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(71) Applicants (*for all designated States except US*):
SMITHKLINE BEECHAM CORPORATION [US/US]; UW2220, 709 Swedeland Road, King of Prussia, PA 19406 (US). **SMITHKLINE BEECHAM PLC** [GB/GB]; New Horizons Court, Great West Road, Brentford, Middlesex TW8-9EP (GB). **GLAXO GROUP LIMITED** [GB/GB]; Glaxo Welcome House, Berkley Ave, Greenford, Middlesex UB6 ONN (GB).

(72) Inventors; and

(75) Inventors/Applicants (*for US only*): **AGARWAL, Pankaj** [IN/US]; E 801, 251 West Dekalb Pike, King of Prussia, PA 19406 (US). **COGSWELL, John, P.** [US/US]; Five Moore Drive, Research Triangle Park, NC 27709 (US). **LAI, Ying-Ta** [CN/US]; 516 Spruce Ave, Upper Darby, PA 19082 (US). **MARTENSEN, Shelby, A.** [US/US]; Five Moore Drive, Research Triangle Park, NC 27709 (US). **RIZVI, Safia, K.** [US/US]; H-610, 4617 Pine Street, Philadelphia, PA 19143 (US). **STRUM, Jay, C.** [US/US]; Five Moore Drive, Research Triangle

Park, NC 27709 (US). **SMITH, Randall, F.** [US/US]; 4138 Presidential Drive, Lafayette Hill, PA 19444 (US). **XIANG, Zhaoying** [CN/US]; 2413 Ridgeway, Fort Lee, NJ 07024 (US). **XIE, Qing** [CN/US]; 4B, 310 Sawmill Lane, Horsham, PA 19044 (US).

(74) Agent: **GIMMI, Edward, R.**; UW2000, 709 Swedeland Road, King Of Prussia, PA 19406 (US).

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(54) Title: NOVEL COMPOUNDS

(57) Abstract: Polypeptides and polynucleotides of the genes set forth in Table I and methods for producing such polypeptides by recombinant techniques are disclosed. Also disclosed are methods for utilizing polypeptides and polynucleotides of the genes set forth in Table I in diagnostic assays.



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Novel Compounds

Field of Invention

This invention relates to newly identified polypeptides and polynucleotides encoding such polypeptides, to their use in diagnosis and in identifying compounds that may be agonists, antagonists that are potentially useful in therapy, and to production of such polypeptides and polynucleotides. The polynucleotides and polypeptides of the present invention also relate to proteins with signal sequences which allow them to be secreted extracellularly or membrane-associated (hereinafter often referred collectively as secreted proteins or secreted polypeptides).

Background of the Invention

The drug discovery process is currently undergoing a fundamental revolution as it embraces "functional genomics", that is, high throughput genome- or gene-based biology. This approach as a means to identify genes and gene products as therapeutic targets is rapidly superseding earlier approaches based on "positional cloning". A phenotype, that is a biological function or genetic disease, would be identified and this would then be tracked back to the responsible gene, based on its genetic map position.

Functional genomics relies heavily on high-throughput DNA sequencing technologies and the various tools of bioinformatics to identify gene sequences of potential interest from the many molecular biology databases now available. There is a continuing need to identify and characterise further genes and their related polypeptides/proteins, as targets for drug discovery.

Proteins and polypeptides that are naturally secreted into blood, lymph and other body fluids, or secreted into the cellular membrane are of primary interest for pharmaceutical research and development. The reason for this interest is the relative ease to target protein therapeutics into their place of action (body fluids or the cellular membrane). The natural pathway for protein secretion into extracellular space is the endoplasmic reticulum in eukaryotes and the inner membrane in prokaryotes (Palade, 1975, Science, 189, 347; Milstein, Brownlee, Harrison, and Mathews, 1972, Nature New Biol., 239, 117; Blobel, and Dobberstein, 1975, J. Cell. Biol., 67, 835). On the other hand, there is no known natural pathway for exporting a protein from the exterior of the cells into the cytosol (with the exception of pinocytosis, a mechanism of snake venom toxin intrusion into cells). Therefore targeting protein therapeutics into cells poses extreme difficulties.

The secreted and membrane-associated proteins include but are not limited

to all peptide hormones and their receptors (including but not limited to insulin, growth hormones, chemokines, cytokines, neuropeptides, integrins, kallikreins, lamins, melanins, natriuretic hormones, neuropsin, neurotrophins, pituitary hormones, pleiotropins, prostaglandins, secretogranins, selectins, thromboglobulins, thymosins), the breast and colon cancer gene products, leptin, the obesity gene protein and its receptors, serum albumin, superoxide dismutase, spliceosome proteins, 7TM (transmembrane) proteins also called as G-protein coupled receptors, immunoglobulins, several families of serine proteinases (including but not limited to proteins of the blood coagulation cascade, digestive enzymes), deoxyribonuclease I, etc.

Therapeutics based on secreted or membrane-associated proteins approved by FDA or foreign agencies include but are not limited to insulin, glucagon, growth hormone, chorionic gonadotropin, follicle stimulating hormone, luteinizing hormone, calcitonin, adrenocorticotrophic hormone (ACTH), vasopressin, interleukines, interferones, immunoglobulins, lactoferrin (diverse products marketed by several companies), tissue-type plasminogen activator (Alteplase by Genentech), hyaluronidase (Wydase by Wyeth-Ayerst), dornase alpha (Pulmozyme) by Genentech, Chymodiactin (chymopapain by Knoll), alglucerase (Ceredase by Genzyme), streptokinase (Kabikinase by Pharmacia) (Streptase by Astra), etc. This indicates that secreted and membrane-associated proteins have an established, proven history as therapeutic targets. Clearly, there is a need for identification and characterization of further secreted and membrane-associated proteins which can play a role in preventing, ameliorating or correcting dysfunction or disease, including but not limited to diabetes, breast-, prostate-, colon cancer and other malignant tumors, hyper- and hypotension, obesity, bulimia, anorexia, growth abnormalities, asthma, manic depression, dementia, delirium, mental retardation, Huntington's disease, Tourette's syndrome, schizophrenia, growth, mental or sexual development disorders, and dysfunctions of the blood cascade system including those leading to stroke. The proteins of the present invention which include the signal sequences are also useful to further elucidate the mechanism of protein transport which at present is not entirely understood, and thus can be used as research tools.

Summary of the Invention

The present invention relates to particular polypeptides and polynucleotides of the genes set forth in Table I, including recombinant materials and methods for their production.

Such polypeptides and polynucleotides are of interest in relation to methods of treatment of certain diseases, including, but not limited to, the diseases set forth in Tables III and V, hereinafter referred to as "diseases of the invention". In a further aspect, the invention relates to methods for identifying agonists and antagonists (*e.g.*, inhibitors) using the materials provided by the invention, and treating conditions associated with imbalance of polypeptides and/or polynucleotides of the genes set forth in Table I with the identified compounds. In still a further aspect, the invention relates to diagnostic assays for detecting diseases associated with inappropriate activity or levels the genes set forth in Table I. Another aspect of the invention concerns a polynucleotide comprising any of the nucleotide sequences set forth in the Sequence Listing and a polypeptide comprising a polypeptide encoded by the nucleotide sequence. In another aspect, the invention relates to a polypeptide comprising any of the polypeptide sequences set forth in the Sequence Listing and recombinant materials and methods for their production. Another aspect of the invention relates to methods for using such polypeptides and polynucleotides. Such uses include the treatment of diseases, abnormalities and disorders (hereinafter simply referred to as diseases) caused by abnormal expression, production, function and or metabolism of the genes of this invention, and such diseases are readily apparent by those skilled in the art from the homology to other proteins disclosed for each attached sequence. In still another aspect, the invention relates to methods to identify agonists and antagonists using the materials provided by the invention, and treating conditions associated with the imbalance with the identified compounds. Yet another aspect of the invention relates to diagnostic assays for detecting diseases associated with inappropriate activity or levels of the secreted proteins of the present invention.

Description of the Invention

In a first aspect, the present invention relates to polypeptides the genes set forth in Table I. Such polypeptides include:

- (a) an isolated polypeptide encoded by a polynucleotide comprising a sequence set forth in the Sequence Listing, herein when referring to polynucleotides or polypeptides of the Sequence Listing, a reference is also made to the Sequence Listing referred to in the Sequence Listing;
- (b) an isolated polypeptide comprising a polypeptide sequence having at least 95%, 96%, 97%, 98%, or 99% identity to a polypeptide sequence set forth in the Sequence Listing;
- (c) an isolated polypeptide comprising a polypeptide sequence set forth in the Sequence Listing;

- (d) an isolated polypeptide having at least 95%, 96%, 97%, 98%, or 99% identity to a polypeptide sequence set forth in the Sequence Listing;
- (e) a polypeptide sequence set forth in the Sequence Listing; and
- (f) an isolated polypeptide having or comprising a polypeptide sequence that has an Identity Index of 0.95, 0.96, 0.97, 0.98, or 0.99 compared to a polypeptide sequence set forth in the Sequence Listing;
- (g) fragments and variants of such polypeptides in (a) to (f).

Polypeptides of the present invention are believed to be members of the gene families set forth in Table II. They are therefore of therapeutic and diagnostic interest for the reasons set forth in Tables III and V. The biological properties of the polypeptides and polynucleotides of the genes set forth in Table I are hereinafter referred to as "the biological activity" of polypeptides and polynucleotides of the genes set forth in Table I. Preferably, a polypeptide of the present invention exhibits at least one biological activity of the genes set forth in Table I.

Polypeptides of the present invention also include variants of the aforementioned polypeptides, including all allelic forms and splice variants. Such polypeptides vary from the reference polypeptide by insertions, deletions, and substitutions that may be conservative or non-conservative, or any combination thereof. Particularly preferred variants are those in which several, for instance from 50 to 30, from 30 to 20, from 20 to 10, from 10 to 5, from 5 to 3, from 3 to 2, from 2 to 1 or 1 amino acids are inserted, substituted, or deleted, in any combination.

Preferred fragments of polypeptides of the present invention include an isolated polypeptide comprising an amino acid sequence having at least 30, 50 or 100 contiguous amino acids from an amino acid sequence set forth in the Sequence Listing, or an isolated polypeptide comprising an amino acid sequence having at least 30, 50 or 100 contiguous amino acids truncated or deleted from an amino acid sequence set forth in the Sequence Listing. Preferred fragments are biologically active fragments that mediate the biological activity of polypeptides and polynucleotides of the genes set forth in Table I, including those with a similar activity or an improved activity, or with a decreased undesirable activity. Also preferred are those fragments that are antigenic or immunogenic in an animal, especially in a human.

Fragments of a polypeptide of the invention may be employed for producing the corresponding full-length polypeptide by peptide synthesis; therefore, these variants may be employed as intermediates for producing the full-length polypeptides of the invention. A polypeptide of the present invention may be in the form of the "mature" protein or may be a

part of a larger protein such as a precursor or a fusion protein. It is often advantageous to include an additional amino acid sequence that contains secretory or leader sequences, pro-sequences, sequences that aid in purification, for instance multiple histidine residues, or an additional sequence for stability during recombinant production.

- 5 Polypeptides of the present invention can be prepared in any suitable manner, for instance by isolation from naturally occurring sources, from genetically engineered host cells comprising expression systems (*vide infra*) or by chemical synthesis, using for instance automated peptide synthesizers, or a combination of such methods. Means for preparing such polypeptides are well understood in the art.
- 10 In a further aspect, the present invention relates to polynucleotides of the genes set forth in Table I. Such polynucleotides include:
- (a) an isolated polynucleotide comprising a polynucleotide sequence having at least 95%, 96%, 97%, 98%, or 99% identity to a polynucleotide sequence set forth in the Sequence Listing;
 - 15 (b) an isolated polynucleotide comprising a polynucleotide set forth in the Sequence Listing;
 - (c) an isolated polynucleotide having at least 95%, 96%, 97%, 98%, or 99% identity to a polynucleotide set forth in the Sequence Listing;
 - (d) an isolated polynucleotide set forth in the Sequence Listing;
 - 20 (e) an isolated polynucleotide comprising a polynucleotide sequence encoding a polypeptide sequence having at least 95%, 96%, 97%, 98%, or 99% identity to a polypeptide sequence set forth in the Sequence Listing;
 - (f) an isolated polynucleotide comprising a polynucleotide sequence encoding a polypeptide set forth in the Sequence Listing;
 - 25 (g) an isolated polynucleotide having a polynucleotide sequence encoding a polypeptide sequence having at least 95%, 96%, 97%, 98%, or 99% identity to a polypeptide sequence set forth in the Sequence Listing;
 - (h) an isolated polynucleotide encoding a polypeptide set forth in the Sequence Listing;
 - (i) an isolated polynucleotide having or comprising a polynucleotide sequence that has an
 - 30 Identity Index of 0.95, 0.96, 0.97, 0.98, or 0.99 compared to a polynucleotide sequence set forth in the Sequence Listing;
 - (j) an isolated polynucleotide having or comprising a polynucleotide sequence encoding a polypeptide sequence that has an Identity Index of 0.95, 0.96, 0.97, 0.98, or 0.99 compared to a polypeptide sequence set forth in the Sequence Listing; and

polynucleotides that are fragments and variants of the above mentioned polynucleotides or that are complementary to above mentioned polynucleotides, over the entire length thereof.

Preferred fragments of polynucleotides of the present invention include an isolated polynucleotide comprising an nucleotide sequence having at least 15, 30, 50 or 100
5 contiguous nucleotides from a sequence set forth in the Sequence Listing, or an isolated polynucleotide comprising a sequence having at least 30, 50 or 100 contiguous nucleotides truncated or deleted from a sequence set forth in the Sequence Listing.

Preferred variants of polynucleotides of the present invention include splice variants, allelic variants, and polymorphisms, including polynucleotides having one or more
10 single nucleotide polymorphisms (SNPs).

Polynucleotides of the present invention also include polynucleotides encoding polypeptide variants that comprise an amino acid sequence set forth in the Sequence Listing and in which several, for instance from 50 to 30, from 30 to 20, from 20 to 10, from 10 to 5, from 5 to 3, from 3 to 2, from 2 to 1 or 1 amino acid residues are substituted, deleted or
15 added, in any combination.

In a further aspect, the present invention provides polynucleotides that are RNA transcripts of the DNA sequences of the present invention. Accordingly, there is provided an RNA polynucleotide that:

(a) comprises an RNA transcript of the DNA sequence encoding a polypeptide set
20 forth in the Sequence Listing;

(b) is a RNA transcript of a DNA sequence encoding a polypeptide set forth in the Sequence Listing;

(c) comprises an RNA transcript of a DNA sequence set forth in the Sequence Listing; or

25 (d) is a RNA transcript of a DNA sequence set forth in the Sequence Listing; and RNA polynucleotides that are complementary thereto.

The polynucleotide sequences set forth in the Sequence Listing show homology with the polynucleotide sequences set forth in Table II. A polynucleotide sequence set forth in the Sequence Listing is a cDNA sequence that encodes a polypeptide set forth in the
30 Sequence Listing. A polynucleotide sequence encoding a polypeptide set forth in the Sequence Listing may be identical to a polypeptide encoding a sequence set forth in the Sequence Listing or it may be a sequence other than a sequence set forth in the Sequence Listing, which, as a result of the redundancy (degeneracy) of the genetic code, also encodes a polypeptide set forth in the Sequence Listing. A polypeptide of a sequence set forth in the
35 Sequence Listing is related to other proteins of the gene families set forth in Table II, having

homology and/or structural similarity with the polypeptides set forth in Table II. Preferred polypeptides and polynucleotides of the present invention are expected to have, *inter alia*, similar biological functions/properties to their homologous polypeptides and polynucleotides. Furthermore, preferred polypeptides and polynucleotides of the present invention have at least one activity of the genes set forth in Table I.

Polynucleotides of the present invention may be obtained using standard cloning and screening techniques from a cDNA library derived from mRNA from the tissues set forth in Table IV (see for instance, Sambrook *et al.*, Molecular Cloning: A Laboratory Manual, 2nd Ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. (1989)). Polynucleotides of the invention can also be obtained from natural sources such as genomic DNA libraries or can be synthesized using well known and commercially available techniques.

When polynucleotides of the present invention are used for the recombinant production of polypeptides of the present invention, the polynucleotide may include the coding sequence for the mature polypeptide, by itself, or the coding sequence for the mature polypeptide in reading frame with other coding sequences, such as those encoding a leader or secretory sequence, a pre-, or pro- or prepro- protein sequence, or other fusion peptide portions. For example, a marker sequence that facilitates purification of the fused polypeptide can be encoded. In certain preferred embodiments of this aspect of the invention, the marker sequence is a hexa-histidine peptide, as provided in the pQE vector (Qiagen, Inc.) and described in Gentz *et al.*, Proc Natl Acad Sci USA (1989) 86:821-824, or is an HA tag. A polynucleotide may also contain non-coding 5' and 3' sequences, such as transcribed, non-translated sequences, splicing and polyadenylation signals, ribosome binding sites and sequences that stabilize mRNA.

Polynucleotides that are identical, or have sufficient identity to a polynucleotide sequence set forth in the Sequence Listing, may be used as hybridization probes for cDNA and genomic DNA or as primers for a nucleic acid amplification reaction (for instance, PCR). Such probes and primers may be used to isolate full-length cDNAs and genomic clones encoding polypeptides of the present invention and to isolate cDNA and genomic clones of other genes (including genes encoding paralogs from human sources and orthologs and paralogs from other species) that have a high sequence similarity to sequences set forth in the Sequence Listing, typically at least 95% identity. Preferred probes and primers will generally comprise at least 15 nucleotides, preferably, at least 30 nucleotides and may have at least 50, if not at least 100 nucleotides. Particularly preferred probes will have between

30 and 50 nucleotides. Particularly preferred primers will have between 20 and 25 nucleotides.

A polynucleotide encoding a polypeptide of the present invention, including homologs from other species, may be obtained by a process comprising the steps of
5 screening a library under stringent hybridization conditions with a labeled probe having a sequence set forth in the Sequence Listing or a fragment thereof, preferably of at least 15 nucleotides; and isolating full-length cDNA and genomic clones containing the polynucleotide sequence set forth in the Sequence Listing. Such hybridization techniques are well known to the skilled artisan. Preferred stringent hybridization conditions include
10 overnight incubation at 42°C in a solution comprising: 50% formamide, 5xSSC (150mM NaCl, 15mM trisodium citrate), 50 mM sodium phosphate (pH 7.6), 5x Denhardt's solution, 10 % dextran sulfate, and 20 microgram/ml denatured, sheared salmon sperm DNA; followed by washing the filters in 0.1x SSC at about 65°C. Thus the present invention also includes isolated polynucleotides, preferably with a nucleotide sequence of at least 100,
15 obtained by screening a library under stringent hybridization conditions with a labeled probe having the sequence set forth in the Sequence Listing or a fragment thereof, preferably of at least 15 nucleotides.

The skilled artisan will appreciate that, in many cases, an isolated cDNA sequence will be incomplete, in that the region coding for the polypeptide does not extend all the way
20 through to the 5' terminus. This is a consequence of reverse transcriptase, an enzyme with inherently low "processivity" (a measure of the ability of the enzyme to remain attached to the template during the polymerisation reaction), failing to complete a DNA copy of the mRNA template during first strand cDNA synthesis.

There are several methods available and well known to those skilled in the art to
25 obtain full-length cDNAs, or extend short cDNAs, for example those based on the method of Rapid Amplification of cDNA ends (RACE) (see, for example, Frohman et al., Proc Nat Acad Sci USA 85, 8998-9002, 1988). Recent modifications of the technique, exemplified by the Marathon (trade mark) technology (Clontech Laboratories Inc.) for example, have significantly simplified the search for longer cDNAs. In the Marathon (trade mark)
30 technology, cDNAs have been prepared from mRNA extracted from a chosen tissue and an 'adaptor' sequence ligated onto each end. Nucleic acid amplification (PCR) is then carried out to amplify the "missing" 5' end of the cDNA using a combination of gene specific and adaptor specific oligonucleotide primers. The PCR reaction is then repeated using 'nested' primers, that is, primers designed to anneal within the amplified product (typically an
35 adapter specific primer that anneals further 3' in the adaptor sequence and a gene specific

primer that anneals further 5' in the known gene sequence). The products of this reaction can then be analyzed by DNA sequencing and a full-length cDNA constructed either by joining the product directly to the existing cDNA to give a complete sequence, or carrying out a separate full-length PCR using the new sequence information for the design of the 5' primer.

Recombinant polypeptides of the present invention may be prepared by processes well known in the art from genetically engineered host cells comprising expression systems. Accordingly, in a further aspect, the present invention relates to expression systems comprising a polynucleotide or polynucleotides of the present invention, to host cells which are genetically engineered with such expression systems and to the production of polypeptides of the invention by recombinant techniques. Cell-free translation systems can also be employed to produce such proteins using RNAs derived from the DNA constructs of the present invention.

For recombinant production, host cells can be genetically engineered to incorporate expression systems or portions thereof for polynucleotides of the present invention. Polynucleotides may be introduced into host cells by methods described in many standard laboratory manuals, such as Davis et al., Basic Methods in Molecular Biology (1986) and Sambrook *et al. (ibid)*. Preferred methods of introducing polynucleotides into host cells include, for instance, calcium phosphate transfection, DEAE-dextran mediated transfection, transfection, micro-injection, cationic lipid-mediated transfection, electroporation, transduction, scrape loading, ballistic introduction or infection.

Representative examples of appropriate hosts include bacterial cells, such as *Streptococci*, *Staphylococci*, *E. coli*, *Streptomyces* and *Bacillus subtilis* cells; fungal cells, such as yeast cells and *Aspergillus* cells; insect cells such as *Drosophila* S2 and *Spodoptera* Sf9 cells; animal cells such as CHO, COS, HeLa, C127, 3T3, BHK, HEK 293 and Bowes melanoma cells; and plant cells.

A great variety of expression systems can be used, for instance, chromosomal, episomal and virus-derived systems, *e.g.*, vectors derived from bacterial plasmids, from bacteriophage, from transposons, from yeast episomes, from insertion elements, from yeast chromosomal elements, from viruses such as baculoviruses, papova viruses, such as SV40, vaccinia viruses, adenoviruses, fowl pox viruses, pseudorabies viruses and retroviruses, and vectors derived from combinations thereof, such as those derived from plasmid and bacteriophage genetic elements, such as cosmids and phagemids. The expression systems may contain control regions that regulate as well as engender expression. Generally, any system or vector that is able to maintain, propagate or express a polynucleotide to produce a

polypeptide in a host may be used. The appropriate polynucleotide sequence may be inserted into an expression system by any of a variety of well-known and routine techniques, such as, for example, those set forth in Sambrook *et al.*, (*ibid*). Appropriate secretion signals may be incorporated into the desired polypeptide to allow secretion of the translated protein into the lumen of the endoplasmic reticulum, the periplasmic space or the extracellular environment. These signals may be endogenous to the polypeptide or they may be heterologous signals.

If a polypeptide of the present invention is to be expressed for use in screening assays, it is generally preferred that the polypeptide be produced at the surface of the cell. In this event, the cells may be harvested prior to use in the screening assay. If the polypeptide is secreted into the medium, the medium can be recovered in order to recover and purify the polypeptide. If produced intracellularly, the cells must first be lysed before the polypeptide is recovered.

Polypeptides of the present invention can be recovered and purified from recombinant cell cultures by well-known methods including ammonium sulfate or ethanol precipitation, acid extraction, anion or cation exchange chromatography, phosphocellulose chromatography, hydrophobic interaction chromatography, affinity chromatography, hydroxylapatite chromatography and lectin chromatography. Most preferably, high performance liquid chromatography is employed for purification. Well known techniques for refolding proteins may be employed to regenerate active conformation when the polypeptide is denatured during intracellular synthesis, isolation and/or purification.

Polynucleotides of the present invention may be used as diagnostic reagents, through detecting mutations in the associated gene. Detection of a mutated form of a gene is characterized by the polynucleotides set forth in the Sequence Listing in the cDNA or genomic sequence and which is associated with a dysfunction. Will provide a diagnostic tool that can add to, or define, a diagnosis of a disease, or susceptibility to a disease, which results from under-expression, over-expression or altered spatial or temporal expression of the gene. Individuals carrying mutations in the gene may be detected at the DNA level by a variety of techniques well known in the art.

Nucleic acids for diagnosis may be obtained from a subject's cells, such as from blood, urine, saliva, tissue biopsy or autopsy material. The genomic DNA may be used directly for detection or it may be amplified enzymatically by using PCR, preferably RT-PCR, or other amplification techniques prior to analysis. RNA or cDNA may also be used in similar fashion. Deletions and insertions can be detected by a change in size of the amplified product in comparison to the normal genotype. Point mutations can be identified

by hybridizing amplified DNA to labeled nucleotide sequences of the genes set forth in Table I. Perfectly matched sequences can be distinguished from mismatched duplexes by RNase digestion or by differences in melting temperatures. DNA sequence difference may also be detected by alterations in the electrophoretic mobility of DNA fragments in gels, with or without denaturing agents, or by direct DNA sequencing (see, for instance, Myers *et al.*, Science (1985) 230:1242). Sequence changes at specific locations may also be revealed by nuclease protection assays, such as RNase and S1 protection or the chemical cleavage method (see Cotton *et al.*, Proc Natl Acad Sci USA (1985) 85: 4397-4401).

An array of oligonucleotides probes comprising polynucleotide sequences or fragments thereof of the genes set forth in Table I can be constructed to conduct efficient screening of *e.g.*, genetic mutations. Such arrays are preferably high density arrays or grids. Array technology methods are well known and have general applicability and can be used to address a variety of questions in molecular genetics including gene expression, genetic linkage, and genetic variability, see, for example, M. Chee *et al.*, Science, 274, 610-613 (1996) and other references cited therein.

Detection of abnormally decreased or increased levels of polypeptide or mRNA expression may also be used for diagnosing or determining susceptibility of a subject to a disease of the invention. Decreased or increased expression can be measured at the RNA level using any of the methods well known in the art for the quantitation of polynucleotides, such as, for example, nucleic acid amplification, for instance PCR, RT-PCR, RNase protection, Northern blotting and other hybridization methods. Assay techniques that can be used to determine levels of a protein, such as a polypeptide of the present invention, in a sample derived from a host are well-known to those of skill in the art. Such assay methods include radio-immunoassays, competitive-binding assays, Western Blot analysis and ELISA assays.

Thus in another aspect, the present invention relates to a diagnostic kit comprising:

- (a) a polynucleotide of the present invention, preferably the nucleotide sequence set forth in the Sequence Listing, or a fragment or an RNA transcript thereof;
- (b) a nucleotide sequence complementary to that of (a);
- (c) a polypeptide of the present invention, preferably the polypeptide set forth in the Sequence Listing or a fragment thereof; or
- (d) an antibody to a polypeptide of the present invention, preferably to the polypeptide set forth in the Sequence Listing.

It will be appreciated that in any such kit, (a), (b), (c) or (d) may comprise a substantial component. Such a kit will be of use in diagnosing a disease or susceptibility to a disease, particularly diseases of the invention, amongst others.

The polynucleotide sequences of the present invention are valuable for chromosome localisation studies. The sequences set forth in the Sequence Listing are specifically targeted to, and can hybridize with, a particular location on an individual human chromosome. The mapping of relevant sequences to chromosomes according to the present invention is an important first step in correlating those sequences with gene associated disease. Once a sequence has been mapped to a precise chromosomal location, the physical position of the sequence on the chromosome can be correlated with genetic map data. Such data are found in, for example, V. McKusick, Mendelian Inheritance in Man (available on-line through Johns Hopkins University Welch Medical Library). The relationship between genes and diseases that have been mapped to the same chromosomal region are then identified through linkage analysis (co-inheritance of physically adjacent genes). Precise human chromosomal localisations for a genomic sequence (gene fragment etc.) can be determined using Radiation Hybrid (RH) Mapping (Walter, M. Spillett, D., Thomas, P., Weissenbach, J., and Goodfellow, P., (1994) A method for constructing radiation hybrid maps of whole genomes, *Nature Genetics* 7, 22-28). A number of RH panels are available from Research Genetics (Huntsville, AL, USA) e.g. the GeneBridge4 RH panel (*Hum Mol Genet* 1996 Mar;5(3):339-46 A radiation hybrid map of the human genome. Gyapay G, Schmitt K, Fizames C, Jones H, Vega-Czarny N, Spillett D, Muselet D, Prud'Homme JF, Dib C, Auffray C, Morissette J, Weissenbach J, Goodfellow PN). To determine the chromosomal location of a gene using this panel, 93 PCRs are performed using primers designed from the gene of interest on RH DNAs. Each of these DNAs contains random human genomic fragments maintained in a hamster background (human / hamster hybrid cell lines). These PCRs result in 93 scores indicating the presence or absence of the PCR product of the gene of interest. These scores are compared with scores created using PCR products from genomic sequences of known location. This comparison is conducted at <http://www.genome.wi.mit.edu/>.

The polynucleotide sequences of the present invention are also valuable tools for tissue expression studies. Such studies allow the determination of expression patterns of polynucleotides of the present invention which may give an indication as to the expression patterns of the encoded polypeptides in tissues, by detecting the mRNAs that encode them. The techniques used are well known in the art and include in situ hybridization techniques to clones arrayed on a grid, such as cDNA microarray hybridization (Schena *et al*, *Science*, 270, 467-470, 1995 and Shalon *et al*, *Genome Res*, 6, 639-645, 1996) and nucleotide amplification techniques such as PCR. A preferred method uses the TAQMAN (Trade mark) technology available from Perkin Elmer. Results from these studies can provide an

indication of the normal function of the polypeptide in the organism. In addition, comparative studies of the normal expression pattern of mRNAs with that of mRNAs encoded by an alternative form of the same gene (for example, one having an alteration in polypeptide coding potential or a regulatory mutation) can provide valuable insights into the role of the polypeptides of the present invention, or that of inappropriate expression thereof in disease. Such inappropriate expression may be of a temporal, spatial or simply quantitative nature.

A further aspect of the present invention relates to antibodies. The polypeptides of the invention or their fragments, or cells expressing them, can be used as immunogens to produce antibodies that are immunospecific for polypeptides of the present invention. The term "immunospecific" means that the antibodies have substantially greater affinity for the polypeptides of the invention than their affinity for other related polypeptides in the prior art.

Antibodies generated against polypeptides of the present invention may be obtained by administering the polypeptides or epitope-bearing fragments, or cells to an animal, preferably a non-human animal, using routine protocols. For preparation of monoclonal antibodies, any technique which provides antibodies produced by continuous cell line cultures can be used. Examples include the hybridoma technique (Kohler, G. and Milstein, C., *Nature* (1975) 256:495-497), the trioma technique, the human B-cell hybridoma technique (Kozbor *et al.*, *Immunology Today* (1983) 4:72) and the EBV-hybridoma technique (Cole *et al.*, *Monoclonal Antibodies and Cancer Therapy*, 77-96, Alan R. Liss, Inc., 1985).

Techniques for the production of single chain antibodies, such as those described in U.S. Patent No. 4,946,778, can also be adapted to produce single chain antibodies to polypeptides of this invention. Also, transgenic mice, or other organisms, including other mammals, may be used to express humanized antibodies.

The above-described antibodies may be employed to isolate or to identify clones expressing the polypeptide or to purify the polypeptides by affinity chromatography. Antibodies against polypeptides of the present invention may also be employed to treat diseases of the invention, amongst others.

Polypeptides and polynucleotides of the present invention may also be used as vaccines. Accordingly, in a further aspect, the present invention relates to a method for inducing an immunological response in a mammal that comprises inoculating the mammal with a polypeptide of the present invention, adequate to produce antibody and/or T cell immune response, including, for example, cytokine-producing T cells or cytotoxic T cells,

to protect said animal from disease, whether that disease is already established within the individual or not. An immunological response in a mammal may also be induced by a method comprises delivering a polypeptide of the present invention *via* a vector directing expression of the polynucleotide and coding for the polypeptide *in vivo* in order to induce
5 such an immunological response to produce antibody to protect said animal from diseases of the invention. One way of administering the vector is by accelerating it into the desired cells as a coating on particles or otherwise. Such nucleic acid vector may comprise DNA, RNA, a modified nucleic acid, or a DNA/RNA hybrid. For use a vaccine, a polypeptide or a nucleic acid vector will be normally provided as a vaccine formulation (composition). The
10 formulation may further comprise a suitable carrier. Since a polypeptide may be broken down in the stomach, it is preferably administered parenterally (for instance, subcutaneous, intra-muscular, intravenous, or intra-dermal injection). Formulations suitable for parenteral administration include aqueous and non-aqueous sterile injection solutions that may contain anti-oxidants, buffers, bacteriostats and solutes that render the formulation isotonic with the
15 blood of the recipient; and aqueous and non-aqueous sterile suspensions that may include suspending agents or thickening agents. The formulations may be presented in unit-dose or multi-dose containers, for example, sealed ampoules and vials and may be stored in a freeze-dried condition requiring only the addition of the sterile liquid carrier immediately prior to use. The vaccine formulation may also include adjuvant systems for enhancing the
20 immunogenicity of the formulation, such as oil-in water systems and other systems known in the art. The dosage will depend on the specific activity of the vaccine and can be readily determined by routine experimentation.

Polypeptides of the present invention have one or more biological functions that are of relevance in one or more disease states, in particular the diseases of the invention
25 hereinbefore mentioned. It is therefore useful to identify compounds that stimulate or inhibit the function or level of the polypeptide. Accordingly, in a further aspect, the present invention provides for a method of screening compounds to identify those that stimulate or inhibit the function or level of the polypeptide. Such methods identify agonists or antagonists that may be employed for therapeutic and prophylactic purposes for such
30 diseases of the invention as hereinbefore mentioned. Compounds may be identified from a variety of sources, for example, cells, cell-free preparations, chemical libraries, collections of chemical compounds, and natural product mixtures. Such agonists or antagonists so-identified may be natural or modified substrates, ligands, receptors, enzymes, etc., as the case may be, of the polypeptide; a structural or functional mimetic thereof (see Coligan *et al.*, Current Protocols in Immunology 1(2):Chapter 5 (1991)) or a small molecule. Such
35

small molecules preferably have a molecular weight below 2,000 daltons, more preferably between 300 and 1,000 daltons, and most preferably between 400 and 700 daltons. It is preferred that these small molecules are organic molecules.

5 The screening method may simply measure the binding of a candidate compound to the polypeptide, or to cells or membranes bearing the polypeptide, or a fusion protein thereof, by means of a label directly or indirectly associated with the candidate compound. Alternatively, the screening method may involve measuring or detecting (qualitatively or quantitatively) the competitive binding of a candidate compound to the polypeptide against a labeled competitor (*e.g.* agonist or antagonist). Further, these screening methods may test 10 whether the candidate compound results in a signal generated by activation or inhibition of the polypeptide, using detection systems appropriate to the cells bearing the polypeptide. Inhibitors of activation are generally assayed in the presence of a known agonist and the effect on activation by the agonist by the presence of the candidate compound is observed. Further, the screening methods may simply comprise the steps of mixing a candidate 15 compound with a solution containing a polypeptide of the present invention, to form a mixture, measuring an activity of the genes set forth in Table I in the mixture, and comparing activity of the mixture of the genes set forth in Table I to a control mixture which contains no candidate compound.

Polypeptides of the present invention may be employed in conventional low 20 capacity screening methods and also in high-throughput screening (HTS) formats. Such HTS formats include not only the well-established use of 96- and, more recently, 384-well micotiter plates but also emerging methods such as the nanowell method described by Schullek et al, *Anal Biochem.*, 246, 20-29, (1997).

Fusion proteins, such as those made from Fc portion and polypeptide of the genes set forth 25 in Table I, as hereinbefore described, can also be used for high-throughput screening assays to identify antagonists for the polypeptide of the present invention (see D. Bennett *et al.*, *J Mol Recognition*, 8:52-58 (1995); and K. Johanson *et al.*, *J Biol Chem*, 270(16):9459-9471 (1995)).

The polynucleotides, polypeptides and antibodies to the polypeptide of the present 30 invention may also be used to configure screening methods for detecting the effect of added compounds on the production of mRNA and polypeptide in cells. For example, an ELISA assay may be constructed for measuring secreted or cell associated levels of polypeptide using monoclonal and polyclonal antibodies by standard methods known in the art. This can be used to discover agents that may inhibit or enhance the production of polypeptide 35 (also called antagonist or agonist, respectively) from suitably manipulated cells or tissues.

A polypeptide of the present invention may be used to identify membrane bound or soluble receptors, if any, through standard receptor binding techniques known in the art. These include, but are not limited to, ligand binding and crosslinking assays in which the polypeptide is labeled with a radioactive isotope (for instance, ^{125}I), chemically modified
5 (for instance, biotinylated), or fused to a peptide sequence suitable for detection or purification, and incubated with a source of the putative receptor (cells, cell membranes, cell supernatants, tissue extracts, bodily fluids). Other methods include biophysical techniques such as surface plasmon resonance and spectroscopy. These screening methods may also be used to identify agonists and antagonists of the polypeptide that compete with the binding of
10 the polypeptide to its receptors, if any. Standard methods for conducting such assays are well understood in the art.

Examples of antagonists of polypeptides of the present invention include antibodies or, in some cases, oligonucleotides or proteins that are closely related to the ligands, substrates, receptors, enzymes, etc., as the case may be, of the polypeptide, *e.g.*, a fragment
15 of the ligands, substrates, receptors, enzymes, etc.; or a small molecule that bind to the polypeptide of the present invention but do not elicit a response, so that the activity of the polypeptide is prevented.

Screening methods may also involve the use of transgenic technology and the genes set forth in Table I. The art of constructing transgenic animals is well established. For
20 example, the genes set forth in Table I may be introduced through microinjection into the male pronucleus of fertilized oocytes, retroviral transfer into pre- or post-implantation embryos, or injection of genetically modified, such as by electroporation, embryonic stem cells into host blastocysts. Particularly useful transgenic animals are so-called "knock-in" animals in which an animal gene is replaced by the human equivalent within the genome of
25 that animal. Knock-in transgenic animals are useful in the drug discovery process, for target validation, where the compound is specific for the human target. Other useful transgenic animals are so-called "knock-out" animals in which the expression of the animal ortholog of a polypeptide of the present invention and encoded by an endogenous DNA sequence in a cell is partially or completely annulled. The gene knock-out may be targeted to specific
30 cells or tissues, may occur only in certain cells or tissues as a consequence of the limitations of the technology, or may occur in all, or substantially all, cells in the animal. Transgenic animal technology also offers a whole animal expression-cloning system in which introduced genes are expressed to give large amounts of polypeptides of the present invention

Screening kits for use in the above described methods form a further aspect of the present invention. Such screening kits comprise:

- (a) a polypeptide of the present invention;
- (b) a recombinant cell expressing a polypeptide of the present invention;
- 5 (c) a cell membrane expressing a polypeptide of the present invention; or
- (d) an antibody to a polypeptide of the present invention;

which polypeptide is preferably that set forth in the Sequence Listing.

It will be appreciated that in any such kit, (a), (b), (c) or (d) may comprise a substantial component.

10

Glossary

The following definitions are provided to facilitate understanding of certain terms used frequently hereinbefore.

- “Antibodies” as used herein includes polyclonal and monoclonal antibodies, chimeric,
15 single chain, and humanized antibodies, as well as Fab fragments, including the products of an

Fab or other immunoglobulin expression library.

- “Isolated” means altered “by the hand of man” from its natural state, *i.e.*, if it occurs in nature, it has been changed or removed from its original environment, or both. For
20 example, a polynucleotide or a polypeptide naturally present in a living organism is not “isolated,” but the same polynucleotide or polypeptide separated from the coexisting materials of its natural state is “isolated”, as the term is employed herein. Moreover, a polynucleotide or polypeptide that is introduced into an organism by transformation, genetic manipulation or by any other recombinant method is “isolated” even if it is still present in
25 said organism, which organism may be living or non-living.

- “Secreted protein activity or secreted polypeptide activity” or “biological activity of the secreted protein or secreted polypeptide” refers to the metabolic or physiologic function of said secreted protein including similar activities or improved activities or these activities with decreased undesirable side-effects. Also included are antigenic and immunogenic
30 activities of said secreted protein.

“Secreted protein gene” refers to a polynucleotide comprising any of the attached nucleotide sequences or allelic variants thereof and/or their complements.

“Polynucleotide” generally refers to any polyribonucleotide (RNA) or polydeoxribonucleotide (DNA), which may be unmodified or modified RNA or DNA.

- 35 “Polynucleotides” include, without limitation, single- and double-stranded DNA, DNA that

is a mixture of single- and double-stranded regions, single- and double-stranded RNA, and RNA that is mixture of single- and double-stranded regions, hybrid molecules comprising DNA and RNA that may be single-stranded or, more typically, double-stranded or a mixture of single- and double-stranded regions. In addition, "polynucleotide" refers to triple-
5 stranded regions comprising RNA or DNA or both RNA and DNA. The term "polynucleotide" also includes DNAs or RNAs containing one or more modified bases and DNAs or RNAs with backbones modified for stability or for other reasons. "Modified" bases include, for example, tritylated bases and unusual bases such as inosine. A variety of modifications may be made to DNA and RNA; thus, "polynucleotide" embraces chemically,
10 enzymatically or metabolically modified forms of polynucleotides as typically found in nature, as well as the chemical forms of DNA and RNA characteristic of viruses and cells. "Polynucleotide" also embraces relatively short polynucleotides, often referred to as oligonucleotides.

"Polypeptide" refers to any polypeptide comprising two or more amino acids joined
15 to each other by peptide bonds or modified peptide bonds, i.e., peptide isosteres. "Polypeptide" refers to both short chains, commonly referred to as peptides, oligopeptides or oligomers, and to longer chains, generally referred to as proteins. Polypeptides may contain amino acids other than the 20 gene-encoded amino acids. "Polypeptides" include amino acid sequences modified either by natural processes, such as post-translational
20 processing, or by chemical modification techniques that are well known in the art. Such modifications are well described in basic texts and in more detailed monographs, as well as in a voluminous research literature. Modifications may occur anywhere in a polypeptide, including the peptide backbone, the amino acid side-chains and the amino or carboxyl termini. It will be appreciated that the same type of modification may be present to the
25 same or varying degrees at several sites in a given polypeptide. Also, a given polypeptide may contain many types of modifications. Polypeptides may be branched as a result of ubiquitination, and they may be cyclic, with or without branching. Cyclic, branched and branched cyclic polypeptides may result from post-translation natural processes or may be made by synthetic methods. Modifications include acetylation, acylation, ADP-
30 ribosylation, amidation, biotinylation, covalent attachment of flavin, covalent attachment of a heme moiety, covalent attachment of a nucleotide or nucleotide derivative, covalent attachment of a lipid or lipid derivative, covalent attachment of phosphatidylinositol, cross-linking, cyclization, disulfide bond formation, demethylation, formation of covalent cross-links, formation of cystine, formation of pyroglutamate, formylation, gamma-carboxylation,
35 glycosylation, GPI anchor formation, hydroxylation, iodination, methylation,

myristoylation, oxidation, proteolytic processing, phosphorylation, prenylation, racemization, selenoylation, sulfation, transfer-RNA mediated addition of amino acids to proteins such as arginylation, and ubiquitination (see, for instance, *Proteins - Structure and Molecular Properties*, 2nd Ed., T. E. Creighton, W. H. Freeman and Company, New York, 1993; Wold, F., *Post-translational Protein Modifications: Perspectives and Prospects*, 1-12, in *Post-translational Covalent Modification of Proteins*, B. C. Johnson, Ed., Academic Press, New York, 1983; Seifter *et al.*, "Analysis for protein modifications and nonprotein cofactors", *Meth Enzymol*, 182, 626-646, 1990, and Rattan *et al.*, "Protein Synthesis: Post-translational Modifications and Aging", *Ann NY Acad Sci*, 663, 48-62, 1992).

10 "Fragment" of a polypeptide sequence refers to a polypeptide sequence that is shorter than the reference sequence but that retains essentially the same biological function or activity as the reference polypeptide. "Fragment" of a polynucleotide sequence refers to a polynucleotide sequence that is shorter than the reference sequence set forth in the Sequence Listing.

15 "Variant" refers to a polynucleotide or polypeptide that differs from a reference polynucleotide or polypeptide, but retains the essential properties thereof. A typical variant of a polynucleotide differs in nucleotide sequence from the reference polynucleotide. Changes in the nucleotide sequence of the variant may or may not alter the amino acid sequence of a polypeptide encoded by the reference polynucleotide. Nucleotide changes
20 may result in amino acid substitutions, additions, deletions, fusions and truncations in the polypeptide encoded by the reference sequence, as discussed below. A typical variant of a polypeptide differs in amino acid sequence from the reference polypeptide. Generally, alterations are limited so that the sequences of the reference polypeptide and the variant are closely similar overall and, in many regions, identical. A variant and reference polypeptide
25 may differ in amino acid sequence by one or more substitutions, insertions, deletions in any combination. A substituted or inserted amino acid residue may or may not be one encoded by the genetic code. Typical conservative substitutions include Gly, Ala; Val, Ile, Leu; Asp, Glu; Asn, Gln; Ser, Thr; Lys, Arg; and Phe and Tyr. A variant of a polynucleotide or polypeptide may be naturally occurring such as an allele, or it may be a variant that is not
30 known to occur naturally. Non-naturally occurring variants of polynucleotides and polypeptides may be made by mutagenesis techniques or by direct synthesis. Also included as variants are polypeptides having one or more post-translational modifications, for instance glycosylation, phosphorylation, methylation, ADP ribosylation and the like. Embodiments include methylation of the N-terminal amino acid, phosphorylations of
35 serines and threonines and modification of C-terminal glycines.

"Allele" refers to one of two or more alternative forms of a gene occurring at a given locus in the genome.

"Polymorphism" refers to a variation in nucleotide sequence (and encoded polypeptide sequence, if relevant) at a given position in the genome within a population.

