852A:B03		M00001345B:E10
	M00003829D:A11		M00001345C:B01
	M00003854C:F01		M00001346B:B07
	M00003856B:C04		M00001405B:E09
	M00003905A:H11		M00001352B:F04
	M00001530A:F11		M00001451C:E01
	M00003840B:E07		M00001361A:H07
	M00003905B:G03		M00001362B:H06
	M00003840B:E08		M00001372C:G12
	M00003855A:C12		M00001375B:G12
	M00003905B:H05		M00001376A:C05
	M00003826B:B04		M00001376B:A08
	M00003851C:B06		M00001377C:E12
	M00003853B:C08		M00001382B:F12
	M00003829A:F03		M00001385A:F12

cDNA Ref No.; ATCC Accession No.	cDNA Ref ES20 ATCC No.	cDNA Ref No. ES27 ATCC No.	cDNA Ref ES28 ATCC No.
	M00001638C:G01		M00001394A:E04
	M00003845D:B02		M00001395A:C09
	M00001653D:G07		M00001396A:H03
	M00001578B:A02		M00001350B:G11
	M00001590B:H10		
	M00001595C:A09		
	M00001596A:E07		
	M00001607A:B06		
	M00001607A:D10		
	M00001652C:B09		
	M00001671B:F02		
	M00001632C:D08		
	M00001638C:H07		
	M00001652D:B09		
	M00001614C:E11		
	M00001633B:B11		
	M00001651C:A04		
	M00001639D:G12		
	M00001671C:F11		
	M00001638A:B04		
	M00001637C:H12		
	M00001669B:H06		
	M00001639D:F02		
	M00001590A:C08		
	M00001636A:C02		
	M00001614A:A04		
	M00001639D:G06		

Table 23. Library Deposited on January 22, 1999

cDNA Ref No.; ATCC Accession No. Clone Names in Library	cDNA Library Ref ES29 ATCC No.	cDNA Library Ref ES30 ATCC No.
	M00001449D:B01	M00001594D:B08
	M00001476D:F03	M00001593A:B07
	M00001456C:B12	M00001594A:C01
	M00001469B:B01	M00001594A:D08
	M00001471A:B04	M00001594A:G09
	M00001472A:D08	M00001595C:B05
	M00001473A:A07	M00001594B:F12
	M00001473C:D09	M00001596D:E03
	M00001475B:C04	M00001594D:C03
	M00001475C:G11	M00001592C:F11
	M00001476A:D11	M00001590D:G07
	M00001476B:D10	M00001595D:A04
	M00001468A:C05	M00001595D:G03
	M00001476C:C11	M00001601A:A06
	M00001467A:H07	M00001590C:F10
	M00001477B:E02	M00001589B:B08
	M00001478B:H08	M00001589C:E06
	M00001479C:E01	M00001611B:A05
	M00001480A:D03	M00001601A:E02
	M00001480C:A05	M00001587A:D01
	M00001481A:H08	M00001591B:B12
	M00001481B:D09	M00001590B:G08
	M00001482A:H05	M00001592C:E05
	M00001482D:H11	M00001591B:B06
	M00001483C:G09	M00001591D:C07
	M00001485A:C05	M00001591D:F06
	M00001476B:F08	M00001592A:E02
	M00001460A:E11	M00001592A:H05
	M00001456C:C11	M00001592B:A04
	M00001457A:C05	M00001587A:B10
	M00001457A:G12	M00001609D:G10
	M00001458A:A11	M00005231D:B09
	M00001458C:D10	M00001614B:E08
	M00001458D:A01	M00005217C:C01
	M00001458D:A02	M00001587A:B01
	M00001458D:C11	M00001613D:B03
	M00001458D:D01	M00001613A:F03
	M00001459B:C11	M00001611C:H11
	M00001468A:H10	M00001611C:C12
	M00001460A:C10	M00001611B:E06
	M00001485B:F05	M00001611B:A09
	M00001460A:H11	M00001610D:D05
	M00001461A:F05	M00001610B:C07
	M00001462A:D03	M00001610C:E07
	M00001464A:B02	M00001610A:E09
	M00001464A:E10	M00001601A:E12
	M00001465A:B12	M00001609B:C09
	M00001465A:C12	M00001608D:D11
	M00001465A:E10	M00001608B:A09