5 "Single Nucleotide Polymorphism" (SNP) refers to the occurrence of nucleotide variability at a single nucleotide position in the genome, within a population. An SNP may occur within a gene or within intergenic regions of the genome. SNPs can be assayed using Allele Specific Amplification (ASA). For the process at least 3 primers are required. A common primer is used in reverse complement to the polymorphism being assayed. This
10 common primer can be between 50 and 1500 bps from the polymorphic base. The other two (or more) primers are identical to each other except that the final 3' base wobbles to match one of the two (or more) alleles that make up the polymorphism. Two (or more) PCR reactions are then conducted on sample DNA, each using the common primer and one of the Allele Specific Primers.

15 "Splice Variant" as used herein refers to cDNA molecules produced from RNA molecules initially transcribed from the same genomic DNA sequence but which have undergone alternative RNA splicing. Alternative RNA splicing occurs when a primary RNA transcript undergoes splicing, generally for the removal of introns, which results in the production of more than one mRNA molecule each of that may encode different amino acid
20 sequences. The term splice variant also refers to the proteins encoded by the above cDNA molecules.

"Identity" reflects a relationship between two or more polypeptide sequences or two or more polynucleotide sequences, determined by comparing the sequences. In general, identity refers to an exact nucleotide to nucleotide or amino acid to amino acid
25 correspondence of the two polynucleotide or two polypeptide sequences, respectively, over the length of the sequences being compared.

"% Identity" - For sequences where there is not an exact correspondence, a "% identity" may be determined. In general, the two sequences to be compared are aligned to give a maximum correlation between the sequences. This may include inserting "gaps" in
30 either one or both sequences, to enhance the degree of alignment. A % identity may be determined over the whole length of each of the sequences being compared (so-called global alignment), that is particularly suitable for sequences of the same or very similar length, or over shorter, defined lengths (so-called local alignment), that is more suitable for sequences of unequal length.

"Similarity" is a further, more sophisticated measure of the relationship between two polypeptide sequences. In general, "similarity" means a comparison between the amino acids of two polypeptide chains, on a residue by residue basis, taking into account not only exact correspondences between a between pairs of residues, one from each of the sequences
5 being compared (as for identity) but also, where there is not an exact correspondence, whether, on an evolutionary basis, one residue is a likely substitute for the other. This likelihood has an associated "score" from which the "% similarity" of the two sequences can then be determined.

Methods for comparing the identity and similarity of two or more sequences are
10 well known in the art. Thus for instance, programs available in the Wisconsin Sequence Analysis Package, version 9.1 (Devereux J et al, Nucleic Acids Res, 12, 387-395, 1984, available from Genetics Computer Group, Madison, Wisconsin, USA), for example the programs BESTFIT and GAP, may be used to determine the % identity between two polynucleotides and the % identity and the % similarity between two polypeptide sequences.
15 BESTFIT uses the "local homology" algorithm of Smith and Waterman (J Mol Biol, 147,195-197, 1981, Advances in Applied Mathematics, 2, 482-489, 1981) and finds the best single region of similarity between two sequences. BESTFIT is more suited to comparing two polynucleotide or two polypeptide sequences that are dissimilar in length, the program assuming that the shorter sequence represents a portion of the longer. In comparison, GAP
20 aligns two sequences, finding a "maximum similarity", according to the algorithm of Needleman and Wunsch (J Mol Biol, 48, 443-453, 1970). GAP is more suited to comparing sequences that are approximately the same length and an alignment is expected over the entire length. Preferably, the parameters "Gap Weight" and "Length Weight" used in each program are 50 and 3, for polynucleotide sequences and 12 and 4 for polypeptide sequences,
25 respectively. Preferably, % identities and similarities are determined when the two sequences being compared are optimally aligned.

Other programs for determining identity and/or similarity between sequences are also known in the art, for instance the BLAST family of programs (Altschul S F et al, J Mol Biol, 215, 403-410, 1990, Altschul S F et al, Nucleic Acids Res., 25:389-3402, 1997,
30 available from the National Center for Biotechnology Information (NCBI), Bethesda, Maryland, USA and accessible through the home page of the NCBI at www.ncbi.nlm.nih.gov) and FASTA (Pearson W R, Methods in Enzymology, 183, 63-99, 1990; Pearson W R and Lipman D J, Proc Nat Acad Sci USA, 85, 2444-2448,1988, available as part of the Wisconsin Sequence Analysis Package).

Preferably, the BLOSUM62 amino acid substitution matrix (Henikoff S and Henikoff J G, Proc. Nat. Acad Sci. USA, 89, 10915-10919, 1992) is used in polypeptide sequence comparisons including where nucleotide sequences are first translated into amino acid sequences before comparison.

- 5 Preferably, the program BESTFIT is used to determine the % identity of a query polynucleotide or a polypeptide sequence with respect to a reference polynucleotide or a polypeptide sequence, the query and the reference sequence being optimally aligned and the parameters of the program set at the default value, as hereinbefore described.

 "Identity Index" is a measure of sequence relatedness which may be used to
10 compare a candidate sequence (polynucleotide or polypeptide) and a reference sequence. Thus, for instance, a candidate polynucleotide sequence having, for example, an Identity Index of 0.95 compared to a reference polynucleotide sequence is identical to the reference sequence except that the candidate polynucleotide sequence may include on average up to
15 five differences per each 100 nucleotides of the reference sequence. Such differences are selected from the group consisting of at least one nucleotide deletion, substitution, including transition and transversion, or insertion. These differences may occur at the 5' or 3' terminal positions of the reference polynucleotide sequence or anywhere between these terminal positions, interspersed either individually among the nucleotides in the reference sequence or in one or more contiguous groups within the reference sequence. In other words, to
20 obtain a polynucleotide sequence having an Identity Index of 0.95 compared to a reference polynucleotide sequence, an average of up to 5 in every 100 of the nucleotides of the in the reference sequence may be deleted, substituted or inserted, or any combination thereof, as hereinbefore described. The same applies *mutatis mutandis* for other values of the Identity Index, for instance 0.96, 0.97, 0.98 and 0.99.

25 Similarly, for a polypeptide, a candidate polypeptide sequence having, for example, an Identity Index of 0.95 compared to a reference polypeptide sequence is identical to the reference sequence except that the polypeptide sequence may include an average of up to five differences per each 100 amino acids of the reference sequence. Such differences are selected from the group consisting of at least one amino acid deletion, substitution,
30 including conservative and non-conservative substitution, or insertion. These differences may occur at the amino- or carboxy-terminal positions of the reference polypeptide sequence or anywhere between these terminal positions, interspersed either individually among the amino acids in the reference sequence or in one or more contiguous groups within the reference sequence. In other words, to obtain a polypeptide sequence having an
35 Identity Index of 0.95 compared to a reference polypeptide sequence, an average of up to 5

in every 100 of the amino acids in the reference sequence may be deleted, substituted or inserted, or any combination thereof, as hereinbefore described. The same applies *mutatis mutandis* for other values of the Identity Index, for instance 0.96, 0.97, 0.98 and 0.99.

5 The relationship between the number of nucleotide or amino acid differences and the Identity Index may be expressed in the following equation:

$$n_a \leq x_a - (x_a \bullet I),$$

in which:

n_a is the number of nucleotide or amino acid differences,

10 x_a is the total number of nucleotides or amino acids in a sequence set forth in the Sequence Listing,

I is the Identity Index,

• is the symbol for the multiplication operator, and

in which any non-integer product of x_a and I is rounded down to the nearest integer prior to subtracting it from x_a .

15 "Homolog" is a generic term used in the art to indicate a polynucleotide or polypeptide sequence possessing a high degree of sequence relatedness to a reference sequence. Such relatedness may be quantified by determining the degree of identity and/or similarity between the two sequences as hereinbefore defined. Falling within this generic term are the terms "ortholog", and "paralog". "Ortholog" refers to a polynucleotide or
20 polypeptide that is the functional equivalent of the polynucleotide or polypeptide in another species. "Paralog" refers to a polynucleotide or polypeptide that within the same species which is functionally similar.

"Fusion protein" refers to a protein encoded by two, often unrelated, fused genes or fragments thereof. In one example, EP-A-0 464 533-A discloses fusion proteins comprising
25 various portions of constant region of immunoglobulin molecules together with another human protein or part thereof. In many cases, employing an immunoglobulin Fc region as a part of a fusion protein is advantageous for use in therapy and diagnosis resulting in, for example, improved pharmacokinetic properties [see, *e.g.*, EP-A 0232 262]. On the other hand, for some uses it would be desirable to be able to delete the Fc part after the fusion
30 protein has been expressed, detected and purified.

All publications and references, including but not limited to patents and patent applications, cited in this specification are herein incorporated by reference in their entirety as if each individual publication or reference were specifically and individually indicated to be incorporated by reference herein as being fully set forth. Any patent application to which

this application claims priority is also incorporated by reference herein in its entirety in the manner described above for publications and references.

Table I

Gene Name	GSK Gene ID	Nucleic Acid SEQ ID NO's	Corresponding Protein SEQ ID NO's
sbg458463PERLAXINa	458463	SEQ ID NO:1 SEQ ID NO:2	SEQ ID NO:29 SEQ ID NO:30
sbg507885RDPa	507885	SEQ ID NO:3 SEQ ID NO:4	SEQ ID NO:31 SEQ ID NO:32
sbg507885RDPb	507885	SEQ ID NO:5	SEQ ID NO:33
SBh511364.NR-CAMa	511364	SEQ ID NO:6 SEQ ID NO:7	SEQ ID NO:34 SEQ ID NO:35
SBh511364.NR-CAMb	511364	SEQ ID NO:8	SEQ ID NO:36
SBh511827.C1q-related factor	511827	SEQ ID NO:9 SEQ ID NO:10	SEQ ID NO:37 SEQ ID NO:38
sbg533677PALSa	533677	SEQ ID NO:11 SEQ ID NO:12	SEQ ID NO:39 SEQ ID NO:40
sbg535067MELAA	535067	SEQ ID NO:13	SEQ ID NO:41
sbg590979THP	590979	SEQ ID NO:14 SEQ ID NO:15	SEQ ID NO:42 SEQ ID NO:43
sbg658629CRF	658629	SEQ ID NO:16 SEQ ID NO:17	SEQ ID NO:44 SEQ ID NO:45
sbg507131mannosidase	507131	SEQ ID NO:18 SEQ ID NO:19	SEQ ID NO:46 SEQ ID NO:47
sbg655871calgizzarin- like	655871	SEQ ID NO:20 SEQ ID NO:21	SEQ ID NO:48 SEQ ID NO:49
sbg506454MPG-1	506454	SEQ ID NO:22 SEQ ID NO:23	SEQ ID NO:50 SEQ ID NO:51
sbg659837OBCAM	659837	SEQ ID NO:24 SEQ ID NO:25	SEQ ID NO:52 SEQ ID NO:53
sbg467870CBP	467870	SEQ ID NO:26	SEQ ID NO:54
sbg514112RNase	514112	SEQ ID NO:27	SEQ ID NO:55
sbg962274FGF-BP	962274	SEQ ID NO:28	SEQ ID NO:56

Table II

Gene Name	Gene Family	Closest Polynucleotide by homology	Closest Polypeptide by homology	Cell localization (by homology)
sbg458463 PERLAXI Na	Periaxin protein	GB:AC010271 Submitted (15-SEP-1999) by Production Sequencing Facility, DOE Joint Genome Institute	Human periaxin, gi:13649706 Submitted (17-APR-2001) by National Center for Biotechnology Information, NIH, Bethesda, MD 20894, USA	Cytosolic
sbg507885 RDPa	Renal dipeptidase	JGI:RPCI-11_331B16 Found at Joint Genome Institute, Department of Energy, USA	Human putative metallopeptidase (family M19), gi:11641273 Submitted (02-NOV-2000) by Chen J.M., MRC Molecular Enzymology Laboratory, The Babraham Institute, Babraham, Cambridge, CB2 4AT, UNITED KINGDOM	Secreted
sbg507885 RDPb	Renal dipeptidase	JGI:RPCI-11_331B16 Found at Joint Genome Institute, Department of Energy, USA	Human putative metallopeptidase (family M19), gi:11641273 Submitted (02-NOV-2000) by Chen J.M., MRC Molecular Enzymology Laboratory, The Babraham Institute, Babraham, Cambridge, CB2 4AT, UNITED KINGDOM	Secreted
SBh511364 .NR-CAMa	Immunoglobulin superfamily, neuron-glia cell adhesion molecule-related protein (Nr-CAM)	EMBL:AC073550 Submitted (22-JUN-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA	Human hypothetical protein, gi:6807875 Submitted (15-JAN-2000) MIPS, Am Klopferspitz 18a, D-82152 Martinsried, GERMANY	Membrane-bound
SBh511364 .NR-CAMb	Neuron-glia cell adhesion molecule-related protein (Nr-CAM)	EMBL:AC073550 Submitted (22-JUN-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA	Human hypothetical protein, gi:13632065 Submitted (17-APR-2001) by National Center for Biotechnology Information, NIH, Bethesda, MD 20894, USA	Cytosolic
SBh511827 .C1q-related factor	Complement-c1q tumor necrosis factor-related protein	GB:AC026707 Submitted (23-MAR-2000) by Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598,	Human complement-c1q tumor necrosis factor-related protein, gi: 13569919 Maeda T, Abe M, Kurisu K, Jikko A and Furukawa S J Biol Chem 2001 Feb 2;276(5):3628-34	Secreted

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Table II (cont)

Gene Name	Gene Family	Closest Polynucleotide by homology	Closest Polypeptide by homology	Cell localization (by homology)
sbg533677 PALSa	Palmitoylated 3 (MAGUK p55 subfamily member 5, proteins associated with Lin-7 (PALs))	GB:AL135978 Submitted (15-MAY-2001) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE	Mouse palmitoylated 3 (MAGUK p55 subfamily member 5), gi: 9625023 Kamberov,E., Makarova,O., Roh,M., Liu,A., Karnak,D., Straight,S. and Margolis,B. J. Biol. Chem. 275 (15), 11425-11431 (2000).	Membrane-bound
sbg535067 MELAa	Melanoma associated protein	SC:AL096827 Submitted (13-SEP-1999) by Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK.	Unidentified human gene, gi:10047249 Submitted (03-AUG-2000) by Osamu Ohara, Kazusa DNA Research Institute, Department of Human Gene Research; 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan	Membrane-bound
sbg590979 THP	Tamm-Horsfall protien (THP)	GB: AC069548 Direct submitted (02-JUN-2000) Genome Therapeutics Corporation, 100 Beaver Street, Waltham, MA 02453, USA	Human pancreatic zymogen granule membrane protein GP2, gi:4504075 Wong,S.M. and Lowe,A.W. Gene 171 (2), 311-312 (1996)	Secreted
sbg658629 CRF	C1q-related factor	GB:AC010173 Direct submitted (15-SEP-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX77030, USA	Human C1q-related factor, gi :5729785 Berube NG, Swanson XH, Bertram MJ, Kittle JD, Didenko V, Baskin DS, Smith JR and Pereira-Smith OM. Brain Res. Mol. Brain Res. 63 (2), 233-240 (1999)	Secreted
sbg507131 mannosidase	Alpha-mannosidase	GB:AC004480 Direct submitted (27-MAR-1998) Department of Genetics, Stanford Human Genome Center, 855 California Avenue, Palo Alto, CA 94304, USA.	Mouse mannosidase 2, alpha B2, gi:6678792 Hiramoto,S., Tamba,M., Kiuchi,S., Jin,Y.Z., Bannai,S., Sugita,Y., Dacheux,F., Dacheux,J.L., Yoshida,M. and Okamura,N. Biochem. Biophys. Res. Commun. 241 (2), 439-445 (1997)	Secreted

Table II (cont)

Gene Name	Gene Family	Closest Polynucleotide by homology	Closest Polypeptide by homology	Cell localization (by homology)
sbg655871 calgizzarin-like	S100 calcium-binding protein	GB:AC027667 Direct submitted (01-APR-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA	Mouse calgizzarin (endothelial monocyte-activating polypeptide), gi: 1710819, Fan,Y., Leung,D., Houck,K.A., Yan,S., Brett,J., Heath,M., Pan,Y., Clauss,M., Kisiel,W., Chabot,J., Logerfo,P., Stern,D. and Kao,J. submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases	Secreted
sbg506454 MPG-1	Macrophage Gene-1 Product (MGP1)	GB:AP000406 Submitted (27-AUG-1999) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555, Japan	Mouse MPS1 protein gi:2137564 Spilsbury,K., O'Mara,M.A., Wu,W.M., Rowe,P.B., Symonds,G. and Takayama,Y. Blood 85 (6), 1620-1629 (1995)	Secreted
sbg659837 OBCAM	Opioid-binding cell adhesion molecule (OBCAM)	GB: AC016769 Submitted (25-MAY-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA	Bovine opioid-binding cell adhesion molecule Schofield,P.R., McFarland,K.C., Hayflick,J.S., Wilcox,J.N., Cho,T.M., Roy,S., Lee,N.M., Loh,H.H. and Seeburg, P.H. EMBO J. 8 (2), 489-495 (1989)	Secreted
sbg467870 CBP	EF-hand protein	GB:AC018638 Direct submitted (15-DEC-1999) Human Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA.	Rat CBP-50 protein, gi:2511701 Submitted (04-OCT-1997) by Hseu M.J., Institute of Biological Chemistry, Academia Sinica, Taiwan, R. O. C., P.O.Box 23-106, Taipei, Taiwan, 10098, REPUBLIC OF CHINA	Endoplasmic reticulum-bound (secreted if C-terminus HDEF were deleted)
sbg514112 RNase	RNase	GB:AL355075 Direct submitted (06-JUN-2000) to the EMBL/GenBank/DDBJ databases by Genoscope.	Mouse putative protein, gi: 12853968 Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Genome Res. 10 (10), 1617-1630 (2000)	Secreted

Table II (cont)

Gene Name	Gene Family	Closest Polynucleotide by homology	Closest Polypeptide by homology	Cell localization (by homology)
sbg962274 FGF-BP	Fibroblast growth factor binding protein	EMBL:AL359198 Found at Sanger Centre and submitted (08-APR-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK.	Mouse putative protein, gi: 12853968 Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Genome Res. 10 (10), 1617-1630 (2000)	Secreted

Table III

Gene Name	Uses	Associated Diseases
sbg458463 PERLAXI Na	An embodiment of the invention is the use of sbg458463PERLAXINa in axon-glia interactions. A close homologue of sbg458463PERLAXINa is the rat periaxin (PRX). Rat periaxin (PRX), a protein of myelinating Schwann cells. Periaxin has a role in axon-glia interactions, possibly by interacting with the cytoplasmic domains of integral membrane proteins such as myelin-associated glycoprotein in the periaxonal regions of the Schwann cell plasma membrane (Gillespie CS, Sherman DL, Blair GE, Brophy PJ. Periaxin, a protein of myelinating Schwann cells with a possible role in axonal ensheathment. Neuron 1994 Mar;12(3):497-508). Prx(-/-) mice develop a severe demyelinating peripheral neuropathy, despite apparently normal initial formation of myelin sheaths. Three unrelated Dejerine-Sottas neuropathy patients with recessive PRX mutations have been identified. It was hypothesized that mutations in PRX could cause human peripheral myelinopathies (Boerkoel,C.F., Takashima,H., Stankiewicz,P., Garcia,C.A., Leber,S.M., Rhee-Morris,L. and Lupski,J.R. Am. J. Hum. Genet. 68 (2), 325-333 (2001)).	Peripheral myelinopathies, infection, cancer, autoimmune disorders, wound healing disorders and hematopoietic disorders
sbg507885 RDPa	An embodiment of the invention is the use of sbg507885RDPa in the renal metabolism. Close homologues of sbg507885RDPa are microsomal dipeptidases. The renal dipeptidase (RDP), previously referred to as microsomal dipeptidase, is a kidney membrane enzyme which hydrolyzes a variety of dipeptides, and is implicated in the renal metabolism. RDP is responsible for hydrolysis of the beta-lactam ring of antibiotics (Campbell BJ, Forrester LJ, Zahler WL, Burks M; 1984; Biol Chem 259:14586-90). The renal dipeptidase has been shown to be a glycosylphosphatidylinositol-anchored ectoenzyme within the renal proximal tubules, and is proposed as a diagnostic enzyme of renal disease (Kang BY, We JS, Choi K, Lee HB, Han HJ, Park H; 1999; Arch Pharm Res 22:367-71).	Cancer, infection, autoimmune disorder, inflammation, and acute renal failure
sbg507885 RDPb	An embodiment of the invention is the use of sbg507885RDPb in the renal metabolism. Close homologues of sbg507885RDPb are microsomal dipeptidases. The renal dipeptidase (RDP), previously referred to as microsomal dipeptidase, is a kidney membrane enzyme which hydrolyzes a variety of dipeptides, and is implicated in the renal metabolism. RDP is responsible for hydrolysis of the beta-lactam ring of antibiotics (Campbell BJ, Forrester LJ, Zahler WL, Burks M; 1984; Biol Chem 259:14586-90). The renal dipeptidase has been shown to be a glycosylphosphatidylinositol-	Cancer, infection, autoimmune disorder, inflammation, and acute renal failure

	anchored ectoenzyme within the renal proximal tubules, and is proposed as a diagnostic enzyme of renal disease (Kang BY, We JS, Choi K, Lee HB, Han HJ, Park H; 1999; Arch Pharm Res 22:367-71).	
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Table III (cont).

Gene Name	Uses	Associated Diseases
SBh511364.NR-CAMa	An embodiment of the invention is the use of SBh511364.NR-CAMa in the pathogenesis and invasive/metastatic behavior of pancreatic cancers. A close homologue of SBh511364.NR-CAMa is neural cell adhesion molecule Nr-CAM protein. Nr-CAM protein has been detected in the brain and normal human pancreas. Its expression was markedly up-regulated in intraductal hyperplasia. Expression was well maintained in well or moderately differentiated carcinoma but was reduced or absent from most poorly differentiated tumors. In addition, 4 of 4 human pancreatic adenocarcinoma cell lines tested demonstrated little or no Nr-CAM expression. This differential regulation of Nr-CAM expression suggests that it may be involved in the pathogenesis and invasive/metastatic behavior of pancreatic cancers (Dhodapkar KM, Friedlander D, Scholes J, Grumet M. Hum Pathol 2001 Apr;32(4):396-400).	Cancer such as pancreatic cancers, infections, autoimmune diseases, and neurological disorders
SBh511364.NR-CAMb	An embodiment of the invention is the use of SBh511364.NR-CAMb as a marker for diagnosing, treating, inhibiting or preventing malignancies like brain cancer, leukemia, B cell lymphoma, premalignant conditions, benign tumors, hyperproliferative disorders or benign dysproliferative disorders. Similar protein's treatment is especially useful for treating glioblastoma, glioma, meningioma, astrocytoma, medulloblastoma, neuroectodermal cancer and neuroblastoma, especially glioblastoma multiforme (WO9955380-A1, 04-NOV-99; Boynton AI, Murphy Gp, Sehgal A. Pacific Northwest Cancer Foundation).	Hematopoietic disorder, wound healing disorders, autoimmune diseases, viral and bacterial infections, cancer such as meningioma, astrocytoma, medulloblastoma, neuroectodermal and neuroblastoma, especially glioblastoma
SBh511827.C1q-related factor	An embodiment of the invention is the use of SBh511827.C1q-related factor in diagnosing and treating lung cancer and neurological disorders such as Parkinson's disease, Alzheimer's disease and schizophrenia as well as . A close homologue of SBh511827.C1q-related factor is collagenous repeat-containing sequence of 26-kDa protein (CORS26). Northern blot analysis revealed that CORS26 mRNA was present at high levels in rib growth plate cartilage and at moderate levels in kidney of adult mice. High levels of CORS26 mRNA were also detected in condensed prechondrocytic cells of cartilage primordia and developing cartilages in mouse embryos between 13 and 15 days postcoitus. Overexpression of CORS26 enhanced the growth of C3H10T1/2 cells in vitro. These data suggested that the CORS26 gene might play an important role in skeletal development. Related polypeptides have been reported useful for diagnosing and treating lung cancer (WO199938973-A2, FRUDAKIS TN, LODES MJ, MOHAMATH R, REED SG; 05-AUG-99; (CORI-) CORIXA CORP), and neurological disorders such as Parkinson's disease, Alzheimer's disease and schizophrenia (WO199942576-A1,	Hematopoietic disorder, skeletal development disorder, wound healing disorders, autoimmune diseases, viral and bacterial infections, lung tumor, cancer and growth abnormalities, parkinson's disease, alzheimer's disease and schizophrenia

	BARNES MR, 26-AUG-99;(SMIK) SMITHKLINE BEECHAM PL.	
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Table III (cont).

Gene Name	Uses	Associated Diseases
sbg533677 PALSa	An embodiment of the invention is the use of sbg533677PALSa in the proper targeting of growth factor receptors to the basolateral surface of epithelial cells. A close homologue of sbg533677PALSa is the mouse protein, Pals. Pals represents a new subfamily of membrane-associated guanylate kinases that allow for multiple targeting complexes containing mLin-7 that is necessary for the proper targeting of the Let-23 growth factor receptor to the basolateral surface of epithelial cells (Kamberov E, Makarova O, Roh M, Liu A, Karnak D, Straight S, Margolis B Molecular cloning and characterization of Pals, proteins associated with mLin-7. J Biol Chem 2000 Apr 14; 275(15):11425-31).	Cancer, infection, autoimmune disorders, wound healing disorders and hematopoietic disorders
sbg535067 MELAA	An embodiment of the invention is the use of sbg535067MELAA in detection, treatment and prevention of cancers, e.g. melanoma. A close homologue of sbg535067MELAA is a human melanoma-associated antigen. Human melanoma-associated antigen may be useful in detection, treatment and prevention of cancers. (Pavitt R. dJ142F18.1 similar to melanoma-associated antigen. Accession no. CAA19928, Submitted (11-FEB-1999) Sanger Centre, Hinxton, Cambridge shire, CB10 1SA, UK)	Melanoma
sbg590979 THP	An embodiment of the invention is the use of sbg590979THP in regulating cytokine circulation. A close homologue of sbg590979THP is a Human Tamm-Horsfall Protein. Human Tamm-Horsfall Protein, a major urinary protein, is linked to membranes via a glycosylphosphatidylinositol (GPI) anchor, and mainly exists at the luminal face of cells of the thick ascending limb of Henle's loop (TAL) and early distal convoluted tubules of nephron. A portion of the Tamm-Horsfall protein is cleaved by the action of proteases, and subsequently is secreted in urine. Since the urinary Tamm-Horsfall protein has a high gel-forming tendency, it has been postulated that it takes part in the water impermeability of TAL. It is also proposed that the Tamm-Horsfall protein may inhibit the colonization of pathogens in the renal mucosa in that the soluble form competes with that exposed at the plasma membrane (Pressac M; 2000; Ann Biol Clin (Paris) 58:167-76)	Cancer, infection, autoimmune disorder, hematopoietic disorder, wound healing disorders, inflammation, diabetic nephropathy, and nephrolithiasis
sbg658629 CRF	An embodiment of the invention is the use of sbg658629CRF in regulating central nervous system functions, e.g. motor functions. A close homologue of sbg658629CRF is C1q. C1q is a subunit of the C1 enzyme complex that activates the serum complement system. It has been shown that human CRF transcript is expressed at highest levels in the brain, particularly in the brainstem. Similarly, in mouse brain CRF transcripts are most abundant in areas of the nervous system involved in motor function (Berube NG, Swanson XH, Bertram MJ, Kittle JD, Didenko V, Baskin DS, Smith JR, and Pereira-Smith OM., 1999, Brain Res. Mol. Brain Res. 63:233-240).	Nervous system disorder

Table III (cont).

Gene Name	Uses	Associated Diseases
sbg507131 mannosidase	An embodiment of the invention is the use of sbg507131mannosidase in cell-cell and cell-substratum interactions affecting processes such as lymphocyte trafficking, immune cell stimulation, embryogenesis, and cancer metastasis. A close homologue of sbg507131mannosidase is Alpha-D-mannosidase. Alpha-D-mannosidase is involved in the catabolism of glycoproteins through the sequential degradation of mannose and complex oligosaccharides. Specific carbohydrate structures are involved in cell-cell and cell-substratum interactions affecting processes such as lymphocyte trafficking, immune cell stimulation, embryogenesis, and cancer metastasis. Therefore, alpha-mannosidase inhibitors have been selected as anticancer agents for clinical tests (Goss PE, Baker MA, Carver JP, Dennis JW; 1995; Clin Cancer Res 1:935-44). Besides, in the human alpha-mannosidosis is an autosomal recessive lysosomal storage disease caused by the deficiency of lysosomal alpha-D-mannosidase activity (Beccari T, Stinchi S, Orlacchio A; 1999; Biosci Rep 19:157-62).	Cancer , infection, autoimmune disorder, hematopoietic disorder, wound healing disorders, inflammation, and aplha- mannosidosis
sbg655871 calgizzarin- like	An embodiment of the invention is the use of sbg655871calgizzarin-like in the regulation of cell transformation and/or differentiation. A close homologue of sbg655871calgizzarin-like is human calgizzarin. The expression of human calgizzarin was remarkably elevated in colorectal cancers (Tanaka M, Adzuma K, Iwami M, Yoshimoto K, Monden Y, Itakura. 1995 Cancer Lett 89:195-200). In addition, it has been reported that calgizzarin, or MLN70, is one of several genes expressed in breast cancer-derived metastatic axillary lymph nodes but not in normal lymph nodes or breast fibroadenomas (Tomasetto C, Regnier C, Moog-Lutz C, Mattei MG, Chenard MP, Lidereau R, Basset P, Rio MC. 1995. Genomics 28:367-76). It is becoming clear that calgizzarin-related proteins may be involved in the regulation of cell transformation and/or differentiation (Moog-Lutz C, Bouillet P, Regnier CH, Tomasetto C, Mattei MG, Chenard MP, Anglard P, Rio MC, Basset P. 1995. Int J Cancer 63:297-303).	Cancer, infection, autoimmune disorder, hematopoietic disorder, wound healing disorders, and inflammation
sbg506454 MPG-1	An embodiment of the invention is the use of sbg506454MPG-1 in regulating the immune system and familial hemophagocytic lymphohistiocytosis. Close homologues of sbg506454MPG-1 are human mpg-1 and perforin. It was shown that the mpg-1 gene may be specifically expressed in macrophages, and it shares a distant ancestry to perforin, a lytic protein found in cytotoxic T lymphocytes and natural killer cells (Spilsbury K, O'Mara MA, Wu WM, Rowe PB, Symonds G, Takayama Y. 1995. Blood 85:1620-9). Analyses of mice deficient in perforin demonstrate that cytolysis is critical for immunity against some infections (Harty JT, Tvinnereim AR, White DW. 2000. Annu Rev Immunol 18:275-30). Mutations in the perforin gene were recently identified in familial hemophagocytic lymphohistiocytosis, a fatal disease of early childhood (Fadeel B, Henter JI, Orrenius S. 2000. Lakartidningen 97:1395-400)	Cancer, infection, autoimmune disorder, hematopoietic disorder, wound healing disorders, and inflammation

Table III (cont).

Gene Name	Uses	Associated Diseases
sbg659837 OBCAM	An embodiment of the invention is the use of sbg659837OBCAM in cell recognition and adhesion. Close homologues of sbg659837OBCAM are opoid-binding proteins. The opoid-binding protein binds opoid alkaloids in the presence of acidic lipids. It has been shown that the opoid-binding protein shares structural homology with members of the immunoglobulin protein superfamily, most notably with cell-adhesion molecules, such as neural cell adhesion molecules (NCAM) and myelin associated glycoproteins (MAG) (Schofield PR, McFarland KC, Hayflick JS, Wilcox JN, Cho TM, Roy S, Lee NM, Loh HH, Seeburg PH. 1989. EMBO J 8:489-95). It has been shown that opoids can modulate cell-cell interactions of monocytes, and support for links between opoids and the immune system (Loh HH, Smith AP.1990; Annu Rev Pharmacol Toxicol 30:123-47).	Cancer, infection, autoimmune disorder, hematopoietic disorder, wound healing disorders, and inflammation
sbg467870 CBP	An embodiment of the invention is the use of sbg467870CBP in tumor cell invasiveness. A close homologue of sbg467870CBP is reticulocalbin. Reticulocalbin is a calcium-binding protein located in the lumen of the ER. The protein contains six conserved regions with similarity to a high affinity calcium-binding motif, the EF-hand (Ozawa M, Muramatsu T. 1993. J Biol Chem 268:699-705). It has been shown that reticulocalbin was overexpressed in highly invasive breast cancer cell lines, but not in poorly invasive ones (Liu Z, Brattain MG, Appert H. 1997. Biochem Biophys Res Commun 231:283-9).	Cancer, infection, autoimmune disorder, hematopoietic disorder, wound healing disorders, and inflammation
sbg514112 RNase	An embodiment of the invention is the use of sbg514112RNase as a tool for anticancer therapy and the antagonist of this RNase may be useful in treating apoptosis-related disorders. A close homologue of sbg514112RNase is human keratinocyte-derived RNase-like protein (AAY44192). It has been shown that a genetic-engineered pancreatic RNase has cytotoxic action on mouse and human tumor cells, but lacks any appreciable toxicity on human and mouse normal cells. This variant of human pancreatic RNase selectively sensitized cells derived from a human thyroid tumor to apoptotic death. Because of its selectivity for tumor cells, and because of its human origin, this protein was thought to represent a promising tool for anticancer therapy (Piccoli R, Di Gaetano S, De Lorenzo C, Grauso M, Monaco C, Spalletti-Cernia D, Laccetti P, Cinatl J, Matousek J, D'Alessio G. 1999. Proc Natl Acad Sci U S A 96:7768-73).	Cancer, infection, autoimmune disorder, hematopoietic disorder, wound healing disorders, and inflammation

Table III (cont).

Gene Name	Uses	Associated Diseases
sbg962274 FGF-BP	An embodiment of the invention is the use of sbg962274FGF-BP as a modulator of FGF in FGF-responsive cells and/or detection, treatment and prevention of cancers. A close homologue of sbg962274FGF-BP is mouse fibroblast growth factor binding protein 1 (gi:7106317). Murine FGF-BP binds to FGF-2 and can function as a modulator of FGF in FGF-responsive cells. FGF-BP mRNA expression in the adult skin was dramatically increased during early stages of carcinogen-induced transformation in vivo and by ras-activation (Kurtz A, Wang HL, Darwiche N, Harris V, Wellstein A. 1997. Oncogene Jun 5;14(22):2671-81). The induction of the angiogenic modulator FGF-BP by epidermal growth factor was mediated through both MEK/ERK and p38 signal transduction pathways (Harris VK, Coticchia CM, Kagan BL, Ahmad S, Wellstein A, Riegel AT. 2000. J Biol Chem Apr 14;275(15):10802-11). Further more, the FGF-BP was upregulated in carcinogen-induced skin tumors, in squamous cell carcinoma (SCC) and in some colon cancer cell lines and tumor samples (Harris VK, Coticchia CM, List HJ, Wellstein A, Riegel AT. 2000. J Biol Chem Jun 27). Finally, human tumors can utilize FGF-BP as an angiogenic switch molecule, the growth and angiogenesis of xenograft tumors in mice was decreased in parallel with the reduction of FGF-BP. These results indicate the role of FGF-BP in tumor metastases (Czubayko F, Liaudet-Coopman ED, Aigner A, Tuveson AT, Berchem GJ, Wellstein A. 1997. Med. Oct;3(10):1137-40,. Jayne DG, Perry SL, Morrison E, Farmery SM, Guillou PJ. 2000. Br J Cancer Mar;82(6):1233-8).	Cancer, infection, autoimmune disorder, hematopoietic disorder, wound healing disorders, inflammation, osteoporosis, Alzheimer's disease, Parkinson's disease, asthma, multiple sclerosis and rheumatoid

Table IV. Quantitative, Tissue-specific mRNA expression detected using SybrMan

- Quantitative, tissue-specific, mRNA expression patterns of the genes were measured using SYBR-Green Quantitative PCR (Applied Biosystems, Foster City, CA; see Schmittgen T.D. et al., Analytical Biochemistry 285:194-204, 2000) and human cDNAs prepared from various human tissues. Gene-specific PCR primers were designed using the first nucleic acid sequence listed in the Sequence List for each gene.
- In each gene's first subset table, two replicate measurements of gene of identification (GOI) mRNA were measured from various human tissues (column 2 and 3). The average GOI mRNA copies of the two replicates were made from each tissue RNA (column 4). The average amount of 18S rRNA from each tissue RNA was measured (column 5) and used for normalization. To make each tissue with the same amount of 50 ng of 18S rRNA, the normalization factor (column 6) was calculated by dividing 50 ng with the amount of 18S rRNA measured from each tissue (column 5). The mRNA copies per 50 ng of total RNA were obtained by multiplying each GOI normalization factor and average mRNA copies (column 7).
- Fold changes shown in each gene's second subset table were only calculated for disease tissues which have a normal counterpart. There are blanks in the fold change column for all samples that do not have counterparts. In addition, the fold change calculations are the fold change in the disease sample as compared to the normal sample. Accordingly, there will not be a fold change calculation next to any of the normal samples. For patient matched cancer pairs (colon, lung, and breast), each tumor is compared to its specific normal counterpart. When patient-matched normal/disease pairs do not exist, each disease sample was compared back to the average of all the normal samples of that same tissue type. For example, normal brain from the same patient that provided Alzheimer's brain is not applicable. Three normal brain samples and 4 Alzheimer's brain samples are used in the fold change. Three normal samples were averaged, and each of the Alzheimer's samples was compared back to that average.

Abbreviations

- ALZ Alzheimer's Disease
 CT CLONTECH (1020 East Meadow Circle Palo Alto, CA 94303-4230, USA)
 KC Sample prepared by GSK investigator
 COPD chronic obstructive pulmonary disease
 endo endothelial
 VEGF vascular endothelial growth factor
 bFGF basic fibroblast growth factor
 BM bone marrow
 osteo osteoblast
 OA osteoarthritis
 RA rheumatoid arthritis
 PBL peripheral blood lymphocytes
 PBMNC peripheral blood mononuclear cells
 HIV human immunodeficiency virus
 HSV Herpes simplex virus
 HPV human papilloma virus

Gene Name sbg458463PERLAXINa

Strongly expressed in brain and lung. Overexpressed in lung tumor (1/4). Downregulated in COPD lung. Overexpressed in Alzheimer's disease.

Sample sbg458463PERLAXINa	Mean GOI copies (sample 1)	Mean GOI copies (sample 2)	Average GOI Copies	18S rRNA (ng)	50 ng/18S rRNA (ng)	copies of mRNA detected/5 0 ng total RNA
Subcutaneous Adipocytes Zenbio	41.23	19.93	41.23	3.06	16.34	673.69
Subcutaneous Adipose Zenbio	0.00	3.77	0.00	0.96	52.36	0.00
Adrenal Gland Clontech	8.11	3.36	8.11	0.61	81.97	664.75
Whole Brain Clontech	1249.19	1199.08	1249.19	7.24	6.91	8627.00
Fetal Brain Clontech	4.03	3.17	4.03	0.48	103.95	418.92
Cerebellum Clontech	29.60	2.26	29.60	2.17	23.04	682.03
Cervix	0.00	3.52	0.00	2.42	20.66	0.00
Colon	10.94	11.43	10.94	2.71	18.45	201.85
Endometrium	19.75	10.39	19.75	0.73	68.21	1347.20
Esophagus	3.42	0.00	3.42	1.37	36.50	124.82
Heart Clontech	5.63	8.28	5.63	1.32	37.88	213.26
Hypothalamus	9.61	3.16	9.61	0.32	155.28	1492.24
Ileum	19.50	0.00	19.50	2.58	19.38	377.91
Jejunum	35.72	32.22	35.72	6.60	7.58	270.61
Kidney	6.42	13.66	6.42	2.12	23.58	151.42
Liver	13.55	3.28	13.55	1.50	33.33	451.67
Fetal Liver Clontech	57.57	94.10	57.57	10.40	4.81	276.78
Lung	124.57	127.73	124.57	2.57	19.46	2423.54
Mammary Gland Clontech	60.58	30.84	60.58	13.00	3.85	233.00
Myometrium	6.30	0.00	6.30	2.34	21.37	134.62
Omentum	3.51	7.21	3.51	3.94	12.69	44.54
Ovary	19.14	33.01	19.14	4.34	11.52	220.51
Pancreas	3.28	0.00	3.28	0.81	61.80	202.72
Head of Pancreas	0.00	5.33	0.00	1.57	31.85	0.00
Parotid Gland	17.05	0.00	17.05	5.48	9.12	155.57
Placenta Clontech	36.77	12.63	36.77	5.26	9.51	349.52
Prostate	4.30	18.25	4.30	3.00	16.67	71.67
Rectum	2.68	22.55	2.68	1.23	40.65	108.94
Salivary Gland Clontech	21.54	10.89	21.54	7.31	6.84	147.33
Skeletal Muscle Clontech	0.00	0.00	0.00	1.26	39.68	0.00
Skin	3.35	0.00	3.35	1.21	41.32	138.43
Small Intestine Clontech	0.00	0.00	0.00	0.98	51.07	0.00
Spleen	4.87	0.00	4.87	4.92	10.16	49.49
Stomach	12.63	21.35	12.63	2.73	18.32	231.32
Testis Clontech	0.00	0.00	0.00	0.57	87.87	0.00
Thymus Clontech	45.02	58.50	45.02	9.89	5.06	227.60
Thyroid	19.37	58.11	19.37	2.77	18.05	349.64
Trachea Clontech	24.52	32.52	24.52	9.71	5.15	126.26
Urinary Bladder	17.48	18.43	17.48	5.47	9.14	159.78
Uterus	27.02	14.43	27.02	5.34	9.36	253.00

Sample sbg458463PERLAXINa	Reg number (GSK identifier)	Mean GOI copies	copies of mRNA detected/50 ng total RNA	Sample	Fold Change in Disease Population
colon normal GW98-167	21941	253.9	507.80	colon normal	
colon tumor GW98-166	21940	228.99	457.98	colon tumor	-1.108782043
colon normal GW98-178	22080	149.04	298.08	colon normal	
colon tumor GW98-177	22060	68.84	137.68	colon tumor	-2.165020337
colon normal GW98-561	23514	61.93	123.86	colon normal	
colon tumor GW98-560	23513	167.95	335.90	colon tumor	2.711932827
colon normal GW98-894	24691	160.94	321.88	colon normal	
colon tumor GW98-893	24690	157.68	315.36	colon tumor	-1.020674784
lung normal GW98-3	20742	4197.38	8394.76	lung normal	
lung tumor GW98-2	20741	176.65	353.30	lung tumor	-23.76099632
lung normal GW97-179	20677	385.26	770.52	lung normal	
lung tumor GW97-178	20676	480.07	960.14	lung tumor	1.246093547
lung normal GW98-165	21922	5999.5	11999.00	lung normal	
lung tumor GW98-164	21921	856.89	1713.78	lung tumor	-7.001482104
lung normal GW98-282	22584	377.61	755.22	lung normal	
lung tumor GW98-281	22583	2559.29	5118.58	lung tumor	6.777601229
breast normal GW00-392	28750	408.18	408.18	breast normal	
breast tumor GW00-391	28746	394.46	788.92	breast tumor	1.932774756
breast normal GW00-413	28798	74.3	74.30	breast normal	
breast tumor GW00-412	28797	258.3	516.60	breast tumor	6.952893674
breast normal GW00-235:238	27592-95	51.75	51.75	breast normal	
breast tumor GW00-231:234	27588-91	238.94	238.94	breast tumor	4.617198068
breast normal GW98-621	23656	556.61	1113.22	breast normal	
breast tumor GW98-620	23655	375.74	751.48	breast tumor	-1.481370096
brain normal BB99-542	25507	94588.67	189177.34	brain normal	
brain normal BB99-406	25509	639.74	1279.48	brain normal	
brain normal BB99-904	25546	230.79	461.58	brain normal	
brain stage 5 ALZ BB99-874	25502	1238.35	2476.70	brain stage 5 ALZ	-25.69526655
brain stage 5 ALZ BB99-887	25503	1317.43	2634.86	brain stage 5 ALZ	-24.15288352
brain stage 5 ALZ BB99-862	25504	1028.9	2057.80	brain stage 5 ALZ	-30.92597272
brain stage 5 ALZ BB99-927	25542	863.06	1726.12	brain stage 5 ALZ	-36.86850663
CT lung KC	normal	3367.92	6735.84	CT lung	
lung 26 KC	normal	95.04	95.04	lung 26	
lung 27 KC	normal	116.4	116.40	lung 27	
lung 24 KC	COPD	44.2	44.20	lung 24	-39.76391403
lung 28 KC	COPD	15.38	15.38	lung 28	-114.2760078
lung 23 KC	COPD	23.06	23.06	lung 23	-76.2170425
lung 25 KC	COPD	82.98	82.98	lung 25	
asthmatic lung ODO3112	29321	2034.33	2034.33	asthmatic lung	1.157470705
asthmatic lung ODO3433	29323	3155.21	6310.42	asthmatic lung	3.590433355

asthmatic lung ODO3397	29322	6352.76	12705.52	asthmatic lung	7.229047005
asthmatic lung ODO4928	29325	2424.25	4848.50	asthmatic lung	2.758646195
endo cells KC	control	41.66	41.66	endo cells	
endo VEGF KC		51.2	51.20	endo VEGF	1.228996639
endo bFGF KC		45.7	45.70	endo bFGF	1.096975516
heart Clontech	normal	63.06	126.12	heart	
heart (T-1) ischemic	29417	479.42	958.84	heart T-1	7.602600698
heart (T-14) non- obstructive DCM	29422	410.97	821.94	heart T-14	6.517126546
heart (T-3399) DCM	29426	486.59	973.18	heart T-3399	7.716301935
adenoid GW99-269	26162	100.09	200.18	adenoid	
tonsil GW98-280	22582	260.2	520.40	tonsil	
T cells PC00314	28453	257.22	514.44	T cells	
PBMNC KC		26.27	26.27	PBMNC	
monocyte KC		33.09	66.18	monocyte	
B cells PC00665	28455	144.41	288.82	B cells	
dendritic cells 28441		159.67	319.34	dendritic cells	
neutrophils	28440	444.77	444.77	neutrophils	
eosinophils	28446	23.29	46.58	eosinophils	
BM unstim KC		9.26	9.26	BM unstim	
BM stim KC		67.52	67.52	BM stim	7.291576674
osteo dif KC		50.27	50.27	osteo dif	
osteo undif KC		9.8	9.80	osteo undif	-5.129591837
chondrocytes		275.5	688.75	chondrocytes	
OA Synovium IP12/01	29462	432.44	432.44	OA Synovium	
OA Synovium NP10/01	29461	315.85	631.70	OA Synovium	
OA Synovium NP57/00	28464	397.41	794.82	OA Synovium	
RA Synovium NP03/01	28466	342.52	685.04	RA Synovium	
RA Synovium NP71/00	28467	439.34	878.68	RA Synovium	
RA Synovium NP45/00	28475	222.07	444.14	RA Synovium	
OA bone (biobank)	29217	152.61	152.61	OA bone (biobank)	
OA bone Sample 1	J. Emory	623.73	1247.46	OA bone	
OA bone Sample 2	J. Emory	330.6	661.20	OA bone	
Cartilage (pool)	Normal	592.05	1184.10	Cartilage (pool)	
Cartilage (pool)	OA	204.82	409.64	Cartilage (pool)	-2.890586857
PBL uninfected	28441	488.95	977.90	PBL uninfected	
PBL HIV IIIB	28442	261.88	523.76	PBL HIV IIIB	-1.867076524
MRC5 uninfected (100%)	29158	476.47	952.94	MRC5 uninfected (100%)	
MRC5 HSV strain F	29178	216.34	432.68	MRC5 HSV strain F	-2.202412869
W12 cells	29179	182.76	365.52	W12 cells	
Keratinocytes	29180	124.58	249.16	Keratinocytes	

Gene Name sbg458463PERLAXINa

Disease tissues	Fold Change in Disease
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	Population Relative to Normal
colon tumor	-1.11
colon tumor	-2.17
colon tumor	2.71
colon tumor	-1.02
lung tumor	-23.76
lung tumor	1.25
lung tumor	-7.00
lung tumor	6.78
breast tumor	1.93
breast tumor	6.95
breast tumor	4.62
breast tumor	-1.48
brain stage 5 ALZ	-25.70
brain stage 5 ALZ	-24.15
brain stage 5 ALZ	-30.93
brain stage 5 ALZ	-36.87
lung 24	-39.76
lung 28	-114.28
lung 23	-76.22
asthmatic lung	1.16
asthmatic lung	3.59
asthmatic lung	7.23
asthmatic lung	2.76
endo VEGF	1.23
endo bFGF	1.10
heart T-1	7.60
heart T-14	6.52
heart T-3399	7.72
BM stim	7.29
osteo undif	-5.13
Cartilage (pool)	-2.89
PBL HIV IIIB	-1.87
MRC5 HSV strain F	-2.20

Gene Name sbg507885RDPa and sbg507885RDPb

Strongly expressed in immune cells. Corroborating expression in OA and RA samples suggesting a role in this disease. Expression in brain outside of cortex, cerebellum, and hypothalamus indicating localized expression in brain.

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Sample sbg507885RDPa and sbg507885RDPb	Mean GOI copies (sample 1)	Mean GOI copies (sample 2)	Average GOI Copies	18S rRNA (ng)	50 ng/18S rRNA (ng)	copies of mRNA detected/ 50 ng total RNA
Subcutaneous Adipocytes Zenbio	0.44	0.00	0.22	3.06	16.34	3.59
Subcutaneous Adipose Zenbio	0.00	1.46	0.73	0.96	52.36	38.22
Adrenal Gland Clontech	2.56	1.63	2.10	0.61	81.97	171.72

Whole Brain Clontech	354.41	170.16	262.29	7.24	6.91	1811.36
Fetal Brain Clontech	1.81	1.98	1.90	0.48	103.95	196.99
Cerebellum Clontech	1.42	4.83	3.13	2.17	23.04	72.00
Cervix	1.00	0.94	0.97	2.42	20.66	20.04
Colon	7.32	3.78	5.55	2.71	18.45	102.40
Endometrium	6.52	0.99	3.76	0.73	68.21	256.14
Esophagus	1.30	0.65	0.98	1.37	36.50	35.58
Heart Clontech	0.45	1.81	1.13	1.32	37.88	42.80
Hypothalamus	0.00	0.00	0.00	0.32	155.28	0.00
Ileum	14.77	2.05	8.41	2.58	19.38	162.98
Jejunum	12.85	18.38	15.62	6.60	7.58	118.30
Kidney	0.71	0.70	0.71	2.12	23.58	16.63
Liver	0.84	14.92	7.88	1.50	33.33	262.67
Fetal Liver Clontech	34.52	48.23	41.38	10.40	4.81	198.92
Lung	0.00	6.12	3.06	2.57	19.46	59.53
Mammary Gland Clontech	6.69	1.13	3.91	13.00	3.85	15.04
Myometrium	0.00	0.00	0.00	2.34	21.37	0.00
Omentum	19.39	22.18	20.79	3.94	12.69	263.77
Ovary	10.10	8.28	9.19	4.34	11.52	105.88
Pancreas	0.62	0.75	0.69	0.81	61.80	42.34
Head of Pancreas	0.51	0.80	0.66	1.57	31.85	20.86
Parotid Gland	0.79	12.98	6.89	5.48	9.12	62.82
Placenta Clontech	5.82	6.21	6.02	5.26	9.51	57.18
Prostate	0.94	0.00	0.47	3.00	16.67	7.83
Rectum	9.47	0.59	5.03	1.23	40.65	204.47
Salivary Gland Clontech	1.06	4.83	2.95	7.31	6.84	20.14
Skeletal Muscle Clontech	0.89	0.00	0.45	1.26	39.68	17.66
Skin	0.70	0.92	0.81	1.21	41.32	33.47
Small Intestine Clontech	2.38	0.00	1.19	0.98	51.07	60.78
Spleen	5.42	0.63	3.03	4.92	10.16	30.74
Stomach	0.00	14.37	7.19	2.73	18.32	131.59
Testis Clontech	29.69	16.00	22.85	0.57	87.87	2007.47
Thymus Clontech	27.94	42.80	35.37	9.89	5.06	178.82
Thyroid	0.00	5.97	2.99	2.77	18.05	53.88
Trachea Clontech	35.39	143.02	89.21	9.71	5.15	459.35
Urinary Bladder	0.56	0.00	0.28	5.47	9.14	2.56
Uterus	6.57	32.58	19.58	5.34	9.36	183.29

Sample sbg507885RDPa and sbg507885RDPb	Reg number (GSK identifier)	Mean GOI copies	copies of mRNA detected/50 ng total RNA	Sample	Fold Change in Disease Population
colon normal GW98-167	21941	45.66	91.32	colon normal	
colon tumor GW98-166	21940	43.18	86.36	colon tumor	-1.057433997
colon normal GW98-178	22080	20.11	40.22	colon normal	
colon tumor GW98-177	22060	10.96	21.92	colon tumor	-1.834854015
colon normal GW98-561	23514	31.65	63.30	colon normal	
colon tumor GW98-560	23513	17.32	34.64	colon tumor	-1.827367206
colon normal GW98-894	24691	47.87	95.74	colon normal	

colon tumor GW98-893	24690	19.49	38.98	colon tumor	-2.456131349
lung normal GW98-3	20742	92.38	184.76	lung normal	
lung tumor GW98-2	20741	0	0.00	lung tumor	-184.76
lung normal GW97-179	20677	118.63	237.26	lung normal	
lung tumor GW97-178	20676	179.06	358.12	lung tumor	1.509398972
lung normal GW98-165	21922	282.77	565.54	lung normal	
lung tumor GW98-164	21921	127.86	255.72	lung tumor	-2.211559518
lung normal GW98-282	22584	34.81	69.62	lung normal	
lung tumor GW98-281	22583	14.9	29.80	lung tumor	-2.336241611
breast normal GW00-392	28750	19.47	19.47	breast normal	
breast tumor GW00-391	28746	21.61	43.22	breast tumor	2.219825372
breast normal GW00-413	28798	19.77	19.77	breast normal	
breast tumor GW00-412	28797	28.47	56.94	breast tumor	2.880121396
breast normal GW00-235:238	27592-95	8.87	8.87	breast normal	
breast tumor GW00-231:234	27588-91	19.37	19.37	breast tumor	2.183765502
breast normal GW98-621	23656	40.14	80.28	breast normal	
breast tumor GW98-620	23655	8.92	17.84	breast tumor	-4.5
brain normal BB99-542	25507	136.73	273.46	brain normal	
brain normal BB99-406	25509	74.17	148.34	brain normal	
brain normal BB99-904	25546	103.79	207.58	brain normal	
brain stage 5 ALZ BB99-874	25502	15.31	30.62	brain stage 5 ALZ	-6.851513172
brain stage 5 ALZ BB99-887	25503	256.01	512.02	brain stage 5 ALZ	2.440592329
brain stage 5 ALZ BB99-862	25504	75.06	150.12	brain stage 5 ALZ	-1.397504219
brain stage 5 ALZ BB99-927	25542	142.17	284.34	brain stage 5 ALZ	1.355333821
CT lung KC	normal	51.66	103.32	CT lung	
lung 26 KC	normal	25.26	25.26	lung 26	
lung 27 KC	normal	0	0.00	lung 27	
lung 24 KC	COPD	8.84	8.84	lung 24	-4.022624434
lung 28 KC	COPD	2.6	2.60	lung 28	-13.67692308
lung 23 KC	COPD	5.92	5.92	lung 23	-6.006756757
lung 25 KC	COPD	13.66	13.66	lung 25	
asthmatic lung ODO3112	29321	22.47	22.47	asthmatic lung	-1.582554517
asthmatic lung ODO3433	29323	72.48	144.96	asthmatic lung	4.076490439
asthmatic lung ODO3397	29322	89.06	178.12	asthmatic lung	5.008998875
asthmatic lung ODO4928	29325	165.77	331.54	asthmatic lung	9.323397075
endo cells KC	control	3.74	3.74	endo cells	
endo VEGF KC		0	0.00	endo VEGF	-3.74
endo bFGF KC		0	0.00	endo bFGF	-3.74
heart Clontech	normal	44.05	88.10	heart	
heart (T-1) ischemic	29417	34.71	69.42	heart T-1	-1.269086719
heart (T-14) non-obstructive DCM	29422	6.78	13.56	heart T-14	-6.497050147
heart (T-3399) DCM	29426	13.42	26.84	heart T-3399	-3.282414307
adenoid GW99-269	26162	79.2	158.40	adenoid	
tonsil GW98-280	22582	92.31	184.62	tonsil	
T cells PC00314	28453	499.1	998.20	T cells	
PBMNC KC		16.17	16.17	PBMNC	
monocyte KC		8.33	16.66	monocyte	

B cells PC00665	28455	1260.77	2521.54	B cells	
dendritic cells 28441		153.63	307.26	dendritic cells	
neutrophils	28440	5938.24	5938.24	neutrophils	
eosinophils	28446	1471.53	2943.06	eosinophils	
BM unstim KC		9.62	9.62	BM unstim	
BM stim KC		31.23	31.23	BM stim	3.246361746
osteo dif KC		0	0.00	osteo dif	
osteo undif KC		0	0.00	osteo undif	0
chondrocytes		0.68	1.70	chondrocytes	
OA Synovium IP12/01	29462	80.64	80.64	OA Synovium	
OA Synovium NP10/01	29461	121	242.00	OA Synovium	
OA Synovium NP57/00	28464	117.75	235.50	OA Synovium	
RA Synovium NP03/01	28466	189.18	378.36	RA Synovium	
RA Synovium NP71/00	28467	313.76	627.52	RA Synovium	
RA Synovium NP45/00	28475	146.34	292.68	RA Synovium	
OA bone (biobank)	29217	171.21	171.21	OA bone (biobank)	
OA bone Sample 1	J. Emory	71.91	143.82	OA bone	
OA bone Sample 2	J. Emory	132.79	265.58	OA bone	
Cartilage (pool)	Normal	19.06	38.12	Cartilage (pool)	
Cartilage (pool)	OA	31.65	63.30	Cartilage (pool)	1.660545645
PBL uninfected	28441	99.28	198.56	PBL uninfected	
PBL HIV IIIB	28442	57.94	115.88	PBL HIV IIIB	-1.713496721
MRC5 uninfected (100%)	29158	0	0.00	MRC5 uninfected (100%)	
MRC5 HSV strain F	29178	206.39	412.78	MRC5 HSV strain F	412.78
W12 cells	29179	0	0.00	W12 cells	
Keratinocytes	29180	4.35	8.70	Keratinocytes	

Gene Name sbg507885RDPa and sbg507885RDPb

Disease tissues	Fold Change in Disease Population Relative to Normal
colon tumor	-1.06
colon tumor	-1.83
colon tumor	-1.83
colon tumor	-2.46
lung tumor	-184.76
lung tumor	1.51
lung tumor	-2.21
lung tumor	-2.34
breast tumor	2.22
breast tumor	2.88
breast tumor	2.18
breast tumor	-4.50
brain stage 5 ALZ	-6.85
brain stage 5 ALZ	2.44
brain stage 5 ALZ	-1.40
brain stage 5 ALZ	1.36
lung 24	-4.02

lung 28	-13.68
lung 23	-6.01
asthmatic lung	-1.58
asthmatic lung	4.08
asthmatic lung	5.01
asthmatic lung	9.32
endo VEGF	-3.74
endo bFGF	-3.74
heart T-1	-1.27
heart T-14	-6.50
heart T-3399	-3.28
BM stim	3.25
osteo undif	0.00
Cartilage (pool)	1.66
PBL HIV IIIB	-1.71
MRC5 HSV strain F	412.78

Gene Name SBh511364.NR-CAMa and SBh511364.NR-CAMb

Strongly expressed in synovium. Specific expression profile and lack of corroborating expression in immune cells indicates that this expression may be derived from synoviocytes. Strongly expressed in brain and to a lesser degree, hypothalamus. Low expression in cortex.

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Sample SBh511364.NR- CAMa and SBh511364.NR- CAMb	Mean GOI copies (sample 1)	Mean GOI copies (sample 2)	Average GOI Copies	18S rRNA (ng)	50 ng/18S rRNA (ng)	copies of mRNA detecte d/50 ng total RNA
Subcutaneous Adipocytes Zenbio	8.81	15.21	12.01	3.06	16.34	196.24
Subcutaneous Adipose Zenbio	0.65	0.60	0.63	0.96	52.36	32.72
Adrenal Gland Clontech	5.82	2.88	4.35	0.61	81.97	356.56
Whole Brain Clontech	745.46	885.20	815.33	7.24	6.91	5630.73
Fetal Brain Clontech	2.54	7.10	4.82	0.48	103.95	501.04
Cerebellum Clontech	2.00	1.60	1.80	2.17	23.04	41.47
Cervix	5.24	5.57	5.41	2.42	20.66	111.67
Colon	19.12	9.91	14.52	2.71	18.45	267.80
Endometrium	5.89	3.09	4.49	0.73	68.21	306.28
Esophagus	3.36	5.73	4.55	1.37	36.50	165.88
Heart Clontech	11.19	4.50	7.85	1.32	37.88	297.16
Hypothalamus	6.23	9.33	7.78	0.32	155.28	1208.07
Ileum	22.13	14.54	18.34	2.58	19.38	355.33
Jejunum	43.08	28.67	35.88	6.60	7.58	271.78
Kidney	6.61	2.38	4.50	2.12	23.58	106.01
Liver	5.71	7.80	6.76	1.50	33.33	225.17
Fetal Liver Clontech	58.58	39.22	48.90	10.40	4.81	235.10
Lung	21.54	14.27	17.91	2.57	19.46	348.35
Mammary Gland Clontech	74.10	70.13	72.12	13.00	3.85	277.37
Myometrium	14.20	14.00	14.10	2.34	21.37	301.28
Omentum	10.02	8.87	9.45	3.94	12.69	119.86

Ovary	18.13	21.78	19.96	4.34	11.52	229.90
Pancreas	5.35	5.01	5.18	0.81	61.80	320.15
Head of Pancreas	15.48	17.71	16.60	1.57	31.85	528.50
Parotid Gland	15.65	18.09	16.87	5.48	9.12	153.92
Placenta Clontech	39.73	32.58	36.16	5.26	9.51	343.68
Prostate	11.18	10.70	10.94	3.00	16.67	182.33
Rectum	13.03	18.25	15.64	1.23	40.65	635.77
Salivary Gland Clontech	45.23	37.40	41.32	7.31	6.84	282.59
Skin	13.36	18.71	16.04	1.21	41.32	662.60
Small Intestine Clontech	9.35	14.90	12.13	0.98	51.07	619.25
Spleen	20.53	16.75	18.64	4.92	10.16	189.43
Stomach	10.15	11.21	10.68	2.73	18.32	195.60
Testis Clontech	4.21	9.04	6.63	0.57	87.87	582.16
Thymus Clontech	107.54	69.67	88.61	9.89	5.06	447.95
Thyroid	16.42	20.77	18.60	2.77	18.05	335.65
Trachea Clontech	45.92	41.96	43.94	9.71	5.15	226.26
Urinary Bladder	32.67	27.42	30.05	5.47	9.14	274.63
Uterus	16.56	13.13	14.85	5.34	9.36	139.00

Sample SBh511364.NR-CAMa and SBh511364.NR- CAMb	Reg number (GSK identifier)	Mean GOI copies	copies of mRNA detected/50 ng total RNA	Sample	Fold Change in Disease Population
colon normal GW98-167	21941	341.84	683.68	colon normal	
colon tumor GW98-166	21940	698.49	1396.98	colon tumor	2.043324362
colon normal GW98-178	22080	173.88	347.76	colon normal	
colon tumor GW98-177	22060	69.79	139.58	colon tumor	-2.491474423
colon normal GW98-561	23514	131.42	262.84	colon normal	
colon tumor GW98-560	23513	89.43	178.86	colon tumor	-1.469529241
colon normal GW98-894	24691	182.2	364.40	colon normal	
colon tumor GW98-893	24690	119.24	238.48	colon tumor	-1.528010735
lung normal GW98-3	20742	366.92	733.84	lung normal	
lung tumor GW98-2	20741	171.96	343.92	lung tumor	-2.133752035
lung normal GW97-179	20677	779.87	1559.74	lung normal	
lung tumor GW97-178	20676	276.89	553.78	lung tumor	-2.816533642
lung normal GW98-165	21922	325.67	651.34	lung normal	
lung tumor GW98-164	21921	1297.39	2594.78	lung tumor	3.983756563
lung normal GW98-282	22584	608.41	1216.82	lung normal	
lung tumor GW98-281	22583	164.45	328.90	lung tumor	-3.699665552
breast normal GW00-392	28750	138.27	138.27	breast normal	
breast tumor GW00-391	28746	181.83	363.66	breast tumor	2.630071599
breast normal GW00-413	28798	38.99	38.99	breast normal	
breast tumor GW00-412	28797	90.26	180.52	breast tumor	4.629905104
breast normal GW00-235:238	27592-95	34.69	34.69	breast normal	
breast tumor GW00-231:234	27588-91	189.47	189.47	breast tumor	5.461804555
breast normal GW98-621	23656	375.65	751.30	breast normal	
breast tumor GW98-620	23655	165.82	331.64	breast tumor	-2.265408274
brain normal BB99-542	25507	193.78	387.56	brain normal	
brain normal BB99-406	25509	90.91	181.82	brain normal	

brain normal BB99-904	25546	106.82	213.64	brain normal	
brain stage 5 ALZ BB99-874	25502	107.53	215.06	brain stage 5 ALZ	-1.213645804
brain stage 5 ALZ BB99-887	25503	178.51	357.02	brain stage 5 ALZ	1.367857781
brain stage 5 ALZ BB99-862	25504	134.36	268.72	brain stage 5 ALZ	1.029552246
brain stage 5 ALZ BB99-927	25542	99.03	198.06	brain stage 5 ALZ	-1.31781615
CT lung KC	normal	260.82	521.64	CT lung	
lung 26 KC	normal	5.72	5.72	lung 26	
lung 27 KC	normal	1.05	1.05	lung 27	
lung 24 KC	COPD	2.04	2.04	lung 24	-64.84803922
lung 28 KC	COPD	2.13	2.13	lung 28	-62.10798122
lung 23 KC	COPD	5.32	5.32	lung 23	-24.86654135
lung 25 KC	COPD	0.75	0.75	lung 25	
asthmatic lung ODO3112	29321	153.45	153.45	asthmatic lung	1.159951621
asthmatic lung ODO3433	29323	324.42	648.84	asthmatic lung	4.904679114
asthmatic lung ODO3397	29322	940.06	1880.12	asthmatic lung	14.21210976
asthmatic lung ODO4928	29325	336.17	672.34	asthmatic lung	5.082319147
endo cells KC	control	17.87	17.87	endo cells	
endo VEGF KC		3.69	3.69	endo VEGF	-4.842818428
endo bFGF KC		1.99	1.99	endo bFGF	-8.979899497
heart Clontech	normal	103.46	206.92	heart	
heart (T-1) ischemic	29417	82.96	165.92	heart T-1	-1.24710704
heart (T-14) non-obstructive DCM	29422	95.28	190.56	heart T-14	-1.085852225
heart (T-3399) DCM	29426	82.5	165.00	heart T-3399	-1.254060606
adenoid GW99-269	26162	194.24	388.48	adenoid	
tonsil GW98-280	22582	229.68	459.36	tonsil	
T cells PC00314	28453	96.61	193.22	T cells	
PBMNC KC		4.33	4.33	PBMNC	
monocyte KC		19.34	38.68	monocyte	
B cells PC00665	28455	87.76	175.52	B cells	
dendritic cells 28441		38.09	76.18	dendritic cells	
neutrophils	28440	37.8	37.80	neutrophils	
eosinophils	28446	55.24	110.48	eosinophils	
BM unstim KC		9.02	9.02	BM unstim	
BM stim KC		5.15	5.15	BM stim	-1.751456311
osteo dif KC		1.36	1.36	osteo dif	
osteo undif KC		1.62	1.62	osteo undif	1.191176471
chondrocytes		15.33	38.33	chondrocytes	
OA Synovium IP12/01	29462	761.5	761.50	OA Synovium	
OA Synovium NP10/01	29461	331.41	662.82	OA Synovium	
OA Synovium NP57/00	28464	1027.35	2054.70	OA Synovium	
RA Synovium NP03/01	28466	1550.08	3100.16	RA Synovium	
RA Synovium NP71/00	28467	1537.93	3075.86	RA Synovium	
RA Synovium NP45/00	28475	2117.45	4234.90	RA Synovium	
OA bone (biobank)	29217	15.14	15.14	OA bone (biobank)	
OA bone Sample 1	J. Emory	147.58	295.16	OA bone	
OA bone Sample 2	J. Emory	78.86	157.72	OA bone	
Cartilage (pool)	Normal	170.3	340.60	Cartilage (pool)	

Cartilage (pool)	OA	107.65	215.30	Cartilage (pool)	-1.581978634
PBL uninfected	28441	23	46.00	PBL uninfected	
PBL HIV IIIB	28442	29.11	58.22	PBL HIV IIIB	1.265652174
MRC5 uninfected (100%)	29158	181.22	362.44	MRC5 uninfected (100%)	
MRC5 HSV strain F	29178	37.26	74.52	MRC5 HSV strain F	-4.863660762
W12 cells	29179	92.73	185.46	W12 cells	
Keratinocytes	29180	55.64	111.28	Keratinocytes	

Gene Name SBh511364.NR-CAMa and SBh511364.NR-CAMb

Disease tissues	Fold Change in Disease Population Relative to Normal
colon tumor	2.04
colon tumor	-2.49
colon tumor	-1.47
colon tumor	-1.53
lung tumor	-2.13
lung tumor	-2.82
lung tumor	3.98
lung tumor	-3.70
breast tumor	2.63
breast tumor	4.63
breast tumor	5.46
breast tumor	-2.27
brain stage 5 ALZ	-1.21
brain stage 5 ALZ	1.37
brain stage 5 ALZ	1.03
brain stage 5 ALZ	-1.32
lung 24	-64.85
lung 28	-62.11
lung 23	-24.87
asthmatic lung	1.16
asthmatic lung	4.90
asthmatic lung	14.21
asthmatic lung	5.08
endo VEGF	-4.84
endo bFGF	-8.98
heart T-1	-1.25
heart T-14	-1.09
heart T-3399	-1.25
BM stim	-1.75
osteo undif	1.19
Cartilage (pool)	-1.58
PBL HIV IIIB	1.27
MRC5 HSV strain F	-4.86

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Gene Name SBh511827.C1q-related factor

Expression in T and B cells. Corroborating expression in OA and RA samples suggesting role in this disease. Expression in tumors may be due to infiltration of immune cells. High brain expression in whole brain and cortex but does not correlate with Alzheimer's disease.

Sample SBh511827.C1q- related factor	Mean GOI copies (sample 1)	Mean GOI copies (sample 2)	Average GOI Copies	18S rRNA (ng)	50 ng/18S rRNA (ng)	copies of mRNA detected/ 50 ng total RNA
Subcutaneous Adipocytes Zenbio	10.01	5.60	7.81	3.06	16.34	127.53
Subcutaneous Adipose Zenbio	0.00	2.57	1.29	0.96	52.36	67.28
Adrenal Gland Clontech	0.00	0.00	0.00	0.61	81.97	0.00
Whole Brain Clontech	5567.93	8662.87	7115.40	7.24	6.91	49139.50
Fetal Brain Clontech	0.00	2.90	1.45	0.48	103.95	150.73
Cerebellum Clontech	16.42	20.36	18.39	2.17	23.04	423.73
Cervix	7.42	5.99	6.71	2.42	20.66	138.53
Colon	48.72	28.04	38.38	2.71	18.45	708.12
Endometrium	2.79	0.00	1.40	0.73	68.21	95.16
Esophagus	0.00	0.00	0.00	1.37	36.50	0.00
Heart Clontech	6.47	0.00	3.24	1.32	37.88	122.54
Hypothalamus	0.66	0.00	0.33	0.32	155.28	51.24
Ileum	93.23	38.67	65.95	2.58	19.38	1278.10
Jejunum	139.58	66.22	102.90	6.60	7.58	779.55
Kidney	3.44	1.90	2.67	2.12	23.58	62.97
Liver	5.92	2.25	4.09	1.50	33.33	136.17
Fetal Liver Clontech	660.71	619.22	639.97	10.40	4.81	3076.75
Lung	8.32	30.50	19.41	2.57	19.46	377.63
Mammary Gland Clontech	83.57	132.39	107.98	13.00	3.85	415.31
Myometrium	3.80	7.92	5.86	2.34	21.37	125.21
Omentum	38.71	144.15	91.43	3.94	12.69	1160.28
Ovary	20.35	30.49	25.42	4.34	11.52	292.86
Pancreas	3.05	6.19	4.62	0.81	61.80	285.54
Head of Pancreas	0.00	0.00	0.00	1.57	31.85	0.00
Parotid Gland	508.91	732.28	620.60	5.48	9.12	5662.36
Placenta Clontech	41.43	20.41	30.92	5.26	9.51	293.92
Prostate	3.11	0.00	1.56	3.00	16.67	25.92
Rectum	32.59	24.20	28.40	1.23	40.65	1154.27
Salivary Gland Clontech	333.69	307.24	320.47	7.31	6.84	2191.96
Skeletal Muscle Clontech	0.00	3.23	1.62	1.26	39.68	64.09
Skin	0.00	0.00	0.00	1.21	41.32	0.00
Small Intestine Clontech	0.00	0.00	0.00	0.98	51.07	0.00
Spleen	6.23	29.09	17.66	4.92	10.16	179.47
Stomach	14.40	28.92	21.66	2.73	18.32	396.70
Testis Clontech	0.00	2.81	1.41	0.57	87.87	123.46
Thymus Clontech	1882.59	1917.19	1899.89	9.89	5.06	9605.11
Thyroid	8.33	5.07	6.70	2.77	18.05	120.94

Trachea Clontech	114.59	259.72	187.16	9.71	5.15	963.72
Urinary Bladder	71.47	89.07	80.27	5.47	9.14	733.73
Uterus	30.66	37.35	34.01	5.34	9.36	318.40

Sample SBh511827.C1q-related factor	Reg number (GSK identifier)	Mean GOI copies	copies of mRNA detected/5 0 ng total RNA	Sample	Fold Change in Disease Population
colon normal GW98-167	21941	5744.02	11488.04	colon normal	
colon tumor GW98-166	21940	6292.52	12585.04	colon tumor	1.095490615
colon normal GW98-178	22080	320.97	641.94	colon normal	
colon tumor GW98-177	22060	1579.81	3159.62	colon tumor	4.921986478
colon normal GW98-561	23514	1441.03	2882.06	colon normal	
colon tumor GW98-560	23513	593.17	1186.34	colon tumor	-2.429371007
colon normal GW98-894	24691	3163.53	6327.06	colon normal	
colon tumor GW98-893	24690	1149.98	2299.96	colon tumor	-2.750943495
lung normal GW98-3	20742	3695.92	7391.84	lung normal	
lung tumor GW98-2	20741	731.09	1462.18	lung tumor	-5.055355702
lung normal GW97-179	20677	1378.74	2757.48	lung normal	
lung tumor GW97-178	20676	1448.64	2897.28	lung tumor	1.050698464
lung normal GW98-165	21922	3139.74	6279.48	lung normal	
lung tumor GW98-164	21921	8081.51	16163.02	lung tumor	2.573942428
lung normal GW98-282	22584	1632.83	3265.66	lung normal	
lung tumor GW98-281	22583	764.62	1529.24	lung tumor	-2.135479061
breast normal GW00-392	28750	2333.36	2333.36	breast normal	
breast tumor GW00-391	28746	2670.09	5340.18	breast tumor	2.288622416
breast normal GW00-413	28798	1982.15	1982.15	breast normal	
breast tumor GW00-412	28797	1739.48	3478.96	breast tumor	1.755144666
breast normal GW00-235:238	27592-95	1835.31	1835.31	breast normal	
breast tumor GW00-231:234	27588-91	9829.72	9829.72	breast tumor	5.35589083
breast normal GW98-621	23656	2824.18	5648.36	breast normal	
breast tumor GW98-620	23655	5401.77	10803.54	breast tumor	1.91268616
brain normal BB99-542	25507	4282.26	8564.52	brain normal	
brain normal BB99-406	25509	5101.69	10203.38	brain normal	
brain normal BB99-904	25546	3412.26	6824.52	brain normal	
brain stage 5 ALZ BB99-874	25502	1341.14	2682.28	brain stage 5 ALZ	-3.180431076
brain stage 5 ALZ BB99-887	25503	7475.28	14950.56	brain stage 5 ALZ	1.752537665
brain stage 5 ALZ BB99-862	25504	4871.16	9742.32	brain stage 5 ALZ	1.142016269
brain stage 5 ALZ BB99-927	25542	4972.65	9945.30	brain stage 5 ALZ	1.165810033
CT lung KC	normal	622.18	1244.36	CT lung	
lung 26 KC	normal	1547.5	1547.50	lung 26	
lung 27 KC	normal	8.75	8.75	lung 27	
lung 24 KC	COPD	45	45.00	lung 24	-15.69138889
lung 28 KC	COPD	107.35	107.35	lung 28	-6.577666511
lung 23 KC	COPD	245.33	245.33	lung 23	-2.878215057
lung 25 KC	COPD	23.84	23.84	lung 25	
asthmatic lung ODO3112	29321	518.92	518.92	asthmatic lung	-1.360734795

asthmatic lung ODO3433	29323	893.67	1787.34	asthmatic lung	2.53123971
asthmatic lung ODO3397	29322	2195.27	4390.54	asthmatic lung	6.217904371
asthmatic lung ODO4928	29325	695.54	1391.08	asthmatic lung	1.970054347
endo cells KC	control	16.49	16.49	endo cells	
endo VEGF KC		119.58	119.58	endo VEGF	7.251667677
endo bFGF KC		17.05	17.05	endo bFGF	1.033959976
heart Clontech	normal	166.69	333.38	heart	
heart (T-1) ischemic	29417	1046.33	2092.66	heart T-1	6.277101206
heart (T-14) non-obstructive DCM	29422	438.65	877.30	heart T-14	2.631531586
heart (T-3399) DCM	29426	634.06	1268.12	heart T-3399	3.803827464
adenoid GW99-269	26162	285.91	571.82	adenoid	
tonsil GW98-280	22582	912.43	1824.86	tonsil	
T cells PC00314	28453	2710.37	5420.74	T cells	
PBMNC KC		53.93	53.93	PBMNC	
monocyte KC		97.03	194.06	monocyte	
B cells PC00665	28455	2096.55	4193.10	B cells	
dendritic cells 28441		307.67	615.34	dendritic cells	
neutrophils	28440	352.93	352.93	neutrophils	
eosinophils	28446	148.18	296.36	eosinophils	
BM unstim KC		44.62	44.62	BM unstim	
BM stim KC		102.28	102.28	BM stim	2.29224563
osteo dif KC		13.17	13.17	osteo dif	
osteo undif KC		9.04	9.04	osteo undif	-1.456858407
chondrocytes		189.54	473.85	chondrocytes	
OA Synovium IP12/01	29462	9850.71	9850.71	OA Synovium	
OA Synovium NP10/01	29461	4627.57	9255.14	OA Synovium	
OA Synovium NP57/00	28464	3568.61	7137.22	OA Synovium	
RA Synovium NP03/01	28466	4452.77	8905.54	RA Synovium	
RA Synovium NP71/00	28467	4479.74	8959.48	RA Synovium	
RA Synovium NP45/00	28475	10746.73	21493.46	RA Synovium	
OA bone (biobank)	29217	468.68	468.68	OA bone (biobank)	
OA bone Sample 1	J. Emory	2277.5	4555.00	OA bone	
OA bone Sample 2	J. Emory	921.91	1843.82	OA bone	
Cartilage (pool)	Normal	9515.61	19031.22	Cartilage (pool)	
Cartilage (pool)	OA	3862.55	7725.10	Cartilage (pool)	-2.463556459
PBL uninfected	28441	2689.77	5379.54	PBL uninfected	
PBL HIV IIIB	28442	1110.9	2221.80	PBL HIV IIIB	-2.421253038
MRC5 uninfected (100%)	29158	163.61	327.22	MRC5 uninfected (100%)	
MRC5 HSV strain F	29178	35.94	71.88	MRC5 HSV strain F	-4.552309405
W12 cells	29179	171.69	343.38	W12 cells	
Keratinocytes	29180	142.68	285.36	Keratinocytes	

Gene Name SBh511827.C1q-related factor

Disease tissues	Fold Change in Disease Population Relative to Normal
colon tumor	1.10
colon tumor	4.92

colon tumor	-2.43
colon tumor	-2.75
lung tumor	-5.06
lung tumor	1.05
lung tumor	2.57
lung tumor	-2.14
breast tumor	2.29
breast tumor	1.76
breast tumor	5.36
breast tumor	1.91
brain stage 5 ALZ	-3.18
brain stage 5 ALZ	1.75
brain stage 5 ALZ	1.14
brain stage 5 ALZ	1.17
lung 24	-15.69
lung 28	-6.58
lung 23	-2.88
asthmatic lung	-1.36
asthmatic lung	2.53
asthmatic lung	6.22
asthmatic lung	1.97
endo VEGF	7.25
endo bFGF	1.03
heart T-1	6.28
heart T-14	2.63
heart T-3399	3.80
BM stim	2.29
osteo undif	-1.46
Cartilage (pool)	-2.46
PBL HIV IIIB	-2.42
MRC5 HSV strain F	-4.55

Gene Name sbg533677PALSa

Expression in immune cells with corroborating expression in asthmatic lung (3/4)

suggesting possible role in Asthma. Overexpressed in heart disease suggesting role in CV

- 5 diseases. Down regulation in HSV infection suggesting possible host cell factor. High brain expression in whole brain and cortex but does not correlate with Alzheimer's disease.

Sample sbg533677PALSa	Mean GOI copies (sample 1)	Mean GOI copies (sample 2)	Average GOI Copies	18S rRNA (ng)	50 ng/18S rRNA (ng)	copies of mRNA detected/ 50 ng total RNA
Subcutaneous Adipocytes Zenbio	51.44	92.64	72.04	3.06	16.34	1177.12
Subcutaneous Adipose Zenbio	5.24	2.42	3.83	0.96	52.36	200.52
Adrenal Gland Clontech	8.53	9.10	8.82	0.61	81.97	722.54
Whole Brain Clontech	15161.45	15339.88	15250.67	7.24	6.91	105322.2 7
Fetal Brain Clontech	18.17	23.22	20.70	0.48	103.95	2151.25
Cerebellum Clontech	219.59	45.25	132.42	2.17	23.04	3051.15

Cervix	122.01	91.28	106.65	2.42	20.66	2203.41
Colon	267.14	172.02	219.58	2.71	18.45	4051.29
Endometrium	18.22	34.03	26.13	0.73	68.21	1782.06
Esophagus	45.23	46.43	45.83	1.37	36.50	1672.63
Heart Clontech	27.22	52.91	40.07	1.32	37.88	1517.61
Hypothalamus	1.28	2.12	1.70	0.32	155.28	263.98
Ileum	94.43	111.58	103.01	2.58	19.38	1996.22
Jejunum	1633.12	2127.36	1880.24	6.60	7.58	14244.24
Kidney	63.84	160.51	112.18	2.12	23.58	2645.64
Liver	29.42	42.03	35.73	1.50	33.33	1190.83
Fetal Liver Clontech	2536.60	2105.61	2321.11	10.40	4.81	11159.16
Lung	136.03	198.77	167.40	2.57	19.46	3256.81
Mammary Gland Clontech	424.73	623.88	524.31	13.00	3.85	2016.56
Myometrium	49.18	119.83	84.51	2.34	21.37	1805.66
Omentum	133.77	211.60	172.69	3.94	12.69	2191.43
Ovary	137.22	102.84	120.03	4.34	11.52	1382.83
Pancreas	24.03	19.46	21.75	0.81	61.80	1343.94
Head of Pancreas	15.98	9.70	12.84	1.57	31.85	408.92
Parotid Gland	164.01	243.65	203.83	5.48	9.12	1859.76
Placenta Clontech	443.13	418.73	430.93	5.26	9.51	4096.29
Prostate	348.78	83.31	216.05	3.00	16.67	3600.75
Rectum	82.65	132.21	107.43	1.23	40.65	4367.07
Salivary Gland Clontech	194.49	469.68	332.09	7.31	6.84	2271.44
Skeletal Muscle Clontech	32.51	69.14	50.83	1.26	39.68	2016.87
Skin	8.94	55.38	32.16	1.21	41.32	1328.93
Small Intestine Clontech	4.50	20.21	12.36	0.98	51.07	631.00
Spleen	115.42	95.13	105.28	4.92	10.16	1069.87
Stomach	58.96	147.19	103.08	2.73	18.32	1887.82
Testis Clontech	28.25	6.42	17.34	0.57	87.87	1523.29
Thymus Clontech	1685.23	1168.51	1426.87	9.89	5.06	7213.70
Thyroid	215.93	210.84	213.39	2.77	18.05	3851.71
Trachea Clontech	195.46	204.92	200.19	9.71	5.15	1030.84
Urinary Bladder	238.82	321.83	280.33	5.47	9.14	2562.39
Uterus	162.57	183.68	173.13	5.34	9.36	1621.02

Sample sbg533677PALSa	Reg number (GSK identifier)	Mean GOI copies	copies of mRNA detected/50 ng total RNA	Sample	Fold Change in Disease Population
colon normal GW98-167	21941	3216.52	6433.04	colon normal	
colon tumor GW98-166	21940	2713.61	5427.22	colon tumor	-1.185328769
colon normal GW98-178	22080	324.52	649.04	colon normal	
colon tumor GW98-177	22060	657.5	1315.00	colon tumor	2.026069272
colon normal GW98-561	23514	2007.12	4014.24	colon normal	
colon tumor GW98-560	23513	1433.27	2866.54	colon tumor	-1.400378156
colon normal GW98-894	24691	5207.11	10414.22	colon normal	
colon tumor GW98-893	24690	3315.88	6631.76	colon tumor	-1.570355381
lung normal GW98-3	20742	2880.6	5761.20	lung normal	
lung tumor GW98-2	20741	729.25	1458.50	lung tumor	-3.950085704

lung normal GW97-179	20677	2554.17	5108.34	lung normal	
lung tumor GW97-178	20676	3737.04	7474.08	lung tumor	1.463113262
lung normal GW98-165	21922	5054.4	10108.80	lung normal	
lung tumor GW98-164	21921	2226.27	4452.54	lung tumor	-2.270344567
lung normal GW98-282	22584	1861.66	3723.32	lung normal	
lung tumor GW98-281	22583	1654.05	3308.10	lung tumor	-1.125516157
breast normal GW00-392	28750	1333.43	1333.43	breast normal	
breast tumor GW00-391	28746	1994.93	3989.86	breast tumor	2.992178067
breast normal GW00-413	28798	860.05	860.05	breast normal	
breast tumor GW00-412	28797	2402.76	4805.52	breast tumor	5.587489099
breast normal GW00-235:238	27592-95	430.22	430.22	breast normal	
breast tumor GW00-231:234	27588-91	1888.17	1888.17	breast tumor	4.388847566
breast normal GW98-621	23656	3330.56	6661.12	breast normal	
breast tumor GW98-620	23655	1697.99	3395.98	breast tumor	-1.961472093
brain normal BB99-542	25507	11126.07	22252.14	brain normal	
brain normal BB99-406	25509	10597	21194.00	brain normal	
brain normal BB99-904	25546	5508.06	11016.12	brain normal	
brain stage 5 ALZ BB99-874	25502	2411.63	4823.26	brain stage 5 ALZ	-3.763862339
brain stage 5 ALZ BB99-887	25503	10009.75	20019.50	brain stage 5 ALZ	1.102754458
brain stage 5 ALZ BB99-862	25504	6223.93	12447.86	brain stage 5 ALZ	-1.458410254
brain stage 5 ALZ BB99-927	25542	6282.02	12564.04	brain stage 5 ALZ	-1.444924297
CT lung KC	normal	824.22	1648.44	CT lung	
lung 26 KC	normal	460.62	460.62	lung 26	
lung 27 KC	normal	256.02	256.02	lung 27	
lung 24 KC	COPD	218.84	218.84	lung 24	-3.806159751
lung 28 KC	COPD	382.73	382.73	lung 28	-2.176312283
lung 23 KC	COPD	251.06	251.06	lung 23	-3.317692982
lung 25 KC	COPD	966.68	966.68	lung 25	
asthmatic lung ODO3112	29321	1431.16	1431.16	asthmatic lung	1.718202992
asthmatic lung ODO3433	29323	3337.62	6675.24	asthmatic lung	8.014070641
asthmatic lung ODO3397	29322	10770.42	21540.84	asthmatic lung	25.86121449
asthmatic lung ODO4928	29325	4890.89	9781.78	asthmatic lung	11.74367902
endo cells KC	control	379.58	379.58	endo cells	
endo VEGF KC		308.3	308.30	endo VEGF	-1.231203373
endo bFGF KC		292.91	292.91	endo bFGF	-1.295892936
heart Clontech	normal	189.25	378.50	heart	
heart (T-1) ischemic	29417	3974.32	7948.64	heart T-1	21.00036988
heart (T-14) non-obstructive DCM	29422	2874.83	5749.66	heart T-14	15.19064729
heart (T-3399) DCM	29426	3931.97	7863.94	heart T-3399	20.77659181
adenoid GW99-269	26162	960.03	1920.06	adenoid	
tonsil GW98-280	22582	2921.82	5843.64	tonsil	
T cells PC00314	28453	4357.56	8715.12	T cells	
PBMNC KC		92.93	92.93	PBMNC	
monocyte KC		109.26	218.52	monocyte	

B cells PC00665	28455	2927.24	5854.48	B cells	
dendritic cells 28441		3972.13	7944.26	dendritic cells	
neutrophils	28440	1995.66	1995.66	neutrophils	
eosinophils	28446	3370.63	6741.26	eosinophils	
BM unstim KC		219.27	219.27	BM unstim	
BM stim KC		305.59	305.59	BM stim	1.393669905
osteo dif KC		1240.85	1240.85	osteo dif	
osteo undif KC		250	250.00	osteo undif	-4.9634
chondrocytes		1932.6	4831.50	chondrocytes	
OA Synovium IP12/01	29462	1711.57	1711.57	OA Synovium	
OA Synovium NP10/01	29461	1029.7	2059.40	OA Synovium	
OA Synovium NP57/00	28464	2112.51	4225.02	OA Synovium	
RA Synovium NP03/01	28466	2679.38	5358.76	RA Synovium	
RA Synovium NP71/00	28467	2419.69	4839.38	RA Synovium	
RA Synovium NP45/00	28475	2917.73	5835.46	RA Synovium	
OA bone (biobank)	29217	254.63	254.63	OA bone (biobank)	
OA bone Sample 1	J. Emory	2069.38	4138.76	OA bone	
OA bone Sample 2	J. Emory	1115.3	2230.60	OA bone	
Cartilage (pool)	Normal	3174.67	6349.34	Cartilage (pool)	
Cartilage (pool)	OA	1272.39	2544.78	Cartilage (pool)	-2.495044758
PBL uninfected	28441	4083.14	8166.28	PBL uninfected	
PBL HIV IIIB	28442	1715.44	3430.88	PBL HIV IIIB	-2.380228979
MRC5 uninfected (100%)	29158	6381.95	12763.90	MRC5 uninfected (100%)	
MRC5 HSV strain F	29178	759.86	1519.72	MRC5 HSV strain F	-8.398849788
W12 cells	29179	4256.48	8512.96	W12 cells	
Keratinocytes	29180	7993.74	15987.48	Keratinocytes	

Gene Name sbg533677PALSa

Disease tissues	Fold Change in Disease Population Relative to Normal
colon tumor	-1.19
colon tumor	2.03
colon tumor	-1.40
colon tumor	-1.57
lung tumor	-3.95
lung tumor	1.46
lung tumor	-2.27
lung tumor	-1.13
breast tumor	2.99
breast tumor	5.59
breast tumor	4.39
breast tumor	-1.96
brain stage 5 ALZ	-3.76
brain stage 5 ALZ	1.10
brain stage 5 ALZ	-1.46
brain stage 5 ALZ	-1.44

lung 24	-3.81
lung 28	-2.18
lung 23	-3.32
asthmatic lung	1.72
asthmatic lung	8.01
asthmatic lung	25.86
asthmatic lung	11.74
endo VEGF	-1.23
endo bFGF	-1.30
heart T-1	21.00
heart T-14	15.19
heart T-3399	20.78
BM stim	1.39
osteo undif	-4.96
Cartilage (pool)	-2.50
PBL HIV IIIB	-2.38
MRC5 HSV strain F	-8.40

Gene Name sbg535067MELAa

- Highest expression in brain (unchanged in alzheimers), fetal liver, and thymus. Downregulated in COPD diseased lung suggesting involvement in this disease. Expression in spleen, T and B cells, neutrophils, and chondrocytes corroborates expression in OA and RA synovium suggesting involvement with OA and RA disease. Upregulated in 3 of 4 asthmatic lung suggesting involvement in asthma. GI tract expression could suggest claims for IBS, IBD, and Crohns disease.