cDNA Ref No.; ATCC Accession No.	cDNA Library Ref ES29 ATCC No.	cDNA Library Ref ES30 ATCC No.
	M00001465A:G06	M00001607D:F06
	M00001466A:F08	M00001607B:C05
	M00001467A:C10	M00001606A:H09
	M00001460A:B12	M00001605A:H03
	M00001545A:B12	M00001605A:E09
	M00001535A:D10	M00001605A:A06
	M00001536A:F11	M00001604A:C11
	M00001537A:H05	M00001604A:C07
	M00001539A:E01	M00001604A:B08
	M00001539A:H02	M00001604A:A09
	M00001539B:G07	M00001610A:H05
	M00001539D:B10	M00005214B:A06
	M00001540D:E02	M00005228A:A09
	M00001541B:E05	M00001567A:B09
	M00001542A:G12	M00001561A:D01
	M00001485B:D09	M00001559A:C08
	M00001545A:B10	M00001559A:A11
	M00001533A:G05	M00001558A:G09
	M00001545A:F02	M00001555A:B12
	M00001545A:G05	M00001554A:A08
	M00001546A:D08	M00001552A:H10
	M00001548A:H04	M00001552A:F06
	M00001550A:E07	M00005231C:B07
	M00001551A:A11	M00005218D:G10
	M00001551A:D06	M00001570A:H01
	M00001551A:H06	M00005214D:D10
	M00001551D:H07	M00001570C:G03
	M00001552A:E10	M00005213C:A01
	M00001450A:B08	M00005212D:F08
	M00001544A:F05	M00005212A:D10
	M00001512A:G05	M00005211C:E09
	M00001483B:D04	M00005211A:E09
	M00001485B:H03	M00005210D:C09
	M00001485C:C08	M00005179D:B03
	M00001486B:D07	M00005179B:H02
	M00001486B:E12	M00005177D:F09
	M00001487B:A11	M00005177C:G04
	M00001487B:E10	M00005177B:H02
	M00001507A:A11	M00001614D:B08
	M00001507A:B02	M00001615A:D06
	M00001507A:C05	M00005216B:D02
	M00001507A:E04	M00001579C:A01
	M00001534A:D03	M00001585B:C03
	M00001511A:G01	M00001585B:A06
	M00001533D:A08	M00001584D:H02
	M00001513A:F05	M00001584A:G03
	M00001514A:G03	M00001583D:B08
	M00001516A:D02	M00001583B:F02
	M00001516A:F06	M00001583A:F07
	M00001517A:B11	M00001583A:A05

cDNA Ref No.; ATCC Accession No.	cDNA Library Ref ES29 ATCC No.	cDNA Library Ref ES30 ATCC No.
	M00001529D:C05	M00001582D:F02
	M00001530A:A09	M00001582D:B01
	M00001530A:E10	M00001582A:A03
	M00001532A:C01	M00001579D:H09
	M00001532D:A06	M00001567D:B03
	M00001485B:D10	M00001579C:H06
	M00001511A:A02	M00001585B:F01
	M00004249D:B08	M00001579B:F04
	M00004185D:E04	M00001579A:E03
	M00004188D:G08	M00001578C:F05
	M00004197C:F03	M00001577D:H06
	M00004198B:D02	M00001577B:F10
	M00004204D:C03	M00001576C:G05
	M00004208B:F05	M00001575D:D12
	M00004208D:B10	M00001575D:B10
	M00004210B:B05	M00001575D:A02
	M00001362D:H01	M00001573B:G08
	M00004216D:D03	M00001573A:E01
	M00004167A:H03	M00001572A:B05
	M00004275A:B03	M00001571D:F05
	M00004285C:A08	M00001579D:F04
	M00004316A:G09	M00001636A:F08
	M00004465B:D04	M00001643B:E05
	M00004493B:D09	M00001642C:G02
	M00001347B:H04	M00001642A:F03
	M00001351C:B06	M00001641D:C04
	M00001360A:G10	M00001641C:H07
	M00004216D:C03	M00001641C:F01
	M00004076D:D04	M00001641C:D02
	M00001484C:A04	M00001641B:F12
	M00001456B:G01	M00001634A:B04
	M00003972D:C09	M00001636B:G11
	M00003974C:E04	M00001649C:D05
	M00003979A:E11	M00001636A:C03
	M00003983C:F03	M00001635D:D05
	M00003989B:F11	M00001635D:C12
	M00004031D:B05	M00001635B:H02
	M00004177C:A01	M00001635B:H01
	M00004076B:G03	M00001634D:G11
	M00004167D:A07	M00001634D:D04
	M00004078A:A06	M00001634A:H05
	M00004085A:B02	M00001641A:A11
	M00004107B:A06	M00001638B:E12
	M00004111C:E11	M00001640A:H02
	M00004130D:H01	M00001614C:E06
	M00004157D:B03	M00001636D:F09
	M00004159C:F09	M00001637A:A03
	M00004162C:A07	M00001637A:A06
	M00004135B:G01	M00001637A:E10
	M00004040A:G12	M00001637A:F10