Sample sbg535067MELAa	Mean GOI copies (sample 1)	Mean GOI copies (sample 2)	Average GOI Copies	18S rRNA (ng)	50 ng/18S rRNA (ng)	copies of mRNA detected/5 0 ng total RNA
Subcutaneous Adipocytes Zenbio	23.74	19.92	21.83	3.06	16.34	356.70
Subcutaneous Adipose Zenbio	15.7	3.58	9.64	0.96	52.36	504.71
Adrenal Gland Clontech	1.19	0.43	0.81	0.61	81.97	66.39
Whole Brain Clontech	1924.36	2038.13	1981.25	7.24	6.91	13682.63
Fetal Brain Clontech	0	0	0.00	0.48	103.95	0.00
Cerebellum Clontech	2.16	5.79	3.98	2.17	23.04	91.59
Cervix	7.08	7.77	7.43	2.42	20.66	153.41
Colon	67.4	68.19	67.80	2.71	18.45	1250.83
Endometrium	4.18	3.42	3.80	0.73	68.21	259.21
Esophagus	15.08	17.4	16.24	1.37	36.50	592.70
Heart Clontech	5.86	14.32	10.09	1.32	37.88	382.20
Hypothalamus	0	0	0.00	0.32	155.28	0.00
Ileum	32.34	66.93	49.64	2.58	19.38	961.92
Jejunum	94.38	105.02	99.70	6.60	7.58	755.30
Kidney	10.77	30.93	20.85	2.12	23.58	491.75

Liver	11.37	10.24	10.81	1.50	33.33	360.17
Fetal Liver Clontech	494.61	735.39	615.00	10.40	4.81	2956.73
Lung	32.92	33.74	33.33	2.57	19.46	648.44
Mammary Gland Clontech	412.57	499.72	456.15	13.00	3.85	1754.40
Myometrium	63.47	115.64	89.56	2.34	21.37	1913.57
Omentum	10.73	13.03	11.88	3.94	12.69	150.76
Ovary	26.09	20.49	23.29	4.34	11.52	268.32
Pancreas	1.74	0.02	0.88	0.81	61.80	54.39
Head of Pancreas	3.26	1.92	2.59	1.57	31.85	82.48
Parotid Gland	19.23	35.41	27.32	5.48	9.12	249.27
Placenta Clontech	117.8	116.55	117.18	5.26	9.51	1113.83
Prostate	10.11	1.88	6.00	3.00	16.67	99.92
Rectum	8.4	8.81	8.61	1.23	40.65	349.80
Salivary Gland Clontech	26.76	14.96	20.86	7.31	6.84	142.68
Skeletal Muscle Clontech	6.71	0	3.36	1.26	39.68	133.13
Skin	11.65	24.94	18.30	1.21	41.32	755.99
Small Intestine Clontech	6.32	11.13	8.73	0.98	51.07	445.61
Spleen	173.46	142.39	157.93	4.92	10.16	1604.93
Stomach	6.64	14.3	10.47	2.73	18.32	191.76
Testis Clontech	8.48	4.71	6.60	0.57	87.87	579.53
Thymus Clontech	544.9	734.52	639.71	9.89	5.06	3234.13
Thyroid	8.81	2.52	5.67	2.77	18.05	102.26
Trachea Clontech	84.46	104.09	94.28	9.71	5.15	485.45
Urinary Bladder	17.47	27.24	22.36	5.47	9.14	204.34
Uterus	40.05	46.49	43.27	5.34	9.36	405.15

Sample sbg535067MELAA	Reg number (GSK identifier)	Mean GOI copies	copies of mRNA detected/50 ng total RNA	Sample	Fold Change in Disease Population
colon normal GW98-167	21941	614.52	1229.04	colon normal	
colon tumor GW98-166	21940	809.88	1619.76	colon tumor	1.32
colon normal GW98-178	22080	339.76	679.52	colon normal	
colon tumor GW98-177	22060	104.5	209.00	colon tumor	-3.25
colon normal GW98-561	23514	235.88	471.76	colon normal	
colon tumor GW98-560	23513	93.21	186.42	colon tumor	-2.53
colon normal GW98-894	24691	309.33	618.66	colon normal	
colon tumor GW98-893	24690	218.62	437.24	colon tumor	-1.41
lung normal GW98-3	20742	558.13	1116.26	lung normal	
lung tumor GW98-2	20741	82.81	165.62	lung tumor	-6.74
lung normal GW97-179	20677	2066.15	4132.30	lung normal	
lung tumor GW97-178	20676	859.79	1719.58	lung tumor	-2.40
lung normal GW98-165	21922	574.92	1149.84	lung normal	
lung tumor GW98-164	21921	845.89	1691.78	lung tumor	1.47

lung normal GW98-282	22584	210.81	421.62	lung normal	
lung tumor GW98-281	22583	346.75	693.50	lung tumor	1.64
breast normal GW00-392	28750	1165.85	1165.85	breast normal	
breast tumor GW00-391	28746	728.17	1456.34	breast tumor	1.25
breast normal GW00-413	28798	836.13	836.13	breast normal	
breast tumor GW00-412	28797	591.76	1183.52	breast tumor	1.42
breast normal GW00-235:238	27592-95	415.79	415.79	breast normal	
breast tumor GW00-231:234	27588-91	1193.03	1193.03	breast tumor	2.87
breast normal GW98-621	23656	1070.75	2141.50	breast normal	
breast tumor GW98-620	23655	1904.41	3808.82	breast tumor	1.78
brain normal BB99-542	25507	22658.63	45317.26	brain normal	
brain normal BB99-406	25509	4463.72	8927.44	brain normal	
brain normal BB99-904	25546	6799.49	13598.98	brain normal	
brain stage 5 ALZ BB99-874	25502	449.53	899.06	brain stage 5 ALZ	-25.15
brain stage 5 ALZ BB99-887	25503	6199.11	12398.22	brain stage 5 ALZ	-1.82
brain stage 5 ALZ BB99-862	25504	4621.76	9243.52	brain stage 5 ALZ	-2.45
brain stage 5 ALZ BB99-927	25542	4859.74	9719.48	brain stage 5 ALZ	-2.33
CT lung KC	normal	527.05	1054.10	CT lung	
lung 26 KC	normal	628.91	628.91	lung 26	
lung 27 KC	normal	66.78	66.78	lung 27	
lung 24 KC	COPD	45.13	45.13	lung 24	-9.96
lung 28 KC	COPD	64.1	64.10	lung 28	-7.01
lung 23 KC	COPD	97.61	97.61	lung 23	-4.61
lung 25 KC	normal	48.69	48.69	lung 25	
asthmatic lung ODO3112	29321	521.43	521.43	asthmatic lung	1.16
asthmatic lung ODO3433	29323	1614.29	3228.58	asthmatic lung	7.18
asthmatic lung ODO3397	29322	2352.95	4705.90	asthmatic lung	10.47
asthmatic lung ODO4928	29325	1560.6	3121.20	asthmatic lung	6.94
endo cells KC	control	187.93	187.93	endo cells	
endo VEGF KC		30.65	30.65	endo VEGF	-6.13
endo bFGF KC		93.32	93.32	endo bFGF	-2.01
heart Clontech	normal	585.46	1170.92	heart	
heart (T-1) ischemic	29417	1546.85	3093.70	heart T-1	2.64
heart (T-14) non-obstructive DCM	29422	1304.67	2609.34	heart T-14	2.23
heart (T-3399) DCM	29426	2208.72	4417.44	heart T-3399	3.77
adenoid GW99-269	26162	896.42	1792.84	adenoid	
tonsil GW98-280	22582	2459.55	4919.10	tonsil	
T cells PC00314	28453	2147.55	4295.10	T cells	
PBMNC KC		143.16	143.16	PBMNC	
monocyte KC		135.21	270.42	monocyte	

B cells PC00665	28455	1305.96	2611.92	B cells	
dendritic cells 28441		118.25	236.50	dendritic cells	
neutrophils	28440	960.88	960.88	neutrophils	
eosinophils	28446	14.31	28.62	eosinophils	
BM unstim KC		132.56	132.56	BM unstim	
BM stim KC		31.27	31.27	BM stim	-4.24
osteo dif KC		127.45	127.45	osteo dif	2.02
osteo undif KC		63.07	63.07	osteo undif	
chondrocytes		771.65	1929.13	chondrocytes	
OA Synovium IP12/01	29462	2214.8	2214.80	OA Synovium	
OA Synovium NP10/01	29461	576.67	1153.34	OA Synovium	
OA Synovium NP57/00	28464	682.06	1364.12	OA Synovium	
RA Synovium NP03/01	28466	499.99	999.98	RA Synovium	
RA Synovium NP71/00	28467	631.41	1262.82	RA Synovium	
RA Synovium NP45/00	28475	551.2	1102.40	RA Synovium	
OA bone (biobank)	29217	224.68	224.68	OA bone (biobank)	
OA bone Sample 1	J. Emory	751.77	1503.54	OA bone	
OA bone Sample 2	J. Emory	633.33	1266.66	OA bone	
Cartilage (pool)	Normal	1863.02	3726.04	Cartilage (pool)	
Cartilage (pool)	OA	1658.1	3316.20	Cartilage (pool)	-1.12
PBL uninfected	28441	4666.52	9333.04	PBL uninfected	
PBL HIV IIIB	28442	2342.79	4685.58	PBL HIV IIIB	-1.99
MRC5 uninfected (100%)	29158	951.75	1903.50	MRC5 uninfected (100%)	
MRC5 HSV strain F	29178	0	0.00	MRC5 HSV strain F	-1903.50
W12 cells	29179	2071.68	4143.36	W12 cells	
Keratinocytes	29180	3752.88	7505.76	Keratinocytes	

Gene Name sbg535067MELAa

Disease tissues	Fold Change in Disease Population Relative to Normal
colon tumor	1.32
colon tumor	-3.25
colon tumor	-2.53
colon tumor	-1.41
lung tumor	-6.74
lung tumor	-2.40
lung tumor	1.47
lung tumor	1.64
breast tumor	1.25
breast tumor	1.42

breast tumor	2.87
breast tumor	1.78
brain stage 5 ALZ	-25.15
brain stage 5 ALZ	-1.82
brain stage 5 ALZ	-2.45
brain stage 5 ALZ	-2.33
lung 24	-9.96
lung 28	-7.01
lung 23	-4.61
asthmatic lung	1.16
asthmatic lung	7.18
asthmatic lung	10.47
asthmatic lung	6.94
endo VEGF	-6.13
endo bFGF	-2.01
heart T-1	2.64
heart T-14	2.23
heart T-3399	3.77
BM stim	-4.24
osteo dif	2.02
Cartilage (pool)	-1.12
PBL HIV IIIB	-1.99
MRC5 HSV strain F	-1903.50

Gene Name sbg590979THP

- 5 High in fetal liver and some expression in adult liver. Expressed in adult and fetal brain. Hypothalamus is a significant fraction of the brain expression suggesting metabolic disease claims related to diabetes, impaired glucose tolerance, metabolic syndrome, and obesity. Significant overexpression in one breast cancer is sufficient for claim in this area (caveat: lack of expression in normal may lead to exaggerated fold-overexpression). Decreased expression in dilated
- 10 cardiomyopathy suggests involvement in this disease. Expression in OA and RA synovium and corroborating expression in immune cells (adenoid, tonsil, T, B, and eosinophils) suggests involvement in both RA and OA disease. Significant decrease in DCM heart suggests involvement in dilated cardiomyopathy.

Sample sbg590979THP	Mean GOI copies (sample 1)	Mean GOI copies (sample 2)	Average GOI Copies	18S rRNA (ng)	50 ng/18S rRNA (ng)	copies of mRNA detecte d/50 ng total RNA
Subcutaneous Adipocytes Zenbio	0	0	0.00	3.06	16.34	0.00
Subcutaneous Adipose Zenbio	0	0	0.00	0.96	52.36	0.00
Adrenal Gland Clontech	0	0	0.00	0.61	81.97	0.00

Whole Brain Clontech	103.17	92.02	97.60	7.24	6.91	674.00
Fetal Brain Clontech	0	5.32	2.66	0.48	103.95	276.51
Cerebellum Clontech	0	0	0.00	2.17	23.04	0.00
Cervix	0	0	0.00	2.42	20.66	0.00
Colon	5.58	4.45	5.02	2.71	18.45	92.53
Endometrium	0	0	0.00	0.73	68.21	0.00
Esophagus	0	0	0.00	1.37	36.50	0.00
Heart Clontech	0	4.11	2.06	1.32	37.88	77.84
Hypothalamus	4.16	0	2.08	0.32	155.28	322.98
Ileum	0	7.16	3.58	2.58	19.38	69.38
Jejunum	3.15	8.34	5.75	6.60	7.58	43.52
Kidney	0	0	0.00	2.12	23.58	0.00
Liver	17.8	29.95	23.88	1.50	33.33	795.83
Fetal Liver Clontech	2349.79	2396.71	2373.25	10.40	4.81	11409.86
Lung	9.75	0	4.88	2.57	19.46	94.84
Mammary Gland Clontech	0	0	0.00	13.00	3.85	0.00
Myometrium	0	0	0.00	2.34	21.37	0.00
Omentum	0	0	0.00	3.94	12.69	0.00
Ovary	12.64	21.85	17.25	4.34	11.52	198.68
Pancreas	0	0	0.00	0.81	61.80	0.00
Head of Pancreas	0	0	0.00	1.57	31.85	0.00
Parotid Gland	17.64	0	8.82	5.48	9.12	80.47
Placenta Clontech	2.66	0	1.33	5.26	9.51	12.64
Prostate	0	0	0.00	3.00	16.67	0.00
Rectum	0	0	0.00	1.23	40.65	0.00
Salivary Gland Clontech	3.58	0	1.79	7.31	6.84	12.24
Skeletal Muscle Clontech	0	0	0.00	1.26	39.68	0.00
Skin	0	0	0.00	1.21	41.32	0.00
Small Intestine Clontech	0	0	0.00	0.98	51.07	0.00
Spleen	14.01	13.8	13.91	4.92	10.16	141.31
Stomach	0	0	0.00	2.73	18.32	0.00
Testis Clontech	0	0	0.00	0.57	87.87	0.00
Thymus Clontech	0	13.24	6.62	9.89	5.06	33.47
Thyroid	10.53	0	5.27	2.77	18.05	95.04
Trachea Clontech	0	9.3	4.65	9.71	5.15	23.94
Urinary Bladder	0	0	0.00	5.47	9.14	0.00
Uterus	13.93	6.43	10.18	5.34	9.36	95.32

Sample sbg590979THP	Reg number (GSK identifier)	Mean GOI copies	copies of mRNA detected/50 ng total RNA	Sample	Fold Change in Disease Population
colon normal GW98-167	21941	148.83	297.66	colon normal	
colon tumor GW98-166	21940	246.62	493.24	colon tumor	1.66
colon normal GW98-178	22080	97.46	194.92	colon normal	
colon tumor GW98-177	22060	68.77	137.54	colon tumor	-1.42

colon normal GW98-561	23514	210.78	421.56	colon normal	
colon tumor GW98-560	23513	76.83	153.66	colon tumor	-2.74
colon normal GW98-894	24691	130.52	261.04	colon normal	
colon tumor GW98-893	24690	89.49	178.98	colon tumor	-1.46
lung normal GW98-3	20742	108.75	217.50	lung normal	
lung tumor GW98-2	20741	9.94	19.88	lung tumor	-10.94
lung normal GW97-179	20677	39.37	78.74	lung normal	
lung tumor GW97-178	20676	34.84	69.68	lung tumor	-1.13
lung normal GW98-165	21922	54.25	108.50	lung normal	
lung tumor GW98-164	21921	153.78	307.56	lung tumor	2.83
lung normal GW98-282	22584	61.06	122.12	lung normal	
lung tumor GW98-281	22583	42.22	84.44	lung tumor	-1.45
breast normal GW00-392	28750	23.64	23.64	breast normal	
breast tumor GW00-391	28746	24.54	49.08	breast tumor	2.08
breast normal GW00-413	28798	0	0.00	breast normal	
breast tumor GW00-412	28797	19.55	39.10	breast tumor	39.10
breast normal GW00-235:238	27592-95	0	0.00	breast normal	
breast tumor GW00-231:234	27588-91	0	0.00	breast tumor	0.00
breast normal GW98-621	23656	18.18	36.36	breast normal	
breast tumor GW98-620	23655	78.46	156.92	breast tumor	4.32
brain normal BB99-542	25507	31.51	63.02	brain normal	
brain normal BB99-406	25509	39.55	79.10	brain normal	
brain normal BB99-904	25546	3.64	7.28	brain normal	
brain stage 5 ALZ BB99-874	25502	25.84	51.68	brain stage 5 ALZ	1.04
brain stage 5 ALZ BB99-887	25503	98.79	197.58	brain stage 5 ALZ	3.97
brain stage 5 ALZ BB99-862	25504	43.27	86.54	brain stage 5 ALZ	1.74
brain stage 5 ALZ BB99-927	25542	56.03	112.06	brain stage 5 ALZ	2.25
CT lung KC	normal	7.59	15.18	CT lung	
lung 26 KC	normal	0	0.00	lung 26	
lung 27 KC	normal	0	0.00	lung 27	
lung 24 KC	COPD	0	0.00	lung 24	-3.80
lung 28 KC	COPD	0	0.00	lung 28	-3.80
lung 23 KC	COPD	3.41	3.41	lung 23	-1.11
lung 25 KC	normal	0	0.00	lung 25	
asthmatic lung ODO3112	29321	0	0.00	asthmatic lung	-3.80
asthmatic lung ODO3433	29323	7	14.00	asthmatic lung	3.69
asthmatic lung ODO3397	29322	14.33	28.66	asthmatic lung	7.55
asthmatic lung ODO4928	29325	7.81	15.62	asthmatic lung	4.12
endo cells KC	control	0	0.00	endo cells	
endo VEGF KC		2.17	2.17	endo VEGF	2.17
endo bFGF KC		0	0.00	endo bFGF	0.00
heart Clontech	normal	58.56	117.12	heart	
heart (T-1) ischemic	29417	40.59	81.18	heart T-1	-1.44

heart (T-14) non-obstructive DCM	29422	180.2	360.40	heart T-14	3.08
heart (T-3399) DCM	29426	0	0.00	heart T-3399	-117.12
adenoid GW99-269	26162	25.38	50.76	adenoid	
tonsil GW98-280	22582	31.19	62.38	tonsil	
T cells PC00314	28453	25.24	50.48	T cells	
PBMNC KC		0	0.00	PBMNC	
monocyte KC		1.43	2.86	monocyte	
B cells PC00665	28455	20.91	41.82	B cells	
dendritic cells 28441		0	0.00	dendritic cells	
neutrophils	28440	20.88	20.88	neutrophils	
eosinophils	28446	31.73	63.46	eosinophils	
BM unstim KC		0	0.00	BM unstim	
BM stim KC		9.9	9.90	BM stim	9.90
osteo dif KC		3.62	3.62	osteo dif	3.62
osteo undif KC		0	0.00	osteo undif	
chondrocytes		26.14	65.35	chondrocytes	
OA Synovium IP12/01	29462	25.64	25.64	OA Synovium	
OA Synovium NP10/01	29461	52	104.00	OA Synovium	
OA Synovium NP57/00	28464	90.32	180.64	OA Synovium	
RA Synovium NP03/01	28466	64.83	129.66	RA Synovium	
RA Synovium NP71/00	28467	321.14	642.28	RA Synovium	
RA Synovium NP45/00	28475	91.05	182.10	RA Synovium	
OA bone (biobank)	29217	10.58	10.58	OA bone (biobank)	
OA bone Sample 1	J. Emory	41.46	82.92	OA bone	
OA bone Sample 2	J. Emory	82	164.00	OA bone	
Cartilage (pool)	Normal	12.72	25.44	Cartilage (pool)	
Cartilage (pool)	OA	45.45	90.90	Cartilage (pool)	3.57
PBL uninfected	28441	18.32	36.64	PBL uninfected	
PBL HIV IIIB	28442	46.38	92.76	PBL HIV IIIB	2.53
MRC5 uninfected (100%)	29158	10.17	20.34	MRC5 uninfected (100%)	
MRC5 HSV strain F	29178	424.91	849.82	MRC5 HSV strain F	41.78
W12 cells	29179	12.35	24.70	W12 cells	
Keratinocytes	29180	11.74	23.48	Keratinocytes	

Gene Name sbg590979THP

Disease tissues	Fold Change in Disease Population Relative to Normal
colon tumor	1.66
colon tumor	-1.42
colon tumor	-2.74
colon tumor	-1.46
lung tumor	-10.94
lung tumor	-1.13

lung tumor	2.83
lung tumor	-1.45
breast tumor	2.08
breast tumor	39.10
breast tumor	0.00
breast tumor	4.32
brain stage 5 ALZ	1.04
brain stage 5 ALZ	3.97
brain stage 5 ALZ	1.74
brain stage 5 ALZ	2.25
lung 24	-3.80
lung 28	-3.80
lung 23	-1.11
asthmatic lung	-3.80
asthmatic lung	3.69
asthmatic lung	7.55
asthmatic lung	4.12
endo VEGF	2.17
endo bFGF	0.00
heart T-1	-1.44
heart T-14	3.08
heart T-3399	-117.12
BM stim	9.90
osteo dif	3.62
Cartilage (pool)	3.57
PBL HIV IIIB	2.53
MRC5 HSV strain F	41.78

Gene Name sbg658629CRF

- 5 Highly expressed in brain. Expression in parotid gland suggest it is secreted.
 Expression in chondrocyte cells consistent with expression in cartilage.
 Downregulated in HSV infected MRC5 cells suggesting possible host factor for HSV infection.

Sample sbg658629CRF	Mean GOI copies (sample 1)	Mean GOI copies (sample 2)	Average GOI Copies	18S rRNA (ng)	50 ng/18S rRNA (ng)	copies of mRNA detected/ 50 ng total RNA
Subcutaneous Adipocytes Zenbio	0.41	0.12	0.27	3.06	16.34	4.33
Subcutaneous Adipose Zenbio	0.26	0	0.13	0.96	52.36	6.81
Adrenal Gland Clontech	0	0.04	0.02	0.61	81.97	1.64
Whole Brain Clontech	8417.5	9519.49	8968.50	7.24	6.91	61937.12
Fetal Brain Clontech	8.6	10.03	9.32	0.48	103.95	968.30
Cerebellum Clontech	12.11	12.1	12.11	2.17	23.04	278.92
Cervix	2.83	5.55	4.19	2.42	20.66	86.57
Colon	4.92	1.31	3.12	2.71	18.45	57.47
Endometrium	5.14	9.68	7.41	0.73	68.21	505.46

Esophagus	0.11	0.14	0.13	1.37	36.50	4.56
Heart Clontech	0	1.03	0.52	1.32	37.88	19.51
Hypothalamus	0	0.27	0.14	0.32	155.28	20.96
Ileum	3.59	1.4	2.50	2.58	19.38	48.35
Jejunum	20.07	31.06	25.57	6.60	7.58	193.67
Kidney	2.83	7.94	5.39	2.12	23.58	127.00
Liver	4.23	7.95	6.09	1.50	33.33	203.00
Fetal Liver Clontech	16.66	25.88	21.27	10.40	4.81	102.26
Lung	1.42	1.64	1.53	2.57	19.46	29.77
Mammary Gland Clontech	3.1	9.56	6.33	13.00	3.85	24.35
Myometrium	2.87	3.05	2.96	2.34	21.37	63.25
Omentum	2.76	3.5	3.13	3.94	12.69	39.72
Ovary	9.43	10.74	10.09	4.34	11.52	116.19
Pancreas	0.88	0.04	0.46	0.81	61.80	28.43
Head of Pancreas	0.04	0.12	0.08	1.57	31.85	2.55
Parotid Gland	368.36	439.47	403.92	5.48	9.12	3685.36
Placenta Clontech	2.99	0.93	1.96	5.26	9.51	18.63
Prostate	0.15	0.06	0.11	3.00	16.67	1.75
Rectum	1.08	1.78	1.43	1.23	40.65	58.13
Salivary Gland Clontech	0.76	1.35	1.06	7.31	6.84	7.22
Skeletal Muscle Clontech	0.2	0.07	0.14	1.26	39.68	5.36
Skin	0.03	0.05	0.04	1.21	41.32	1.65
Small Intestine Clontech	7.1	0.03	3.57	0.98	51.07	182.07
Spleen	2.3	0.03	1.23	4.92	10.16	12.45
Stomach	3.63	4.6	4.12	2.73	18.32	75.37
Testis Clontech	8.57	4.18	6.38	0.57	87.87	560.19
Thymus Clontech	5.54	16.02	10.78	9.89	5.06	54.50
Thyroid	12.12	4.34	8.23	2.77	18.05	148.56
Trachea Clontech	3.97	17.75	10.86	9.71	5.15	55.92
Urinary Bladder	5.08	8.59	6.84	5.47	9.14	62.48
Uterus	24.16	29.46	26.81	5.34	9.36	251.03

Sample sbg658629CRF	Reg number (GSK identifier)	Mean GOI copies	copies of mRNA detected/50 ng total RNA	Sample	Fold Change in Disease Population
colon normal GW98-167	21941	758.1	1516.20	colon normal	
colon tumor GW98-166	21940	77.72	155.44	colon tumor	-9.75
colon normal GW98-178	22080	364.17	728.34	colon normal	
colon tumor GW98-177	22060	85.55	171.10	colon tumor	-4.26
colon normal GW98-561	23514	227.04	454.08	colon normal	
colon tumor GW98-560	23513	294.95	589.90	colon tumor	1.30
colon normal GW98-894	24691	521.04	1042.08	colon normal	
colon tumor GW98-893	24690	194.26	388.52	colon tumor	-2.68
lung normal GW98-3	20742	86.31	172.62	lung normal	
lung tumor GW98-2	20741	158.3	316.60	lung tumor	1.83

lung normal GW97-179	20677	3312.4	6624.80	lung normal	
lung tumor GW97-178	20676	27.8	55.60	lung tumor	-119.15
lung normal GW98-165	21922	17.58	35.16	lung normal	
lung tumor GW98-164	21921	56.57	113.14	lung tumor	3.22
lung normal GW98-282	22584	48.66	97.32	lung normal	
lung tumor GW98-281	22583	30.43	60.86	lung tumor	-1.60
breast normal GW00-392	28750	226.72	226.72	breast normal	
breast tumor GW00-391	28746	181.98	363.96	breast tumor	1.61
breast normal GW00-413	28798	84.66	84.66	breast normal	
breast tumor GW00-412	28797	43.27	86.54	breast tumor	1.02
breast normal GW00-235:238	27592-95	266.41	266.41	breast normal	
breast tumor GW00-231:234	27588-91	71.99	71.99	breast tumor	-3.70
breast normal GW98-621	23656	167.13	334.26	breast normal	
breast tumor GW98-620	23655	63.98	127.96	breast tumor	-2.61
brain normal BB99-542	25507	2057.45	4114.90	brain normal	
brain normal BB99-406	25509	1914.41	3828.82	brain normal	
brain normal BB99-904	25546	1209.14	2418.28	brain normal	
brain stage 5 ALZ BB99-874	25502	1126.82	2253.64	brain stage 5 ALZ	-1.53
brain stage 5 ALZ BB99-887	25503	4130.76	8261.52	brain stage 5 ALZ	2.39
brain stage 5 ALZ BB99-862	25504	3025.26	6050.52	brain stage 5 ALZ	1.75
brain stage 5 ALZ BB99-927	25542	1582.92	3165.84	brain stage 5 ALZ	-1.09
CT lung KC	normal	26.49	52.98	CT lung	
lung 26 KC	normal	10.85	10.85	lung 26	
lung 27 KC	normal	0	0.00	lung 27	
lung 24 KC	COPD	0	0.00	lung 24	-16.04
lung 28 KC	COPD	0.74	0.74	lung 28	-21.68
lung 23 KC	COPD	0	0.00	lung 23	-16.04
lung 25 KC	normal	0.33	0.33	lung 25	
asthmatic lung ODO3112	29321	5.95	5.95	asthmatic lung	-2.70
asthmatic lung ODO3433	29323	16.33	32.66	asthmatic lung	2.04
asthmatic lung ODO3397	29322	25.26	50.52	asthmatic lung	3.15
asthmatic lung ODO4928	29325	20.78	41.56	asthmatic lung	2.59
endo cells KC	control	15.55	15.55	endo cells	
endo VEGF KC		6.35	6.35	endo VEGF	-2.45
endo bFGF KC		19.16	19.16	endo bFGF	1.23
heart Clontech	normal	312.58	625.16	heart	
heart (T-1) ischemic	29417	107.41	214.82	heart T-1	-2.91
heart (T-14) non-obstructive DCM	29422	65.45	130.90	heart T-14	-4.78
heart (T-3399) DCM	29426	80.9	161.80	heart T-3399	-3.86
adenoid GW99-269	26162	11.42	22.84	adenoid	
tonsil GW98-280	22582	58.08	116.16	tonsil	
T cells PC00314	28453	13.31	26.62	T cells	

PBMNC KC		0.18	0.18	PBMNC	
monocyte KC		0.45	0.90	monocyte	
B cells PC00665	28455	2.47	4.94	B cells	
dendritic cells 28441		19.58	39.16	dendritic cells	
neutrophils	28440	4.52	4.52	neutrophils	
eosinophils	28446	7.41	14.82	eosinophils	
BM unstim KC		0	0.00	BM unstim	
BM stim KC		8.97	8.97	BM stim	8.97
osteo dif KC		0.56	0.56	osteo dif	-1.43
osteo undif KC		0.8	0.80	osteo undif	
chondrocytes		547.4	1368.50	chondrocytes	
OA Synovium IP12/01	29462	157.16	157.16	OA Synovium	
OA Synovium NP10/01	29461	46.09	92.18	OA Synovium	
OA Synovium NP57/00	28464	63.76	127.52	OA Synovium	
RA Synovium NP03/01	28466	64.6	129.20	RA Synovium	
RA Synovium NP71/00	28467	200.22	400.44	RA Synovium	
RA Synovium NP45/00	28475	189.2	378.40	RA Synovium	
OA bone (biobank)	29217	34.76	34.76	OA bone (biobank)	
OA bone Sample 1	J. Emory	114.88	229.76	OA bone	
OA bone Sample 2	J. Emory	34.93	69.86	OA bone	
Cartilage (pool)	Normal	750.07	1500.14	Cartilage (pool)	
Cartilage (pool)	OA	107.9	215.80	Cartilage (pool)	-6.95
PBL uninfected	28441	196.14	392.28	PBL uninfected	
PBL HIV IIIB	28442	120.64	241.28	PBL HIV IIIB	-1.63
MRC5 uninfected (100%)	29158	1065.06	2130.12	MRC5 uninfected (100%)	
MRC5 HSV strain F	29178	179.4	358.80	MRC5 HSV strain F	-5.94
W12 cells	29179	127.4	254.80	W12 cells	
Keratinocytes	29180	92.44	184.88	Keratinocytes	

Gene Name sbg658629CRF

Disease tissues	Fold Change in Disease Population Relative to Normal
colon tumor	-9.75
colon tumor	-4.26
colon tumor	1.30
colon tumor	-2.68
lung tumor	1.83
lung tumor	-119.15
lung tumor	3.22
lung tumor	-1.60
breast tumor	1.61
breast tumor	1.02
breast tumor	-3.70

breast tumor	-2.61
brain stage 5 ALZ	-1.53
brain stage 5 ALZ	2.39
brain stage 5 ALZ	1.75
brain stage 5 ALZ	-1.09
lung 24	-16.04
lung 28	-21.68
lung 23	-16.04
asthmatic lung	-2.70
asthmatic lung	2.04
asthmatic lung	3.15
asthmatic lung	2.59
endo VEGF	-2.45
endo bFGF	1.23
heart T-1	-2.91
heart T-14	-4.78
heart T-3399	-3.86
BM stim	8.97
osteo dif	-1.43
Cartilage (pool)	-6.95
PBL HIV IIIB	-1.63
MRC5 HSV strain F	-5.94

Gene Name sbg507131mannosidase

Expressed in brain, especially cortex, but not changed in alzheimers. Expressed in subcutaneous adipose and adipocytes. Expression in fetal liver, thymus, and immune cell populations (adenoid, tonsil, eosinophils, neutrophils, T cells, B cells, and dendritic cells) suggest some involvement in immune cell functions. Expression in asthmatic lung although not significantly upregulated compared to clontech pool. Expressed in OA and RA synovium, OA bone, cartilage, and chondrocytes suggests involvement in OA and RA. Significantly downregulated in HSV lung cell line suggests possible host factor for HSV infection. Expression in subcutaneous adipose suggests claim for dyslipidemia and obesity.

Sample sbg507131mannosidase	Mean GOI copies (sample 1)	Mean GOI copies (sample 2)	Average GOI Copies	18S rRNA (ng)	50 ng/18S rRNA (ng)	copies of mRNA detected/ 50 ng total RNA
Subcutaneous Adipocytes Zenbio	157.3	180.21	168.76	3.06	16.34	2757.43
Subcutaneous Adipose Zenbio	27.08	7.08	17.08	0.96	52.36	894.24
Adrenal Gland Clontech	0	0	0.00	0.61	81.97	0.00
Whole Brain Clontech	8341.44	12017.65	10179.55	7.24	6.91	70300.73
Fetal Brain Clontech	11.48	15.85	13.67	0.48	103.95	1420.48
Cerebellum Clontech	10.53	9.03	9.78	2.17	23.04	225.35
Cervix	23.6	11.58	17.59	2.42	20.66	363.43
Colon	38.31	72.55	55.43	2.71	18.45	1022.69
Endometrium	15.99	21.62	18.81	0.73	68.21	1282.74
Esophagus	6.27	7.28	6.78	1.37	36.50	247.26
Heart Clontech	0	8.15	4.08	1.32	37.88	154.36
Hypothalamus	0	0	0.00	0.32	155.28	0.00
Ileum	6.58	11.07	8.83	2.58	19.38	171.03

Jejunum	38.74	51.43	45.09	6.60	7.58	341.55
Kidney	20.7	26.62	23.66	2.12	23.58	558.02
Liver	16.74	15.49	16.12	1.50	33.33	537.17
Fetal Liver Clontech	876.2	881.14	878.67	10.40	4.81	4224.38
Lung	0	9.21	4.61	2.57	19.46	89.59
Mammary Gland Clontech	168.63	218.21	193.42	13.00	3.85	743.92
Myometrium	30.45	12.65	21.55	2.34	21.37	460.47
Omentum	10.92	0	5.46	3.94	12.69	69.29
Ovary	78.21	48.52	63.37	4.34	11.52	730.01
Pancreas	0.83	0.38	0.61	0.81	61.80	37.39
Head of Pancreas	0.45	0	0.23	1.57	31.85	7.17
Parotid Gland	28.48	86.17	57.33	5.48	9.12	523.04
Placenta Clontech	49.24	92.67	70.96	5.26	9.51	674.48
Prostate	31.41	22.64	27.03	3.00	16.67	450.42
Rectum	27.38	23.01	25.20	1.23	40.65	1024.19
Salivary Gland Clontech	64.88	84.19	74.54	7.31	6.84	509.82
Skeletal Muscle Clontech	0.88	0.38	0.63	1.26	39.68	25.00
Skin	0	0.44	0.22	1.21	41.32	9.09
Small Intestine Clontech	0	0	0.00	0.98	51.07	0.00
Spleen	28.32	10.16	19.24	4.92	10.16	195.53
Stomach	0.49	11.86	6.18	2.73	18.32	113.10
Testis Clontech	0	0	0.00	0.57	87.87	0.00
Thymus Clontech	992.36	1311.32	1151.84	9.89	5.06	5823.26
Thyroid	5.25	29.51	17.38	2.77	18.05	313.72
Trachea Clontech	96.02	82.56	89.29	9.71	5.15	459.78
Urinary Bladder	22.05	34.45	28.25	5.47	9.14	258.23
Uterus	74.02	95.43	84.73	5.34	9.36	793.31

Sample sbg507131mannosidase	Reg number (GSK identifier)	Mean GOI copies	copies of mRNA detected/50 ng total RNA	Sample	Fold Change in Disease Population
colon normal GW98-167	21941	9614.3	19228.60	colon normal	
colon tumor GW98-166	21940	16103.87	32207.74	colon tumor	1.67
colon normal GW98-178	22080	2303.04	4606.08	colon normal	
colon tumor GW98-177	22060	5088.22	10176.44	colon tumor	2.21
colon normal GW98-561	23514	9405.12	18810.24	colon normal	
colon tumor GW98-560	23513	7410.97	14821.94	colon tumor	-1.27
colon normal GW98-894	24691	17796.08	35592.16	colon normal	
colon tumor GW98-893	24690	11212.12	22424.24	colon tumor	-1.59
lung normal GW98-3	20742	27285.1	54570.20	lung normal	
lung tumor GW98-2	20741	4815.29	9630.58	lung tumor	-5.67
lung normal GW97-179	20677	10640.73	21281.46	lung normal	
lung tumor GW97-178	20676	13513.23	27026.46	lung tumor	1.27
lung normal GW98-165	21922	9994.82	19989.64	lung normal	
lung tumor GW98-164	21921	10116.17	20232.34	lung tumor	1.01

lung normal GW98-282	22584	3301.07	6602.14	lung normal	
lung tumor GW98-281	22583	4877.02	9754.04	lung tumor	1.48
breast normal GW00-392	28750	4720.46	4720.46	breast normal	
breast tumor GW00-391	28746	4546.76	9093.52	breast tumor	1.93
breast normal GW00-413	28798	2621.82	2621.82	breast normal	
breast tumor GW00-412	28797	6120.14	12240.28	breast tumor	4.67
breast normal GW00-235:238	27592-95	1687.45	1687.45	breast normal	
breast tumor GW00-231:234	27588-91	5583.72	5583.72	breast tumor	3.31
breast normal GW98-621	23656	5377.79	10755.58	breast normal	
breast tumor GW98-620	23655	4502.23	9004.46	breast tumor	-1.19
brain normal BB99-542	25507	6715.69	13431.38	brain normal	
brain normal BB99-406	25509	5048.43	10096.86	brain normal	
brain normal BB99-904	25546	5145.09	10290.18	brain normal	
brain stage 5 ALZ BB99-874	25502	2895.87	5791.74	brain stage 5 ALZ	-1.95
brain stage 5 ALZ BB99-887	25503	7573.41	15146.82	brain stage 5 ALZ	1.34
brain stage 5 ALZ BB99-862	25504	5549.18	11098.36	brain stage 5 ALZ	-1.02
brain stage 5 ALZ BB99-927	25542	7409.43	14818.86	brain stage 5 ALZ	1.31
CT lung KC	normal	5550.23	11100.46	CT lung	
lung 26 KC	normal	148.79	148.79	lung 26	
lung 27 KC	normal	69.13	69.13	lung 27	
lung 24 KC	COPD	85.09	85.09	lung 24	-33.61
lung 28 KC	COPD	122.28	122.28	lung 28	-23.39
lung 23 KC	COPD	83.08	83.08	lung 23	-34.42
lung 25 KC	normal	121.14	121.14	lung 25	
asthmatic lung ODO3112	29321	2772.08	2772.08	asthmatic lung	-1.03
asthmatic lung ODO3433	29323	4996.38	9992.76	asthmatic lung	3.49
asthmatic lung ODO3397	29322	9994.38	19988.76	asthmatic lung	6.99
asthmatic lung ODO4928	29325	6018.96	12037.92	asthmatic lung	4.21
endo cells KC	control	428.24	428.24	endo cells	
endo VEGF KC		535	535.00	endo VEGF	1.25
endo bFGF KC		323.01	323.01	endo bFGF	-1.33
heart Clontech	normal	2610.15	5220.30	heart	
heart (T-1) ischemic	29417	4004.99	8009.98	heart T-1	1.53
heart (T-14) non-obstructive DCM	29422	5596.98	11193.96	heart T-14	2.14
heart (T-3399) DCM	29426	9381.53	18763.06	heart T-3399	3.59
adenoid GW99-269	26162	4435.48	8870.96	adenoid	
tonsil GW98-280	22582	7399.53	14799.06	tonsil	
T cells PC00314	28453	6576.4	13152.80	T cells	
PBMNC KC		139.42	139.42	PBMNC	
monocyte KC		126.02	252.04	monocyte	
B cells PC00665	28455	9735.42	19470.84	B cells	
dendritic cells 28441		15293.67	30587.34	dendritic cells	

neutrophils	28440	13487.07	13487.07	neutrophils	
eosinophils	28446	13111.46	26222.92	eosinophils	
BM unstim KC		332.7	332.70	BM unstim	
BM stim KC		379.27	379.27	BM stim	1.14
osteo dif KC		427.84	427.84	osteo dif	1.60
osteo undif KC		267.96	267.96	osteo undif	
chondrocytes		7063.55	17658.88	chondrocytes	
OA Synovium IP12/01	29462	9069.17	9069.17	OA Synovium	
OA Synovium NP10/01	29461	4247.36	8494.72	OA Synovium	
OA Synovium NP57/00	28464	4826.09	9652.18	OA Synovium	
RA Synovium NP03/01	28466	6003.36	12006.72	RA Synovium	
RA Synovium NP71/00	28467	6850.62	13701.24	RA Synovium	
RA Synovium NP45/00	28475	8737.59	17475.18	RA Synovium	
OA bone (biobank)	29217	3479.78	3479.78	OA bone (biobank)	
OA bone Sample 1	J. Emory	2992.04	5984.08	OA bone	
OA bone Sample 2	J. Emory	5164.14	10328.28	OA bone	
Cartilage (pool)	Normal	7859.28	15718.56	Cartilage (pool)	
Cartilage (pool)	OA	4341.01	8682.02	Cartilage (pool)	-1.81
PBL uninfected	28441	16983.2	33966.40	PBL uninfected	
PBL HIV IIIB	28442	9427.01	18854.02	PBL HIV IIIB	-1.80
MRC5 uninfected (100%)	29158	17734.85	35469.70	MRC5 uninfected (100%)	
MRC5 HSV strain F	29178	670.02	1340.04	MRC5 HSV strain F	-26.47
W12 cells	29179	3619.54	7239.08	W12 cells	
Keratinocytes	29180	4955.73	9911.46	Keratinocytes	

Gene Name sbg507131mannosidase

Disease tissues	Fold Change in Disease Population Relative to Normal
colon tumor	1.67
colon tumor	2.21
colon tumor	-1.27
colon tumor	-1.59
lung tumor	-5.67
lung tumor	1.27
lung tumor	1.01
lung tumor	1.48
breast tumor	1.93
breast tumor	4.67
breast tumor	3.31
breast tumor	-1.19
brain stage 5 ALZ	-1.95
brain stage 5 ALZ	1.34
brain stage 5 ALZ	-1.02
brain stage 5 ALZ	1.31

lung 24	-33.61
lung 28	-23.39
lung 23	-34.42
asthmatic lung	-1.03
asthmatic lung	3.49
asthmatic lung	6.99
asthmatic lung	4.21
endo VEGF	1.25
endo bFGF	-1.33
heart T-1	1.53
heart T-14	2.14
heart T-3399	3.59
BM stim	1.14
osteo dif	1.60
Cartilage (pool)	-1.81
PBL HIV IIIB	-1.80
MRC5 HSV strain F	-26.47

Gene Name sbg655871calgizzarin-like

- High expression in brain. Expression in intestines along with immune expression suggest claims for IBS, IBD, and crohn's disease. Fetal liver, thymus, adenoid, tonsil, T and
- 5 B cells and monocytes corroborates immune cell expression. Expression in RA and OA synovium and OA bone suggests involvement in these diseases. Significant overexpression in one breast tumor is sufficient to claim breast cancer (caveat: undetectable expression in normal may lead to exaggerated fold-overexpression). Consistently higher expression in normal adjacent and tumor tissue compared to tissues on normal masterplate is also
- 10 consistent with expression in activated immune cells.