cDNA Ref No.; ATCC Accession No.	cDNA Library Ref ES29 ATCC No.	cDNA Library Ref ES30 ATCC No.
	M00001453B:H12	M00001637C:C06
	M00001448A:E11	M00001644A:H01
	M00001448B:F09	M00001638B:E03
	M00001448B:H05	M00001649A:E11
	M00001448C:E11	M00001638B:F10
	M00001448C:F10	M00001639A:C03
	M00001448D:F12	M00001639A:G07
	M00001449B:B03	M00001639B:H01
	M00001449C:C05	M00001639B:H05
	M00001449D:G10	M00001639C:A09
	M00001448A:B12	M00001639C:C02
	M00001453A:D08	M00001649C:E11
	M00001451B:A04	M00001649C:H10
	M00001454A:F11	M00001637C:E03
	M00001454A:G03	M00001617A:A08
	M00001455A:F04	M00001622A:H12
	M00001455B:E07	M00001621C:H12
	M00001455D:A06	M00001621B:G05
	M00001364B:B06	M00001620D:H02
	M00004117A:G01	M00001620D:G11
	M00001455D:D11	M00001619D:D10
	M00001456B:A06	M00001619C:C07
	M00001451A:C10	M00001619A:E05
	M00001395A:E03	M00001623A:F04
	M00001366D:C06	M00001618A:A03
	M00001365A:H10	M00001618B:D09
	M00001366D:C12	M00001617A:A01
	M00001373D:B03	M00001616D:C11
	M00001453B:F08	M00001615C:G05
	M00001444D:C01	M00001615C:A11
	M00001375B:C06	M00001615B:G07
	M00001392C:D05	M00001633D:H06
	M00001395A:A12	M00001639C:A10
	M00001395A:H02	M00001615B:A09
	M00001397D:G08	M00001615B:G01
	M00001434A:B10	M00001618A:F10
	M00001416A:D09	M00001632C:H07
	M00001433C:F10	M00001633D:D12
	M00001416A:H02	M00001633D:D09
	M00001428D:B10	M00001618A:F08
	M00001428B:D01	M00001633D:G09
	M00001426D:D12	M00001624A:A03
	M00001400C:D02	M00001633C:F09
	M00001427C:D01	M00001633C:H05
		M00001633C:B09
		M00001633A:E06
		M00001633C:H11
		M00001632C:B10
		M00001625D:G10
		M00001631D:G05

cDNA Ref No.; ATCC Accession No.	cDNA Library Ref ES29 ATCC No.	cDNA Library Ref ES30 ATCC No.
		M00001629C:E07
		M00001629B:B08
		M00001626C:E04
		M00001626C:C11
		M00001632A:B10
		M00001624B:B10
		M00001633C:A05
		M00001625C:G05

Table 24. Clones Deposited on January 22, 1999

cDNA Ref No.; ATCC Accession No. Clone Names in Library	cDNA Ref ES31 ATCC No.	cDNA Ref No. ES32 ATCC No.	cDNA Ref ES33 ATCC No.
	M00003843A:E04	M00003906A:F12	M00005254D:A10
	M00003842C:G03	M00003906B:H06	M00005260B:E11
	M00003842A:A03	M00003906C:C05	M00005260A:F04
	M00003841D:A04	M00003907A:F01	M00005260A:A12
	M00003841B:E06	M00003907B:C03	M00005259B:D12
	M00003841C:H11	M00003907B:D05	M00005257D:H11
	M00003844A:A11	M00003918A:D08	M00005257D:G07
	M00003841C:F01	M00003918A:F09	M00005257D:A06
	M00003841C:H08	M00003918C:H10	M00005257C:G01
	M00003841C:D07	M00003924A:D08	M00005257A:H11
	M00003844D:A07	M00003958B:E11	M00005236B:H10
	M00003845D:G08	M00003958B:H08	M00005236B:G03
	M00003852C:B06	M00003960A:G07	M00005257C:E05
	M00003854B:A07	M00003971B:A10	M00001608C:D02
	M00003854B:D04	M00003972D:H02	M00001608C:G04
	M00003859D:C05	M00003973C:C03	M00001608D:F11
	M00003860B:F11	M00003974B:B11	M00001609C:A12
	M00003867B:G07	M00003974D:F02	M00001609C:G05
	M00003867B:G08	M00003974D:H04	M00001610C:B07
	M00003841B:E03	M00003975C:F07	M00001612D:D12
	M00003822D:B10	M00003977C:A06	M00001612D:F06
	M00003867D:A06	M00003977C:B03	M00001613A:D02
	M00003868B:G06	M00003977D:A03	M00001614A:B10
	M00003867B:D10	M00003977D:A06	M00001614C:G07
	M00003831C:G05	M00003977D:D04	M00001615C:E07
	M00003901C:B01	M00003978D:G04	M00001625C:F10
	M00003868C:C07	M00003980A:F04	M00001626D:A02
	M00003820A:A08	M00003980B:C11	M00001629A:H09
	M00003820B:D07	M00003981C:B04	M00001629D:B10
	M00003820B:D10	M00003982A:B12	M00001629D:D10
	M00003822D:C06	M00003982C:G04	M00001630C:F09
	M00003823B:F07	M00003984D:B08	M00001631A:D03
	M00003824C:D07	M00003985B:G04	M00001631A:F06
	M00003825B:B10	M00003985D:E10	M00001631A:F12
	M00003825B:B11	M00003986B:A08	M00001631B:H04
	M00003828A:D05	M00003986C:D09	M00001633A:F11
	M00003822D:D04	M00003986D:C08	M00001633A:G10
	M00003830C:A03	M00003987B:E12	M00001633B:A12
	M00003840D:H10	M00003987B:F08	M00001633B:E03
	M00003832A:A09	M00003987C:G03	M00001633C:A08
	M00003833B:B03	M00003988D:A08	M00001633C:E12
	M00003833B:C12	M00003989C:D03	M00001635B:B02
	M00003834B:G04	M00003989C:G05	M00001636A:H12
	M00003835A:A09	M00003989D:F12	M00001638A:C08
	M00003835B:H11	M00004029B:F01	M00001638B:C08
	M00003835D:G06	M00004029C:C05	M00001639D:C12
	M00003837C:E05	M00004029C:G10	M00001640A:F05
	M00003837C:F10	M00004030D:F11	M00001642D:G08

cDNA Ref No.; ATCC Accession No.	cDNA Ref ES31 ATCC No.	cDNA Ref No. ES32 ATCC No.	cDNA Ref ES33 ATCC No.
	M00003839A:D07	M00004034A:A01	M00001647D:G07
	M00003839D:E11	M00004034C:G02	M00001649A:E10
	M00003829C:H05	M00004034D:E09	M00001650D:D10
	M00003901B:C03	M00004035B:H09	M00001650D:F11
	M00003878C:F06	M00004036D:B04	M00001651C:D11
	M00003878C:G08	M00004036D:B09	M00001651C:G12
	M00003879A:A02	M00004038A:F02	M00001652B:D06
	M00003879A:B08	M00004038D:G06	M00001652D:G02
	M00003879A:C11	M00004039A:C03	M00001652D:G06
	M00003879A:D02	M00004039A:H11	M00001653A:A05
	M00003879B:G02	M00004039B:A05	M00001653D:H07
	M00003880B:D11	M00004039B:E12	M00001654A:E08
	M00003880C:E11	M00004040C:A01	M00001654B:A01
	M00003880C:H03	M00004051D:E01	M00001654C:D10
	M00003901B:F10	M00004072D:F09	M00001654C:G07
	M00003890B:C08	M00004073A:D10	M00001654C:G09
	M00003877C:A11	M00004075B:G09	M00001655C:C07
	M00003819D:B01	M00004076A:D12	M00001655D:E08
	M00003901B:G11	M00004076D:H07	M00001655D:H11
	M00001692A:G06	M00004078A:C11	M00001656A:H12
	M00003903C:C05	M00004078A:E05	M00001656C:C04
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	M00003903D:C12	M00004078B:C11	M00001657C:C11
	M00003903D:D10	M00004078B:F12	M00001657D:A10
	M00003903D:H11	M00004079D:G08	M00001659D:A09
	M00003904A:C04	M00004081A:E02	M00001661D:D05
	M00003904B:C03	M00004081A:G01	M00001664B:E08
	M00003904C:A08	M00004081C:A10	M00001664B:F06
	M00003881B:F10	M00004083A:E08	M00001669B:C12
	M00003871D:G06	M00004083B:C01	M00001669C:B09
	M00003868D:D09	M00004086D:G08	M00001670A:F09
	M00003868D:D11	M00004087B:A12	M00001678C:F09
	M00003870C:A01	M00004087C:A01	M00001693A:H06
	M00003870C:A10	M00004088C:F01	M00003805D:E06
	M00003870C:E10	M00004088D:A11	M00003806C:A06
	M00003871A:A02	M00004088D:B05	M00003809B:A03
	M00003871A:B09	M00004088D:B10	M00003810A:A02
	M00003871A:C11	M00004090B:B04	M00003810B:B11
	M00003871A:G09	M00004090B:H06	M00003810C:B06
	M00003871C:E04	M00004092B:E05	M00003810D:H09
	M00003871C:F12	M00004093C:C02	M00003811C:C02
	M00003878C:D08	M00004096D:H03	M00003813B:F02
	M00003871D:E11	M00004099D:F01	M00003813C:H08
	M00003877C:G12	M00004100B:C07	M00003813D:B12
	M00003875A:A07	M00004103B:E09	M00003813D:C02
	M00003875A:B01	M00004105C:B05	M00003813D:G06
	M00003875B:F12	M00004105C:C08	M00003814B:C01
	M00003875C:A01	M00004107A:A12	M00003817C:A10
	M00003875C:A09	M00004107B:D07	M00003817C:G06
	M00003875C:G02	M00004108B:B02	M00003817D:D12