Sample sbg655871calgizzarin-like	Mean GOI copies (sample 1)	Mean GOI copies (sample 2)	Average GOI Copies	18S rRNA (ng)	50 ng/18S rRNA (ng)	copies of mRNA detecte d/50 ng total RNA
Subcutaneous Adipocytes Zenbio	0	0	0.00	3.06	16.34	0.00
Subcutaneous Adipose Zenbio	0	0	0.00	0.96	52.36	0.00
Adrenal Gland Clontech	0	0	0.00	0.61	81.97	0.00
Whole Brain Clontech	537.46	799.45	668.46	7.24	6.91	4616.40
Fetal Brain Clontech	0	0	0.00	0.48	103.95	0.00
Cerebellum Clontech	29.9	13.65	21.78	2.17	23.04	501.73
Cervix	0	0	0.00	2.42	20.66	0.00
Colon	15.41	16.6	16.01	2.71	18.45	295.30
Endometrium	0	0	0.00	0.73	68.21	0.00
Esophagus	0	0	0.00	1.37	36.50	0.00
Heart Clontech	0	0	0.00	1.32	37.88	0.00

Hypothalamus	0	0	0.00	0.32	155.28	0.00
Ileum	0	15.15	7.58	2.58	19.38	146.80
Jejunum	40.86	16.79	28.83	6.60	7.58	218.37
Kidney	0	0	0.00	2.12	23.58	0.00
Liver	0	12.5	6.25	1.50	33.33	208.33
Fetal Liver Clontech	293.5	393.13	343.32	10.40	4.81	1650.55
Lung	0	0	0.00	2.57	19.46	0.00
Mammary Gland Clontech	91.08	118.14	104.61	13.00	3.85	402.35
Myometrium	0	26.43	13.22	2.34	21.37	282.37
Omentum	0	0	0.00	3.94	12.69	0.00
Ovary	22.65	12.76	17.71	4.34	11.52	203.97
Pancreas	0	0	0.00	0.81	61.80	0.00
Head of Pancreas	0	0	0.00	1.57	31.85	0.00
Parotid Gland	23.32	24.07	23.70	5.48	9.12	216.20
Placenta Clontech	28.2	34.71	31.46	5.26	9.51	299.00
Prostate	0	0	0.00	3.00	16.67	0.00
Rectum	0	0	0.00	1.23	40.65	0.00
Salivary Gland Clontech	52.48	55.96	54.22	7.31	6.84	370.86
Skeletal Muscle Clontech	0	0	0.00	1.26	39.68	0.00
Skin	0	0	0.00	1.21	41.32	0.00
Small Intestine Clontech	0	0	0.00	0.98	51.07	0.00
Spleen	13.83	0	6.92	4.92	10.16	70.27
Stomach	0	0	0.00	2.73	18.32	0.00
Testis Clontech	0	0	0.00	0.57	87.87	0.00
Thymus Clontech	409.4	502.34	455.87	9.89	5.06	2304.70
Thyroid	22.55	17.24	19.90	2.77	18.05	359.12
Trachea Clontech	73.02	52.6	62.81	9.71	5.15	323.43
Urinary Bladder	0	0	0.00	5.47	9.14	0.00
Uterus	0	24.54	12.27	5.34	9.36	114.89

Sample sbg655871calgizzarin- like	Reg number (GSK identifier)	Mean GOI copies	copies of mRNA detected/50 ng total RNA	Sample	Fold Change in Disease Population
colon normal GW98-167	21941	263.68	527.36	colon normal	
colon tumor GW98-166	21940	566.89	1133.78	colon tumor	2.15
colon normal GW98-178	22080	48.87	97.74	colon normal	
colon tumor GW98-177	22060	188.64	377.28	colon tumor	3.86
colon normal GW98-561	23514	113.25	226.50	colon normal	
colon tumor GW98-560	23513	196.14	392.28	colon tumor	1.73
colon normal GW98-894	24691	318.81	637.62	colon normal	
colon tumor GW98-893	24690	460.8	921.60	colon tumor	1.45
lung normal GW98-3	20742	508.76	1017.52	lung normal	

lung tumor GW98-2	20741	124.1	248.20	lung tumor	-4.10
lung normal GW97-179	20677	601.78	1203.56	lung normal	
lung tumor GW97-178	20676	316.85	633.70	lung tumor	-1.90
lung normal GW98-165	21922	913.61	1827.22	lung normal	
lung tumor GW98-164	21921	747.36	1494.72	lung tumor	-1.22
lung normal GW98-282	22584	216.1	432.20	lung normal	
lung tumor GW98-281	22583	177.97	355.94	lung tumor	-1.21
breast normal GW00-392	28750	186.88	186.88	breast normal	
breast tumor GW00-391	28746	278.12	556.24	breast tumor	2.98
breast normal GW00-413	28798	0	0.00	breast normal	
breast tumor GW00-412	28797	804.19	1608.38	breast tumor	1608.38
breast normal GW00-235:238	27592-95	0	0.00	breast normal	
breast tumor GW00-231:234	27588-91	0	0.00	breast tumor	0.00
breast normal GW98-621	23656	716.41	1432.82	breast normal	
breast tumor GW98-620	23655	436.65	873.30	breast tumor	-1.64
brain normal BB99-542	25507	404.96	809.92	brain normal	
brain normal BB99-406	25509	496.2	992.40	brain normal	
brain normal BB99-904	25546	90.22	180.44	brain normal	
brain stage 5 ALZ BB99-874	25502	90.86	181.72	brain stage 5 ALZ	-3.64
brain stage 5 ALZ BB99-887	25503	379.2	758.40	brain stage 5 ALZ	1.15
brain stage 5 ALZ BB99-862	25504	278.99	557.98	brain stage 5 ALZ	-1.18
brain stage 5 ALZ BB99-927	25542	316.21	632.42	brain stage 5 ALZ	-1.05
CT lung KC	normal	260.58	521.16	CT lung	
lung 26 KC	normal	0	0.00	lung 26	
lung 27 KC	normal	0	0.00	lung 27	
lung 24 KC	COPD	0	0.00	lung 24	-130.29
lung 28 KC	COPD	0	0.00	lung 28	-130.29
lung 23 KC	COPD	0	0.00	lung 23	-130.29
lung 25 KC	normal	0	0.00	lung 25	
asthmatic lung ODO3112	29321	0	0.00	asthmatic lung	-130.29
asthmatic lung ODO3433	29323	25.9	51.80	asthmatic lung	-2.52
asthmatic lung ODO3397	29322	274.29	548.58	asthmatic lung	4.21
asthmatic lung ODO4928	29325	76.05	152.10	asthmatic lung	1.17
endo cells KC	control	0	0.00	endo cells	
endo VEGF KC		15.57	15.57	endo VEGF	15.57
endo bFGF KC		24.36	24.36	endo bFGF	24.36
heart Clontech	normal	0	0.00	heart	
heart (T-1) ischemic	29417	286.72	573.44	heart T-1	573.44
heart (T-14) non-obstructive DCM	29422	160.22	320.44	heart T-14	320.44
heart (T-3399) DCM	29426	212.95	425.90	heart T-3399	425.90
adenoid GW99-269	26162	404.24	808.48	adenoid	
tonsil GW98-280	22582	1077.53	2155.06	tonsil	

T cells PC00314	28453	562.08	1124.16	T cells	
PBMNC KC		0	0.00	PBMNC	
monocyte KC		0	0.00	monocyte	
B cells PC00665	28455	925.74	1851.48	B cells	
dendritic cells 28441		56.59	113.18	dendritic cells	
neutrophils	28440	83.29	83.29	neutrophils	
eosinophils	28446	399.07	798.14	eosinophils	
BM unstim KC		0	0.00	BM unstim	
BM stim KC		24.03	24.03	BM stim	24.03
osteo dif KC		0	0.00	osteo dif	0.00
osteo undif KC		0	0.00	osteo undif	
chondrocytes		59.55	148.88	chondrocytes	
OA Synovium IP12/01	29462	17.31	17.31	OA Synovium	
OA Synovium NP10/01	29461	222.82	445.64	OA Synovium	
OA Synovium NP57/00	28464	267.63	535.26	OA Synovium	
RA Synovium NP03/01	28466	227.09	454.18	RA Synovium	
RA Synovium NP71/00	28467	638.53	1277.06	RA Synovium	
RA Synovium NP45/00	28475	1088.59	2177.18	RA Synovium	
OA bone (biobank)	29217	66.45	66.45	OA bone (biobank)	
OA bone Sample 1	J. Emory	205.74	411.48	OA bone	
OA bone Sample 2	J. Emory	679.55	1359.10	OA bone	
Cartilage (pool)	Normal	736.08	1472.16	Cartilage (pool)	
Cartilage (pool)	OA	286.47	572.94	Cartilage (pool)	-2.57
PBL uninfected	28441	1155.62	2311.24	PBL uninfected	
PBL HIV IIIB	28442	763.53	1527.06	PBL HIV IIIB	-1.51
MRC5 uninfected (100%)	29158	97.19	194.38	MRC5 uninfected (100%)	
MRC5 HSV strain F	29178	30.38	60.76	MRC5 HSV strain F	-3.20
W12 cells	29179	182.95	365.90	W12 cells	
Keratinocytes	29180	211.73	423.46	Keratinocytes	

Gene Name sbg655871calgizzarin-like

Disease tissues	Fold Change in Disease Population Relative to Normal
colon tumor	2.15
colon tumor	3.86
colon tumor	1.73
colon tumor	1.45
lung tumor	-4.10
lung tumor	-1.90
lung tumor	-1.22
lung tumor	-1.21
breast tumor	2.98
breast tumor	1608.38

breast tumor	0.00
breast tumor	-1.64
brain stage 5 ALZ	-3.64
brain stage 5 ALZ	1.15
brain stage 5 ALZ	-1.18
brain stage 5 ALZ	-1.05
lung 24	-130.29
lung 28	-130.29
lung 23	-130.29
asthmatic lung	-130.29
asthmatic lung	-2.52
asthmatic lung	4.21
asthmatic lung	1.17
endo VEGF	15.57
endo bFGF	24.36
heart T-1	573.44
heart T-14	320.44
heart T-3399	425.90
BM stim	24.03
osteo dif	0.00
Cartilage (pool)	-2.57
PBL HIV IIIB	-1.51
MRC5 HSV strain F	-3.20

Gene Name sbg506454MPG-1

Significant upregulation in one breast adenocarcinoma sufficient to make a claim for breast cancer. Widespread expression in immune cell populations, upregulated expression in 3 of 4 asthmatic lungs and high expression in RA and OA synovium, OA bone and cartilage suggest involvement in asthma, OA, and RA disease. Expression in GI tract as well as subcutaneous adipose suggest claims in IBS, IBD, and crohn's diseases. Expression in subcutaneous adipose and omentum (a fat depot) suggests claim for dyslipidemia and obesity.

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Sample sbg506454MPG-1	Mean GOI copies (sample 1)	Mean GOI copies (sample 2)	Average GOI Copies	18S rRNA (ng)	50 ng/18S rRNA (ng)	copies of mRNA detected/ 50 ng total RNA
Subcutaneous Adipocytes Zenbio	32.46	22.02	27.24	3.06	16.34	445.10
Subcutaneous Adipose Zenbio	0	0	0.00	0.96	52.36	0.00
Adrenal Gland Clontech	0	0	0.00	0.61	81.97	0.00
Whole Brain Clontech	9195.49	12359.11	10777.30	7.24	6.91	74428.87
Fetal Brain Clontech	8.14	12.95	10.55	0.48	103.95	1096.15
Cerebellum Clontech	161.39	87.85	124.62	2.17	23.04	2871.43
Cervix	58.73	35.95	47.34	2.42	20.66	978.10
Colon	11.75	41.67	26.71	2.71	18.45	492.80

Endometrium	0	15.54	7.77	0.73	68.21	530.01
Esophagus	0	12.09	6.05	1.37	36.50	220.62
Heart Clontech	0	0	0.00	1.32	37.88	0.00
Hypothalamus	0	10.73	5.37	0.32	155.28	833.07
Ileum	16.49	23.89	20.19	2.58	19.38	391.28
Jejunum	82.08	38.94	60.51	6.60	7.58	458.41
Kidney	39.06	10.72	24.89	2.12	23.58	587.03
Liver	41.23	28.71	34.97	1.50	33.33	1165.67
Fetal Liver Clontech	100.26	139.8	120.03	10.40	4.81	577.07
Lung	4.2	0	2.10	2.57	19.46	40.86
Mammary Gland Clontech	75.84	122.26	99.05	13.00	3.85	380.96
Myometrium	15.76	59.25	37.51	2.34	21.37	801.39
Omentum	35.05	66.71	50.88	3.94	12.69	645.69
Ovary	96.27	189.21	142.74	4.34	11.52	1644.47
Pancreas	4.98	0	2.49	0.81	61.80	153.89
Head of Pancreas	0	0	0.00	1.57	31.85	0.00
Parotid Gland	13.16	107.03	60.10	5.48	9.12	548.31
Placenta Clontech	0	0	0.00	5.26	9.51	0.00
Prostate	0	0	0.00	3.00	16.67	0.00
Rectum	27.68	15.44	21.56	1.23	40.65	876.42
Salivary Gland Clontech	31.31	47.7	39.51	7.31	6.84	270.21
Skeletal Muscle Clontech	0	8.62	4.31	1.26	39.68	171.03
Skin	23.3	4.31	13.81	1.21	41.32	570.45
Small Intestine Clontech	0	0	0.00	0.98	51.07	0.00
Spleen	30.6	0	15.30	4.92	10.16	155.49
Stomach	22.74	37.71	30.23	2.73	18.32	553.57
Testis Clontech	0	0	0.00	0.57	87.87	0.00
Thymus Clontech	437.25	466.27	451.76	9.89	5.06	2283.92
Thyroid	29.73	11.51	20.62	2.77	18.05	372.20
Trachea Clontech	32.38	84.84	58.61	9.71	5.15	301.80
Urinary Bladder	49.96	72.21	61.09	5.47	9.14	558.36
Uterus	138.38	160.37	149.38	5.34	9.36	1398.64

Sample sbg506454MPG-1	Reg number (GSK identifier)	Mean GOI copies	copies of mRNA detected/50 ng total RNA	Sample	Fold Change in Disease Population
colon normal GW98-167	21941	2762.2	5524.40	colon normal	
colon tumor GW98-166	21940	4187.4	8374.80	colon tumor	1.52
colon normal GW98-178	22080	304.95	609.90	colon normal	
colon tumor GW98-177	22060	591.09	1182.18	colon tumor	1.94
colon normal GW98-561	23514	1334.04	2668.08	colon normal	
colon tumor GW98-560	23513	773.62	1547.24	colon tumor	-1.72
colon normal GW98-894	24691	5252.81	10505.62	colon normal	

colon tumor GW98-893	24690	1582.61	3165.22	colon tumor	-3.32
lung normal GW98-3	20742	5609.71	11219.42	lung normal	
lung tumor GW98-2	20741	244.73	489.46	lung tumor	-22.92
lung normal GW97-179	20677	5225.63	10451.26	lung normal	
lung tumor GW97-178	20676	3397.1	6794.20	lung tumor	-1.54
lung normal GW98-165	21922	4925.8	9851.60	lung normal	
lung tumor GW98-164	21921	3628.09	7256.18	lung tumor	-1.36
lung normal GW98-282	22584	1689.76	3379.52	lung normal	
lung tumor GW98-281	22583	2126.38	4252.76	lung tumor	1.26
breast normal GW00-392	28750	919.61	919.61	breast normal	
breast tumor GW00-391	28746	844.85	1689.70	breast tumor	1.84
breast normal GW00-413	28798	402.44	402.44	breast normal	
breast tumor GW00-412	28797	4379.69	8759.38	breast tumor	21.77
breast normal GW00-235:238	27592-95	59.61	59.61	breast normal	
breast tumor GW00-231:234	27588-91	182.62	182.62	breast tumor	3.06
breast normal GW98-621	23656	1437.56	2875.12	breast normal	
breast tumor GW98-620	23655	1973.41	3946.82	breast tumor	1.37
brain normal BB99-542	25507	151.01	302.02	brain normal	
brain normal BB99-406	25509	220.06	440.12	brain normal	
brain normal BB99-904	25546	118	236.00	brain normal	
brain stage 5 ALZ BB99-874	25502	37.44	74.88	brain stage 5 ALZ	-4.35
brain stage 5 ALZ BB99-887	25503	475.99	951.98	brain stage 5 ALZ	2.92
brain stage 5 ALZ BB99-862	25504	175.26	350.52	brain stage 5 ALZ	1.08
brain stage 5 ALZ BB99-927	25542	127.66	255.32	brain stage 5 ALZ	-1.28
CT lung KC	normal	2040.92	4081.84	CT lung	
lung 26 KC	normal	304.9	304.90	lung 26	
lung 27 KC	normal	97.51	97.51	lung 27	
lung 24 KC	COPD	179.61	179.61	lung 24	-6.45
lung 28 KC	COPD	345.33	345.33	lung 28	-3.35
lung 23 KC	COPD	181.29	181.29	lung 23	-6.39
lung 25 KC	normal	147.65	147.65	lung 25	
asthmatic lung ODO3112	29321	299.26	299.26	asthmatic lung	-3.87
asthmatic lung ODO3433	29323	6700	13400.00	asthmatic lung	11.57
asthmatic lung ODO3397	29322	10865.43	21730.86	asthmatic lung	18.77
asthmatic lung ODO4928	29325	5532.73	11065.46	asthmatic lung	9.56
endo cells KC	control	0	0.00	endo cells	
endo VEGF KC		0	0.00	endo VEGF	0.00
endo bFGF KC		0	0.00	endo bFGF	0.00
heart Clontech	normal	4533.27	9066.54	heart	
heart (T-1) ischemic	29417	996.35	1992.70	heart T-1	-4.55
heart (T-14) non-obstructive DCM	29422	787.37	1574.74	heart T-14	-5.76
heart (T-3399) DCM	29426	1496.18	2992.36	heart T-3399	-3.03

adenoid GW99-269	26162	7988.69	15977.38	adenoid	
tonsil GW98-280	22582	9400.6	18801.20	tonsil	
T cells PC00314	28453	1806.51	3613.02	T cells	
PBMNC KC		1206.11	1206.11	PBMNC	
monocyte KC		2460.19	4920.38	monocyte	
B cells PC00665	28455	24529.33	49058.66	B cells	
dendritic cells 28441		57867.91	115735.82	dendritic cells	
neutrophils	28440	34334.73	34334.73	neutrophils	
eosinophils	28446	7309.05	14618.10	eosinophils	
BM unstim KC		592.73	592.73	BM unstim	
BM stim KC		2305.64	2305.64	BM stim	3.89
osteo dif KC		0	0.00	osteo dif	0.00
osteo undif KC		0	0.00	osteo undif	
chondrocytes		3.91	9.78	chondrocytes	
OA Synovium IP12/01	29462	4075.04	4075.04	OA Synovium	
OA Synovium NP10/01	29461	3058.76	6117.52	OA Synovium	
OA Synovium NP57/00	28464	10311.73	20623.46	OA Synovium	
RA Synovium NP03/01	28466	15610.63	31221.26	RA Synovium	
RA Synovium NP71/00	28467	16336.72	32673.44	RA Synovium	
RA Synovium NP45/00	28475	25648.1	51296.20	RA Synovium	
OA bone (biobank)	29217	2045.31	2045.31	OA bone (biobank)	
OA bone Sample 1	J. Emory	8940.89	17881.78	OA bone	
OA bone Sample 2	J. Emory	10348.45	20696.90	OA bone	
Cartilage (pool)	Normal	4762.29	9524.58	Cartilage (pool)	
Cartilage (pool)	OA	2412.92	4825.84	Cartilage (pool)	-1.97
PBL uninfected	28441	3559.78	7119.56	PBL uninfected	
PBL HIV IIIB	28442	10815.58	21631.16	PBL HIV IIIB	3.04
MRC5 uninfected (100%)	29158	72.21	144.42	MRC5 uninfected (100%)	
MRC5 HSV strain F	29178	133.55	267.10	MRC5 HSV strain F	1.85
W12 cells	29179	6.74	13.48	W12 cells	
Keratinocytes	29180	3.55	7.10	Keratinocytes	

Gene Name sbg506454MPG-1

Disease tissues	Fold Change in Disease Population Relative to Normal
colon tumor	1.52
colon tumor	1.94
colon tumor	-1.72
colon tumor	-3.32
lung tumor	-22.92
lung tumor	-1.54

lung tumor	-1.36
lung tumor	1.26
breast tumor	1.84
breast tumor	21.77
breast tumor	3.06
breast tumor	1.37
brain stage 5 ALZ	-4.35
brain stage 5 ALZ	2.92
brain stage 5 ALZ	1.08
brain stage 5 ALZ	-1.28
lung 24	-6.45
lung 28	-3.35
lung 23	-6.39
asthmatic lung	-3.87
asthmatic lung	11.57
asthmatic lung	18.77
asthmatic lung	9.56
endo VEGF	0.00
endo bFGF	0.00
heart T-1	-4.55
heart T-14	-5.76
heart T-3399	-3.03
BM stim	3.89
osteo dif	0.00
Cartilage (pool)	-1.97
PBL HIV IIIB	3.04
MRC5 HSV strain F	1.85

Gene Name sbg659837OBCAM

Highest in brain but not changed in alzheimers. Significantly increased expression in one tumor each of colon and lung sufficient to claim colon and lung cancer.

- 5 Upregulated expression in ischemic and non-obstructive DCM suggesting possible roles in these diseases

Sample sbg659837OBCAM	Mean GOI copies (sample 1)	Mean GOI copies (sample 2)	Average GOI Copies	18S rRNA (ng)	50 ng/18S rRNA (ng)	copies of mRNA detected/ 50 ng total RNA
Subcutaneous Adipocytes Zenbio	1.15	5.28	3.22	3.06	16.34	52.53
Subcutaneous Adipose Zenbio	5.25	5.54	5.40	0.96	52.36	282.46
Adrenal Gland Clontech	0	0.47	0.24	0.61	81.97	19.26
Whole Brain Clontech	7004	8885.24	7944.62	7.24	6.91	54866.16
Fetal Brain Clontech	63.3	31.88	47.59	0.48	103.95	4946.99
Cerebellum Clontech	113.86	99.7	106.78	2.17	23.04	2460.37

Cervix	0	0.9	0.45	2.42	20.66	9.30
Colon	9.45	0	4.73	2.71	18.45	87.18
Endometrium	0.95	9.52	5.24	0.73	68.21	357.09
Esophagus	0.93	0.41	0.67	1.37	36.50	24.45
Heart Clontech	2.38	1.46	1.92	1.32	37.88	72.73
Hypothalamus	15.19	3.03	9.11	0.32	155.28	1414.60
Ileum	0	0.17	0.09	2.58	19.38	1.65
Jejunum	8.83	9.37	9.10	6.60	7.58	68.94
Kidney	1.88	0.13	1.01	2.12	23.58	23.70
Liver	0.5	19.09	9.80	1.50	33.33	326.50
Fetal Liver Clontech	29.24	24.47	26.86	10.40	4.81	129.11
Lung	1.59	0.57	1.08	2.57	19.46	21.01
Mammary Gland Clontech	18.83	15.4	17.12	13.00	3.85	65.83
Myometrium	1.61	0.47	1.04	2.34	21.37	22.22
Omentum	5.14	0.36	2.75	3.94	12.69	34.90
Ovary	7.55	9.8	8.68	4.34	11.52	99.94
Pancreas	0.15	0	0.08	0.81	61.80	4.64
Head of Pancreas	7.79	0	3.90	1.57	31.85	124.04
Parotid Gland	15.83	17.02	16.43	5.48	9.12	149.86
Placenta Clontech	0.11	12.02	6.07	5.26	9.51	57.65
Prostate	0.39	2.26	1.33	3.00	16.67	22.08
Rectum	2.79	0.43	1.61	1.23	40.65	65.45
Salivary Gland Clontech	0.48	4.21	2.35	7.31	6.84	16.04
Skeletal Muscle Clontech	0.4	0	0.20	1.26	39.68	7.94
Skin	8.94	0.49	4.72	1.21	41.32	194.83
Small Intestine Clontech	0.56	0.68	0.62	0.98	51.07	31.66
Spleen	0.17	9.76	4.97	4.92	10.16	50.46
Stomach	0.47	10.35	5.41	2.73	18.32	99.08
Testis Clontech	16.85	2.95	9.90	0.57	87.87	869.95
Thymus Clontech	9.87	19.27	14.57	9.89	5.06	73.66
Thyroid	0	0	0.00	2.77	18.05	0.00
Trachea Clontech	2.61	21.88	12.25	9.71	5.15	63.05
Urinary Bladder	0.49	5.2	2.85	5.47	9.14	26.01
Uterus	15.14	10.84	12.99	5.34	9.36	121.63

Sample sbg659837OBCAM	Reg number (GSK identifier)	Mean GOI copies	copies of mRNA detected/5 0 ng total RNA	Sample	Fold Change in Disease Population
colon normal GW98-167	21941	61.2	122.40	colon normal	
colon tumor GW98-166	21940	220.5	441.00	colon tumor	3.60
colon normal GW98-178	22080	12.34	24.68	colon normal	
colon tumor GW98-177	22060	11.21	22.42	colon tumor	-1.10

colon normal GW98-561	23514	15.49	30.98	colon normal	
colon tumor GW98-560	23513	146.12	292.24	colon tumor	9.43
colon normal GW98-894	24691	7.27	14.54	colon normal	
colon tumor GW98-893	24690	20.83	41.66	colon tumor	2.87
lung normal GW98-3	20742	12.55	25.10	lung normal	
lung tumor GW98-2	20741	19.34	38.68	lung tumor	1.54
lung normal GW97-179	20677	934.94	1869.88	lung normal	
lung tumor GW97-178	20676	3.9	7.80	lung tumor	-239.73
lung normal GW98-165	21922	0.96	1.92	lung normal	
lung tumor GW98-164	21921	108.12	216.24	lung tumor	112.63
lung normal GW98-282	22584	8.25	16.50	lung normal	
lung tumor GW98-281	22583	6.21	12.42	lung tumor	-1.33
breast normal GW00-392	28750	9.43	9.43	breast normal	
breast tumor GW00-391	28746	18.02	36.04	breast tumor	3.82
breast normal GW00-413	28798	13.42	13.42	breast normal	
breast tumor GW00-412	28797	1.94	3.88	breast tumor	-3.46
breast normal GW00-235:238	27592-95	4.61	4.61	breast normal	
breast tumor GW00-231:234	27588-91	10.16	10.16	breast tumor	2.20
breast normal GW98-621	23656	18.65	37.30	breast normal	
breast tumor GW98-620	23655	13.96	27.92	breast tumor	-1.34
brain normal BB99-542	25507	812.47	1624.94	brain normal	
brain normal BB99-406	25509	231.81	463.62	brain normal	
brain normal BB99-904	25546	583.17	1166.34	brain normal	
brain stage 5 ALZ BB99-874	25502	200.73	401.46	brain stage 5 ALZ	-2.70
brain stage 5 ALZ BB99-887	25503	685.93	1371.86	brain stage 5 ALZ	1.26
brain stage 5 ALZ BB99-862	25504	585.8	1171.60	brain stage 5 ALZ	1.08
brain stage 5 ALZ BB99-927	25542	329.32	658.64	brain stage 5 ALZ	-1.65
CT lung KC	normal	17.5	35.00	CT lung	
lung 26 KC	normal	8.07	8.07	lung 26	
lung 27 KC	normal	0.3	0.30	lung 27	
lung 24 KC	COPD	0.45	0.45	lung 24	-24.09
lung 28 KC	COPD	0.22	0.22	lung 28	-49.28
lung 23 KC	COPD	0	0.00	lung 23	-10.84
lung 25 KC	normal	0	0.00	lung 25	
asthmatic lung ODO3112	29321	0.52	0.52	asthmatic lung	-20.85
asthmatic lung ODO3433	29323	0.7	1.40	asthmatic lung	-7.74
asthmatic lung ODO3397	29322	1.96	3.92	asthmatic lung	-2.77
asthmatic lung ODO4928	29325	6.35	12.70	asthmatic lung	1.17
endo cells KC	control	0	0.00	endo cells	
endo VEGF KC		0	0.00	endo VEGF	0.00
endo bFGF KC		0.9	0.90	endo bFGF	0.90
heart Clontech	normal	0	0.00	heart	
heart (T-1) ischemic	29417	12.89	25.78	heart T-1	25.78

heart (T-14) non-obstructive DCM	29422	12.27	24.54	heart T-14	24.54
heart (T-3399) DCM	29426	0	0.00	heart T-3399	0.00
adenoid GW99-269	26162	4.88	9.76	adenoid	
tonsil GW98-280	22582	1.13	2.26	tonsil	
T cells PC00314	28453	5.99	11.98	T cells	
PBMNC KC		0	0.00	PBMNC	
monocyte KC		0.15	0.30	monocyte	
B cells PC00665	28455	4.62	9.24	B cells	
dendritic cells 28441		1.33	2.66	dendritic cells	
neutrophils	28440	1.86	1.86	neutrophils	
eosinophils	28446	3.76	7.52	eosinophils	
BM unstim KC		0.15	0.15	BM unstim	
BM stim KC		0.99	0.99	BM stim	6.60
osteo dif KC		0	0.00	osteo dif	0.00
osteo undif KC		0	0.00	osteo undif	
chondrocytes		6.09	15.23	chondrocytes	
OA Synovium IP12/01	29462	29.16	29.16	OA Synovium	
OA Synovium NP10/01	29461	7.61	15.22	OA Synovium	
OA Synovium NP57/00	28464	10.65	21.30	OA Synovium	
RA Synovium NP03/01	28466	0.84	1.68	RA Synovium	
RA Synovium NP71/00	28467	10.01	20.02	RA Synovium	
RA Synovium NP45/00	28475	3.77	7.54	RA Synovium	
OA bone (biobank)	29217	1.34	1.34	OA bone (biobank)	
OA bone Sample 1	J. Emory	13.96	27.92	OA bone	
OA bone Sample 2	J. Emory	5.82	11.64	OA bone	
Cartilage (pool)	Normal	8.9	17.80	Cartilage (pool)	
Cartilage (pool)	OA	5.88	11.76	Cartilage (pool)	-1.51
PBL uninfected	28441	37.23	74.46	PBL uninfected	
PBL HIV IIIB	28442	12.75	25.50	PBL HIV IIIB	-2.92
MRC5 uninfected (100%)	29158	1.88	3.76	MRC5 uninfected (100%)	
MRC5 HSV strain F	29178	4.71	9.42	MRC5 HSV strain F	2.51
W12 cells	29179	2.4	4.80	W12 cells	
Keratinocytes	29180	0.47	0.94	Keratinocytes	

Gene Name sbg659837OBCAM

Disease tissues	Fold Change in Disease Population Relative to Normal
colon tumor	3.60
colon tumor	-1.10
colon tumor	9.43
colon tumor	2.87

lung tumor	1.54
lung tumor	-239.73
lung tumor	112.63
lung tumor	-1.33
breast tumor	3.82
breast tumor	-3.46
breast tumor	2.20
breast tumor	-1.34
brain stage 5 ALZ	-2.70
brain stage 5 ALZ	1.26
brain stage 5 ALZ	1.08
brain stage 5 ALZ	-1.65
lung 24	-24.09
lung 28	-49.28
lung 23	-10.84
asthmatic lung	-20.85
asthmatic lung	-7.74
asthmatic lung	-2.77
asthmatic lung	1.17
endo VEGF	0.00
endo bFGF	0.90
heart T-1	25.78
heart T-14	24.54
heart T-3399	0.00
BM stim	6.60
osteo dif	0.00
Cartilage (pool)	-1.51
PBL HIV IIIB	-2.92
MRC5 HSV strain F	2.51

Gene Name sbg467870CBP

Expression in fetal liver, thymus, monocytes, adenoid, and tonsil consistent with role in I inflammation. Upregulated in 2 of 4 asthmatic lungs, expression in OA and RA synovium, chondrocyte cells and cartilage, OA bone, and RA synovia suggest involvement in asthma, osteoarthritis, and rheumatoid arthritis. Upregulated in differentiated osteoblasts and expression in OA bone suggests possible involvement in bone disease such as osteoporosis. Down-regulated expression in HSV infected lung cell line suggest possible host factor for HSV infection. Expressed in brain but not changed in alzheimers disease.

Sample sbg467870CBP	Mean GOI copies (sample 1)	Mean GOI copies (sample 2)	Average GOI Copies	18S rRNA (ng)	50 ng/18S rRNA (ng)	copies of mRNA detected/ 50 ng total RNA
Subcutaneous Adipocytes Zenbio	122.51	171.63	147.07	3.06	16.34	2403.10
Subcutaneous Adipose Zenbio	1.45	13.47	7.46	0.96	52.36	390.58
Adrenal Gland Clontech	0	0	0.00	0.61	81.97	0.00

Whole Brain Clontech	3940.12	4641.93	4291.03	7.24	6.91	29634.15
Fetal Brain Clontech	3.53	0	1.77	0.48	103.95	183.47
Cerebellum Clontech	22.75	10.04	16.40	2.17	23.04	377.76
Cervix	29.81	35.43	32.62	2.42	20.66	673.97
Colon	28.29	54.06	41.18	2.71	18.45	759.69
Endometrium	30.56	34.68	32.62	0.73	68.21	2225.10
Esophagus	17.68	20.49	19.09	1.37	36.50	696.53
Heart Clontech	28.33	8.29	18.31	1.32	37.88	693.56
Hypothalamus	3.33	0	1.67	0.32	155.28	258.54
Ileum	61.25	51.5	56.38	2.58	19.38	1092.54
Jejunum	67.83	122.15	94.99	6.60	7.58	719.62
Kidney	16.18	62.83	39.51	2.12	23.58	931.72
Liver	18.1	47.12	32.61	1.50	33.33	1087.00
Fetal Liver Clontech	2254.06	1918.75	2086.41	10.40	4.81	10030.79
Lung	22.15	21.19	21.67	2.57	19.46	421.60
Mammary Gland Clontech	601.21	800.88	701.05	13.00	3.85	2696.33
Myometrium	111.87	92.21	102.04	2.34	21.37	2180.34
Omentum	127.05	139.02	133.04	3.94	12.69	1688.26
Ovary	101.56	83.66	92.61	4.34	11.52	1066.94
Pancreas	0	5.97	2.99	0.81	61.80	184.49
Head of Pancreas	1	6.97	3.99	1.57	31.85	126.91
Parotid Gland	73.96	99.31	86.64	5.48	9.12	790.47
Placenta Clontech	418.31	231.45	324.88	5.26	9.51	3088.21
Prostate	48.01	84.04	66.03	3.00	16.67	1100.42
Rectum	36.56	53.99	45.28	1.23	40.65	1840.45
Salivary Gland Clontech	121.88	154.83	138.36	7.31	6.84	946.34
Skeletal Muscle Clontech	21.46	0	10.73	1.26	39.68	425.79
Skin	28.31	20.63	24.47	1.21	41.32	1011.16
Small Intestine Clontech	11.03	5.84	8.44	0.98	51.07	430.80
Spleen	25.2	33.24	29.22	4.92	10.16	296.95
Stomach	31.15	51.9	41.53	2.73	18.32	760.53
Testis Clontech	0	6.47	3.24	0.57	87.87	284.27
Thymus Clontech	2456.56	2161.41	2308.99	9.89	5.06	11673.33
Thyroid	32.73	62.2	47.47	2.77	18.05	856.77
Trachea Clontech	129.76	145.42	137.59	9.71	5.15	708.50
Urinary Bladder	137.82	144.51	141.17	5.47	9.14	1290.36
Uterus	166.73	180.21	173.47	5.34	9.36	1624.25

Sample sbg467870CBP	Reg number (GSK identifier)	Mean GOI copies	copies of mRNA detected/50 ng total RNA	Sample	Fold Change in Disease Population
colon normal GW98-167	21941	5005.21	10010.42	colon normal	

colon tumor GW98-166	21940	15849.6	31699.20	colon tumor	3.17
colon normal GW98-178	22080	1796.63	3593.26	colon normal	
colon tumor GW98-177	22060	2527.09	5054.18	colon tumor	1.41
colon normal GW98-561	23514	1769.84	3539.68	colon normal	
colon tumor GW98-560	23513	4004.28	8008.56	colon tumor	2.26
colon normal GW98-894	24691	2496.8	4993.60	colon normal	
colon tumor GW98-893	24690	5145.92	10291.84	colon tumor	2.06
lung normal GW98-3	20742	2177.03	4354.06	lung normal	
lung tumor GW98-2	20741	2751.54	5503.08	lung tumor	1.26
lung normal GW97-179	20677	5925.16	11850.32	lung normal	
lung tumor GW97-178	20676	5250.96	10501.92	lung tumor	-1.13
lung normal GW98-165	21922	2705.56	5411.12	lung normal	
lung tumor GW98-164	21921	10468.54	20937.08	lung tumor	3.87
lung normal GW98-282	22584	1959.86	3919.72	lung normal	
lung tumor GW98-281	22583	937.14	1874.28	lung tumor	-2.09
breast normal GW00-392	28750	4102.06	4102.06	breast normal	
breast tumor GW00-391	28746	2805.02	5610.04	breast tumor	1.37
breast normal GW00-413	28798	4564.07	4564.07	breast normal	
breast tumor GW00-412	28797	5045.72	10091.44	breast tumor	2.21
breast normal GW00-235:238	27592-95	3527.38	3527.38	breast normal	
breast tumor GW00-231:234	27588-91	4475.08	4475.08	breast tumor	1.27
breast normal GW98-621	23656	5436.38	10872.76	breast normal	
breast tumor GW98-620	23655	7555.65	15111.30	breast tumor	1.39
brain normal BB99-542	25507	4185.89	8371.78	brain normal	
brain normal BB99-406	25509	1474.43	2948.86	brain normal	
brain normal BB99-904	25546	824.95	1649.90	brain normal	
brain stage 5 ALZ BB99-874	25502	439.29	878.58	brain stage 5 ALZ	-4.92
brain stage 5 ALZ BB99-887	25503	1034.44	2068.88	brain stage 5 ALZ	-2.09
brain stage 5 ALZ BB99-862	25504	2189.42	4378.84	brain stage 5 ALZ	1.01
brain stage 5 ALZ BB99-927	25542	2009.16	4018.32	brain stage 5 ALZ	-1.08
CT lung KC	normal	2111.76	4223.52	CT lung	
lung 26 KC	normal	308.92	308.92	lung 26	
lung 27 KC	normal	11.77	11.77	lung 27	
lung 24 KC	COPD	23.05	23.05	lung 24	-49.55
lung 28 KC	COPD	217.04	217.04	lung 28	-5.26
lung 23 KC	COPD	66.62	66.62	lung 23	-17.15
lung 25 KC	normal	24.66	24.66	lung 25	
asthmatic lung ODO3112	29321	3982.98	3982.98	asthmatic lung	3.49
asthmatic lung ODO3433	29323	2535.37	5070.74	asthmatic lung	4.44
asthmatic lung ODO3397	29322	10395.55	20791.10	asthmatic lung	18.20
asthmatic lung ODO4928	29325	5044.21	10088.42	asthmatic	8.83

				lung	
endo cells KC	control	724.08	724.08	endo cells	
endo VEGF KC		607.05	607.05	endo VEGF	-1.19
endo bFGF KC		346.88	346.88	endo bFGF	-2.09
heart Clontech	normal	338.3	676.60	heart	
heart (T-1) ischemic	29417	7198.62	14397.24	heart T-1	21.28
heart (T-14) non-obstructive DCM	29422	1634.96	3269.92	heart T-14	4.83
heart (T-3399) DCM	29426	8987.22	17974.44	heart T-3399	26.57
adenoid GW99-269	26162	1327.73	2655.46	adenoid	
tonsil GW98-280	22582	3389.07	6778.14	tonsil	
T cells PC00314	28453	2349.93	4699.86	T cells	
PBMNC KC		41.03	41.03	PBMNC	
monocyte KC		21.32	42.64	monocyte	
B cells PC00665	28455	1181.61	2363.22	B cells	
dendritic cells 28441		7521.93	15043.86	dendritic cells	
neutrophils	28440	248.9	248.90	neutrophils	
eosinophils	28446	874.14	1748.28	eosinophils	
BM unstim KC		142.11	142.11	BM unstim	
BM stim KC		635.4	635.40	BM stim	4.47
osteo dif KC		2464.77	2464.77	osteo dif	5.45
osteo undif KC		452.56	452.56	osteo undif	
chondrocytes		24737.56	61843.90	chondrocytes	
OA Synovium IP12/01	29462	1788.87	1788.87	OA Synovium	
OA Synovium NP10/01	29461	7842.79	15685.58	OA Synovium	
OA Synovium NP57/00	28464	11577.91	23155.82	OA Synovium	
RA Synovium NP03/01	28466	19643.98	39287.96	RA Synovium	
RA Synovium NP71/00	28467	22772.86	45545.72	RA Synovium	
RA Synovium NP45/00	28475	16068.31	32136.62	RA Synovium	
OA bone (biobank)	29217	1829.84	1829.84	OA bone (biobank)	
OA bone Sample 1	J. Emory	11770.26	23540.52	OA bone	
OA bone Sample 2	J. Emory	2525.12	5050.24	OA bone	
Cartilage (pool)	Normal	18001.36	36002.72	Cartilage (pool)	
Cartilage (pool)	OA	7463.95	14927.90	Cartilage (pool)	-2.41
PBL uninfected	28441	3136.91	6273.82	PBL uninfected	
PBL HIV IIIB	28442	2830.85	5661.70	PBL HIV IIIB	-1.11
MRC5 uninfected (100%)	29158	25933.25	51866.50	MRC5 uninfected (100%)	
MRC5 HSV strain F	29178	279.28	558.56	MRC5 HSV strain F	-92.86
W12 cells	29179	6771.87	13543.74	W12 cells	
Keratinocytes	29180	22577.2	45154.40	Keratinocytes	

Gene Name sbg467870CBP

Disease tissues	Fold Change in Disease Population Relative to Normal
colon tumor	3.17
colon tumor	1.41
colon tumor	2.26
colon tumor	2.06
lung tumor	1.26
lung tumor	-1.13
lung tumor	3.87
lung tumor	-2.09
breast tumor	1.37
breast tumor	2.21
breast tumor	1.27
breast tumor	1.39
brain stage 5 ALZ	-4.92
brain stage 5 ALZ	-2.09
brain stage 5 ALZ	1.01
brain stage 5 ALZ	-1.08
lung 24	-49.55
lung 28	-5.26
lung 23	-17.15
asthmatic lung	3.49
asthmatic lung	4.44
asthmatic lung	18.20
asthmatic lung	8.83
endo VEGF	-1.19
endo bFGF	-2.09
heart T-1	21.28
heart T-14	4.83
heart T-3399	26.57
BM stim	4.47
osteo dif	5.45
Cartilage (pool)	-2.41
PBL HIV IIIB	-1.11
MRC5 HSV strain F	-92.86

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Gene Name sbg514112RNase

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Low expression overall. Upregulated in 4 of 4 colon adenocarcinomas, 2 of 4 lung carcinomas, and 2 of 4 breast carcinomas suggesting claim for all cancers. Expression in spleen, PHA stimulated T and B cells, dendritic cells corroborates expression RA and OA synovium suggesting involvement in RA and OA diseases. Upregulated expression in 2 of 4 asthmatic lungs suggesting role in asthma. Upregulated in ischemic heart suggests possible involvement in ischemic heart disease. Strongly upregulated expression in HSV infected cell line.

Sample sbg514112RNase	Mean GOI copies (sample 1)	Mean GOI copies (sample 2)	Average GOI Copies	18S rRNA (ng)	50 ng/18S rRNA (ng)	copies of mRNA detected/ 50 ng total RNA
Subcutaneous Adipocytes Zenbio	2.22	3	2.61	3.06	16.34	42.65
Subcutaneous Adipose Zenbio	0	0	0.00	0.96	52.36	0.00
Adrenal Gland Clontech	2.31	1.85	2.08	0.61	81.97	170.49
Whole Brain Clontech	53.95	74.45	64.20	7.24	6.91	443.37
Fetal Brain Clontech	0	1.4	0.70	0.48	103.95	72.77
Cerebellum Clontech	0.7	1.99	1.35	2.17	23.04	30.99
Cervix	10.35	8.54	9.45	2.42	20.66	195.14
Colon	2.09	0.84	1.47	2.71	18.45	27.03
Endometrium	3.8	2.54	3.17	0.73	68.21	216.23
Esophagus	3.19	3.42	3.31	1.37	36.50	120.62
Heart Clontech	5.21	1.04	3.13	1.32	37.88	118.37
Hypothalamus	0.95	0.96	0.96	0.32	155.28	148.29
Ileum	2.04	1.5	1.77	2.58	19.38	34.30
Jejunum	10.27	2.15	6.21	6.60	7.58	47.05
Kidney	2.89	1.11	2.00	2.12	23.58	47.17
Liver	20.9	19.22	20.06	1.50	33.33	668.67
Fetal Liver Clontech	1.38	18.45	9.92	10.40	4.81	47.67
Lung	2.86	1.11	1.99	2.57	19.46	38.62
Mammary Gland Clontech	1.19	1.72	1.46	13.00	3.85	5.60
Myometrium	1.48	1.95	1.72	2.34	21.37	36.65
Omentum	13.35	0.72	7.04	3.94	12.69	89.28
Ovary	10.88	17.35	14.12	4.34	11.52	162.62
Pancreas	0.66	1.29	0.98	0.81	61.80	60.26
Head of Pancreas	1.31	7.17	4.24	1.57	31.85	135.03
Parotid Gland	2.19	0	1.10	5.48	9.12	9.99
Placenta Clontech	0.68	16.07	8.38	5.26	9.51	79.61
Prostate	1.1	0.95	1.03	3.00	16.67	17.08
Rectum	1.84	4.04	2.94	1.23	40.65	119.51
Salivary Gland Clontech	1.52	0.91	1.22	7.31	6.84	8.31
Skeletal Muscle Clontech	1.79	0.91	1.35	1.26	39.68	53.57
Skin	1.19	0.86	1.03	1.21	41.32	42.36
Small Intestine Clontech	3.14	1.72	2.43	0.98	51.07	124.11
Spleen	0.9	34.95	17.93	4.92	10.16	182.16
Stomach	0.72	2.21	1.47	2.73	18.32	26.83
Testis Clontech	0.69	1.82	1.26	0.57	87.87	110.28
Thymus Clontech	1.66	17.77	9.72	9.89	5.06	49.12
Thyroid	0.71	1.47	1.09	2.77	18.05	19.68
Trachea Clontech	18.75	19.05	18.90	9.71	5.15	97.32

Urinary Bladder	29.84	1.96	15.90	5.47	9.14	145.34
Uterus	10.06	46.86	28.46	5.34	9.36	266.48

Sample sbg514112RNase	Reg number (GSK identifier)	Mean GOI copies	copies of mRNA detected/50 ng total RNA	Sample	Fold Change in Disease Population
colon normal GW98-167	21941	6.61	13.22	colon normal	
colon tumor GW98-166	21940	102.54	205.08	colon tumor	15.51
colon normal GW98-178	22080	0.47	0.94	colon normal	
colon tumor GW98-177	22060	13.57	27.14	colon tumor	28.87
colon normal GW98-561	23514	4.51	9.02	colon normal	
colon tumor GW98-560	23513	25.13	50.26	colon tumor	5.57
colon normal GW98-894	24691	0.55	1.10	colon normal	
colon tumor GW98-893	24690	23.36	46.72	colon tumor	42.47
lung normal GW98-3	20742	9.59	19.18	lung normal	
lung tumor GW98-2	20741	48.18	96.36	lung tumor	5.02
lung normal GW97-179	20677	121.59	243.18	lung normal	
lung tumor GW97-178	20676	1.08	2.16	lung tumor	-112.58
lung normal GW98-165	21922	1.7	3.40	lung normal	
lung tumor GW98-164	21921	25.45	50.90	lung tumor	14.97
lung normal GW98-282	22584	62.77	125.54	lung normal	
lung tumor GW98-281	22583	0.31	0.62	lung tumor	-202.48
breast normal GW00-392	28750	20.59	20.59	breast normal	
breast tumor GW00-391	28746	13.93	27.86	breast tumor	1.35
breast normal GW00-413	28798	6.64	6.64	breast normal	
breast tumor GW00-412	28797	21.99	43.98	breast tumor	6.62
breast normal GW00-235:238	27592-95	4.32	4.32	breast normal	
breast tumor GW00-231:234	27588-91	31.59	31.59	breast tumor	7.31
breast normal GW98-621	23656	24.05	48.10	breast normal	
breast tumor GW98-620	23655	57.33	114.66	breast tumor	2.38
brain normal BB99-542	25507	34.49	68.98	brain normal	
brain normal BB99-406	25509	15.34	30.68	brain normal	
brain normal BB99-904	25546	12.44	24.88	brain normal	
brain stage 5 ALZ BB99-874	25502	22.56	45.12	brain stage 5 ALZ	1.09
brain stage 5 ALZ BB99-887	25503	39.16	78.32	brain stage 5 ALZ	1.89
brain stage 5 ALZ BB99-862	25504	7.79	15.58	brain stage 5 ALZ	-2.66
brain stage 5 ALZ BB99-927	25542	17.31	34.62	brain stage 5 ALZ	-1.20
CT lung KC	normal	0.54	1.08	CT lung	
lung 26 KC	normal	6.44	6.44	lung 26	
lung 27 KC	normal	2.29	2.29	lung 27	
lung 24 KC	COPD	2.85	2.85	lung 24	1.12

lung 28 KC	COPD	2.33	2.33	lung 28	-1.09
lung 23 KC	COPD	1.04	1.04	lung 23	-2.44
lung 25 KC	normal	0.33	0.33	lung 25	
asthmatic lung ODO3112	29321	3.37	3.37	asthmatic lung	1.33
asthmatic lung ODO3433	29323	2.7	5.40	asthmatic lung	2.13
asthmatic lung ODO3397	29322	5.75	11.50	asthmatic lung	4.54
asthmatic lung ODO4928	29325	11.16	22.32	asthmatic lung	8.80
endo cells KC	control	26.26	26.26	endo cells	
endo VEGF KC		50.21	50.21	endo VEGF	1.91
endo bFGF KC		11.98	11.98	endo bFGF	-2.19
heart Clontech	normal	3.65	7.30	heart	
heart (T-1) ischemic	29417	37.58	75.16	heart T-1	10.30
heart (T-14) non-obstructive DCM	29422	7.85	15.70	heart T-14	2.15
heart (T-3399) DCM	29426	25.01	50.02	heart T-3399	6.85
adenoid GW99-269	26162	6.35	12.70	adenoid	
tonsil GW98-280	22582	29.12	58.24	tonsil	
T cells PC00314	28453	28.13	56.26	T cells	
PBMNC KC		0.68	0.68	PBMNC	
monocyte KC		0.48	0.96	monocyte	
B cells PC00665	28455	68.51	137.02	B cells	
dendritic cells 28441		59	118.00	dendritic cells	
neutrophils	28440	0.5	0.50	neutrophils	
eosinophils	28446	0	0.00	eosinophils	
BM unstim KC		3.41	3.41	BM unstim	
BM stim KC		0.37	0.37	BM stim	-9.22
osteo dif KC		0	0.00	osteo dif	0.00
osteo undif KC		0	0.00	osteo undif	
chondrocytes		0.51	1.28	chondrocytes	
OA Synovium IP12/01	29462	9.81	9.81	OA Synovium	
OA Synovium NP10/01	29461	0.85	1.70	OA Synovium	
OA Synovium NP57/00	28464	30.2	60.40	OA Synovium	
RA Synovium NP03/01	28466	8.15	16.30	RA Synovium	
RA Synovium NP71/00	28467	34.68	69.36	RA Synovium	
RA Synovium NP45/00	28475	49.69	99.38	RA Synovium	
OA bone (biobank)	29217	0.63	0.63	OA bone (biobank)	
OA bone Sample 1	J. Emory	23.54	47.08	OA bone	
OA bone Sample 2	J. Emory	37.19	74.38	OA bone	
Cartilage (pool)	Normal	20.02	40.04	Cartilage (pool)	
Cartilage (pool)	OA	6.66	13.32	Cartilage (pool)	-3.01
PBL uninfected	28441	21.95	43.90	PBL uninfected	
PBL HIV IIIB	28442	7	14.00	PBL HIV IIIB	-3.14
MRC5 uninfected (100%)	29158	0	0.00	MRC5 uninfected (100%)	
MRC5 HSV strain F	29178	501.82	1003.64	MRC5 HSV strain F	1003.64
W12 cells	29179	3.76	7.52	W12 cells	

Keratinocytes	29180	0.28	0.56	Keratinocytes	
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Gene Name sbg514112RNase

Disease tissues	Fold Change in Disease Population Relative to Normal
colon tumor	15.51
colon tumor	28.87
colon tumor	5.57
colon tumor	42.47
lung tumor	5.02
lung tumor	-112.58
lung tumor	14.97
lung tumor	-202.48
breast tumor	1.35
breast tumor	6.62
breast tumor	7.31
breast tumor	2.38
brain stage 5 ALZ	1.09
brain stage 5 ALZ	1.89
brain stage 5 ALZ	-2.66
brain stage 5 ALZ	-1.20
lung 24	1.12
lung 28	-1.09
lung 23	-2.44
asthmatic lung	1.33
asthmatic lung	2.13
asthmatic lung	4.54
asthmatic lung	8.80
endo VEGF	1.91
endo bFGF	-2.19
heart T-1	10.30
heart T-14	2.15
heart T-3399	6.85
BM stim	-9.22
osteo undif	0.00
Cartilage (pool)	-3.01
PBL HIV IIIB	-3.14
MRC5 HSV strain F	1003.64

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Gene Name sbg962274FGF-BP

Expressed in brain with highest expression in fetal tissues. Significant expression in hypothalamus and thyroid suggests claims in thyroid disease and and metabolic disease claims related to diabetes, impaired glucose tolerance, metabolic syndrome, and obesity. Upregulated expression in all three heart diseases suggests involvement in non-obstructive DCM, DCM, and ischemic heart disease. Overexpression in one of four breast tumors suggests claim for breast cancer (caveat: undetectable expression in normal adjacent may lead to exaggerated fold overexpression). Immune cell

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expression in T and B cells, dendritic cells, chondrocytes and stimulated bone marrow consistent with expression in RA and OA synovium, OA bone, and cartilage and suggests involvement in OA and RA diseases.

Sample sbg962274FGF-BP	Mean GOI copies (sample 1)	Mean GOI copies (sample 2)	Average GOI Copies	18S rRNA (ng)	50 ng/18S rRNA (ng)	copies of mRNA detected/ 50 ng total RNA
Subcutaneous Adipocytes Zenbio	0	0	0.00	3.06	16.34	0.00
Subcutaneous Adipose Zenbio	0	0	0.00	0.96	52.36	0.00
Adrenal Gland Clontech	0	0	0.00	0.61	81.97	0.00
Whole Brain Clontech	455.56	624.29	539.93	7.24	6.91	3728.76
Fetal Brain Clontech	164.47	320.73	242.60	0.48	103.95	25218.30
Cerebellum Clontech	99.48	123.78	111.63	2.17	23.04	2572.12
Cervix	63.34	61.46	62.40	2.42	20.66	1289.26
Colon	110.4	0	55.20	2.71	18.45	1018.45
Endometrium	0	0	0.00	0.73	68.21	0.00
Esophagus	0	0	0.00	1.37	36.50	0.00
Heart Clontech	0	0	0.00	1.32	37.88	0.00
Hypothalamus	0	58.72	29.36	0.32	155.28	4559.01
Ileum	69.65	0	34.83	2.58	19.38	674.90
Jejunum	59.87	0	29.94	6.60	7.58	226.78
Kidney	0	0	0.00	2.12	23.58	0.00
Liver	0	0	0.00	1.50	33.33	0.00
Fetal Liver Clontech	562.37	739.81	651.09	10.40	4.81	3130.24
Lung	0	78.59	39.30	2.57	19.46	764.49
Mammary Gland Clontech	237.04	320.2	278.62	13.00	3.85	1071.62
Myometrium	91.84	179.02	135.43	2.34	21.37	2893.80
Omentum	159.45	158.28	158.87	3.94	12.69	2016.05
Ovary	70.3	0	35.15	4.34	11.52	404.95
Pancreas	0	0	0.00	0.81	61.80	0.00
Head of Pancreas	0	0	0.00	1.57	31.85	0.00
Parotid Gland	230.22	319.65	274.94	5.48	9.12	2508.53
Placenta Clontech	103.93	101.53	102.73	5.26	9.51	976.52
Prostate	88.39	90.06	89.23	3.00	16.67	1487.08
Rectum	0	70.56	35.28	1.23	40.65	1434.15
Salivary Gland Clontech	218.67	151.81	185.24	7.31	6.84	1267.03
Skeletal Muscle Clontech	0	0	0.00	1.26	39.68	0.00
Skin	0	0	0.00	1.21	41.32	0.00
Small Intestine Clontech	0	0	0.00	0.98	51.07	0.00
Spleen	0	0	0.00	4.92	10.16	0.00
Stomach	0	0	0.00	2.73	18.32	0.00
Testis Clontech	0	0	0.00	0.57	87.87	0.00

Thymus Clontech	493.89	500.57	497.23	9.89	5.06	2513.80
Thyroid	237.11	201.59	219.35	2.77	18.05	3959.39
Trachea Clontech	124.53	114.49	119.51	9.71	5.15	615.40
Urinary Bladder	72.14	92.61	82.38	5.47	9.14	752.97
Uterus	0	115.86	57.93	5.34	9.36	542.42

Sample sbg962274FGF-BP	Reg number (GSK identifier)	Mean GOI copies	copies of mRNA detected/50 ng total RNA	Sample	Fold Change in Disease Population
colon normal GW98-167	21941	532.51	1065.02	colon normal	
colon tumor GW98-166	21940	597.14	1194.28	colon tumor	1.12
colon normal GW98-178	22080	108.63	217.26	colon normal	
colon tumor GW98-177	22060	433.99	867.98	colon tumor	4.00
colon normal GW98-561	23514	346.17	692.34	colon normal	
colon tumor GW98-560	23513	485.16	970.32	colon tumor	1.40
colon normal GW98-894	24691	318.86	637.72	colon normal	
colon tumor GW98-893	24690	711.68	1423.36	colon tumor	2.23
lung normal GW98-3	20742	447.66	895.32	lung normal	
lung tumor GW98-2	20741	376.57	753.14	lung tumor	-1.19
lung normal GW97-179	20677	1066.58	2133.16	lung normal	
lung tumor GW97-178	20676	426.93	853.86	lung tumor	-2.50
lung normal GW98-165	21922	947.52	1895.04	lung normal	
lung tumor GW98-164	21921	539.95	1079.90	lung tumor	-1.75
lung normal GW98-282	22584	358.48	716.96	lung normal	
lung tumor GW98-281	22583	494.08	988.16	lung tumor	1.38
breast normal GW00-392	28750	293.27	293.27	breast normal	
breast tumor GW00-391	28746	556.69	1113.38	breast tumor	3.80
breast normal GW00-413	28798	0	0.00	breast normal	
breast tumor GW00-412	28797	493.54	987.08	breast tumor	987.08
breast normal GW00-235:238	27592-95	0	0.00	breast normal	
breast tumor GW00-231:234	27588-91	0	0.00	breast tumor	0.00
breast normal GW98-621	23656	646.3	1292.60	breast normal	
breast tumor GW98-620	23655	519.35	1038.70	breast tumor	-1.24
brain normal BB99-542	25507	2558.99	5117.98	brain normal	
brain normal BB99-406	25509	1640.03	3280.06	brain normal	
brain normal BB99-904	25546	1519.52	3039.04	brain normal	
brain stage 5 ALZ BB99-874	25502	696.08	1392.16	brain stage 5 ALZ	-2.74
brain stage 5 ALZ BB99-887	25503	1796.62	3593.24	brain stage 5 ALZ	-1.06
brain stage 5 ALZ BB99-862	25504	1654.65	3309.30	brain stage 5 ALZ	-1.15
brain stage 5 ALZ BB99-927	25542	651.31	1302.62	brain stage 5 ALZ	-2.93
CT lung KC	normal	280.34	560.68	CT lung	
lung 26 KC	normal	0	0.00	lung 26	

lung 27 KC	normal	0	0.00	lung 27	
lung 24 KC	COPD	0	0.00	lung 24	-156.37
lung 28 KC	COPD	0	0.00	lung 28	-156.37
lung 23 KC	COPD	131.98	131.98	lung 23	-1.18
lung 25 KC	normal	64.81	64.81	lung 25	
asthmatic lung ODO3112	29321	35.77	35.77	asthmatic lung	-4.37
asthmatic lung ODO3433	29323	323.27	646.54	asthmatic lung	4.13
asthmatic lung ODO3397	29322	614.8	1229.60	asthmatic lung	7.86
asthmatic lung ODO4928	29325	337.93	675.86	asthmatic lung	4.32
endo cells KC	control	0	0.00	endo cells	
endo VEGF KC		0	0.00	endo VEGF	0.00
endo bFGF KC		0	0.00	endo bFGF	0.00
heart Clontech	normal	103.42	206.84	heart	
heart (T-1) ischemic	29417	326.36	652.72	heart T-1	3.16
heart (T-14) non-obstructive DCM	29422	799.11	1598.22	heart T-14	7.73
heart (T-3399) DCM	29426	885.7	1771.40	heart T-3399	8.56
adenoid GW99-269	26162	1005.58	2011.16	adenoid	
tonsil GW98-280	22582	979.88	1959.76	tonsil	
T cells PC00314	28453	1516.14	3032.28	T cells	
PBMNC KC		179.43	179.43	PBMNC	
monocyte KC		338.32	676.64	monocyte	
B cells PC00665	28455	550.97	1101.94	B cells	
dendritic cells 28441		619.32	1238.64	dendritic cells	
neutrophils	28440	104.25	104.25	neutrophils	
eosinophils	28446	63.57	127.14	eosinophils	
BM unstim KC		0	0.00	BM unstim	
BM stim KC		981.8	981.80	BM stim	981.80
osteo dif KC		275.28	275.28	osteo dif	1.47
osteo undif KC		187.39	187.39	osteo undif	
chondrocytes		1165.74	2914.35	chondrocytes	
OA Synovium IP12/01	29462	277.86	277.86	OA Synovium	
OA Synovium NP10/01	29461	523.26	1046.52	OA Synovium	
OA Synovium NP57/00	28464	445.78	891.56	OA Synovium	
RA Synovium NP03/01	28466	604.66	1209.32	RA Synovium	
RA Synovium NP71/00	28467	567.56	1135.12	RA Synovium	
RA Synovium NP45/00	28475	466.75	933.50	RA Synovium	
OA bone (biobank)	29217	72.67	72.67	OA bone (biobank)	
OA bone Sample 1	J. Emory	321.31	642.62	OA bone	
OA bone Sample 2	J. Emory	817.43	1634.86	OA bone	
Cartilage (pool)	Normal	1280.04	2560.08	Cartilage (pool)	
Cartilage (pool)	OA	876.26	1752.52	Cartilage (pool)	-1.46
PBL uninfected	28441	1589.59	3179.18	PBL uninfected	
PBL HIV IIIB	28442	1286.53	2573.06	PBL HIV IIIB	-1.24
MRC5 uninfected (100%)	29158	578.8	1157.60	MRC5 uninfected (100%)	

MRC5 HSV strain F	29178	184.2	368.40	MRC5 HSV strain F	-3.14
W12 cells	29179	383.66	767.32	W12 cells	
Keratinocytes	29180	326.35	652.70	Keratinocytes	

Gene Name sbg962274FGF-BP

Disease tissues	Fold Change in Disease Population Relative to Normal
colon tumor	1.12
colon tumor	4.00
colon tumor	1.40
colon tumor	2.23
lung tumor	-1.19
lung tumor	-2.50
lung tumor	-1.75
lung tumor	1.38
breast tumor	3.80
breast tumor	987.08
breast tumor	0.00
breast tumor	-1.24
brain stage 5 ALZ	-2.74
brain stage 5 ALZ	-1.06
brain stage 5 ALZ	-1.15
brain stage 5 ALZ	-2.93
lung 24	-156.37
lung 28	-156.37
lung 23	-1.18
asthmatic lung	-4.37
asthmatic lung	4.13
asthmatic lung	7.86
asthmatic lung	4.32
endo VEGF	0.00
endo bFGF	0.00
heart T-1	3.16
heart T-14	7.73
heart T-3399	8.56
BM stim	981.80
osteo dif	1.47
Cartilage (pool)	-1.46
PBL HIV IIIB	-1.24
MRC5 HSV strain F	-3.14

Table V. Additional diseases based on mRNA expression in specific tissues

Tissue Expression	Additional Diseases
Brain	Neurological and psychiatric diseases, including Alzheimers, parasupranuclear palsey, Huntington's disease, myotonic dystrophy, anorexia, depression, schizophrenia, headache, amnesias, anxiety disorders, sleep disorders, multiple sclerosis
Heart	Cardiovascular diseases, including congestive heart failure, dilated cardiomyopathy, cardiac arrhythmias, Hodgson's Disease, myocardial infarction, cardiac arrhythmias
Lung	Respiratory diseases, including asthma, Chronic Obstructive Pulmonary Disease, cystic fibrosis, acute bronchitis, adult respiratory distress syndrome
Liver	Dyslipidemia, hypercholesterolemia, hypertriglyceridemia, cirrhosis, hepatic encephalopathy, fatty hepatocirrhosis, viral and nonviral hepatitis, Type II Diabetes Mellitis, impaired glucose tolerance
Kidney	Renal diseases, including acute and chronic renal failure, acute tubular necrosis, cystinuria, Fanconi's Syndrome, glomerulonephritis, renal cell carcinoma, renovascular hypertension
Skeletal muscle	Eulenburg's Disease, hypoglycemia, obesity, tendinitis, periodic paralyses, malignant hyperthermia, paramyotonia congenita, myotonia congenita
Intestine	Gastrointestinal diseases, including Myotonia congenita, Ileus, Intestinal Obstruction, Tropical Sprue, Pseudomembranous Enterocolitis
Spleen/lymph	Lymphangiectasia, hypersplenism, angiomas, ankylosing spondylitis, Hodgkin's Disease, macroglobulinemia, malignant lymphomas, rheumatoid arthritis
Placenta	Choriocarcinoma, hydatidiform mole, placenta previa
Testis	Testicular cancer, male reproductive diseases, including low testosterone and male infertility
Pancreas	Diabetic ketoacidosis, Type 1 & 2 diabetes, obesity, impaired glucose tolerance

What is claimed is:

1. An isolated polypeptide selected from the group consisting of:
 - 5 (a) an isolated polypeptide encoded by a polynucleotide comprising a sequence set forth in Table I;
 - (b) an isolated polypeptide comprising a polypeptide sequence set forth in Table I; and
 - (c) a polypeptide sequence of a gene set forth in Table I.
- 10 2. An isolated polynucleotide selected from the group consisting of:
 - (a) an isolated polynucleotide comprising a polynucleotide sequence set forth in Table I;
 - (b) an isolated polynucleotide of a gene set forth in Table I;
 - (c) an isolated polynucleotide comprising a polynucleotide sequence encoding a polypeptide set forth in Table I;
 - 15 (d) an isolated polynucleotide encoding a polypeptide set forth in Table I;
 - (e) a polynucleotide which is an RNA equivalent of the polynucleotide of (a) to (d); or a polynucleotide sequence complementary to said isolated polynucleotide.
- 20 3. An expression vector comprising a polynucleotide capable of producing a polypeptide of claim 1 when said expression vector is present in a compatible host cell.
4. A process for producing a recombinant host cell which comprises the step of introducing an expression vector comprising a polynucleotide capable of producing a polypeptide of claim 1 into a cell such that the host cell, under appropriate culture conditions, produces said
25 polypeptide.
5. A recombinant host cell produced by the process of claim 4.
6. A membrane of a recombinant host cell of claim 5 expressing said polypeptide.
- 30 7. A process for producing a polypeptide which comprises culturing a host cell of claim 5 under conditions sufficient for the production of said polypeptide and recovering said polypeptide from the culture.

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SMITHKLINE BEECHAM p.l.c.
GLAXO GROUP LIMITED

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<213> Homo sapiens

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<213> Homo sapiens

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<212> DNA

<213> Homo sapiens

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<211> 309

<212> DNA

<213> Homo sapiens

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<212> DNA

<213> Homo sapiens

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<211> 2199

<212> DNA

<213> Homo sapiens

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<212> DNA

<213> Homo sapiens

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<212> DNA

<213> Homo sapiens

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<211> 948

<212> DNA

<213> Homo sapiens

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225					230					235					240
Val	Glu	Ala	Glu	Val	Ala	Ala	Gly	Ala	Arg	Phe	Thr	Ala	Pro	Gln	Val
				245					250					255	
Glu	Leu	Val	Gly	Pro	Arg	Leu	Pro	Gly	Ala	Glu	Val	Gly	Val	Pro	Gln
			260					265					270		
Val	Ser	Ala	Pro	Lys	Ala	Ala	Pro	Ser	Ala	Glu	Ala	Ala	Gly	Gly	Phe
	275						280					285			
Ala	Leu	His	Leu	Pro	Thr	Leu	Gly	Leu	Gly	Ala	Pro	Ala	Pro	Pro	Ala
	290					295					300				
Val	Glu	Ala	Pro	Ala	Val	Gly	Ile	Gln	Val	Pro	Gln	Val	Glu	Leu	Pro
305					310					315					320
Ala	Leu	Pro	Ser	Leu	Pro	Thr	Leu	Pro	Thr	Leu	Pro	Cys	Leu	Glu	Thr
				325					330					335	
Arg	Glu	Gly	Ala	Val	Ser	Val	Val	Val	Pro	Thr	Leu	Asp	Val	Ala	Ala
			340					345					350		
Pro	Thr	Val	Gly	Val	Asp	Leu	Ala	Leu	Pro	Gly	Ala	Glu	Val	Glu	Ala
		355					360					365			
Arg	Gly	Glu	Ala	Pro	Glu	Val	Ala	Leu	Lys	Met	Pro	Arg	Leu	Ser	Phe
	370					375					380				
Pro	Arg	Phe	Gly	Ala	Arg	Ala	Lys	Glu	Val	Ala	Glu	Ala	Lys	Val	Ala
385					390					395					400
Lys	Val	Ser	Pro	Glu	Ala	Arg	Val	Lys	Gly	Pro	Arg	Leu	Arg	Met	Pro
				405					410					415	
Thr	Phe	Gly	Leu	Ser	Leu	Leu	Glu	Pro	Arg	Pro	Ala	Ala	Pro	Glu	Val
			420					425					430		
Val	Glu	Ser	Lys	Leu	Lys	Leu	Pro	Thr	Ile	Lys	Met	Pro	Ser	Leu	Gly
	435						440					445			
Ile	Gly	Val	Ser	Gly	Pro	Glu	Val	Lys	Val	Pro	Lys	Gly	Pro	Glu	Val
	450					455					460				
Lys	Leu	Pro	Lys	Ala	Pro	Glu	Val	Lys	Leu	Pro	Lys	Val	Pro	Glu	Ala
465					470					475					480
Ala	Leu	Pro	Glu	Val	Arg	Leu	Pro	Glu	Val	Glu	Leu	Pro	Lys	Val	Ser
				485					490					495	
Glu	Met	Lys	Leu	Pro	Lys	Val	Pro	Glu	Met	Ala	Val	Pro	Glu	Val	Arg
			500					505					510		
Leu	Pro	Glu	Val	Glu	Leu	Pro	Lys	Val	Ser	Glu	Met	Lys	Leu	Pro	Lys
	515						520					525			
Val	Pro	Glu	Met	Ala	Val	Pro	Glu	Val	Arg	Leu	Pro	Glu	Val	Gln	Leu
	530					535					540				
Leu	Lys	Val	Ser	Glu	Met	Lys	Leu	Pro	Lys	Val	Pro	Glu	Met	Ala	Val

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Pro Glu Val Arg	Leu Pro Glu Val Gln	Leu Pro Lys Val Ser	Glu Met			
	565		570			575
Lys Leu Pro Glu	Val Ser Glu Val Ala	Val Pro Glu Val Arg	Leu Pro			
	580		585			590
Glu Val Gln Leu	Pro Lys Val Pro Glu	Met Lys Val Pro Glu	Met Lys			
	595		600			605
Leu Pro Lys Val	Pro Glu Met Lys Leu	Pro Glu Met Lys Leu	Pro Glu			
	610		615			620
Val Gln Leu Pro	Lys Val Pro Glu Met	Ala Val Pro Asp	Val His Leu			
	625		630			635
Pro Glu Val Gln	Leu Pro Lys Val Pro	Glu Met Lys Leu	Pro Glu			
	645		650			655
Lys Leu Pro Glu	Val Lys Leu Pro Lys	Val Pro Glu Met	Ala Val Pro			
	660		665			670
Asp Val His Leu	Pro Glu Val Gln Leu	Pro Lys Val Pro	Glu Met Lys			
	675		680			685
Leu Pro Lys Met	Pro Glu Met Ala	Val Pro Glu Val	Arg Leu Pro			
	690		695			700
Val Gln Leu Pro	Lys Val Ser Glu Met	Lys Leu Pro Lys	Val Pro Glu			
	705		710			715
Met Ala Val Pro	Asp Val His Leu Pro	Glu Val Gln Leu	Pro Lys Val			
	725		730			735
Cys Glu Met Lys	Val Pro Asp Met Lys	Leu Pro Glu Ile	Lys Leu Pro			
	740		745			750
Lys Val Pro Glu	Met Ala Val Pro Asp	Val His Leu Pro	Glu Val Gln			
	755		760			765
Leu Pro Lys Val	Ser Glu Ile Arg Leu	Pro Glu Met Gln	Val Pro Lys			
	770		775			780
Val Pro Asp Val	His Leu Pro Lys Ala	Pro Glu Val Lys	Leu Pro Arg			
	785		790			800
Ala Pro Glu Val	Gln Leu Lys Ala Thr	Lys Ala Glu Gln	Ala Glu Gly			
	805		810			815
Met Glu Phe Gly	Phe Lys Met Pro Lys	Met Thr Met Pro	Lys Leu Gly			
	820		825			830
Arg Ala Glu Ser	Pro Ser Arg Gly Lys	Pro Gly Glu Ala	Gly Ala Glu			
	835		840			845
Val Ser Gly Lys	Leu Val Thr Leu Pro	Cys Leu Gln Pro	Glu Val Asp			
	850		855			860
Gly Glu Ala His	Val Gly Val Pro Ser	Leu Thr Leu Pro	Ser Val Glu			
	865		870			875
Leu Asp Leu Pro	Gly Ala Leu Gly Leu	Gln Gly Gln Val	Pro Ala Ala			
	885		890			895
Lys Met Gly Lys	Gly Glu Arg Val Glu	Gly Pro Glu Val	Ala Ala Gly			
	900		905			910
Val Arg Glu Val	Gly Phe Arg Val Pro	Ser Val Glu Ile	Val Thr Pro			
	915		920			925
Gln Leu Pro Ala	Val Glu Ile Glu Glu	Gly Arg Leu Glu	Met Ile Glu			
	930		935			940
Thr Lys Val Lys	Pro Ser Ser Lys Phe	Ser Leu Pro Lys	Phe Gly Leu			
	945		950			955
Ser Gly Pro Lys	Val Ala Lys Ala Glu	Ala Glu Gly Ala	Gly Arg Ala			
	965		970			975
Thr Lys Leu Lys	Val Ser Lys Phe Ala	Ile Ser Leu Pro	Lys Ala Arg			
	980		985			990
Val Gly Ala Glu	Ala Glu Ala Lys Gly	Ala Gly Glu Ala	Gly Leu Leu			
	995		1000			1005
Pro Ala Leu Asp	Leu Ser Ile Pro Gln	Leu Ser Leu Asp	Ala His Leu			
	1010		1015			1020

Pro Ser Gly Lys Val Glu Val Ala Gly Ala Asp Leu Lys Phe Lys Gly
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 Pro Arg Phe Ala Leu Pro Lys Phe Gly Val Arg Gly Arg Asp Thr Glu
 1045 1050 1055
 Ala Ala Glu Leu Val Pro Gly Val Ala Glu Leu Glu Gly Lys Gly Trp
 1060 1065 1070
 Gly Trp Asp Gly Arg Val Lys Met Pro Lys Leu Lys Met Pro Ser Phe
 1075 1080 1085
 Gly Leu Ala Arg Gly Lys Glu Ala Glu Val Gln Gly Asp Arg Ala Ser
 1090 1095 1100
 Pro Gly Glu Lys Ala Glu Ser Thr Ala Val Gln Leu Lys Ile Pro Glu
 1105 1110 1115 1120
 Val Glu Leu Val Thr Leu Gly Ala Gln Glu Glu Gly Arg Ala Glu Gly
 1125 1130 1135
 Ala Val Ala Val Ser Gly Met Gln Leu Ser Gly Leu Lys Val Ser Thr
 1140 1145 1150
 Ala Gly Gln Val Val Thr Glu Gly His Asp Ala Gly Leu Arg Met Pro
 1155 1160 1165
 Pro Leu Gly Ile Ser Leu Pro Gln Val Glu Leu Thr Gly Phe Gly Glu
 1170 1175 1180
 Ala Gly Thr Pro Gly Gln Gln Ala Gln Ser Thr Val Pro Ser Ala Glu
 1185 1190 1195 1200
 Gly Thr Ala Gly Tyr Arg Val Gln Val Pro Gln Val Thr Leu Ser Leu
 1205 1210 1215
 Pro Gly Ala Gln Val Ala Gly Gly Glu Leu Leu Val Gly Glu Gly Val
 1220 1225 1230
 Phe Lys Met Pro Thr Val Thr Val Pro Gln Leu Glu Leu Asp Val Gly
 1235 1240 1245
 Leu Ser Arg Glu Ala Gln Ala Gly Glu Ala Ala Thr Gly Glu Gly Gly
 1250 1255 1260
 Leu Arg Leu Lys Leu Pro Thr Leu Gly Ala Arg Ala Arg Val Gly Gly
 1265 1270 1275 1280
 Glu Gly Ala Glu Glu Gln Pro Pro Gly Ala Glu Arg Thr Phe Cys Leu
 1285 1290 1295
 Ser Leu Pro Asp Val Glu Leu Ser Pro Ser Gly Gly Asn His Ala Glu
 1300 1305 1310
 Tyr Gln Val Ala Glu Gly Glu Gly Glu Ala Gly His Lys Leu Lys Val
 1315 1320 1325
 Arg Leu Pro Arg Phe Gly Leu Val Arg Ala Lys Glu Gly Ala Glu Glu
 1330 1335 1340
 Gly Glu Lys Ala Lys Ser Pro Lys Leu Arg Leu Pro Arg Val Gly Phe
 1345 1350 1355 1360
 Ser Gln Ser Glu Met Val Thr Gly Glu Gly Ser Pro Ser Pro Glu Glu
 1365 1370 1375
 Glu Glu Glu Glu Glu Glu Gly Ser Gly Glu Gly Ala Ser Gly Arg
 1380 1385 1390
 Arg Gly Arg Val Arg Val Arg Leu Pro Arg Val Gly Leu Ala Ala Pro
 1395 1400 1405
 Ser Lys Ala Ser Arg Gly Gln Glu Gly Asp Ala Ala Pro Lys Ser Pro
 1410 1415 1420
 Val Arg Glu Lys Ser Pro Lys Phe Arg Phe Pro Arg Val Ser Leu Ser
 1425 1430 1435 1440
 Pro Lys Ala Arg Ser Gly Ser Gly Asp Gln Glu Glu Gly Gly Leu Arg
 1445 1450 1455
 Val Arg Leu Pro Ser Val Gly Phe Ser Glu Thr Gly Ala Pro Gly Pro
 1460 1465 1470
 Ala Arg Met Glu Gly Ala Gln Ala Ala Ala Val
 1475 1480

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 <211> 1461
 <212> PRT
 <213> Homo sapiens

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 Asn Val Ala Gly Gly Gly Lys Glu Gly Ile Phe Val Arg Glu Leu Arg
 35 40 45
 Glu Asp Ser Pro Ala Ala Arg Ser Leu Ser Leu Gln Glu Gly Asp Gln
 50 55 60
 Leu Leu Ser Ala Arg Val Phe Phe Glu Asn Phe Lys Tyr Glu Asp Ala
 65 70 75 80
 Leu Arg Leu Leu Gln Cys Ala Glu Pro Tyr Lys Val Ser Phe Cys Leu
 85 90 95
 Lys Arg Thr Val Pro Thr Gly Asp Leu Ala Leu Arg Pro Gly Thr Val
 100 105 110
 Ser Gly Tyr Glu Ile Lys Gly Pro Arg Ala Lys Val Ala Lys Leu Asn
 115 120 125
 Ile Gln Ser Leu Ser Pro Val Lys Lys Lys Lys Met Val Pro Gly Ala
 130 135 140
 Leu Gly Val Pro Ala Asp Leu Ala Pro Val Asp Val Glu Phe Ser Phe
 145 150 155 160
 Pro Lys Phe Ser Arg Leu Arg Arg Gly Leu Lys Ala Glu Ala Val Lys
 165 170 175
 Gly Pro Val Pro Ala Ala Pro Ala Arg Arg Arg Leu Gln Leu Pro Arg
 180 185 190
 Leu Arg Val Arg Glu Val Ala Glu Ala Gln Ala Ala Arg Leu Ala
 195 200 205
 Ala Ala Ala Pro Pro Pro Arg Lys Ala Lys Val Glu Ala Glu Val Ala
 210 215 220
 Ala Gly Ala Arg Phe Thr Ala Pro Gln Val Glu Leu Val Gly Pro Arg
 225 230 235 240
 Leu Pro Gly Ala Glu Val Gly Val Pro Gln Val Ser Ala Pro Lys Ala
 245 250 255
 Ala Pro Ser Ala Glu Ala Ala Gly Gly Phe Ala Leu His Leu Pro Thr
 260 265 270
 Leu Gly Leu Gly Ala Pro Ala Pro Pro Ala Val Glu Ala Pro Ala Val
 275 280 285
 Gly Ile Gln Val Pro Gln Val Glu Leu Pro Ala Leu Pro Ser Leu Pro
 290 295 300
 Thr Leu Pro Thr Leu Pro Cys Leu Glu Thr Arg Glu Gly Ala Val Ser
 305 310 315 320
 Val Val Val Pro Thr Leu Asp Val Ala Ala Pro Thr Val Gly Val Asp
 325 330 335
 Leu Ala Leu Pro Gly Ala Glu Val Glu Ala Arg Gly Glu Ala Pro Glu
 340 345 350
 Val Ala Leu Lys Met Pro Arg Leu Ser Phe Pro Arg Phe Gly Ala Arg
 355 360 365
 Ala Lys Glu Val Ala Glu Ala Lys Val Ala Lys Val Ser Pro Glu Ala
 370 375 380
 Arg Val Lys Gly Pro Arg Leu Arg Met Pro Thr Phe Gly Leu Ser Leu
 385 390 395 400
 Leu Glu Pro Arg Pro Ala Ala Pro Glu Val Val Glu Ser Lys Leu Lys
 405 410 415
 Leu Pro Thr Ile Lys Met Pro Ser Leu Gly Ile Gly Val Ser Gly Pro

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Arg Val Pro Ser Val Glu Ile Val Thr Pro Gln Leu Pro Ala Val Glu
 900 905 910
 Ile Glu Glu Gly Arg Leu Glu Met Ile Glu Thr Lys Val Lys Pro Ser
 915 920 925
 Ser Lys Phe Ser Leu Pro Lys Phe Gly Leu Ser Gly Pro Lys Val Ala
 930 935 940
 Lys Ala Glu Ala Glu Gly Ala Gly Arg Ala Thr Lys Leu Lys Val Ser
 945 950 955 960
 Lys Phe Ala Ile Ser Leu Pro Lys Ala Arg Val Gly Ala Glu Ala Glu
 965 970 975
 Ala Lys Gly Ala Gly Glu Ala Gly Leu Leu Pro Ala Leu Asp Leu Ser
 980 985 990
 Ile Pro Gln Leu Ser Leu Asp Ala His Leu Pro Ser Gly Lys Val Glu
 995 1000 1005
 Val Ala Gly Ala Asp Leu Lys Phe Lys Gly Pro Arg Phe Ala Leu Pro
 1010 1015 1020
 Lys Phe Gly Val Arg Gly Arg Asp Thr Glu Ala Ala Glu Leu Val Pro
 1025 1030 1035 1040
 Gly Val Ala Glu Leu Glu Gly Lys Gly Trp Gly Trp Asp Gly Arg Val
 1045 1050 1055
 Lys Met Pro Lys Leu Lys Met Pro Ser Phe Gly Leu Ala Arg Gly Lys
 1060 1065 1070
 Glu Ala Glu Val Gln Gly Asp Arg Ala Ser Pro Gly Glu Lys Ala Glu
 1075 1080 1085
 Ser Thr Ala Val Gln Leu Lys Ile Pro Glu Val Glu Leu Val Thr Leu
 1090 1095 1100
 Gly Ala Gln Glu Glu Gly Arg Ala Glu Gly Ala Val Ala Val Ser Gly
 1105 1110 1115 1120
 Met Gln Leu Ser Gly Leu Lys Val Ser Thr Ala Gly Gln Val Val Thr
 1125 1130 1135
 Glu Gly His Asp Ala Gly Leu Arg Met Pro Pro Leu Gly Ile Ser Leu
 1140 1145 1150
 Pro Gln Val Glu Leu Thr Gly Phe Gly Glu Ala Gly Thr Pro Gly Gln
 1155 1160 1165
 Gln Ala Gln Ser Thr Val Pro Ser Ala Glu Gly Thr Ala Gly Tyr Arg
 1170 1175 1180
 Val Gln Val Pro Gln Val Thr Leu Ser Leu Pro Gly Ala Gln Val Ala
 1185 1190 1195 1200
 Gly Gly Glu Leu Leu Val Gly Glu Gly Val Phe Lys Met Pro Thr Val
 1205 1210 1215
 Thr Val Pro Gln Leu Glu Leu Asp Val Gly Leu Ser Arg Glu Ala Gln
 1220 1225 1230
 Ala Gly Glu Ala Ala Thr Gly Glu Gly Gly Leu Arg Leu Lys Leu Pro
 1235 1240 1245
 Thr Leu Gly Ala Arg Ala Arg Val Gly Gly Glu Gly Ala Glu Glu Gln
 1250 1255 1260
 Pro Pro Gly Ala Glu Arg Thr Phe Cys Leu Ser Leu Pro Asp Val Glu
 1265 1270 1275 1280
 Leu Ser Pro Ser Gly Gly Asn His Ala Glu Tyr Gln Val Ala Glu Gly
 1285 1290 1295
 Glu Gly Glu Ala Gly His Lys Leu Lys Val Arg Leu Pro Arg Phe Gly
 1300 1305 1310
 Leu Val Arg Ala Lys Glu Gly Ala Glu Glu Gly Glu Lys Ala Lys Ser
 1315 1320 1325
 Pro Lys Leu Arg Leu Pro Arg Val Gly Phe Ser Gln Ser Glu Met Val
 1330 1335 1340
 Thr Gly Glu Gly Ser Pro Ser Pro Glu Glu Glu Glu Glu Glu Glu
 1345 1350 1355 1360
 Glu Gly Ser Gly Glu Gly Ala Ser Gly Arg Gly Arg Val Arg Val

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<210> 31
<211> 491
<212> PRT
<213> Homo sapiens
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<400> 31															
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			20					25					30		
Val	Thr	Arg	Ala	Glu	Thr	Thr	Pro	Gly	Ala	Pro	Arg	Ala	Leu	Ser	Thr
		35					40					45			
Leu	Gly	Ser	Pro	Ser	Leu	Phe	Thr	Thr	Pro	Gly	Val	Pro	Ser	Ala	Leu
	50					55					60				
Thr	Thr	Pro	Gly	Leu	Thr	Thr	Pro	Gly	Thr	Pro	Lys	Thr	Leu	Asp	Leu
65					70					75					80
Arg	Gly	Arg	Ala	Gln	Ala	Leu	Met	Arg	Ser	Phe	Pro	Leu	Val	Asp	Gly
				85					90					95	
His	Asn	Asp	Leu	Pro	Gln	Val	Leu	Arg	Gln	Arg	Tyr	Lys	Asn	Val	Leu
			100					105					110		
Gln	Asp	Val	Asn	Leu	Arg	Asn	Phe	Ser	His	Gly	Gln	Thr	Ser	Leu	Asp
		115					120					125			
Arg	Leu	Arg	Asp	Gly	Leu	Val	Gly	Ala	Gln	Val	Pro	Gln	Gly	His	Thr
		130				135					140				
Gly	Cys	His	Ser	Met	Ala	Ala	Gly	Gly	Cys	Trp	Gly	His	Arg	Asn	Leu
145				150						155					160
Gly	Ser	Gln	Asp	Val	Thr	Leu	Glu	Val	Leu	Phe	Leu	Gly	Ser	Asn	His
			165						170					175	
Leu	Thr	Leu	Tyr	Leu	Leu	Leu	Gly	Leu	Asn	Ser	Ser	Gln	Lys	Leu	Ala
			180					185					190		
Cys	Leu	Ile	Gly	Val	Glu	Gly	Gly	His	Ser	Leu	Asp	Ser	Ser	Leu	Ser
		195					200					205			
Val	Leu	Arg	Ser	Phe	Tyr	Val	Leu	Gly	Val	Arg	Tyr	Leu	Thr	Leu	Thr
	210					215					220				
Phe	Thr	Cys	Ser	Thr	Pro	Trp	Ala	Glu	Ser	Ser	Thr	Lys	Phe	Arg	His
225					230					235					240
His	Met	Tyr	Thr	Asn	Val	Ser	Gly	Leu	Thr	Ser	Phe	Gly	Glu	Lys	Val
				245					250					255	
Val	Glu	Glu	Leu	Asn	Arg	Leu	Gly	Met	Met	Ile	Asp	Leu	Ser	Tyr	Ala
			260					265				270			
Ser	Asp	Thr	Leu	Ile	Arg	Arg	Val	Leu	Glu	Val	Ser	Gln	Ala	Pro	Val
		275					280					285			
Ile	Phe	Ser	His	Ser	Ala	Ala	Arg	Ala	Val	Cys	Asp	Asn	Leu	Leu	Asn
	290					295					300				
Val	Pro	Asp	Asp	Ile	Leu	Gln	Leu	Leu	Lys	Lys	Asn	Gly	Gly	Ile	Val

305					310					315				320
Met	Val	Thr	Leu	Ser	Met	Gly	Val	Leu	Gln	Cys	Asn	Leu	Leu	Ala
				325					330					335
Val	Ser	Thr	Val	Ala	Asp	Asp	Ser	Asn	Arg	Cys	Ser	Val	Pro	Val
			340					345					350	
Gly	Ser	Glu	Phe	Ile	Gly	Ile	Gly	Gly	Asn	Tyr	Asp	Gly	Thr	Gly
		355					360					365		
Phe	Pro	Gln	Gly	Leu	Glu	Asp	Val	Ser	Thr	Tyr	Pro	Val	Leu	Ile
		370				375					380			
Glu	Leu	Leu	Ser	Arg	Ser	Trp	Ser	Glu	Glu	Glu	Leu	Gln	Gly	Val
385					390					395				400
Arg	Gly	Asn	Leu	Leu	Arg	Val	Phe	Arg	Gln	Val	Glu	Lys	Val	Arg
			405						410					415
Glu	Ser	Arg	Ala	Gln	Ser	Pro	Val	Glu	Ala	Glu	Phe	Pro	Tyr	Gly
			420					425					430	
Leu	Ser	Thr	Ser	Cys	His	Ser	His	Leu	Val	Pro	Gln	Asn	Gly	His
		435					440					445		
Ala	Thr	His	Leu	Glu	Val	Thr	Lys	Gln	Pro	Thr	Asn	Arg	Val	Pro
		450				455					460			
Arg	Ser	Ser	Asn	Ala	Ser	Pro	Tyr	Leu	Val	Pro	Gly	Leu	Val	Ala
465					470					475				480
Ala	Thr	Ile	Pro	Thr	Phe	Thr	Gln	Trp	Leu	Cys				
				485					490					