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	M00003876B:C05	M00004108D:E07	M00003821A:H09
	M00003876C:D02	M00004108D:G04	M00003822B:G12
	M00003876C:F02	M00004110A:A10	M00003822C:A07
	M00003877B:H10	M00004110B:A07	M00003823C:B01
	M00003868D:B09	M00004118B:A03	M00003823C:C04
	M00003871D:A10	M00004118B:F01	M00003824A:G11
	M00001669D:D06	M00004118D:B05	M00003824B:C09
	M00001661A:B11	M00004119A:C09	M00003824C:A10
	M00001661B:F06	M00004136D:B02	M00003824D:D08
	M00001662A:C07	M00004137A:D06	M00003825B:F10
	M00001662A:G01	M00004139C:A12	M00003825D:F01
	M00001662B:F06	M00004149C:B02	M00003826C:F05
	M00001663C:F12	M00004159C:G12	M00003829A:B08
	M00001664A:F08	M00004169D:B11	M00003829C:E08
	M00001664D:F04	M00004187D:H06	M00003829D:D12
	M00001661A:E06	M00004228C:H03	M00003829D:F03
	M00001669A:B02	M00004244C:G07	M00003830D:B11
	M00001669B:B12	M00004358D:C02	M00003830D:H11
	M00001669C:C08	M00004690A:G08	M00003833D:H08
	M00001675A:G10	M00004891B:D01	M00003833D:H10
	M00001669D:C03	M00004891C:D04	M00003840A:C10
	M00001660B:E03	M00004895B:E12	M00003840B:F05
	M00001669D:F05	M00004895B:G04	M00003840C:C02
	M00001670B:G12	M00004895D:G07	M00003845C:D04
	M00001671A:A10	M00004898C:F03	M00003845D:A04
	M00001671B:G05	M00004899D:G06	M00003846B:C05
	M00001671C:C11	M00004959D:H12	M00003846C:F08
	M00001672D:E08	M00004960A:B08	M00003848B:E07
	M00001673A:G08	M00004960C:E10	M00003848D:G02
	M00001673B:B07	M00005100A:B02	M00003850C:G09
	M00001673B:F07	M00005100A:C01	M00003851A:A06
	M00001673D:D06	M00005101C:E12	M00003851B:D03
	M00001673D:F10	M00005102C:D03	M00003851B:E01
	M00001674A:G07	M00005134B:E08	M00003851C:F09
	M00001692D:B01	M00005139A:H03	M00003851D:H11
	M00001669C:D09	M00005140C:B10	M00003852B:G04
	M00001655C:E01	M00005140D:C06	M00003852C:F07
	M00001649D:A08	M00005178D:H04	M00003853B:C10
	M00001650A:C11	M00005210A:E06	M00003854C:C09
	M00001651A:H11	M00005212B:E01	M00003855A:A01
	M00001652A:A01	M00005212C:C03	M00003855A:F01
	M00001652B:G10	M00005212C:D02	M00003855B:B09
	M00001652D:E05	M00005212C:H02	M00003856A:G04
	M00001652D:E09	M00005212D:D09	M00003856B:A12
	M00001653B:C06	M00005212D:H01	M00003857A:E12
	M00001653B:G10	M00005216A:D09	M00003857A:H10
	M00001653C:D10	M00005216A:H01	M00003857C:E05
	M00001654D:A03	M00005217B:A06	M00003858B:G02
	M00001654D:E12	M00005218A:F09	M00003860D:E06
	M00001654D:F11	M00005228A:B03	M00003905C:F12