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<211> 489

<212> PRT

<213> Homo sapiens

<400> 32

Ala	Met	Gln	Pro	Thr	Gly	Arg	Glu	Gly	Ser	Arg	Ala	Leu	Ser	Arg	Arg
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Tyr	Leu	Arg	Arg	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Arg	Gln
			20					25					30		
Pro	Val	Thr	Arg	Ala	Glu	Thr	Thr	Pro	Gly	Ala	Pro	Arg	Ala	Leu	Ser
		35				40					45				
Thr	Leu	Gly	Ser	Pro	Ser	Leu	Phe	Thr	Thr	Pro	Gly	Val	Pro	Ser	Ala
	50					55				60					
Leu	Thr	Thr	Pro	Gly	Leu	Thr	Thr	Pro	Gly	Thr	Pro	Lys	Thr	Leu	Asp
65					70				75					80	
Leu	Arg	Gly	Arg	Ala	Gln	Ala	Leu	Met	Arg	Ser	Phe	Pro	Leu	Val	Asp
			85					90						95	
Gly	His	Asn	Asp	Leu	Pro	Gln	Val	Leu	Arg	Gln	Arg	Tyr	Lys	Asn	Val
		100					105					110			
Leu	Gln	Asp	Val	Asn	Leu	Arg	Asn	Phe	Ser	His	Gly	Gln	Thr	Ser	Leu
		115				120						125			
Asp	Arg	Leu	Arg	Asp	Gly	Leu	Val	Gly	Ala	Gln	Phe	Trp	Ser	Ala	Ser
	130					135					140				
Val	Ser	Cys	Gln	Ser	Gln	Asp	Gln	Thr	Ala	Val	Arg	Leu	Ala	Leu	Glu
145					150					155					160
Gln	Ile	Asp	Leu	Ile	His	Arg	Met	Cys	Ala	Ser	Tyr	Ser	Glu	Leu	Glu
			165					170						175	
Leu	Val	Thr	Ser	Ala	Glu	Gly	Leu	Asn	Ser	Ser	Gln	Lys	Leu	Ala	Cys
		180					185					190			
Leu	Ile	Gly	Val	Glu	Gly	Gly	His	Ser	Leu	Asp	Ser	Ser	Leu	Ser	Val
	195					200					205				
Leu	Arg	Ser	Phe	Tyr	Val	Leu	Gly	Val	Arg	Tyr	Leu	Thr	Leu	Thr	Phe
	210					215				220					
Thr	Cys	Ser	Thr	Pro	Trp	Ala	Glu	Ser	Ser	Thr	Lys	Phe	Arg	His	His

225		230		235		240									
Met	Tyr	Thr	Asn	Val	Ser	Gly	Leu	Thr	Ser	Phe	Gly	Glu	Lys	Val	Val
				245					250					255	
Glu	Glu	Leu	Asn	Arg	Leu	Gly	Met	Met	Ile	Asp	Leu	Ser	Tyr	Ala	Ser
			260					265					270		
Asp	Thr	Leu	Ile	Arg	Arg	Val	Leu	Glu	Val	Ser	Gln	Ala	Pro	Val	Ile
		275					280					285			
Phe	Ser	His	Ser	Ala	Ala	Arg	Ala	Val	Cys	Asp	Asn	Leu	Leu	Asn	Val
	290					295				300					
Pro	Asp	Asp	Ile	Leu	Gln	Leu	Leu	Lys	Lys	Asn	Gly	Gly	Ile	Val	Met
305					310					315				320	
Val	Thr	Leu	Ser	Met	Gly	Val	Leu	Gln	Cys	Asn	Leu	Leu	Ala	Asn	Val
			325						330					335	
Ser	Thr	Val	Ala	Asp	His	Phe	Asp	His	Ile	Lys	Ala	Val	Ile	Gly	Ser
		340					345						350		
Lys	Phe	Ile	Gly	Ile	Gly	Gly	Asp	Tyr	Asp	Gly	Ala	Gly	Lys	Phe	Pro
	355				360					365					
Gln	Gly	Leu	Glu	Asp	Val	Ser	Thr	Tyr	Pro	Val	Leu	Ile	Glu	Glu	Leu
	370				375					380					
Leu	Ser	Arg	Ser	Trp	Ser	Glu	Glu	Glu	Leu	Gln	Gly	Val	Leu	Arg	Gly
385					390					395				400	
Asn	Leu	Leu	Arg	Val	Phe	Arg	Gln	Val	Glu	Lys	Val	Arg	Glu	Glu	Ser
			405						410					415	
Arg	Ala	Gln	Ser	Pro	Val	Glu	Ala	Glu	Phe	Pro	Tyr	Gly	Gln	Leu	Ser
		420					425						430		
Thr	Ser	Cys	His	Ser	His	Leu	Val	Pro	Gln	Asn	Gly	His	Gln	Ala	Thr
	435					440					445				
His	Leu	Glu	Val	Thr	Lys	Gln	Pro	Thr	Asn	Arg	Val	Pro	Trp	Arg	Ser
	450				455					460					
Ser	Asn	Ala	Ser	Pro	Tyr	Leu	Val	Pro	Gly	Leu	Val	Ala	Ala	Ala	Thr
465					470					475				480	
Ile	Pro	Thr	Phe	Thr	Gln	Trp	Leu	Cys							
			485												

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 <212> PRT
 <213> Homo sapiens

<400> 33
Asx Met Ile Arg Thr Pro Leu Ser Ala Ser Ala His Arg Leu Leu Leu
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Glu Gly Ser Arg Ala Leu Ser Arg Arg Tyr Leu Arg Arg Leu Leu Leu
35 40 45
Leu Leu Leu Leu Leu Leu Leu Arg Gln Pro Val Thr Arg Ala Glu Thr
50 55 60
Thr Pro Gly Ala Pro Arg Ala Leu Ser Thr Leu Gly Ser Pro Ser Leu
65 70 75 80
Phe Thr Thr Pro Gly Val Pro Ser Ala Leu Thr Thr Pro Gly Leu Thr
85 90 95
Thr Pro Gly Thr Pro Lys Thr Leu Asp Leu Arg Gly Arg Ala Gln Ala
100 105 110
Leu Met Arg Ser Phe Pro Leu Val Asp Gly His Asn Asp Leu Pro Gln
115 120 125
Val Leu Arg Gln Arg Tyr Lys Asn Val Leu Gln Asp Val Asn Leu Arg
130 135 140
Asn Phe Ser His Gly Gln Thr Ser Leu Asp Arg Leu Arg Asp Gly Leu

145 150 155 160
 Val Gly Ala Gln Phe Trp Ser Ala Ser Val Ser Cys Gln Ser Gln Asp
 165 170 175
 Gln Thr Ala Val Arg Leu Ala Leu Glu Gln Ile Asp Leu Ile His Arg
 180 185 190
 Met Cys Ala Ser Tyr Ser Glu Leu Glu Leu Val Thr Ser Ala Glu Gly
 195 200 205
 Leu Asn Ser Ser Gln Lys Leu Ala Cys Leu Ile Gly Val Glu Gly Gly
 210 215 220
 His Ser Leu Asp Ser Ser Leu Ser Val Leu Arg Ser Phe Tyr Val Leu
 225 230 235 240
 Gly Val Arg Tyr Leu Thr Leu Thr Phe Thr Cys Ser Thr Pro Trp Ala
 245 250 255
 Glu Ser Ser Thr Lys Phe Arg His His Met Tyr Thr Asn Val Ser Gly
 260 265 270
 Leu Thr Ser Phe Gly Glu Lys Val Glu Glu Leu Asn Arg Leu Gly
 275 280 285
 Met Met Ile Asp Leu Ser Tyr Ala Ser Asp Thr Leu Ile Arg Arg Val
 290 295 300
 Leu Glu Val Ser Gln Ala Pro Val Ile Phe Ser His Ser Ala Ala Arg
 305 310 315 320
 Ala Val Cys Asp Asn Leu Leu Asn Val Pro Asp Asp Ile Leu Gln Leu
 325 330 335
 Leu Lys Lys Asn Gly Gly Ile Val Met Val Thr Leu Ser Met Gly Val
 340 345 350
 Leu Gln Cys Asn Leu Leu Ala Asn Val Ser Thr Val Ala Asp His Phe
 355 360 365
 Asp His Ile Lys Ala Val Ile Gly Ser Lys Phe Ile Gly Ile Gly Gly
 370 375 380
 Asp Tyr Asp Gly Ala Gly Lys Phe Pro Gln Gly Leu Glu Asp Val Ser
 385 390 395 400
 Thr Tyr Pro Val Leu Ile Glu Glu Leu Leu Ser Arg Ser Trp Ser Glu
 405 410 415
 Glu Glu Leu Gln Gly Val Leu Arg Gly Asn Leu Leu Arg Val Phe Arg
 420 425 430
 Gln Val Glu Lys Val Arg Glu Glu Ser Arg Ala Gln Ser Pro Val Glu
 435 440 445
 Ala Glu Phe Pro Tyr Gly Gln Leu Ser Thr Ser Cys His Ser His Leu
 450 455 460
 Val Pro Gln Asn Gly His Gln Ala Thr His Leu Glu Val Thr Lys Gln
 465 470 475 480
 Pro Thr Asn Arg Val Pro Trp Arg Ser Ser Asn Ala Ser Pro Tyr Leu
 485 490 495
 Val Pro Gly Leu Val Ala Ala Ala Thr Ile Pro Thr Phe Thr Gln Trp
 500 505 510
 Leu Cys

<210> 34
 <211> 512
 <212> PRT
 <213> Homo sapiens

<400> 34
 Met Thr Ala Tyr Asn Ile Ile Gly Glu Ser Pro Ala Ser Ala Pro Val
 1 5 10 15
 Glu Val Phe Val Gly Glu Ala Ala Pro Ala Met Ala Pro Gln Asn Val
 20 25 30
 Gln Val Thr Pro Leu Thr Ala Ser Gln Leu Glu Val Thr Trp Asp Pro

		35						40					45						
Pro 60	Pro 50	Pro	Glu	Ser	Gln	Asn	Gly	Asn	Ile	Gln	Gly	Tyr	Lys	Ala	Arg				
Pro 65	Sér	Arg	Ala	Ile	Tyr	Tyr	Trp	Glu	Ala	Asp	Ser	Gln	Asn	Glu	Thr 80				
Glu	Lys	Met	Lys	Val	Leu	Phe	Leu	Pro	Glu	Pro	Val	Val	Arg	Leu	Lys 95				
Asn	Leu	Thr	Ser	His	Thr	Lys	Tyr	Leu	Val	Ser	Ile	Ser	Ala	Phe	Asn				
Ala	Ala	Gly	Asp	Gly	Pro	Lys	Ser	Asp	Pro	Gln	Gln	Gly	Arg	Thr	His				
Gln	Ala	Ala	Pro	Gly	Ala	Pro	Ser	Phe	Leu	Ala	Phe	Ser	Glu	Ile	Thr				
Ser 145	Thr	Thr	Leu	Asn	Val	Ser	Trp	Gly	Glu	Pro	Ala	Ala	Ala	Asn	Gly 160				
Ile	Leu	Gln	Gly	Tyr	Arg	Val	Val	Tyr	Glu	Pro	Leu	Ala	Pro	Val	Gln 175				
Gly	Val	Ser	Lys	Val	Val	Thr	Val	Glu	Val	Arg	Gly	Asn	Trp	Gln	Arg				
Trp	Leu	Lys	Val	Arg	Asp	Leu	Thr	Lys	Gly	Val	Thr	Tyr	Phe	Phe	Arg				
Val	Gln	Ala	Arg	Thr	Ile	Thr	Tyr	Gly	Pro	Glu	Leu	Gln	Ala	Asn	Ile				
Thr 225	Ala	Gly	Pro	Ala	Glu	Gly	Ser	Pro	Gly	Ser	Pro	Arg	Asp	Val	Leu 240				
Val	Thr	Lys	Ser	Ala	Ser	Glu	Leu	Thr	Leu	Gln	Trp	Thr	Glu	Gly	His 255				
Ser	Gly	Asp	Thr	Pro	Thr	Thr	Gly	Tyr	Val	Ile	Glu	Ala	Arg	Pro	Ser				
Asp	Glu	Gly	Leu	Trp	Asp	Met	Phe	Val	Lys	Asp	Ile	Pro	Arg	Ser	Ala				
Thr	Ser	Tyr	Thr	Leu	Ser	Leu	Asp	Lys	Leu	Arg	Gln	Gly	Val	Thr	Tyr				
Glu 305	Phe	Arg	Val	Val	Ala	Val	Asn	Glu	Ala	Gly	Tyr	Gly	Glu	Pro	Ser 320				
Asn	Pro	Ser	Thr	Ala	Val	Ser	Ala	Gln	Val	Glu	Ala	Pro	Phe	Tyr	Glu				
Glu	Trp	Trp	Phe	Leu	Leu	Val	Met	Ala	Leu	Ser	Ser	Leu	Ile	Val	Ile				
Leu	Leu	Val	Val	Phe	Ala	Leu	Val	Leu	His	Gly	Gln	Asn	Lys	Lys	Tyr				
Lys	Asn	Cys	Ser	Thr	Gly	Ala	Gly	Lys	Gly	Ile	Ser	Thr	Met	Glu	Glu				
Ser 385	Val	Thr	Leu	Asp	Asn	Gly	Gly	Phe	Ala	Ala	Leu	Glu	Leu	Ser	Ser 400				
Arg	His	Leu	Asn	Val	Lys	Ser	Thr	Phe	Ser	Lys	Lys	Asn	Gly	Thr	Ser				
Met	Gly	Pro	His	Pro	Arg	Ser	Pro	Pro	Arg	Pro	Ser	Pro	Gly	Gly	Leu				
His	Tyr	Ser	Asp	Glu	Asp	Ile	Cys	Asn	Lys	Tyr	Asn	Gly	Ala	Val	Leu				
Thr	Glu	Ser	Val	Ser	Leu	Lys	Glu	Lys	Ser	Ala	Asp	Ala	Ser	Glu	Ser				
Glu 465	Val	Ser	Val	Gly	Ala	Tyr	Phe	Arg	Ala	Val	Thr	Ile	Ser	Pro	Tyr 480				
Phe	Cys	Lys	Asp	Ala	Gly	Phe	Ala	Val	Arg	Thr	Ile	Ala	Leu	Gly	Leu				
Ala	Glu	Thr	Ala	Gly	Ser	Lys	Ala	Asp	Ala	Arg	Lys	Gly	Thr	Phe	Val				

<210> 35
 <211> 1152
 <212> PRT
 <213> Homo sapiens

<400> 35
 Ala Met Leu Ser Met Leu Ala Ala Gly Leu Leu Cys Val Pro Trp Val
 1 5 10 15
 Pro Gln Ser His Thr Ala Thr Arg Asn Gln Ser Leu Leu Val Met Gly
 20 25 30
 Leu Gln Arg Ser Pro Lys Met Ser Ser Arg Ala Leu Leu Val Gly Ala
 35 40 45
 Ile Gly Asp Glu Glu Glu Trp Val Thr Leu Tyr Glu Glu Glu Asn Glu
 50 55 60
 Pro Asp Ala Gln Met Leu Glu Ile Pro Asn Leu Thr Pro Tyr Thr His
 65 70 75 80
 Tyr Arg Phe Arg Met Lys Gln Val Asn Ile Val Gly Pro Ser Pro Tyr
 85 90 95
 Ser Pro Ser Ser Arg Val Ile Gln Thr Leu Gln Ala Pro Pro Asp Val
 100 105 110
 Ala Pro Thr Ser Val Thr Val Arg Thr Ala Ser Glu Thr Ser Leu Arg
 115 120 125
 Leu Arg Trp Val Pro Leu Pro Asp Ser Gln Tyr Asn Gly Asn Pro Glu
 130 135 140
 Ser Val Gly Tyr Arg Ile Lys Tyr Trp Arg Ser Asp Leu Gln Ser Ser
 145 150 155 160
 Ala Val Ala Gln Val Val Ser Asp Arg Leu Glu Arg Glu Phe Thr Ile
 165 170 175
 Glu Glu Leu Glu Glu Trp Met Glu Tyr Glu Leu Gln Met Gln Ala Phe
 180 185 190
 Asn Ala Val Gly Ala Gly Pro Trp Ser Glu Val Val Arg Gly Arg Thr
 195 200 205
 Arg Glu Ser Val Pro Ser Ala Ala Pro Glu Asn Val Ser Ala Glu Ala
 210 215 220
 Val Ser Ser Thr Gln Ile Leu Leu Thr Trp Thr Ser Val Pro Glu Gln
 225 230 235 240
 Asp Gln Asn Gly Leu Ile Leu Gly Tyr Lys Ile Leu Phe Arg Ala Lys
 245 250 255
 Asp Leu Asp Pro Glu Pro Arg Ser His Ile Val Arg Gly Asn His Thr
 260 265 270
 Gln Ser Ala Leu Leu Ala Gly Leu Arg Lys Phe Val Leu Tyr Glu Leu
 275 280 285
 Gln Val Leu Ala Phe Thr Arg Ile Gly Asn Gly Val Pro Ser Thr Pro
 290 295 300
 Leu Ile Leu Glu Arg Thr Lys Asp Asp Ala Pro Gly Pro Pro Val Arg
 305 310 315 320
 Leu Val Phe Pro Glu Val Arg Leu Thr Ser Val Arg Ile Val Trp Gln
 325 330 335
 Pro Pro Glu Glu Pro Asn Gly Ile Ile Leu Gly Tyr Gln Ile Ala Tyr
 340 345 350
 Arg Leu Ala Ser Ser Ser Pro His Thr Phe Thr Thr Val Glu Val Gly
 355 360 365
 Ala Thr Val Arg Gln Phe Thr Ala Thr Asp Leu Ala Pro Glu Ser Ala
 370 375 380
 Tyr Ile Phe Arg Leu Ser Ala Lys Thr Arg Gln Gly Trp Gly Glu Pro
 385 390 395 400
 Leu Glu Ala Thr Val Ile Thr Thr Glu Lys Arg Glu Arg Pro Ala Pro
 405 410 415

Pro Arg Glu Leu Leu Val Pro Gln Ala Glu Val Thr Ala Arg Ser Leu
 420 425 430
 Arg Leu Gln Trp Val Pro Gly Ser Asp Gly Ala Ser Pro Ile Arg Tyr
 435 440 445
 Phe Thr Met Gln Val Arg Glu Leu Pro Arg Gly Glu Trp Gln Thr Tyr
 450 455 460
 Ser Ser Ser Ile Ser His Glu Ala Thr Ala Cys Val Val Asp Arg Leu
 465 470 475 480
 Arg Pro Phe Thr Ser Tyr Lys Leu Arg Leu Lys Ala Thr Asn Asp Ile
 485 490 495
 Gly Asp Ser Asp Phe Ser Ser Glu Thr Glu Ala Val Thr Thr Leu Gln
 500 505 510
 Asp Val Pro Gly Glu Pro Pro Gly Ser Val Ser Ala Thr Pro His Thr
 515 520 525
 Thr Ser Ser Val Leu Ile Gln Trp Gln Pro Pro Arg Asp Glu Ser Leu
 530 535 540
 Asn Gly Leu Leu Gln Gly Tyr Arg Ile Tyr Tyr Arg Glu Leu Glu Tyr
 545 550 555 560
 Glu Ala Gly Ser Gly Thr Glu Ala Lys Thr Leu Lys Asn Pro Ile Ala
 565 570 575
 Leu His Ala Glu Leu Thr Ala Gln Ser Ser Phe Lys Thr Val Asn Ser
 580 585 590
 Ser Ser Thr Ser Thr Met Cys Glu Leu Thr His Leu Lys Lys Tyr Arg
 595 600 605
 Arg Tyr Glu Val Ile Met Thr Ala Tyr Asn Ile Ile Gly Glu Ser Pro
 610 615 620
 Ala Ser Ala Pro Val Glu Val Phe Val Gly Glu Ala Ala Pro Ala Met
 625 630 635 640
 Ala Pro Gln Asn Val Gln Val Thr Pro Leu Thr Ala Ser Gln Leu Glu
 645 650 655
 Val Thr Trp Asp Pro Pro Pro Pro Glu Ser Gln Asn Gly Asn Ile Gln
 660 665 670
 Gly Tyr Lys Ile Tyr Tyr Trp Glu Ala Asp Ser Gln Asn Glu Thr Glu
 675 680 685
 Lys Met Lys Val Leu Phe Leu Pro Glu Pro Val Val Arg Leu Lys Asn
 690 695 700
 Leu Thr Ser His Thr Lys Tyr Leu Val Ser Ile Ser Ala Phe Asn Ala
 705 710 715 720
 Ala Gly Asp Gly Pro Lys Ser Asp Pro Gln Gln Gly Arg Thr His Gln
 725 730 735
 Ala Ala Pro Gly Ala Pro Ser Phe Leu Ala Phe Ser Glu Ile Thr Ser
 740 745 750
 Thr Thr Leu Asn Val Ser Trp Gly Glu Pro Ala Ala Ala Asn Gly Ile
 755 760 765
 Leu Gln Gly Tyr Arg Val Val Tyr Glu Pro Leu Ala Pro Val Gln Gly
 770 775 780
 Val Ser Lys Val Val Thr Val Glu Val Arg Gly Asn Trp Gln Arg Trp
 785 790 795 800
 Leu Lys Val Arg Asp Leu Thr Lys Gly Val Thr Tyr Phe Phe Arg Val
 805 810 815
 Gln Ala Arg Thr Ile Thr Tyr Gly Pro Glu Leu Gln Ala Asn Ile Thr
 820 825 830
 Ala Gly Pro Ala Glu Gly Ser Pro Gly Ser Pro Arg Asp Val Leu Val
 835 840 845
 Thr Lys Ser Ala Ser Glu Leu Thr Leu Gln Trp Thr Glu Gly His Ser
 850 855 860
 Gly Asp Thr Pro Thr Thr Gly Tyr Val Ile Glu Ala Arg Pro Ser Asp
 865 870 875 880
 Glu Gly Leu Trp Asp Met Phe Val Lys Asp Ile Pro Arg Ser Ala Thr

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<210> 36
<211> 540
<212> PRT
<213> Homo sapiens
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	<400> 36														
Asx	Met	Thr	Ala	Tyr	Asn	Ile	Ile	Gly	Glu	Ser	Pro	Ala	Ser	Ala	Pro
1				5					10					15	
Val	Glu	Val	Phe	Val	Gly	Glu	Ala	Ala	Pro	Ala	Met	Ala	Pro	Gln	Asn
			20					25					30		
Val	Gln	Val	Thr	Pro	Leu	Thr	Ala	Ser	Gln	Leu	Glu	Val	Thr	Trp	Asp
		35					40					45			
Pro	Pro	Pro	Pro	Glu	Ser	Gln	Asn	Gly	Asn	Ile	Gln	Gly	Tyr	Lys	Ile
	50					55					60				
Tyr	Tyr	Trp	Glu	Ala	Asp	Ser	Gln	Asn	Glu	Thr	Glu	Lys	Met	Lys	Val
65					70					75				80	
Leu	Phe	Leu	Pro	Glu	Pro	Val	Val	Arg	Leu	Lys	Asn	Leu	Thr	Ser	His
				85					90					95	
Thr	Lys	Tyr	Leu	Val	Ser	Ile	Ser	Ala	Phe	Asn	Ala	Ala	Gly	Asp	Gly
			100					105					110		
Pro	Lys	Ser	Asp	Pro	Gln	Gln	Gly	Arg	Thr	His	Gln	Ala	Ala	Pro	Gly
		115					120					125			
Ala	Pro	Ser	Phe	Leu	Ala	Phe	Ser	Glu	Ile	Thr	Ser	Thr	Thr	Leu	Asn
	130					135					140				
Val	Ser	Trp	Gly	Glu	Pro	Ala	Ala	Ala	Asn	Gly	Ile	Leu	Gln	Gly	Tyr

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145          150          155          160
Arg Val Val Tyr Glu Pro Leu Ala Pro Val Gln Gly Val Ser Lys Val
          165          170          175
Val Thr Val Glu Val Arg Gly Asn Trp Gln Arg Trp Leu Lys Val Arg
          180          185          190
Asp Leu Thr Lys Gly Val Thr Tyr Phe Phe Arg Val Gln Ala Arg Thr
          195          200          205
Ile Thr Tyr Gly Pro Glu Leu Gln Ala Asn Ile Thr Ala Gly Pro Ala
          210          215          220
Glu Gly Ser Pro Gly Ser Pro Arg Asp Val Leu Val Thr Lys Ser Ala
225          230          235          240
Ser Glu Leu Thr Leu Gln Trp Thr Glu Gly His Ser Gly Asp Thr Pro
          245          250          255
Thr Thr Gly Tyr Val Ile Glu Ala Arg Pro Ser Asp Glu Gly Leu Trp
          260          265          270
Asp Met Phe Val Lys Asp Ile Pro Arg Ser Ala Thr Ser Tyr Thr Leu
          275          280          285
Ser Leu Asp Lys Leu Arg Gln Gly Val Thr Tyr Glu Phe Arg Val Val
          290          295          300
Ala Val Asn Glu Ala Gly Tyr Gly Glu Pro Ser Asn Pro Ser Thr Ala
305          310          315          320
Val Ser Ala Gln Val Glu Ala Pro Phe Tyr Glu Glu Trp Trp Phe Leu
          325          330          335
Leu Val Met Ala Leu Ser Ser Leu Ile Val Ile Leu Leu Val Val Phe
          340          345          350
Ala Leu Val Leu His Gly Gln Asn Lys Lys Tyr Lys Asn Cys Ser Thr
          355          360          365
Gly Ala Gly Lys Gly Ile Ser Thr Met Glu Glu Ser Val Thr Leu Asp
          370          375          380
Asn Gly Gly Phe Ala Ala Leu Glu Leu Ser Ser Arg His Leu Asn Val
385          390          395          400
Lys Ser Thr Phe Ser Lys Lys Asn Gly Thr Arg Ser Pro Pro Arg Pro
          405          410          415
Ser Pro Gly Gly Leu His Tyr Ser Asp Glu Asp Ile Cys Asn Lys Tyr
          420          425          430
Asn Gly Ala Val Leu Thr Glu Ser Val Ser Leu Lys Glu Lys Ser Ala
          435          440          445
Asp Ala Ser Glu Ser Glu Ala Thr Asp Ser Asp Tyr Glu Asp Ala Leu
          450          455          460
Pro Lys His Ser Phe Val Asn His Tyr Met Ser Asp Pro Thr Tyr Tyr
465          470          475          480
Asn Ser Trp Lys Arg Arg Ala Gln Gly Arg Ala Pro Ala Pro His Arg
          485          490          495
Tyr Glu Ala Val Ala Gly Ser Glu Ala Gly Ala Gln Leu His Pro Val
          500          505          510
Ile Thr Thr Gln Ser Ala Gly Gly Val Tyr Thr Pro Ala Gly Pro Gly
          515          520          525
Ala Arg Thr Pro Leu Thr Gly Phe Ser Ser Phe Val
          530          535          540

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<210> 37

<211> 319

<212> PRT

<213> Homo sapiens

<400> 37

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Met Leu Trp Arg Gln Leu Ile Tyr Trp Gln Leu Leu Ala Leu Phe Phe
 1          5          10          15
Leu Pro Phe Cys Leu Cys Gln Asp Glu Tyr Met Glu Val Ser Gly Arg

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<210> 38
<211> 246
<212> PRT
<213> Homo sapiens
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<400> 38															
Met	Leu	Trp	Arg	Gln	Leu	Ile	Tyr	Trp	Gln	Leu	Leu	Ala	Leu	Phe	Phe
1				5					10					15	
Leu	Pro	Phe	Cys	Leu	Cys	Gln	Asp	Glu	Tyr	Met	Glu	Ser	Pro	Gln	Thr
			20					25					30		
Gly	Gly	Leu	Pro	Pro	Asp	Cys	Ser	Lys	Cys	Cys	His	Gly	Asp	Tyr	Ser
		35				40						45			
Phe	Arg	Gly	Tyr	Gln	Gly	Pro	Pro	Gly	Pro	Pro	Gly	Pro	Pro	Gly	Ile
	50				55						60				
Pro	Gly	Asn	His	Gly	Asn	Asn	Gly	Asn	Asn	Gly	Ala	Thr	Gly	His	Glu
65				70						75				80	
Gly	Ala	Lys	Gly	Glu	Lys	Gly	Asp	Lys	Gly	Asp	Leu	Gly	Pro	Arg	Gly
			85						90					95	
Glu	Arg	Gly	Gln	His	Gly	Pro	Lys	Gly	Glu	Lys	Gly	Tyr	Pro	Gly	Ile
			100					105					110		
Pro	Pro	Glu	Leu	Gln	Ile	Ala	Phe	Met	Ala	Ser	Leu	Ala	Thr	His	Phe

115	120	125
Ser Asn Gln Asn Ser Gly Ile Ile Phe Ser Ser Val Glu Thr Asn Ile		
130	135	140
Gly Asn Phe Phe Asp Val Met Thr Gly Arg Phe Gly Ala Pro Val Ser		
145	150	155
Gly Val Tyr Phe Phe Thr Phe Ser Met Met Lys His Glu Asp Val Glu		
	165	170
Glu Val Tyr Val Tyr Leu Met His Asn Gly Asn Thr Val Phe Ser Met		
	180	185
Tyr Ser Tyr Glu Met Lys Gly Lys Ser Asp Thr Ser Ser Asn His Ala		
	195	200
Val Leu Lys Leu Ala Lys Gly Asp Glu Val Trp Leu Arg Met Gly Asn		
	210	215
Gly Ala Leu His Gly Asp His Gln Arg Phe Ser Thr Phe Ala Gly Phe		
225	230	235
Leu Leu Phe Glu Thr Lys		240
	245	

<210> 39
 <211> 675
 <212> PRT
 <213> Homo sapiens

<400> 39

Met Thr Thr Ser His Met Asn Gly His Val Thr Glu Glu Ser Asp Ser	
1	5
Glu Val Lys Asn Val Asp Leu Ala Ser Pro Glu Glu His Gln Lys His	
	20
Arg Glu Met Ala Val Asp Cys Pro Gly Asp Leu Gly Thr Arg Met Met	
	35
Pro Ile Arg Arg Ser Ala Gln Leu Glu Arg Ile Arg Gln Gln Gln Glu	
	50
Asp Met Arg Arg Arg Arg Glu Glu Glu Gly Lys Lys Gln Glu Leu Asp	
65	70
Leu Asn Ser Ser Met Arg Leu Lys Lys Leu Ala Gln Ile Pro Pro Lys	
	85
Thr Gly Ile Asp Asn Pro Met Phe Asp Thr Glu Glu Gly Ile Val Leu	
	100
Glu Ser Pro His Tyr Ala Val Lys Ile Leu Glu Ile Glu Asp Leu Phe	
	115
Ser Ser Leu Lys His Ile Gln His Thr Leu Val Asp Ser Gln Ser Gln	
	130
Glu Asp Ile Ser Leu Leu Gln Leu Val Gln Asn Lys Asp Phe Gln	
145	150
Asn Ala Phe Lys Ile His Asn Ala Ile Thr Val His Met Asn Lys Ala	
	165
Ser Pro Pro Phe Pro Leu Ile Ser Asn Ala Gln Asp Leu Ala Gln Glu	
	180
Val Gln Thr Val Leu Lys Pro Val His His Lys Glu Gly Gln Glu Leu	
	195
Thr Ala Leu Leu Asn Thr Pro His Ile Gln Ala Leu Leu Leu Ala His	
	210
Asp Lys Val Ala Glu Gln Glu Met Gln Leu Glu Pro Ile Thr Asp Glu	
225	230
Arg Val Tyr Glu Ser Ile Gly Gln Tyr Gly Gly Glu Thr Val Lys Ile	
	245
Val Arg Ile Glu Lys Ala Arg Asp Ile Pro Leu Gly Ala Thr Val Arg	
	260
Asn Glu Met Asp Ser Val Ile Ile Ser Arg Ile Val Lys Gly Gly Ala	
	265
	270

275	280	285
Ala Glu Lys Ser Gly Leu Leu His Glu Gly Asp Glu Val Leu Glu Ile		
290	295	300
Asn Gly Ile Glu Ile Arg Gly Lys Asp Val Asn Glu Val Phe Asp Leu		
305	310	315
Leu Ser Asp Met His Gly Thr Leu Thr Phe Val Leu Ile Pro Ser Gln		
	325	330
Gln Ile Lys Pro Pro Pro Ala Lys Glu Thr Val Ile His Val Lys Ala		
	340	345
His Phe Asp Tyr Asp Pro Ser Asp Asp Pro Tyr Val Pro Cys Arg Glu		
	355	360
Leu Gly Leu Ser Phe Gln Lys Gly Asp Ile Leu His Val Ile Ser Gln		
	370	375
Glu Asp Pro Asn Trp Trp Gln Ala Tyr Arg Glu Gly Asp Glu Asp Asn		
385	390	395
Gln Pro Leu Ala Gly Leu Val Pro Gly Lys Ser Phe Gln Gln Gln Arg		
	405	410
Glu Ala Met Lys Gln Thr Ile Glu Glu Asp Lys Glu Pro Glu Lys Ser		
	420	425
Gly Lys Leu Trp Cys Ala Lys Lys Asn Lys Lys Lys Arg Lys Lys Val		
	435	440
Leu Tyr Asn Ala Asn Lys Asn Asp Asp Tyr Asp Asn Glu Glu Ile Leu		
	450	455
Thr Tyr Glu Glu Met Ser Leu Tyr His Gln Pro Ala Asn Arg Lys Arg		
465	470	475
Pro Ile Ile Leu Ile Gly Pro Gln Asn Cys Gly Gln Asn Glu Leu Arg		
	485	490
Gln Arg Leu Met Asn Lys Glu Lys Asp Arg Phe Ala Ser Ala Val Pro		
	500	505
His Thr Thr Arg Ser Arg Arg Asp Gln Glu Val Ala Gly Arg Asp Tyr		
	515	520
His Phe Val Ser Arg Gln Ala Phe Glu Ala Asp Ile Ala Ala Gly Lys		
	530	535
Phe Ile Glu His Gly Glu Phe Glu Lys Asn Leu Tyr Gly Thr Ser Ile		
545	550	555
Asp Ser Val Arg Gln Val Ile Asn Ser Gly Lys Ile Cys Leu Leu Ser		
	565	570
Leu Arg Thr Gln Ser Leu Lys Thr Leu Arg Asn Ser Asp Leu Lys Pro		
	580	585
Tyr Ile Ile Phe Ile Ala Pro Pro Ser Gln Glu Arg Leu Arg Ala Leu		
	595	600
Leu Ala Lys Glu Gly Lys Asn Pro Lys Pro Glu Glu Leu Arg Glu Ile		
	610	615
Ile Glu Lys Thr Arg Glu Met Glu Gln Asn Asn Gly His Tyr Phe Asp		
625	630	635
Thr Ala Ile Val Asn Ser Asp Leu Asp Lys Ala Tyr Gln Glu Leu Leu		
	645	650
Arg Leu Ile Asn Lys Leu Asp Thr Glu Pro Gln Trp Val Pro Ser Thr		
	660	665
Trp Leu Arg		670
675		

<210> 40

<211> 675

<212> PRT

<213> Homo sapiens

<400> 40

Met Thr Thr Ser His Met Asn Gly His Val Thr Glu Glu Ser Asp Ser

1				5					10				15		
Glu	Val	Lys	Asn	Val	Asp	Leu	Ala	Ser	Pro	Glu	Glu	His	Gln	Lys	His
			20					25					30		
Arg	Glu	Met	Ala	Val	Asp	Cys	Pro	Gly	Asp	Leu	Gly	Thr	Arg	Met	Met
		35					40					45			
Pro	Ile	Arg	Arg	Ser	Ala	Gln	Leu	Glu	Arg	Ile	Arg	Gln	Gln	Gln	Glu
	50					55					60				
Asp	Met	Arg	Arg	Arg	Arg	Glu	Glu	Glu	Gly	Lys	Lys	Gln	Glu	Leu	Asp
65					70					75					80
Leu	Asn	Ser	Ser	Met	Arg	Leu	Lys	Lys	Leu	Ala	Gln	Ile	Pro	Pro	Lys
				85					90					95	
Thr	Gly	Ile	Asp	Asn	Pro	Met	Phe	Asp	Thr	Glu	Glu	Gly	Ile	Val	Leu
			100					105					110		
Glu	Ser	Pro	His	Tyr	Ala	Val	Lys	Ile	Leu	Glu	Ile	Glu	Asp	Leu	Phe
		115					120					125			
Ser	Ser	Leu	Lys	His	Ile	Gln	His	Thr	Leu	Val	Asp	Ser	Gln	Ser	Gln
	130					135					140				
Glu	Asp	Ile	Ser	Leu	Leu	Gln	Leu	Val	Gln	Asn	Lys	Asp	Phe	Gln	
145					150				155					160	
Asn	Ala	Phe	Lys	Ile	His	Asn	Ala	Ile	Thr	Val	His	Met	Asn	Lys	Ala
				165					170					175	
Ser	Pro	Pro	Phe	Pro	Leu	Ile	Ser	Asn	Ala	Gln	Asp	Leu	Ala	Gln	Glu
			180					185					190		
Val	Gln	Thr	Val	Leu	Lys	Pro	Val	His	His	Lys	Glu	Gly	Gln	Glu	Leu
		195					200					205			
Thr	Ala	Leu	Leu	Asn	Thr	Pro	His	Ile	Gln	Ala	Leu	Leu	Leu	Ala	His
	210					215					220				
Asp	Lys	Val	Ala	Glu	Gln	Glu	Met	Gln	Leu	Glu	Pro	Ile	Thr	Asp	Glu
225					230					235				240	
Arg	Val	Tyr	Glu	Ser	Ile	Gly	Gln	Tyr	Gly	Gly	Glu	Thr	Val	Lys	Ile
			245						250					255	
Val	Arg	Ile	Glu	Lys	Ala	Arg	Asp	Ile	Pro	Leu	Gly	Ala	Thr	Val	Arg
			260					265					270		
Asn	Glu	Met	Asp	Ser	Val	Ile	Ile	Ser	Arg	Ile	Val	Lys	Gly	Gly	Ala
		275					280					285			
Ala	Glu	Lys	Ser	Gly	Leu	Leu	His	Glu	Gly	Asp	Glu	Val	Leu	Glu	Ile
	290					295					300				
Asn	Gly	Ile	Glu	Ile	Arg	Gly	Lys	Asp	Val	Asn	Glu	Val	Phe	Asp	Leu
305					310					315				320	
Leu	Ser	Asp	Met	His	Gly	Thr	Leu	Thr	Phe	Val	Leu	Ile	Pro	Ser	Gln
				325					330					335	
Gln	Ile	Lys	Pro	Pro	Pro	Ala	Lys	Glu	Thr	Val	Ile	His	Val	Lys	Ala
			340					345					350		
His	Phe	Asp	Tyr	Asp	Pro	Ser	Asp	Asp	Pro	Tyr	Val	Pro	Cys	Arg	Glu
	355						360					365			
Leu	Gly	Leu	Ser	Phe	Gln	Lys	Gly	Asp	Ile	Leu	His	Val	Ile	Ser	Gln
	370					375					380				
Glu	Asp	Pro	Asn	Trp	Trp	Gln	Ala	Tyr	Arg	Glu	Gly	Asp	Glu	Asp	Asn
385					390					395				400	
Gln	Pro	Leu	Ala	Gly	Leu	Val	Pro	Gly	Lys	Ser	Phe	Gln	Gln	Gln	Arg
				405					410					415	
Glu	Ala	Met	Lys	Gln	Thr	Ile	Glu	Glu	Asp	Lys	Glu	Pro	Glu	Lys	Ser
			420					425					430		
Gly	Lys	Leu	Trp	Cys	Ala	Lys	Lys	Asn	Lys	Lys	Lys	Arg	Lys	Lys	Val
	435						440					445			
Leu	Tyr	Asn	Ala	Asn	Lys	Asn	Asp	Asp	Tyr	Asp	Asn	Glu	Glu	Ile	Leu
	450					455					460				
Thr	Tyr	Glu	Glu	Met	Ser	Leu	Tyr	His	Gln	Pro	Ala	Asn	Arg	Lys	Arg
465					470					475					480

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<210> 41
<211> 957
<212> PRT
<213> Homo sapiens
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<400> 41															
Met 1	Ser	Leu	Val	Ser 5	Gln	Asn	Ser	Arg	Arg 10	Arg	Arg	Arg	Arg	Val 15	Ala
Lys	Ala	Thr	Ala 20	His	Asn	Ser	Ser	Trp 25	Gly	Glu	Met	Gln	Ala 30	Pro	Asn
Ala	Pro	Gly 35	Leu	Pro	Ala	Asp 40	Val	Pro	Gly	Ser	Asp 45	Val	Pro	Gln	Gly
Pro 50	Ser	Asp	Ser	Gln	Ile	Leu 55	Gln	Gly	Leu	Cys	Ala 60	Ser	Glu	Gly	Pro
Ser 65	Thr	Ser	Val	Leu 70	Pro	Thr	Ser	Ala	Glu	Gly 75	Pro	Ser	Thr	Phe	Val 80
Pro	Pro	Thr	Ile 85	Ser	Glu	Ala	Ser	Ser	Ala 90	Ser	Gly	Gln	Pro	Thr	Ile 95
Ser	Glu	Gly 100	Pro	Gly	Thr	Ser	Val	Leu 105	Pro	Thr	Pro	Ser	Glu	Gly	Leu 110
Ser	Thr	Ser 115	Gly	Pro	Pro	Thr	Ile	Ser 120	Lys	Gly	Leu	Cys	Thr	Ser	Val 125
Thr	Leu	Ala 130	Ala	Ser	Glu	Gly 135	Arg	Asn	Thr	Ser	Arg	Pro	Pro	Thr	Ser 140
Ser 145	Glu	Glu	Pro	Ser	Thr	Ser 150	Val	Pro	Pro	Thr	Ala	Ser	Glu	Val	Pro 160
Ser	Thr	Ser	Leu 165	Pro	Pro	Thr	Pro	Gly	Glu	Gly 170	Thr	Ser	Thr	Ser	Val 175
Pro	Pro	Thr	Ala 180	Tyr	Glu	Gly	Pro	Ser 185	Thr	Ser	Val	Val	Pro	Thr	Pro 190
Asp	Glu	Gly 195	Pro	Ser	Thr	Ser	Val	Leu 200	Pro	Thr	Pro	Gly	Glu	Gly	Pro 205

Gly	Thr	Ser	Val	Pro	Leu	Ala	Ala	Thr	Glu	Gly	Leu	Ser	Thr	Ser	Val
210						215					220				
Gln	Ala	Thr	Pro	Asp	Glu	Gly	Pro	Ser	Thr	Ser	Val	Pro	Pro	Thr	Ala
225					230					235					240
Thr	Glu	Gly	Leu	Ser	Thr	Pro	Val	Pro	Pro	Thr	Arg	Asp	Glu	Gly	Pro
				245					250					255	
Ser	Thr	Ser	Val	Pro	Ala	Thr	Pro	Gly	Glu	Gly	Pro	Ser	Thr	Ser	Val
			260					265					270		
Leu	Pro	Ala	Ala	Ser	Asp	Gly	Gln	Ser	Ile	Ser	Leu	Val	Pro	Thr	Arg
		275					280					285			
Gly	Lys	Gly	Ser	Ser	Thr	Ser	Val	Pro	Pro	Thr	Ala	Thr	Glu	Gly	Leu
290						295					300				
Ser	Thr	Ser	Val	Gln	Pro	Thr	Ala	Gly	Glu	Gly	Ser	Ser	Thr	Ser	Val
305					310					315					320
Pro	Pro	Thr	Pro	Gly	Gly	Gly	Leu	Ser	Thr	Ser	Val	Pro	Pro	Thr	Ala
				325					330					335	
Thr	Glu	Glu	Leu	Ser	Thr	Ser	Val	Pro	Pro	Thr	Pro	Gly	Glu	Gly	Pro
			340					345					350		
Ser	Thr	Ser	Val	Leu	Pro	Ile	Pro	Gly	Glu	Gly	Leu	Ser	Thr	Ser	Val
		355					360					365			
Pro	Pro	Thr	Ala	Ser	Asp	Gly	Ser	Asp	Thr	Ser	Val	Pro	Pro	Thr	Pro
		370				375					380				
Gly	Glu	Gly	Ala	Ser	Thr	Leu	Val	Gln	Pro	Thr	Ala	Pro	Asp	Gly	Pro
385					390					395					400
Gly	Ser	Ser	Val	Leu	Pro	Asn	Pro	Gly	Glu	Gly	Pro	Ser	Thr	Leu	Phe
			405						410					415	
Ser	Ser	Ser	Ala	Ser	Val	Asp	Arg	Asn	Pro	Ser	Lys	Cys	Ser	Leu	Val
			420					425					430		
Leu	Pro	Ser	Pro	Arg	Val	Thr	Lys	Ala	Ser	Val	Asp	Ser	Asp	Ser	Glu
		435					440					445			
Gly	Pro	Lys	Gly	Ala	Glu	Gly	Pro	Ile	Glu	Phe	Glu	Val	Leu	Arg	Asp
450						455				460					
Cys	Glu	Ser	Pro	Asn	Ser	Ile	Ser	Ile	Met	Gly	Leu	Asn	Thr	Ser	Arg
465					470					475					480
Val	Ala	Ile	Thr	Leu	Lys	Pro	Gln	Asp	Pro	Met	Glu	Gln	Asn	Val	Ala
			485						490					495	
Glu	Leu	Leu	Gln	Phe	Leu	Leu	Val	Lys	Asp	Gln	Ser	Lys	Tyr	Pro	Ile
			500					505					510		
Arg	Glu	Ser	Glu	Met	Arg	Glu	Tyr	Ile	Val	Lys	Glu	Tyr	Arg	Asn	Gln
		515					520					525			
Phe	Pro	Glu	Ile	Leu	Arg	Arg	Ala	Ala	Ala	His	Leu	Glu	Cys	Ile	Phe
530						535					540				
Arg	Phe	Glu	Leu	Arg	Glu	Leu	Asp	Pro	Glu	Ala	His	Thr	Tyr	Ile	Leu
545					550					555					560
Leu	Asn	Lys	Leu	Gly	Pro	Val	Pro	Phe	Glu	Gly	Leu	Glu	Glu	Ser	Pro
				565					570					575	
Asn	Gly	Pro	Lys	Met	Gly	Leu	Leu	Met	Ile	Leu	Gly	Gln	Ile	Phe	
			580					585					590		
Leu	Asn	Gly	Asn	Gln	Ala	Lys	Glu	Ala	Glu	Ile	Trp	Glu	Met	Leu	Trp
		595					600					605			
Arg	Met	Gly	Val	Gln	Arg	Glu	Arg	Arg	Leu	Ser	Ile	Phe	Gly	Asn	Pro
610						615					620				
Lys	Arg	Leu	Leu	Ser	Val	Glu	Phe	Val	Trp	Gln	Arg	Tyr	Leu	Asp	Tyr
625					630					635					640
Arg	Pro	Val	Thr	Asp	Cys	Lys	Pro	Val	Glu	Tyr	Glu	Phe	Phe	Trp	Gly
			645						650					655	
Pro	Arg	Ser	His	Leu	Glu	Thr	Thr	Lys	Met	Lys	Ile	Leu	Lys	Phe	Met
			660					665					670		
Ala	Lys	Ile	Tyr	Asn	Lys	Asp	Pro	Met	Asp	Trp	Pro	Glu	Lys	Tyr	Asn