cDNA Ref No.; ATCC Accession No.	cDNA Ref ES31 ATCC No.	cDNA Ref No. ES32 ATCC No.	cDNA Ref ES33 ATCC No.
	M00001660C:B06	M00005228C:C05	M00003911A:D12
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	M00001675C:A04	M00005229B:H04	M00003966C:A12
	M00001660B:D03	M00005229B:H06	M00003966C:F03
	M00001660B:A09	M00005229D:H03	M00003973D:F08
	M00001659D:C09	M00005230B:H09	M00003974D:E01
	M00001659D:B05	M00005232A:H12	M00003974D:H07
	M00001654D:F12	M00005233B:D04	M00003976B:E06
	M00001659A:D12	M00005233D:H07	M00003976B:H07
	M00001655A:B11	M00005235B:F10	M00003978A:E01
	M00001658B:A07	M00005236A:E04	M00003978A:E09
	M00001658A:G09	M00005236A:G10	M00003978C:A12
	M00001657D:A04	M00005236B:A12	M00003980C:E12
	M00001657B:B04	M00001448B:A07	M00003980C:F12
	M00001656B:E01	M00001448B:G07	M00003981A:A07
	M00001660B:E04	M00001448D:E11	M00003981B:B12
	M00001659C:F10	M00001455A:D10	M00003982A:G03
	M00003808C:A05	M00001455A:E11	M00003982B:C10
	M00001694D:C12	M00001476D:F12	M00003982B:H10
	M00003746C:E02	M00001478A:F12	M00003983A:D02
	M00003779D:E08	M00001482C:F09	M00003983A:F06
	M00003792A:B10	M00001485C:D07	M00003983A:G02
	M00003793D:A11	M00001485C:G06	M00003983D:E08
	M00003794D:G03	M00001485D:A05	M00003983D:H02
	M00003797A:C11	M00001487C:A11	M00003985A:C01
	M00003797A:D06	M00001487C:G09	M00003986C:G11
	M00003797A:G03	M00001530A:B02	M00003986D:H12
	M00003800B:F03	M00001530A:H05	M00004027A:A08
	M00003805A:F02	M00001530D:A11	M00004028A:B10
	M00003806B:C09	M00001539B:B10	M00004028A:G03
	M00001674A:G11	M00001567A:C04	M00004029B:A01
	M00003806D:D11	M00001567A:C11	M00004029B:A06
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	M00003809B:E10	M00001573B:A06	M00004030C:A08
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	M00003813B:E09	M00001575B:C01	M00004035B:F05
	M00003814B:C12	M00001576C:H02	M00004036A:A11
	M00003814B:F12	M00001577A:A03	M00004037C:D04
	M00003815C:C06	M00001578B:A06	M00004038A:E05
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	M00003817B:C04	M00001582C:C04	M00004039C:E02
	M00003806B:G05	M00001582C:G02	M00004039D:B10
	M00001679A:D10	M00001584A:A07	M00004040A:A07
	M00001675C:C03	M00001584D:B06	M00004040A:B04
	M00001675C:D12	M00001584D:C11	M00004040A:C08

cDNA Ref No.; ATCC Accession No.	cDNA Ref ES31 ATCC No.	cDNA Ref No. ES32 ATCC No.	cDNA Ref ES33 ATCC No.
	M00001675D:E10	M00001585D:B12	M00004040B:C05
	M00001676B:B09	M00001586C:H07	M00004040B:F07
	M00001676B:E01	M00001589D:A01	M00004069A:E12
	M00001676C:A04	M00001590D:B04	M00004069C:C08
	M00001676C:E07	M00001592B:B02	M00004077A:G12
	M00001676D:A02	M00001592D:H02	M00004085B:G01
	M00001676D:B02	M00001594C:E05	M00004087A:B05
	M00001677A:G11	M00001594C:H03	M00004090D:F12
	M00001677B:A12	M00001594D:G11	M00004092C:D08
	M00001677B:B04	M00001595A:C07	M00004097C:E03
	M00001677D:B01	M00001595A:D12	M00004097C:H08
	M00001678D:B11	M00001595A:E07	M00004097D:B05
	M00001681C:A08	M00001595B:G07	
	M00003819B:G01	M00001595B:G10	
	M00001693C:E09	M00001595B:H11	
	M00001693C:C12	M00001595C:A01	
	M00001692B:E01	M00001595C:A05	
	M00001692A:B06	M00001595C:B12	
	M00001678B:H01	M00001595C:E05	
	M00001681D:C12	M00001595C:E09	
	M00001694A:E03	M00001595D:C11	
	M00001680B:D02	M00001596A:A02	
	M00001680A:B02	M00001596A:D01	
	M00001679D:F02	M00001596C:G05	
	M00001679D:B02	M00001607A:A01	
	M00001679A:G06		

We Claim:

1. A library of polynucleotides, the library comprising the sequence information of at least one of SEQ ID NOS:1-3544, 3546-4510, 4512-4725, 4727-4748, and 4750-5252.

2. The library of claim 1, wherein the library is provided on a nucleic acid array.

3. The library of claim 1, wherein the library is provided in a computer-readable format.

4. The library of claim 1, wherein the library comprises a differentially expressed polynucleotide comprising a sequence selected from the group consisting of SEQ ID NOS:65, 174, 203, 252, 253, 387, 419, 420, 491, 552, 560, 581, 590, 648, 693, 726, 746, 990, 1095, 1124, 1205, 1354, 1387, 1780, 1899, 1915, 1979, 2007, 2024, 2245, and 2325.