675	680	685
Glu Ala Leu Glu Glu Asp	Ala Ala Arg Ala Phe	Ala Glu Gly Trp Gln
690	695	700
Ala Leu Pro His Phe Arg	Arg Pro Phe Phe Glu	Glu Ala Ala Ala Glu
705	710	715
Val Pro Ser Pro Asp Ser	Glu Val Ser Ser Tyr	Ser Ser Lys Tyr Ala
725	730	735
Pro His Ser Trp Pro Glu	Ser Arg Leu Glu Ser	Lys Ala Arg Lys Leu
740	745	750
Val Gln Leu Phe Leu Leu	Met Asp Ser Thr Lys	Leu Pro Ile Pro Lys
755	760	765
Lys Gly Ile Leu Tyr Tyr	Ile Gly Arg Glu Cys	Ser Lys Val Phe Pro
770	775	780
Asp Leu Leu Asn Arg Ala	Ala Arg Thr Leu Asn	His Val Tyr Gly Thr
785	790	795
Glu Leu Val Val Leu Asp	Pro Arg Asn His Ser	Tyr Thr Leu Tyr Asn
805	810	815
Arg Arg Glu Met Glu Glu	Thr Glu Glu Ile Val	Asp Ser Pro Asn Arg
820	825	830
Pro Gly Asn Asn Phe Leu	Met Gln Val Leu Ser	Phe Ile Phe Ile Met
835	840	845
Gly Asn His Ala Arg Glu	Ser Ala Val Trp Ala	Phe Leu Arg Gly Leu
850	855	860
Gly Val Gln Ala Gly Arg	Lys His Val Ile Thr	Cys Arg Tyr Leu Ser
865	870	875
Gln Arg Tyr Ile Asp Ser	Leu Arg Val Pro Asp	Ser Asp Pro Val Gln
885	890	895
Tyr Glu Phe Val Trp Gly	Pro Arg Ala Arg Leu	Glu Thr Ser Lys Met
900	905	910
Lys Ala Leu Arg Tyr Val	Ala Arg Ile His Arg	Lys Glu Pro Gln Asp
915	920	925
Trp Pro Gln Gln Tyr Arg	Glu Ala Met Glu Asp	Glu Ala Asn Arg Ala
930	935	940
Asp Val Gly His Arg Gln	Ile Phe Val His Asn	Phe Arg
945	950	955

<210> 42
 <211> 294
 <212> PRT
 <213> Homo sapiens

<400> 42
Met Pro Pro Phe Leu Leu Thr Cys Leu Phe Ile Thr Gly Thr Ser
1 5 10 15
Val Ser Pro Val Ala Leu Asp Pro Cys Ser Ala Tyr Ile Ser Leu Asn
20 25 30
Glu Pro Trp Arg Asn Thr Asp His Gln Leu Asp Glu Ser Gln Gly Pro
35 40 45
Pro Leu Cys Asp Asn His Val Asn Gly Glu Trp Tyr His Phe Thr Gly
50 55 60
Met Ala Gly Asp Ala Met Pro Thr Phe Cys Ile Pro Glu Asn His Cys
65 70 75 80
Gly Thr His Ala Pro Val Trp Leu Asn Gly Ser His Pro Leu Glu Gly
85 90 95
Asp Gly Ile Val Gln Arg Gln Ala Cys Ala Ser Phe Asn Gly Asn Cys
100 105 110
Cys Leu Trp Asn Thr Thr Val Glu Val Lys Ala Cys Pro Gly Gly Tyr
115 120 125
Tyr Val Tyr Arg Leu Thr Lys Pro Ser Val Cys Phe His Val Tyr Cys

130		135		140
Gly His Phe Tyr Asp Ile Cys Asp Glu Asp Cys His Gly Ser Cys Ser				
145		150		155
Asp Thr Ser Glu Cys Thr Cys Ala Pro Gly Thr Val Leu Gly Pro Asp				
	165		170	175
Arg Gln Thr Cys Phe Gly Lys Lys Leu Ile Lys Asp Glu Asn Glu Cys				
	180		185	190
Glu Gln Asn Asn Gly Gly Cys Ser Glu Ile Cys Val Asn Leu Lys Asn				
	195		200	205
Ser Tyr Arg Cys Glu Cys Gly Val Gly Arg Val Leu Arg Ser Asp Gly				
	210		215	220
Lys Thr Cys Glu Gly Glu Asn Gly Gln Lys Gly Thr Gln Ile Lys Ser				
225		230		235
Pro Glu Glu Ala Thr Gly Leu Phe Ser Asp Val Gln Glu Thr Ala Leu				
	245		250	255
Val Ser Glu Glu Ser Asn Arg Leu Ala Val Gln Arg Asn Asp Lys Arg				
	260		265	270
Arg Ser Ser Thr Leu Arg Ile Leu Thr Leu Trp Thr Glu Phe Ser Phe				
	275		280	285
Asp Phe Val Ser Lys Ile				
290				

<210> 43
 <211> 468
 <212> PRT
 <213> Homo sapiens

<400> 43
Met Pro Pro Phe Leu Leu Leu Thr Cys Leu Phe Ile Thr Gly Thr Ser
1 5 10 15
Val Ser Pro Val Ala Leu Asp Pro Cys Ser Ala Tyr Ile Ser Leu Asn
20 25 30
Glu Pro Trp Arg Asn Thr Asp His Gln Leu Asp Glu Ser Gln Gly Pro
35 40 45
Pro Leu Cys Asp Asn His Val Asn Gly Glu Trp Tyr His Phe Thr Gly
50 55 60
Met Ala Gly Asp Ala Met Pro Thr Phe Cys Ile Pro Glu Asn His Cys
65 70 75 80
Gly Thr His Ala Pro Val Trp Leu Asn Gly Ser His Pro Leu Glu Gly
85 90 95
Asp Gly Ile Val Gln Arg Gln Ala Cys Ala Ser Phe Asn Gly Asn Cys
100 105 110
Cys Leu Trp Asn Thr Thr Val Glu Val Lys Ala Cys Pro Gly Gly Tyr
115 120 125
Tyr Val Tyr Arg Leu Thr Lys Pro Ser Val Cys Phe His Val Tyr Cys
130 135 140
Gly His Val Glu Gly Cys His Asn Asn Asn Gly Gly Cys Ser His Ser
145 150 155 160
Cys Leu Gly Ser Glu Lys Gly Tyr Gln Cys Glu Cys Pro Arg Gly Leu
165 170 175
Val Leu Ser Glu Asp Asn His Thr Cys Gln Val Pro Val Leu Cys Lys
180 185 190
Ser Asn Ala Ile Glu Val Asn Ile Pro Arg Glu Leu Val Gly Gly Leu
195 200 205
Glu Leu Phe Leu Thr Asn Thr Ser Cys Arg Gly Val Ser Asn Gly Thr
210 215 220
His Val Asn Ile Leu Phe Ser Leu Lys Thr Cys Gly Thr Val Val Asp
225 230 235 240
Val Val Asn Asp Lys Ile Val Ala Ser Asn Leu Val Thr Gly Leu Pro

```

                245                250                255
Lys Gln Thr Pro Gly Ser Ser Gly Asp Phe Ile Ile Arg Thr Ser Lys
                260                265                270
Leu Leu Ile Pro Val Thr Cys Glu Phe Pro Arg Leu Tyr Thr Ile Ser
                275                280                285
Glu Gly Tyr Val Pro Asn Leu Arg Asn Ser Pro Leu Glu Ile Met Ser
                290                295                300
Arg Asn His Gly Ile Phe Pro Phe Thr Leu Glu Ile Phe Lys Asp Asn
305                310                315                320
Glu Phe Glu Glu Pro Tyr Arg Glu Ala Leu Pro Thr Leu Lys Leu Arg
                325                330                335
Asp Ser Leu Tyr Phe Gly Ile Glu Pro Val Val His Val Ser Gly Leu
                340                345                350
Glu Ser Leu Val Glu Ser Cys Phe Ala Thr Pro Thr Ser Lys Ile Asp
                355                360                365
Glu Val Leu Lys Tyr Tyr Leu Ile Arg Asp Gly Cys Val Ser Asp Asp
370                375                380
Ser Val Lys Gln Tyr Thr Ser Arg Asp His Leu Ala Lys His Phe Gln
385                390                395                400
Val Pro Val Phe Lys Phe Val Gly Lys Asp His Lys Glu Val Phe Leu
                405                410                415
His Cys Arg Val Leu Val Cys Gly Val Leu Asp Glu Arg Ser Arg Cys
                420                425                430
Ala Gln Gly Cys His Arg Arg Met Arg Arg Gly Ala Gly Gly Glu Asp
                435                440                445
Ser Ala Gly Leu Gln Gly Gln Thr Leu Thr Gly Gly Pro Ile Arg Ile
450                455                460
Asp Trp Glu Asp
465

```

<210> 44

<211> 238

<212> PRT

<213> Homo sapiens

<400> 44

```

Met Val Leu Leu Leu Leu Val Ala Ile Pro Leu Leu Val His Ser Ser
1                5                10                15
Arg Gly Pro Ala His Tyr Glu Met Leu Gly Arg Cys Arg Met Val Cys
                20                25                30
Asp Pro His Gly Pro Arg Gly Pro Gly Pro Asp Gly Ala Pro Ala Ser
35                40                45
Val Pro Pro Phe Pro Pro Gly Ala Lys Gly Glu Val Gly Arg Arg Gly
50                55                60
Lys Ala Gly Leu Arg Gly Pro Pro Gly Pro Pro Gly Pro Arg Gly Pro
65                70                75                80
Pro Gly Glu Pro Gly Arg Pro Gly Pro Pro Gly Pro Pro Gly Pro Gly
85                90                95
Pro Gly Gly Val Ala Pro Ala Ala Gly Tyr Val Pro Arg Ile Ala Phe
100                105                110
Tyr Ala Gly Leu Arg Arg Pro His Glu Gly Tyr Glu Val Leu Arg Phe
115                120                125
Asp Asp Val Val Thr Asn Val Gly Asn Ala Tyr Glu Ala Ala Ser Gly
130                135                140
Lys Phe Thr Cys Pro Met Pro Gly Val Tyr Phe Phe Ala Tyr His Val
145                150                155                160
Leu Met Arg Gly Gly Asp Gly Thr Ser Met Trp Ala Asp Leu Met Lys
                165                170                175
Asn Gly Gln Val Arg Ala Ser Ala Ile Ala Gln Asp Ala Asp Gln Asn

```

```
<210> 45
<211> 267
<212> PRT
<213> Homo sapiens
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```
<210> 46
<211> 157
<212> PRT
<213> Homo sapiens
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	<400>	46													
Met	Gly	Gln	Leu	Cys	Trp	Leu	Pro	Leu	Leu	Ala	Pro	Leu	Leu	Leu	Leu
1				5					10					15	
Arg	Pro	Pro	Gly	Val	Gln	Ser	Ala	Gly	Pro	Ile	Arg	Ala	Phe	Val	Val
			20					25					30		

```

Pro His Ser His Met Asp Val Gly Trp Val Tyr Thr Val Gln Glu Ser
    35          40          45
Met Arg Ala Tyr Ala Ala Asn Val Tyr Thr Ser Val Val Glu Glu Leu
    50          55          60
Ala Arg Gly Gln Gln Arg Arg Phe Ile Ala Val Glu Gln Glu Phe Phe
    65          70          75          80
Arg Leu Trp Trp Asp Gly Val Ala Ser Asp Gln Gln Lys Tyr Gln Val
    85          90          95
Arg Gln Leu Leu Glu Glu Gly Arg Leu Glu Phe Val Ile Gly Gly Gln
    100          105          110
Val Met His Asp Glu Ala Val Thr His Leu Asp Asp Gln Ile Leu Gln
    115          120          125
Leu Thr Gly Leu Ala Thr Leu Pro Cys Thr Gln Gly Pro Ser Gly Pro
    130          135          140
Pro Val Gly Leu Gly His Gly Ile Arg Thr Pro Arg Phe
    145          150          155

```

```

<210> 47
<211> 1009
<212> PRT
<213> Homo sapiens

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```

<400> 47
Met Gly Gln Leu Cys Trp Leu Pro Leu Leu Ala Pro Leu Leu Leu Leu
  1          5          10          15
Arg Pro Pro Gly Val Gln Ser Ala Gly Pro Ile Arg Ala Phe Val Val
    20          25          30
Pro His Ser His Met Asp Val Gly Trp Val Tyr Thr Val Gln Glu Ser
    35          40          45
Met Arg Ala Tyr Ala Ala Asn Val Tyr Thr Ser Val Val Glu Glu Leu
    50          55          60
Ala Arg Gly Gln Gln Arg Arg Phe Ile Ala Val Glu Gln Glu Phe Phe
    65          70          75          80
Arg Leu Trp Trp Asp Gly Val Ala Ser Asp Gln Gln Lys Tyr Gln Val
    85          90          95
Arg Gln Leu Leu Glu Glu Gly Arg Leu Glu Phe Val Ile Gly Gly Gln
    100          105          110
Val Met His Asp Glu Ala Val Thr His Leu Asp Asp Gln Ile Leu Gln
    115          120          125
Leu Thr Glu Gly His Gly Phe Leu Tyr Glu Thr Phe Gly Ile Arg Pro
    130          135          140
Gln Phe Ser Trp His Val Asp Pro Phe Gly Ala Ser Ala Thr Thr Pro
    145          150          155          160
Thr Leu Phe Ala Leu Ala Gly Phe Asn Ala His Leu Gly Ser Arg Ile
    165          170          175
Asp Tyr Asp Leu Lys Ala Ala Met Gln Glu Ala Arg Gly Leu Gln Phe
    180          185          190
Val Trp Arg Gly Ser Pro Ser Leu Ser Glu Arg Gln Glu Ile Phe Thr
    195          200          205
His Ile Met Asp Gln Tyr Ser Tyr Cys Thr Pro Ser His Ile Pro Phe
    210          215          220
Ser Asn Arg Ser Gly Phe Tyr Trp Asn Gly Val Ala Val Phe Pro Lys
    225          230          235          240
Pro Pro Gln Asp Gly Val Tyr Pro Asn Met Ser Glu Pro Val Thr Pro
    245          250          255
Ala Asn Ile Asn Leu Tyr Ala Glu Ala Leu Val Ala Asn Val Lys Gln
    260          265          270
Arg Ala Ala Trp Phe Arg Thr Pro His Val Leu Trp Pro Trp Gly Cys
    275          280          285

```

Asp	Lys	Gln	Phe	Phe	Asn	Ala	Ser	Val	Gln	Phe	Ala	Asn	Met	Asp	Pro
290						295					300				
Leu	Leu	Asp	His	Ile	Asn	Ser	His	Ala	Ala	Glu	Leu	Gly	Val	Ser	Val
305					310					315					320
Gln	Tyr	Ala	Thr	Leu	Gly	Asp	Tyr	Phe	Arg	Ala	Leu	His	Ala	Leu	Asn
				325					330						335
Val	Thr	Trp	Arg	Val	Arg	Asp	His	His	Asp	Phe	Leu	Pro	Tyr	Ser	Thr
			340					345						350	
Glu	Pro	Phe	Gln	Ala	Trp	Thr	Gly	Phe	Tyr	Thr	Ser	Arg	Ser	Ser	Leu
		355					360					365			
Lys	Gly	Leu	Ala	Arg	Arg	Ala	Ser	Ala	Leu	Leu	Tyr	Ala	Gly	Glu	Ser
370						375					380				
Met	Phe	Thr	Arg	Tyr	Leu	Trp	Pro	Ala	Pro	Arg	Gly	His	Leu	Asp	Pro
385					390					395					400
Thr	Trp	Ala	Leu	Gln	Gln	Leu	Gln	Gln	Leu	Arg	Trp	Ala	Val	Ser	Glu
				405					410						415
Val	Gln	His	His	Asp	Ala	Ile	Thr	Gly	Thr	Glu	Ser	Pro	Lys	Val	Arg
			420					425					430		
Asp	Met	Tyr	Ala	Thr	His	Leu	Ala	Ser	Gly	Met	Leu	Gly	Met	Arg	Lys
	435						440					445			
Leu	Met	Ala	Ser	Ile	Val	Leu	Asp	Glu	Leu	Gln	Pro	Gln	Ala	Pro	Met
450						455					460				
Ala	Ala	Ser	Ser	Asp	Ala	Gly	Pro	Ala	Gly	His	Phe	Ala	Ser	Val	Tyr
465					470					475					480
Asn	Pro	Leu	Ala	Trp	Thr	Val	Thr	Thr	Ile	Val	Thr	Leu	Thr	Val	Gly
				485					490						495
Phe	Pro	Gly	Val	Arg	Val	Thr	Asp	Glu	Ala	Gly	His	Pro	Val	Pro	Ser
			500					505					510		
Gln	Ile	Gln	Asn	Ser	Thr	Glu	Thr	Pro	Ser	Ala	Tyr	Asp	Leu	Leu	Ile
	515						520					525			
Leu	Thr	Thr	Ile	Pro	Gly	Leu	Ser	Tyr	Arg	His	Tyr	Asn	Ile	Arg	Pro
530						535					540				
Thr	Ala	Gly	Ala	Gln	Glu	Gly	Thr	Gln	Glu	Pro	Ala	Ala	Thr	Val	Ala
545					550					555					560
Ser	Thr	Leu	Gln	Phe	Gly	Arg	Arg	Leu	Arg	Arg	Arg	Thr	Ser	His	Ala
				565					570					575	
Gly	Arg	Tyr	Leu	Val	Pro	Val	Ala	Asn	Asp	Cys	Tyr	Ile	Val	Leu	Leu
			580					585					590		
Asp	Gln	Asp	Thr	Asn	Leu	Met	His	Ser	Ile	Trp	Glu	Arg	Gln	Ser	Asn
	595					600						605			
Arg	Thr	Val	Arg	Val	Thr	Gln	Glu	Phe	Leu	Glu	Tyr	His	Val	Asn	Gly
	610					615					620				
Asp	Val	Lys	Gln	Gly	Pro	Ile	Ser	Asp	Asn	Tyr	Leu	Phe	Thr	Pro	Gly
625					630					635					640
Lys	Ala	Ala	Val	Pro	Ala	Trp	Glu	Ala	Val	Glu	Met	Glu	Ile	Val	Ala
				645					650					655	
Gly	Gln	Leu	Val	Thr	Glu	Ile	Arg	Gln	Tyr	Phe	Tyr	Arg	Asn	Met	Thr
			660					665					670		
Ala	Gln	Asn	Tyr	Thr	Tyr	Ala	Ile	Arg	Ser	Arg	Leu	Thr	His	Val	Pro
	675						680					685			
Gln	Gly	His	Asp	Gly	Glu	Leu	Leu	Cys	His	Arg	Ile	Glu	Gln	Glu	Tyr
	690					695					700				
Gln	Ala	Gly	Pro	Leu	Glu	Leu	Asn	Arg	Glu	Ala	Val	Leu	Arg	Thr	Ser
705					710					715					720
Thr	Asn	Leu	Asn	Ser	Gln	Gln	Val	Ile	Tyr	Ser	Asp	Asn	Asn	Gly	Tyr
				725					730					735	
Gln	Met	Gln	Arg	Arg	Pro	Tyr	Val	Ser	Tyr	Val	Asn	Asn	Ser	Ile	Ala
			740					745					750		
Arg	Asn	Tyr	Tyr	Pro	Met	Val	Gln	Ser	Ala	Phe	Met	Glu	Asp	Gly	Lys

755	760	765
Ser Arg Leu Val Leu Leu	Ser Glu Arg Ala His Gly	Ile Ser Ser Gln
770	775	780
Gly Asn Gly Gln Val Glu	Val Met Leu His Arg Arg	Leu Trp Asn Asn
785	790	795
Phe Asp Trp Asp Leu Gly	Tyr Asn Leu Thr Leu	Asn Asp Thr Ser Val
805	810	815
Val His Pro Val Leu Trp	Leu Leu Leu Gly Ser	Trp Ser Leu Thr Thr
820	825	830
Ala Leu Arg Gln Arg Ser	Ala Leu Ala Leu Gln	His Arg Pro Val Val
835	840	845
Leu Phe Gly Asp Leu Ala	Gly Thr Ala Pro Lys	Leu Pro Gly Pro Gln
850	855	860
Gln Gln Glu Ala Val Thr	Leu Pro Pro Asn Leu	His Leu Gln Ile Leu
865	870	875
Ser Ile Pro Gly Trp Arg	Tyr Ser Ser Asn His	Thr Glu His Ser Gln
885	890	895
Asn Leu Arg Lys Gly His	Arg Gly Glu Ala Gln	Ala Asp Leu Arg Arg
900	905	910
Val Leu Leu Arg Leu Tyr	His Leu Tyr Glu Val	Gly Glu Asp Pro Val
915	920	925
Leu Ser Gln Pro Val Thr	Val Asn Leu Glu Ala	Val Leu Gln Ala Leu
930	935	940
Gly Ser Val Val Ala Val	Glu Glu Arg Ser Leu	Thr Gly Thr Trp Asp
945	950	955
Leu Ser Met Leu His Arg	Trp Ser Trp Arg Thr	Gly Pro Gly Arg His
965	970	975
Arg Gly Asp Thr Thr Ser	Pro Ser Arg Pro Pro	Gly Gly Pro Ile Ile
980	985	990
Thr Val His Pro Lys Glu	Ile Arg Thr Phe Phe	Ile His Phe Gln Gln
995	1000	1005
Gln		

<210> 48
 <211> 104
 <212> PRT
 <213> Homo sapiens

<400> 48
Met Ala Lys Ile Ser Phe Ser Thr Glu Thr Ala Arg Cys Ile Glu Ser
1 5 10 15
Leu Ile Ala Val Phe Gln Lys Tyr Ala Gly Lys Asp Gly Tyr Asn Cys
20 25 30
Asn Leu Ser Lys Thr Glu Phe Pro Ser Phe Met Asn Lys Glu Leu Ala
35 40 45
Ala Phe Thr Lys Asn Gln Lys Asp Pro Gly Val Leu Asp Arg Met Lys
50 55 60
Lys Leu Ala Val Ser Ser Asp Gly Lys Leu Asp Phe Pro Lys Phe Leu
65 70 75 80
Asn Leu Ile Gly Gly Leu Ala Ala Ala Cys His Asp Ser Phe Leu Lys
85 90 95
Ala Val Pro Ser Gln Lys Trp Asn
100

<210> 49
 <211> 102
 <212> PRT
 <213> Homo sapiens

<400> 49
 Met Glu Lys Phe Ser Ser Pro Thr Glu Thr Glu Gln Cys Ile Lys Ser
 1 5 10 15
 Leu Ile Ala Ile Phe Gln Glu Asp Ala Gly Lys Asp Val Thr Thr Ala
 20 25 30
 Asn Ser Pro Arg Gly Glu Pro Leu Ser Phe Met Asn Thr Glu Leu Ala
 35 40 45
 Ala Leu Thr Gln Asn His Lys Asp Ala Gly Val Leu Asp His Met Met
 50 55 60
 Lys Lys Leu Asp Leu Asn Cys Asp Arg Gln Leu Asp Phe Gln Glu Leu
 65 70 75 80
 Leu Asn Leu Phe Cys Phe Pro His Leu Arg Leu Lys Asn Phe Leu Ile
 85 90 95
 Leu Leu Ala Ala Trp Pro
 100

<210> 50
 <211> 716
 <212> PRT
 <213> Homo sapiens

<400> 50
 Met Asn Ser Phe Arg Ala Ala Ile Leu Phe Trp Thr Val Ala Ala Trp
 1 5 10 15
 Val Thr Ser Gly Lys Pro Leu Gly Glu Thr Asp Glu Val Gly Phe Gln
 20 25 30
 Lys Cys Lys Asp Ala Trp Lys Leu Pro Ile Leu Glu Val Leu Ser Gly
 35 40 45
 Gly Gly Trp Asp Asn Leu Arg Asn Val Asp Met Gly Trp Val Met Asp
 50 55 60
 Leu Thr Tyr Thr Asn Cys Arg Thr Thr Glu Asp Gly Gln Tyr Ile Ile
 65 70 75 80
 Pro Asp Glu Ile Phe Thr Ile Leu Gln Lys Gln Ser Asn Leu Glu Met
 85 90 95
 Asn Ser Glu Ile Leu Glu Ser Trp Val Asn Tyr Gln Arg Ser Ile Ser
 100 105 110
 Tyr Tyr Ile Asn Thr Asp Leu Cys Leu Tyr Ser Lys Val Asn Ala Lys
 115 120 125
 Phe Ser Ala Glu Phe Gln Arg Met Lys Thr Leu Gln Val Lys Asp Lys
 130 135 140
 Ala Ile Thr Thr Arg Val Gln Val Arg Asn Leu Val Tyr Thr Val Lys
 145 150 155 160
 Ile Asn Pro Thr Leu Glu Leu Ser Ser Gly Phe Arg Lys Glu Leu Leu
 165 170 175
 Asp Ile Ser Asp Cys Leu Glu Asn Asn Gln Arg Arg Met Ala Thr Tyr
 180 185 190
 Leu Ala Glu Leu Leu Val Leu Asn Tyr Gly Thr His Val Ile Thr Ser
 195 200 205
 Val Asp Ala Gly Ala Ala Leu Ile Gln Glu Asp His Ile Lys Ala Ser
 210 215 220
 Phe Phe Gln Asp Ser Gln Ser Ser Arg Ser Ala Val Thr Ala Ser Ala
 225 230 235 240
 Gly Leu Ala Phe Gln Asn Thr Val Asn Phe Thr Phe Glu Glu Asn His
 245 250 255
 Thr Ser Glu Asn Val Leu Thr Lys Ser Tyr Leu Ser Asn Arg Thr Asn
 260 265 270
 Ser Arg Val Gln Ser Ile Gly Gly Val Pro Phe Tyr Pro Gly Ile Thr
 275 280 285

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Leu Gln Ala Trp Gln Gln Gly Ile Thr Asn His Leu Val Ala Ile Asp
 290                295                300
Arg Ser Gly Leu Pro Leu His Phe Phe Ile Asn Pro Asn Met Leu Pro
305                310                315                320
Asp Leu Pro Gly Pro Leu Val Lys Lys Val Ser Lys Thr Val Glu Thr
                325                330                335
Ala Val Lys Arg Tyr Tyr Thr Phe Asn Thr Asn Pro Gly Cys Thr Asp
                340                345                350
Leu Asn Ser Pro Tyr Phe Asn Phe Gln Ala Asn Thr Asp Asp Val Ser
                355                360                365
Cys Glu Gly Lys Met Thr Asn Phe Ser Phe Val Gly Val Tyr Gln Lys
 370                375                380
Cys Ser Gln Phe Ser Gly Asn Lys Asn Val Val Leu Cys Pro Lys Leu
385                390                395                400
Glu Gln Lys Asn Pro Leu Thr Gly Asp Phe Ser Cys Pro Ser Gly Cys
                405                410                415
Ser Ser Val His Leu Leu Ser Lys Thr Cys Glu Glu Cys Cys Asn His
                420                425                430
Leu Glu Cys His Lys Lys Cys Thr Leu Leu Val Phe Cys Lys Thr Val
                435                440                445
Cys Glu Asp Val Phe Gln Ala Ala Lys Gly Glu Phe Arg Ala Phe Trp
 450                455                460
Cys Val Ala Ser Ser Gln Val Pro Asp Asn Ser Gly Leu Leu Phe Arg
465                470                475                480
Gly Leu Phe Asn Ser Lys Ser Ile Asn Pro Met Thr Asn Ala Gln Ser
                485                490                495
Cys Pro Thr Gly Tyr Phe Pro Trp Arg Leu Phe Glu Asn Leu Lys Val
                500                505                510
Cys Val Ser Gln Asp Tyr Glu Leu Gly Ser Arg Phe Ala Val Pro Phe
                515                520                525
Gly Gly Phe Phe Ser Cys Thr Val Gly Asn Pro Leu Val Val Pro Ala
 530                535                540
Thr Ser Lys Asp Leu Gly Ala Pro Ser Leu Lys Lys Cys Pro Arg Gly
545                550                555                560
Phe Ser Gln His Leu Ala Leu Ile Ser Asn Gly Cys Gln Val Ser Tyr
                565                570                575
Cys Val Lys Ala Gly Leu Phe Thr Glu Lys Phe Leu Pro Pro Ala Ser
                580                585                590
Leu Pro Pro Phe Thr Gln Pro Pro Leu Met Ser Glu Ala Asp Ala Asn
                595                600                605
Thr Val Ile Val Thr Ser Ser Glu Asn Ala Arg Ser Trp Ile Lys Asp
 610                615                620
Ser Gln Thr His Gln Trp Arg Leu Gly Glu Gln Leu Glu Leu Arg Ser
625                630                635                640
Thr Met Ser Ala Ile His Lys Asp Gly Gly Glu Leu Ser Gly Gly Ala
                645                650                655
Thr Ala Gly Ile Val Val Gly Ala Thr Thr Ile Leu Ala Val Val Ile
                660                665                670
Thr Leu Ala Ile Cys Gly Thr Arg Lys Phe Lys Lys Arg Gly Tyr Leu
                675                680                685
Ala Phe Trp Lys Arg Gln Ser Leu Val Pro Gly Thr Ala Ala Thr Gly
 690                695                700
Asp Asn Pro Asp Glu Glu Gln Gly Gln Ser Pro Ala
705                710                715

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<210> 51
 <211> 732
 <212> PRT
 <213> Homo sapiens

<400> 51
Met Asn Asn Phe Arg Ala Thr Ile Leu Phe Trp Ala Ala Ala Ala Trp
1 5 10 15
Ala Lys Ser Gly Lys Pro Ser Gly Glu Met Asp Glu Val Gly Val Gln
20 25 30
Lys Cys Lys Asn Ala Leu Lys Leu Pro Val Leu Glu Val Leu Pro Gly
35 40 45
Gly Gly Trp Asp Asn Leu Arg Asn Val Asp Met Gly Arg Val Met Glu
50 55 60
Leu Thr Tyr Ser Asn Cys Arg Thr Thr Glu Asp Gly Gln Tyr Ile Ile
65 70 75 80
Pro Asp Glu Ile Phe Thr Ile Pro Gln Lys Gln Ser Asn Leu Glu Met
85 90 95
Asn Ser Glu Ile Leu Glu Ser Trp Ala Asn Tyr Gln Ser Ser Thr Ser
100 105 110
Tyr Ser Ile Asn Thr Glu Leu Ser Leu Phe Ser Lys Val Asn Gly Lys
115 120 125
Phe Ser Thr Glu Phe Gln Arg Met Lys Thr Leu Gln Val Lys Asp Gln
130 135 140
Ala Ile Thr Thr Arg Val Gln Val Arg Asn Leu Val Tyr Thr Val Lys
145 150 155 160
Ile Asn Pro Thr Leu Glu Leu Ser Ser Gly Phe Arg Lys Glu Leu Leu
165 170 175
Asp Ile Ser Asp Arg Leu Glu Asn Asn Gln Thr Arg Met Ala Thr Tyr
180 185 190
Leu Ala Glu Leu Leu Val Leu Asn Tyr Gly Thr His Val Thr Thr Ser
195 200 205
Val Asp Ala Gly Ala Ala Leu Ile Gln Glu Asp His Leu Arg Ala Ser
210 215 220
Phe Leu Gln Asp Ser Gln Ser Ser Arg Ser Ala Val Thr Ala Ser Ala
225 230 235 240
Gly Leu Ala Phe Gln Asn Thr Val Asn Phe Lys Phe Glu Glu Asn Tyr
245 250 255
Thr Ser Gln Asn Val Leu Thr Lys Ser Tyr Leu Ser Asn Arg Thr Asn
260 265 270
Ser Arg Val Gln Ser Ile Gly Gly Val Pro Phe Tyr Pro Gly Ile Thr
275 280 285
Leu Gln Ala Trp Gln Gln Gly Ile Thr Asn His Leu Val Ala Ile Asp
290 295 300
Arg Ser Gly Leu Pro Leu His Phe Phe Ile Asn Pro Asn Met Leu Pro
305 310 315 320
Asp Leu Pro Gly Pro Leu Val Lys Lys Val Ser Lys Thr Val Glu Thr
325 330 335
Ala Val Lys Arg Tyr Tyr Thr Phe Asn Thr Tyr Pro Gly Cys Thr Asp
340 345 350
Leu Asn Ser Pro Asn Phe Asn Phe Gln Ala Asn Thr Asp Asp Gly Ser
355 360 365
Cys Glu Gly Lys Met Thr Asn Phe Ser Phe Gly Gly Val Tyr Gln Glu
370 375 380
Cys Thr Gln Leu Ser Gly Asn Arg Asp Val Leu Leu Cys Gln Lys Leu
385 390 395 400
Glu Gln Lys Asn Pro Leu Thr Gly Asp Phe Ser Cys Pro Ser Gly Tyr
405 410 415
Ser Pro Val His Leu Leu Ser Gln Ile His Glu Glu Gly Tyr Asn His
420 425 430
Leu Glu Cys His Arg Lys Cys Thr Leu Leu Val Phe Cys Lys Thr Val
435 440 445
Cys Glu Asp Val Phe Gln Val Ala Lys Ala Glu Phe Arg Ala Phe Trp

450	455	460
Cys Val Thr Ser Ser Gln Val Pro Glu Asn Ser Gly Leu Leu Phe Gly		
465	470	475
Gly Leu Phe Ser Ser Lys Ser Ile Asn Pro Met Thr Asn Ala Gln Ser		480
	485	490
Cys Pro Ala Gly Tyr Phe Pro Leu Arg Leu Phe Glu Asn Leu Lys Val		495
	500	505
Cys Val Ser Gln Asp Tyr Glu Leu Gly Ser Arg Phe Ala Val Pro Phe		510
	515	520
Gly Gly Phe Phe Ser Cys Thr Val Gly Asn Pro Leu Val Asp Pro Ala		525
	530	535
Ile Ser Arg Asp Leu Gly Ala Pro Ser Leu Lys Lys Cys Pro Gly Gly		540
545	550	555
Phe Ser Gln His Pro Ala Leu Ile Ser Asp Gly Cys Gln Val Ser Tyr		560
	565	570
Cys Val Lys Ser Gly Leu Phe Thr Gly Ser Leu Pro Pro Ala Arg		575
	580	585
Leu Pro Pro Phe Thr Arg Pro Pro Leu Met Ser Gln Ala Ala Thr Asn		590
	595	600
Thr Val Ile Val Thr Asn Ser Glu Asn Ala Arg Ser Trp Ile Lys Asp		605
	610	615
Ser Gln Thr His Gln Trp Arg Leu Gly Glu Pro Ile Glu Leu Arg Arg		620
625	630	635
Ala Met Asn Val Ile His Gly Met Val Val Val Cys Gln Glu Gly Leu		640
	645	650
Gln Leu Gly Ser Gln Trp Gly Ser Pro Pro Phe Trp Leu Leu Leu Ser		655
	660	665
Pro Trp Pro Ser Thr Ala Pro Gly Ser Ser Arg Arg Lys His Ile Arg		670
	675	680
Gln Leu Arg Lys Gly Arg Val Trp Phe Gln Ala Leu Gln Gln Leu Glu		685
	690	695
Thr Pro Leu Thr Lys Ser Arg Gly Arg Val Gln Leu Lys Ser Leu Pro		700
705	710	715
Glu Asn Gly Phe Ser His Leu Gln Cys Gly His Cys		720
	725	730

<210> 52

<211> 351

<212> PRT

<213> Homo sapiens

<400> 52

Met Arg Trp Pro Pro Ser Pro Thr His His Pro Arg Trp Gly Lys Pro		
1	5	10
Gln Ala Gly Trp Val Glu Lys Asn Leu Pro Thr His Ser Pro Cys Ser		15
	20	25
Cys Phe Ile Asp Glu His Val Thr Arg Val Ala Trp Leu Asn Arg Ser		30
	35	40
Asn Ile Leu Tyr Ala Gly Asn Asp Arg Trp Thr Ser Asp Pro Arg Val		45
	50	55
Arg Leu Leu Ile Asn Thr Pro Glu Glu Phe Ser Ile Leu Ile Thr Glu		60
65	70	75
Val Gly Leu Gly Asp Glu Gly Leu Tyr Thr Cys Ser Phe Gln Thr Arg		80
	85	90
His Gln Pro Tyr Thr Thr Gln Val Tyr Leu Ile Val His Val Pro Ala		95
	100	105
Arg Ile Val Asn Ile Ser Ser Pro Val Thr Val Asn Glu Gly Gly Asn		110
	115	120
Val Asn Leu Leu Cys Leu Ala Val Gly Arg Pro Glu Pro Thr Val Thr		125

130	135	140
Trp Arg Gln Leu Arg	Gly Glu Asp Pro Ile	Pro Asp Gly Phe Thr Ser
145	150	155
Glu Gly Glu Ile Leu	Glu Ile Ser Asp Ile	Gln Arg Gly Gln Ala Gly
165	170	175
Glu Tyr Glu Cys Val	Thr His Asn Gly Val	Asn Ser Ala Pro Asp Ser
180	185	190
Arg Arg Val Leu Val	Thr Val Asn Tyr Pro	Pro Thr Ile Thr Asp Val
195	200	205
Thr Ser Ala Arg Thr	Ala Leu Gly Arg Ala	Ala Leu Leu Arg Cys Glu
210	215	220
Ala Met Ala Val Pro	Pro Ala Asp Phe Gln	Trp Tyr Lys Asp Asp Arg
225	230	235
Leu Leu Ser Ser Gly	Thr Ala Glu Gly Leu	Lys Val Gln Thr Glu Arg
245	250	255
Thr Arg Ser Met Leu	Leu Phe Ala Lys Arg	Glu Arg Pro Ala Leu Arg
260	265	270
Asn Tyr Thr Cys Arg	Ala Ser His Arg Leu	Gly Ala Ser Ser Ala Ser
275	280	285
Met Arg Leu Leu Arg	Ala Ser Ser Gly Gly	Ala Gly Pro Gly Arg Gly
290	295	300
Pro Gln Ala Lys Ser	Glu Arg Asn Gly Gly	Ala Arg Ala Val Gly Leu
305	310	315
Val Gly Ala Glu Glu	Leu Ser Ala Thr Lys	Glu Glu Glu Arg Gly Glu
325	330	335
Glu Glu Glu Ala Glu	Glu Glu Glu Arg Ser	Ser Ser Glu Asn Pro Ser Leu
340	345	350

<210> 53
 <211> 336
 <212> PRT
 <213> Homo sapiens

<400> 53

Met Pro Pro Ala Ala	Pro Gly Ala Arg	Leu Arg Leu Leu	Ala Ala Ala
1	5	10	15
Ala Leu Ala Gly Leu	Ala Val Ile Ser	Arg Gly Leu Leu	Ser Gln Arg
20	25	30	
Leu Glu Phe Asn Ser	Pro Ala Asp Asn	Tyr Thr Val Cys	Glu Gly Asp
35	40	45	
Asn Ala Thr Leu Ser	Cys Phe Met Asp	Glu His Val Thr	Arg Val Ala
50	55	60	
Trp Leu Asn Arg Ser	Asn Ile Leu Tyr	Ala Gly Asn Asp	Arg Arg Thr
65	70	75	80
Arg Asp Pro Arg Val	Arg Leu Leu Ile	Asn Thr Pro Glu	Glu Phe Ser
85	90	95	
Ile Leu Val Thr Glu	Val Gly Leu Gly	Asp Glu Gly Leu	Tyr Thr Cys
100	105	110	
Ser Phe Gln Thr Arg	His Gln Pro Tyr	Thr Thr Gln Val	Tyr Leu Ile
115	120	125	
Val His Val Pro Ala	Arg Val Val Asn	Ile Ser Ser Pro	Val Met Val
130	135	140	
Asn Glu Gly Gly Asn	Val Asn Leu Leu	Cys Leu Ala Val	Gly Arg Pro
145	150	155	160
Glu Pro Thr Val Thr	Trp Arg Gln Leu	Arg Asp Gly Phe	Thr Ser Glu
165	170	175	
Gly Glu Ile Leu Glu	Ile Ser Asp Ile	Leu Arg Gly Gln	Ala Gly Glu
180	185	190	
Tyr Glu Cys Val Thr	His Asn Gly Val	Asn Ser Ala Pro	Asp Ser Arg

195	200	205
Arg Val Leu Val Thr Val Asn Tyr Pro Pro Thr Ile Thr Asp Val Thr		
210	215	220
Ser Ala Arg Thr Ala Leu Gly Arg Ala Ala Leu Leu Arg Cys Glu Ala		
225	230	235
Met Ala Val Ser Pro Ala Asp Phe Gln Trp Tyr Lys Asp Asp Arg Leu		
245	250	255
Leu Ser Ser Gly Thr Ala Glu Gly Leu Lys Val Gln Met Glu Arg Thr		
260	265	270
Arg Ser Met Leu Leu Phe Ala Asn Met Ser Ala Arg His Tyr Gly Asn		
275	280	285
Tyr Thr Cys Cys Ala Ala Asn Arg Leu Gly Ala Ser Ser Ala Ser Met		
290	295	300
Arg Leu Leu Cys Pro Gly Ser Leu Glu Asn Ser Ala Pro Arg Pro Pro		
305	310	315
Gly Pro Leu Ala Leu Leu Ser Ala Leu Gly Trp Leu Trp Trp Arg Met		
325	330	335

<210> 54

<211> 315

<212> PRT

<213> Homo sapiens

<400> 54

Met Asp Leu Arg Gln Phe Leu Met Cys Leu Ser Leu Cys Thr Ala Phe	
1	5
Ala Leu Ser Lys Pro Thr Glu Lys Lys Asp Arg Val His His Glu Pro	
20	25
Gln Leu Ser Asp Lys Val His Asn Asp Ala Gln Ser Phe Asp Tyr Asp	
35	40
His Asp Ala Phe Leu Gly Ala Glu Glu Ala Lys Thr Phe Asp Gln Leu	
50	55
Thr Pro Glu Glu Ser Lys Glu Arg Leu Gly Met Ile Val Asp Lys Ile	
65	70
Asp Ala Asp Lys Asp Gly Phe Val Thr Glu Gly Glu Leu Lys Ser Trp	
85	90
Ile Lys His Ala Gln Lys Lys Tyr Ile Tyr Asp Asn Val Glu Asn Gln	
100	105
Trp Gln Glu Phe Asp Met Asn Gln Asp Gly Leu Ile Ser Trp Asp Glu	
115	120
Tyr Arg Asn Val Thr Tyr Gly Thr Tyr Leu Asp Asp Pro Asp Pro Asp	
130	135
Asp Gly Phe Asn Tyr Lys Gln Met Met Val Arg Asp Glu Arg Arg Phe	
145	150
Lys Met Ala Asp Lys Asp Gly Asp Leu Ile Ala Thr Lys Glu Glu Phe	
165	170
Thr Ala Phe Leu His Pro Glu Glu Tyr Asp Tyr Met Lys Asp Ile Val	
180	185
Val Gln Glu Thr Met Glu Asp Ile Asp Lys Asn Ala Asp Gly Phe Ile	
195	200
Asp Leu Glu Glu Tyr Ile Gly Asp Met Tyr Ser His Asp Gly Asn Thr	
210	215
Asp Glu Pro Glu Trp Val Lys Thr Glu Arg Glu Gln Phe Val Glu Phe	
225	230
Arg Asp Lys Asn Arg Asp Gly Lys Met Asp Lys Glu Glu Thr Lys Asp	
245	250
Trp Ile Leu Pro Ser Asp Tyr Asp His Ala Glu Ala Glu Ala Arg His	
260	265
Leu Val Tyr Glu Ser Asp Gln Asn Lys Asp Gly Lys Leu Thr Lys Glu	

Glu	Arg	Cys	Ala	Ala	Tyr	Ala	Ala	Arg	Arg	Ala	His	Phe	Trp	Lys	Gln
			100					105					110		
Val	Leu	Gly	Gly	Leu	Arg	Lys	Lys	Arg	Arg	Pro	Cys	His	Asp	Pro	Ala
		115					120					125			
Pro	Leu	Gln	Ala	Arg	Leu	Cys	Ala	Gly	Lys	Lys	Gly	His	Gly	Ala	Glu
	130					135					140				
Leu	Arg	Leu	Val	Pro	Arg	Ala	Ser	Pro	Pro	Ala	Arg	Pro	Thr	Val	Ala
145					150					155					160
Gly	Phe	Ala	Gly	Glu	Ser	Lys	Pro	Arg	Ala	Arg	Asn	Arg	Gly	Arg	Thr
			165						170					175	
Arg	Glu	Arg	Ala	Ser	Gly	Pro	Ala	Ala	Gly	Thr	Pro	Pro	Pro	Gln	Ser
			180					185					190		
Ala	Pro	Pro	Lys	Glu	Asn	Pro	Ser	Glu	Arg	Lys	Thr	Asn	Glu	Gly	Lys
	195					200						205			
Arg	Lys	Ala	Ala	Leu	Val	Pro	Asn	Glu	Glu	Arg	Pro	Met	Gly	Thr	Gly
	210					215					220				
Pro	Asp	Pro	Asp	Gly	Leu	Asp	Gly	Asn	Ala	Glu	Leu	Thr	Glu	Thr	Tyr
225					230					235					240
Cys	Ala	Glu	Lys	Trp	His	Ser	Leu	Cys	Asn	Phe	Phe	Val	Asn	Phe	Trp
			245					250						255	
Asn	Gly														