5. The library of claim 1, wherein the library comprises a polynucleotide differentially expressed in a human breast cancer cell, where the polynucleotide comprises a sequence selected from the group consisting of SEQ ID NOS:15, 36, 44, 45, 89, 146, 154, 159, 165, 174, 172, 183, 203, 261, 364, 366, 387, 419, 420, 496, 503, 510, 512, 529, 552, 560, 564, 570, 590, 606, 644, 646, 693, 707, 711, 726, 746, 754, 756, 875, 902, 921, 942, 990, 1095, 1104, 1122, 1131, 1142, 1170, 1184, 1205, 1286, 1289, 1354, 1387, 1435, 1535, 1751, 1764, 1777, 1795, 1860, 1869, 1882, 1890, 1915, 1933, 1934, 1979, 1980, 2007, 2023, 2040, 2059, 2223, 2245, 2300, 2325, 2409, 2462, 2486, 2488, and 2492.

6. The library of claim 1, wherein the library comprises a polynucleotide differentially expressed in a human colon cancer cell, where the polynucleotide comprises a sequence selected from the group consisting of SEQ ID NOS:33, 65, 228, 250, 252, 253, 280, 282, 355, 370, 387, 443, 460, 491, 545, 560, 581, 603, 680, 693, 703, 704, 716, 726, 746, 752, 753, 1095, 1104, 1205, 1241, 1264, 1354, 1387, 1401, 1442, 1514, 1734, 1742, 1780, 1851, 1899, 1915, 1954, 2024, 2066, 2262, and 2325.



7. The library of claim 1, wherein the library comprises a polynucleotide differentially expressed in a human lung cancer cell, where the polynucleotide comprises a sequence selected from the group consisting of SEQ ID NOS: 10, 54, 65, 171, 174, 203, 252, 253, 254, 285, 419, 420, 466, , 491, 525, 526, 552, 571, 574, 590, 693, 700, 726, 742, 746, 861, 990, 922, 1088, 1288, 1355, 1417, 1422, 1444, 1454, 1570, 1597, 1979, 2007, 2024, 2034, 2038, 2126, and 2245.

8. The library of claim 1, wherein the library comprises a polynucleotide differentially expressed in a human cancer cell, where the polynucleotide comprises a sequence selected from the group consisting of SEQ ID NOS:648 and1899.

9. An isolated polynucleotide comprising a nucleotide sequence having at least 90% sequence identity to an identifying sequence of SEQ ID NOS:1-3544, 3546-4510, 4512-4725, 4727-4748, and 4750-5252, or a degenerate variant or fragment thereof.

10. The polynucleotide of claim 9, wherein the polynucleotide comprises a sequence of one of SEQ ID NOS:2503, 2504, 2550, 2555, 2578, 2656, 2667, 2712, 2723, 2728, 2738, 2734, 2754, 2758, 2760, 2832, 2835, 2842, 2843, 2849, 2893, 2933, 2956, 2971, 2981, 3009, 3018, 3019, 3046, 3084, 3190, 3129, 3173, 3226, 3227, 3274, 3290, 3356, 3365, 3377, 3381, 3390, 3391, 3404, 3407, 3408, 3409, 3418, 3419, 3451, 3597, 3600, 3618, 3632, 3635, 3646, 3648, 3657, 3665, 3669, 3670, 3671, 3656, 3680, 3686, 3695, 3696, 3700, 3710, 3736, 3762, 3763, 3774, 3775, 3791, 3804, 3806, 3836, 3895, 3905, 3919, 3920, 3927, 3936, 3951, 3974, 3998, 4036, 4038, 4044, 4056, 4072, 4117, 4119, 4152, 4153, 4154, 4172, 4175, 4159, 4175, 4205, 4216, 4223, 4228, 4238, 4241, 4243, 4251, 4253, 4261, 4263,4278, 4288, 4322, 4330, 4343, 4359, 4363, 4364, 4365, 4373, 4375, 4384, 4385, 4406, 4409, 4431, 4434, 4441, 4442, 4444, 4455, 4469, 4473, 4477, 4482, 4489, 4495, 4496, 4498, 4525, 4535, 4536, 4540, 4560, 4616, 4562, 4586, 4605, 4629, 4653, 4654, 4658, 4659, 4660, 4661, 4664, 4665, 4668, 4684, 4682, 4688, 4689, 4710, 4718, 4733, 4724, 4733, 4746, 4755, 4760, 4710, 4777, 4785, 4792, 4794, 4801, 4807, 4821, 4822, 4847, 4850, 4854, 4856, 4866, 4885, 4900, 4901, 4905, 4914, 4925, 4929, 4931, 4943, 4944, 4959, 5111, 5020, 5041, 5046, 5059, 5083, 5090, 5094, 5102, 5125, 5174, 5197, 5208, 5217, 5237, 5239, 5241, 5243, 5248, and 5252.

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11. A recombinant host cell containing the polynucleotide of claim 9.

12. An isolated polypeptide encoded by the polynucleotide of claim 9.

13. An antibody that specifically binds a polypeptide of claim 12.

14. A vector comprising the polynucleotide of claim 9.

15. A polynucleotide comprising the nucleotide sequence of an insert contained in a clone deposited as ATCC accession number xx, xx, xx, xx, xx, xx, xx, xx, or xx.

16. A method of detecting differentially expressed genes correlated with a cancerous state of a mammalian cell, the method comprising the step of:

detecting at least one differentially expressed gene product in a test sample derived from a cell suspected of being cancerous, where the gene product is encoded by a gene corresponding to a sequence of at least one of SEQ ID NOS:10, 15, 33, 36, 44, 45, 54, 65, 89, 146, 154, 159, 165, 171, 172, 174, 183, 203, 228, 250, 252, 253, 254, 261, 280, 282, 285, 355, 364, 366, 370, 387, 419, 420, 443, 460, 466, 491, 496, 503, 510, 512, 525, 526, 529, 545, 552, 560, 564, 570, 571, 574, 581, 590, 603, 606, 644, 646, 648, 680, 693, 700, 703, 704, 707, 711, 716, 726, 742, 746, 752, 753, 754, 756, 861, 875, 902, 921, 922, 942, 990, 1088, 1095, 1104, 1122, 1131, 1142, 1170, 1184, 1205, 1286, 1288, 1289, 1354, 1355, 1387, 1417, 1435, 1444, 1454, 1535, 1570, 1597, 1734, 1742, 1751, 1764, 1777, 1780, 1795, 1860, 1869, 1882, 1890, 1899, 1915, 1933, 1934, 1954, 1979, 1980, 2007, 2023, 2024, 2034, 2040, 2059, 2126, 2223, 2245, 2262, 2300, 2325, 2409, 2486, 2462, 2488, 2492, 1241, 1264, 1401, 1422, 1442, 1514, 1851, 1915, 2007, 2024, 2038, 2066, and 2245;

wherein detection of the differentially expressed gene product is correlated with a cancerous state of the cell from which the test sample was derived.

17. The method of claim 16, wherein said detecting step is by hybridization of the test sample to a reference array, wherein the reference array comprises an identifying sequence of at least one of SEQ ID NOS: 65, 174, 203, 252, 253, 387, 419, 420, 491, 552,

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560, 581, 590, 648, 693, 726, 746, 990, 1095, 1124, 1205, 1354, 1387, 1780, 1899, 1915, 1979, 2007, 2024, 2325, and 2245.

18. The method of claim 16, wherein the cell is a breast tissue derived cell, and the differentially expressed gene product is encoded by a gene corresponding to a sequence of at least one of SEQ ID NOS:36, 44, 45, 89, 146, 154, 159, 165, 172, 174, 183, 203, 261, 364, 366, 387, 419, 420, 496, 503, 510, 512, 529, 552, 560,564, 570, 590, 606, 644, 646, 693, 707, 711, 726, 746, 754, 756, 875, 902, 921, 942, 990, 1095, 1104, 1122, 1131, 1142, 1170, 1184, 1205, 1286, 1289, 1354, 1387, 1435, 1535, 1751, 1764, 1777, 1795, 1860, 1869, 1882, 1890, 1915, 1933, 1934, 1979, 1980, 2007, 2023, 2040, 2059, 2223, 2245, 2300, 2325, 2409, 2462, 2486, 2488, and 2492.

19. The method of claim 16, wherein the cell is a colon tissue derived cell, and the differentially expressed gene product is encoded by a gene corresponding to a sequence of at least one of SEQ ID NOS:33, 65, 228, 250, 252, 253, 280, 282, 355, 370, 387, 443, 460, 491, 545, 560, 581, 603, 680, 693, 703, 704, 716, 726, 746, 752, 753, 1095, 1104, 1205, 1241, 1264, 1354, 1387, 1401, 1442, 1514, 1734, 1742, 1780, 1851, 1899, 1915, 1954, 2024, 2066, 2262, and 2325.

20. The method of claim 16, wherein the cell is a lung tissue derived cell, and the differentially expressed gene product is encoded by a gene corresponding to a sequence of at least one of SEQ ID NOS: 10, 54, 65, 171, 174, 203, 252, 253, 254, 285, 419, 420, 466, 491, 525, 526, 552, 571, 574, 590, 693, 700, 726, 742, 746, 861, 922, 990, 1088, 1288, 1355, 1417, 1422, 1444, 1454, 1570, 1597, 1979, 2007, 2024, 2034, 2038, 2126, and 2245.

21. The method of claim 16, wherein the differentially expressed gene product is encoded by a gene corresponding to a sequence of at least one of SEQ ID NOS:648 and 1899.

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